CAUTION: >80 PRINTED PAGES

Supporting Table 1A: Detailed List of Detected Peptides and Proteins

(pages 1-89)

The color-coded columns list the peptides and proteins detected in one out of four replicate experiments for each DE condition. Proteins (named by NCBI accession numbers) are grouped by their frequency of detection in each experiment ("proteins detected in all runs" are listed first, followed by "proteins detected in n-1 runs", and so on). Proteins identified by the same set of peptides are grouped together.
On the accession number rows are reported the protein sequence coverage (%) achieved in each run.
Under the protein IDs, are listed the peptides leading to this identification. The dots "." represent the protease cleavage sites. +1, +2 or +3 at the end of the peptide sequence stands for the charge state. Oxidized methionines are reported as "M*" within the peptide sequences.
On the peptide rows are reported the SEQUEST cross-correlation scores for the best spectrum matching a particular peptide in each run.

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|10383781|ref|NP_009938.2|	60.6	72.4	68.8	65.6	64.2	68	68.3	64.2	72.4	56	60.3	71.9	73.3	78.6	76	75	66.8	59.6	60.6	77.4	35.3	36.1	48.3	44.2	3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphate of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme in glycolysis and gluconeogenesis; Pgk1p [Saccharomyces cerevisiae]
K.ALENPTRPFLAILGGAK.V +2		4.5574	4.1511	3.8195									2.9277	3.7841	4.0786	4.5429			4.7191	3.3901					
K.ALENPTRPFLAILGGAK.V +3		4.556		4.0831										3.9538	4.138	3.841			4.2527	3.8213					
K.ALLDEVVK.S +1	2.0575	2.3171	2.2084	2.1368	2.228	2.2853	2.3005	2.2134	2.0909	2.2805	2.4256	1.8796	2.153	2.1918	2.1503	2.2108	2.0824	2.1463		2.1418		2.2046	2.0026		
K.ALLDEVVK.S +2	2.7612	2.636	2.6743	2.6598	2.8114	2.7724	2.8603	2.7512	2.5794	2.6576	2.6907														
K.ASAPGSVILLENLR.Y +1									3.3784		2.4539	2.7051	2.9572	2.8797	2.8485	3.2212	3.2308			2.6868	3.2451				
K.ASAPGSVILLENLR.Y +2	5.0479	4.855	4.6972	4.6155	4.9727	4.7789	4.7424	4.7561	4.6122	4.6304	4.661	4.5416	4.5093	4.3964	4.2059	4.0402	4.4211	3.8525	3.7483	4.3629	4.4963		4.2425	3.4572	
K.ASAPGSVILLENLR.Y +3							4.2384		4.5727	4.5664		4.9843	4.8874	4.9618	4.787	5.0038	4.7585	4.6518	4.969	5.0575	4.828		4.8985	5.0185	
K.DVTFLNDCVGPEVEAAVK.A +2	6.4029	6.4666	6.4641	5.7507	6.3829	6.2993	6.2823	6.2371	6.0224	6.05	6.1738	6.0572	5.7882	5.708	5.547	6.0453	5.537	5.9497	5.8415	6.1963	3.5975	5.8896	5.6744	5.7456	
K.DVTFLNDCVGPEVEAAVK.A +3										4.8722	4.4973	4.6545	4.0287	5.4454	5.0655	5.2669					4.6664	4.3867			
K.EGIPAGWQGLDNGPESR.K +2	4.6411	4.5846	4.5608	4.5963	4.7673	4.7739	4.459	4.6573	4.5411	4.5009	4.607	4.5491	4.4538	4.5976	4.3228	4.5115	4.6513	3.9557		4.6792	4.0479	4.0636	4.2145	3.9345	
K.EGIPAGWQGLDNGPESR.K +3												3.9949	4.8913	3.9393		4.784									
K.EGIPAGWQGLDNGPESRK.L +2																	2.9674								
K.ELPGVAFLSEK.K +1					2.9524	2.6854		2.2428	2.9229		3.1266		2.9242	3.0384	2.8759	3.396	2.6727	2.6004	2.7212	3.0619		2.7074		2.1518	
K.ELPGVAFLSEK.K +2	3.0114	3.0716	3.0873	3.0654	3.1913	2.9608	2.9524	2.9485	2.9115	3.1673	3.0987	2.9235	2.8211	3.0812	2.8553	2.8899	2.6396	2.7793	2.506		2.8011		2.9145		
K.ELPGVAFLSEKK.- +2		3.5897	3.3309	3.5464													3.2683		3.2434	3.2739					
K.ELQSLLGK.D +1	2.0366						1.9945																		
K.ELQSLLGK.D +2						2.5008			2.5408		2.5332														
K.GVEVVLPVDFIIADAFSADANTK.T +2		7.4693	7.4152	7.4166	7.5655	7.4013	7.5843	7.5358	7.3089	3.8484	7.1284	7.4873	7.1476	7.136	6.8825	7.3436	2.6704	6.2928	6.1933	6.8584			2.8623	4.6487	
K.GVEVVLPVDFIIADAFSADANTK.T +3			5.1966	5.7516	5.4711	4.9339	5.5901	5.219	5.067		4.1644	5.1515	5.1331	5.0137	4.7439	5.1335			4.0507	4.7729					
K.IQLIDNLLDK.V +1					2.4764				2.8321		2.628		2.9247	2.542	2.4873	2.78	2.2613	2.4556		2.6627					
K.IQLIDNLLDK.V +2	3.165	3.0755	3.3696	3.7567	3.1266	3.217	3.1223	3.1796	3.2204	3.155	3.5524	2.9512	3.2335	3.1592	3.0251	3.1981					3.0733				
K.ISHVSTGGGASLELLEGK.E +2	6.1443	6.3461	6.073	5.504	3.8262	3.2866	3.462	6.2769	6.1352			5.3634	5.9018	6.1212	6.1251	5.5274	4.7595	5.4385	5.6214	5.9414					
K.ISHVSTGGGASLELLEGK.E +3	3.9797	4.3863	4.1377										4.3891	4.0475	4.2393	3.636			5.5897	3.8828					
K.KVLENTEIGDSIFDK.A +2		5.5604	5.6155	5.717					5.4191				5.465	5.4693	5.136	4.1709	5.3239	4.3055	5.2807	5.5912					
K.LFAATVAK.A +1	2.1986	2.0547	1.9925	2.0981	1.8448	1.9889	2.1569	1.9402	2.0556	2.0365	2.0045		1.8042	2.0892	1.8249			2.0623						1.8809	
K.LSVQDLDLK.D +1			2.4764								2.1291								2.3471						
K.LSVQDLDLK.D +2	3.2799	3.0531	3.161	3.229	3.1854	3.239	3.0591	3.2447	3.0414	3.1941	3.1787	3.2427	2.9095	2.9802	2.9714	3.1219	2.8636	3.0937	3.0226		2.7137	2.8921	2.8726	3.0758	
K.LSVQDLDLKDK.R +2														2.9623			3.3315		3.2275	3.5011					
K.SSAAGNTVIIGGGDTATVAK.K +2	5.4822	5.5717	5.6039	5.3407	5.4589	5.544	5.4787	5.426	5.2631	5.4716	5.2515	5.2855	5.2561	5.4367	5.4115	5.1463	5.2713	5.3603	5.1707	5.438	5.3844	5.5827	5.3597	5.3591	
K.SSAAGNTVIIGGGDTATVAK.K +3									4.2744	3.929		4.3116				3.6514		5.7455				5.1209			
K.SSAAGNTVIIGGGDTATVAKK.Y +2																	4.2543	4.1015							
K.TIVWNGPPGVFEFEK.F +2	5.2454	5.1407	5.1456	5.0534	5.2023	5.0836	5.2106	5.1623	4.9062	4.787	4.8725	5.1241	4.9745	5.0305	4.7778	4.9021	4.7616	4.7367	4.8148	4.944	3.5186		3.0399	4.2693	
K.TIVWNGPPGVFEFEK.F +3													3.7118						3.7267						
K.TVTDKEGIPAGWQGLDNGPESR.K +2													4.1521	4.0467	3.899	3.7504									
K.TVTDKEGIPAGWQGLDNGPESR.K +3													3.9821	4.4893		3.9756									
K.VDSIIIGGGM*AFTFK.K +2					3.7889	4.2248			4.8225			4.2615	5.0819	5.1282	4.7757	4.8811	3.397		3.53	4.6609					
K.VDSIIIGGGMAFTFK.K +2	3.1679	3.138			4.8892	5.0584	4.392	3.8128	5.3151			3.9681	3.3284	3.8519	4.6513	4.0397			5.2232	5.1851					
K.VLENTEIGDSIFDK.A +1					4.0902	3.9011	3.6661	3.9296	3.7705			2.7792	3.782	3.899	3.6521	3.6754	1.9966		2.0067						
K.VLENTEIGDSIFDK.A +2	5.015	5.0944	5.2329	5.133	5.3071	5.2285	5.4445	5.3292	5.2126	5.2216	5.3752	5.3025	5.0062	4.9898	4.6013	5.07	3.7264	4.1778	4.3803	4.5128	5.1617	4.9737	4.3826	5.2076	
K.YSLAPVAK.E +1	2.2401	2.1554	2.1499	2.0498	2.2353	2.138	2.0943	2.144	2.229	1.9256	2.1727		1.8166	1.9629	2.1723		2.2525	1.9853		2.0735			2.2245		
K.YVLEHHPR.Y +1																			1.9925						
K.YVLEHHPR.Y +2	2.9646	3.4408	3.2738		3.1449	3.3365	2.9743	3.3645	3.2256	2.6781	3.0138	3.1639	3.0662	3.2309	3.1614	3.2753	3.0382		3.0272	3.1237		3.068	2.8507	3.2195	
R.AAGFLLEK.E +2	2.9372	3.0935	3.0122	3.0277	2.9525	2.9068	2.9278	2.9634	2.8848	3.1081	2.9829	2.834	2.8508	3.0696	3.023	3.0177				2.9153		2.8646	2.9983	2.9104	
R.AHSSM*VGFDLPQR.A +2	3.4583	4.1202	4.0459	4.1649	3.2968	2.5247	2.994	4.0226	4.0068	2.9045	2.9369	3.9229	4.1296	3.8248	3.735	4.2188	3.2831	3.4184	3.3273	3.765					
R.AHSSM*VGFDLPQR.A +3													4.0172	3.7927											
R.AHSSMVGFDLPQR.A +1															2.5449	3.0881				2.2627					
R.AHSSMVGFDLPQR.A +2	4.595	4.6542	4.5605	4.437					3.8376			3.9907	4.3322	4.2546	4.3324	4.2447	3.911	3.7466	3.4768	4.4762					
R.AHSSMVGFDLPQR.A +3		4.9581	4.2449	4.1927									4.5248	4.5019		4.5282	4.4725			4.6355					
R.HELSSLADVYINDAFGTAHR.A +2												2.5363		6.6438	3.3316					3.5986					
R.HELSSLADVYINDAFGTAHR.A +3														5.7837	5.3689	4.3641				3.9729					
R.IVAALPTIK.Y +1	2.7121	2.6485	2.6282	2.6489	2.6508	2.5914	2.6557	2.6656	2.4057	2.5378	2.3852	2.6559	2.6409	2.5146	2.4185	2.4123		2.2329	2.2439	2.5733	2.6099	1.9613	2.8029	2.6601	
R.IVAALPTIK.Y +2		2.5539	2.5559	2.6044	2.6951	2.6813	2.591	2.6914						2.5756			2.5398								
R.KLFAATVAK.A +1			2.3945						2.4642				2.8109	2.5773	2.689	2.4852	2.5613	2.2318	2.5479	2.4835		2.409			
R.KLFAATVAK.A +2	3.2333	3.1196	3.3131	3.1738	2.6231		3.1572	3.2295	2.7982		2.9555	3.2378			2.5828	2.9307									
R.PFLAILGGAK.V +1													3.2531	2.9844	3.1912					2.6494					
R.PFLAILGGAK.V +2									3.437			3.802	3.8525	3.6651	3.6762	3.8657			3.0936	3.1089					
R.VDFNVPLDGK.K +1		2.665	2.2296	2.8256	2.8175	2.9927	2.9531	2.945	2.6733	2.3558	2.5322	2.5747	2.7011	3.0439	2.7915	2.617	2.5454	2.5674	3.0159	2.5136	2.1522	2.9769	2.7246	2.5752	
R.VDFNVPLDGK.K +2	3.8634	3.7532	3.8845	3.9655	3.8377	3.8253	3.8448	3.836	3.8156	3.8798	3.7901	3.6841	3.733	3.9638	3.6344	3.7719	3.7291	3.0219		3.7463	3.5381	3.9395	3.8078	3.7109	
R.VDFNVPLDGKK.I +2		3.6444	3.7303	3.6769	3.8889			3.7568	3.6324	3.4586		3.2396	3.8113	3.5381	3.5925	3.5173		3.2703	2.8984						
R.YHIEEEGSR.K +1																	3.0593								
R.YHIEEEGSR.K +2		3.3926	3.1338	3.2565	2.9966	2.9349	2.8751	2.9742	3.0176	2.9837	2.9617	2.7502	2.7734	2.82		2.79	2.7866	2.7211	2.7627	2.7785		2.5613	2.8804		
R.YVVLASHLGR.P +1									2.2775				2.6816	2.5527	2.3937	2.5388	2.3248	2.4627							
R.YVVLASHLGR.P +2	3.1715	3.2867	3.3846	3.2077		3.2002	2.9329		3.3354		3.2524	3.1131	3.2757	3.2076	3.14	3.1865									
R.YVVLASHLGRPNGER.N +2		3.8819	3.7739						2.5906				2.8899	3.0368	2.9925		2.6741		3.6362	3.3741					
gi|10383793|ref|NP_009960.2|	24.8	46	48.2	48.2	51.1	51.1	51.1	58.4	53.3	38	38	51.1	60.6	60.6	53.3	60.6	30.7	22.6	46	46	21.2	38	28.5	21.2	Ribosomal protein 59 of the small subunit, required for ribosome assembly and 20S pre-rRNA processing; mutations confer cryptopleurine resistance; nearly identical to Rps14Bp and similar to E. coli S11 and rat S14 ribosomal proteins; Rps14ap [Saccharomyces cerevisiae]
gi|6322270|ref|NP_012344.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	Ribosomal protein 59 of the small subunit, required for ribosome assembly and 20S pre-rRNA processing; mutations confer cryptopleurine resistance; nearly identical to Rps14Ap and similar to E. coli S11 and rat S14 ribosomal proteins; Rps14bp [Saccharomyces cerevisiae]
K.ADRDESSPYAAM*LAAQDVAAK.C +2													4.9854					3.6229	5.3783	3.805					
K.ADRDESSPYAAM*LAAQDVAAK.C +3													5.3462	4.8584				3.6418							
K.ADRDESSPYAAMLAAQDVAAK.C +2									5.3626				5.0895	5.6081	5.3448	5.8701	5.6971	5.1618		4.9789					
K.ADRDESSPYAAMLAAQDVAAK.C +3			3.9938	4.9797					3.7078				4.1827	4.1912	3.8169	3.8675	3.5876	3.8319	4.3291	4.3255					
K.EVGITAVHVK.I +1													2.4083					2.2947	2.2246				2.3445		
K.EVGITAVHVK.I +2		2.9471	3.0417	3.008				2.5754					2.656	2.7508	2.9766	2.8803	2.8279	2.838							
K.TPGPGGQAALR.A +1					1.9274																				
K.TPGPGGQAALR.A +2	3.5244	3.312	3.5483	3.1717	3.6393	3.6494	3.5743	3.5487	3.3569	3.5263	3.2078	3.4309	3.4893	3.5037	2.5007	3.4142	2.789			2.8834	2.8108	3.3067	3.3591	3.2085	
R.DESSPYAAM*LAAQDVAAK.C +2										4.9654	4.7111	5.242									5.0031	5.154			
R.DESSPYAAMLAAQDVAAK.C +2					6.2382	6.0082	6.1373	6.2393	5.8989	5.589	5.8169	5.2373	5.6206	5.0048	4.2189	5.5699	4.56				4.852	4.7643	5.7413	3.3951	
R.DESSPYAAMLAAQDVAAK.C +3														3.8973											
R.DNSQVFGVAR.I +2	3.776	3.641	3.5864	3.6425			3.5438	3.6106		3.4744	3.545	3.2472		3.1535		2.9178				3.5348					
R.DNSQVFGARIYASFNDTFVHVTDLSGK.E +3					4.8715	4.4703	4.8799	4.4576	4.3785			4.4224	3.9834	4.2502		5.4019									
R.IEDVTPVPSDSTR.K +1											2.0701			2.2806											
R.IEDVTPVPSDSTR.K +2	4.141	4.137	3.9854	3.8608	4.2855	4.1109	4.1176	4.1971	4.2284	3.9384	4.0669	3.8842	3.8091	3.7555	3.9607	4.1343				4.0279					
R.IEDVTPVPSDSTRK.K +2		3.812	3.4794	3.3953															3.1456						
R.IYASFNDTFVHVTDLSGK.E +2		5.0701											5.1818	5.7067	4.7406	3.517			5.0248	5.1736					
gi|14318479|ref|NP_116614.1|	21.1	33.6	30.4	37.9	31.7	29.3	29.3	31.5	38.4	22.4	22.7	31.2	50.7	49.3	32.8	40	32.5	39.5	32	44.3	18.9	9.9	29.3	18.1	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions; Act1p [Saccharomyces cerevisiae]
K.AGFAGDDAPR.A +1													2.2736												
K.AGFAGDDAPR.A +2	3.1143				2.7619	3.4971	2.9086		2.6063	2.6255		2.8056	3.1552	2.9647	2.9002	3.2185		2.9166					2.5377		
K.DSYVGDEAQSK.R +1																							2.3988		
K.DSYVGDEAQSK.R +2	3.8582	3.7987	3.6051		3.474	3.5252	3.5151	3.2345	2.7794	3.1218	3.3953	2.7949	3.0807	3.2004	3.0173	3.0211							3.3891		
K.EITALAPSSM*K.V +2									2.8701																
K.EITALAPSSMK.V +1											2.3071						2.785	2.8792		2.6761	2.4672		2.4171		
K.EITALAPSSMK.V +2	2.7442	2.8526	2.7293	2.5968	2.8872	2.8095	2.7742	2.6178		2.6271	2.5603									2.798		2.6604			
K.ELYGNIVM*SGGTTM*FPGIAER.M +2									2.6174				4.4754	4.7194	3.977			2.5284	4.8209	3.3476	4.306		3.4276	3.323	
K.ELYGNIVM*SGGTTM*FPGIAER.M +3													3.6376	4.3796											
K.ELYGNIVM*SGGTTMFPGIAER.M +2																		3.7261			2.5451		3.7121		
K.ELYGNIVMSGGTTM*FPGIAER.M +2									4.085		2.5125				4.807		3.3277		4.6119	4.7603	3.2815		4.3211	3.9643	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ELYGNIVMSGGTTMFPGIAER.M +2	4.1132	4.3634	5.1167	2.5671	4.8488	4.608	4.7474	4.586	4.512		3.5771	3.9795			4.3386	4.2757	5.0466		3.6369	4.8048			4.4683	2.6132	
K.IWHHTFYNELR.V +2																				3.0684					
K.LCYVALDFEQEM*QTAAQSSSIEK.S +2									2.5869									4.7511			5.7776		2.9345	2.7874	
K.LCYVALDFEQEM*QTAAQSSSIEK.S +3													5.5618	4.9399	6.0394										
K.LCYVALDFEQEMQTAAQSSSIEK.S +2					5.4845	3.331	5.9389	6.4091	6.6229			4.8222					4.9845	3.5142	3.8735	4.6146	4.0675		3.6401		
K.LCYVALDFEQEMQTAAQSSSIEK.S +3					3.9484				4.0508											5.0985					
K.QEYDESGPSIVHHK.C +2				2.8776									2.7505	2.8396				2.6557	2.8283						
K.SYELPDGQVITIGNER.F +2	4.858	5.0041	4.9785	4.8505	5.0614	4.9104	4.9494	4.8846	4.6784	4.7183	4.8762	4.5352	4.7023	4.7993	4.5082	4.6352	4.2495	4.4875		3.9608	2.9718	4.1377	2.7807	4.8826	
R.APEALFHPSVLGLESAGIDQTTYNSIM*K.C +2														3.9139											
R.APEALFHPSVLGLESAGIDQTTYNSIM*K.C +3													5.2347	7.542		4.2821			5.3885						
R.APEALFHPSVLGLESAGIDQTTYNSIMK.C +3		6.3404		5.1064																6.2451					
R.AVFPSIVGR.P +2					2.5138									2.7285			2.7476								
R.AVFPSIVGRPR.H +2		3.1789	3.3805										2.7664			2.7572		2.5392		2.6951					
R.DLTDYLMK.I +1										1.8607															
R.DLTDYLMK.I +1				2.4425	2.357	2.4399	2.4485	2.4764	2.4093		2.0563	2.3057		2.4682	2.2	2.1711	2.2628	2.0159							
R.DLTDYLMK.I +2						2.8301	2.5464					2.6837												2.6805	
R.GYSFSTTAER.E +2	3.1775	3.3607	3.4226	3.4274	3.4156	3.1133	3.5544	3.4811	2.6889	3.0327		3.1977	3.0827									3.5268			
R.HQGIM*VGMGQK.D +2														3.0257		2.6806									
R.HQGIMVGM*GQK.D +2													2.9203												
R.HQGIMVGMGQK.D +2																3.0932				3.0244					
R.KELYGNIVM*SGGTTM*FPGIAER.M +3													4.3654												
R.VAPEEHPVLLTEAPM*NPK.S +2				4.1274						4.1274		3.7433	4.085	4.1508	3.6191	3.7405		3.8004	2.8082				3.0975		
R.VAPEEHPVLLTEAPM*NPK.S +3													4.248												
R.VAPEEHPVLLTEAPMNPK.S +2		4.9383	4.8851	5.0291				4.7909	4.0804		3.9424			4.3202	3.8902	4.1164	4.4558			4.3141					
R.YPIEHGIVTNWDDM*EK.I +2									4.9015				5.6694	5.5434	4.4081	4.7623	3.8111		4.8429	4.4667					
R.YPIEHGIVTNWDDM*EK.I +3													4.7227	3.9883		3.8666		3.6873							
R.YPIEHGIVTNWDDMEK.I +2			6.2569	6.1397					3.5085						4.9633	3.2195	5.2244			5.7874					
gi|14318555|ref|NP_116688.1|	27.2	27.2	27.6	27.2	4.3	4.3	4.3	4.3	15.4	4.3	15.4	15.4	26.4	35.4	35	15.4	15.7	11	15.7	11.4	4.3	4.3	4.3	4.3	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. coli L2 and rat L8 ribosomal proteins; Rpl2ap [Saccharomyces cerevisiae]
K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G +2														3.7093											
K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G +3	3.5991	4.6164	4.3625	4.7975										4.5665	4.6197										
K.GAGSIFTSHTR.L +2	3.3415	3.6527	3.5029	3.5376					2.853		3.0735	2.6478	3.4484	3.3678	3.3035	3.5987			3.4692						
R.ASGNYVIIIGHNPDENK.T +2	5.0885	5.3957	5.3937	5.4939					5.2334		4.0955	4.1589	5.3903	5.2496	5.3677	5.1041	5.072	3.8964	5.2743	5.2702					
R.EEIFIANEGVHTGQFIYAGK.K +2													5.3617	4.9931	3.1931										
R.EEIFIANEGVHTGQFIYAGK.K +3													3.7258	4.0173											
R.GVIGVIAGGGR.V +1	2.7447	3.0928	2.9411	3.0785	2.543	3.0479	2.8071		2.8193	1.8761	2.7434	1.9505					2.9162		3.0465		2.8231	2.7613	2.7158	2.4517	
R.GVIGVIAGGGR.V +2	3.9323		3.951	4.1814	4.1869	4.0528	4.1405	4.0649	4.1074	4.0153	3.8713	4.0092	4.1152	3.9505	4.1757	4.0054	4.1189	4.1436	4.2439		3.6956	3.8914	2.8834	4.1091	
R.KGAGSIFTSHTR.L +2			3.8629										3.3673	3.6201			2.7952		3.1887	3.8026					
R.TLDYAER.H +1													1.8233												
gi|14318578|ref|NP_116711.1|	1.6	5.4	8.9	3.5	12.2	19	23.5	16.7	32.4	13	24.5	21.2	41.2	42.7	27.4	38.6	24.9	26.2	20.8	25.8	19	22.9	21.4	21.2	Hexokinase isoenzyme 1, a cytosolic protein that catalyzes phosphorylation of glucose during glucose metabolism; expression is highest during growth on non-glucose carbon sources; glucose-induced repression involves the hexokinase Hxk2p; Hxk1p [Saccharomyces cerevisiae]
K.DFM*VEQELLNTK.D +2										3.0885	3.022	3.225	3.599	4.3618	4.2641				4.0962		2.9042	2.5585		3.1306	
K.DFMVEQELLNTK.D +2															4.4933	4.4702	4.5634	4.6778		3.6687		4.6558	4.5377		
K.DPITIVPAEDGSGAGAAVIAALSEK.R +2						4.6845			4.0864							5.1144	5.307	2.5017	5.4435	3.8062	3.6034			3.8553	
K.DPITIVPAEDGSGAGAAVIAALSEK.R +3							4.1621		4.5563				5.2212	5.2242	5.3763	4.9322	4.742	4.8957	4.6625		4.6479	4.5398	5.172	4.9341	
K.DTLPLGFTFSYPASQNK.I +2			4.4272		4.5432	4.4467	4.4483	4.5039	4.553	3.478	3.7404	4.3722	4.1704	4.2676	3.7562	4.6435	4.2124	3.7835	4.3068	3.8844	4.8789	4.3075	4.1884	4.2247	
K.ESGNYLAIDLGGTNLR.V +2					4.049	3.9611	4.1412	4.1152	4.0017		2.9052	3.3043	4.8284	4.2642	4.5241	4.4894			3.9797	3.5712					
K.INEGILQR.W +1																					2.0241				
K.INEGILQR.W +2	3.149	3.069	3.0979	3.0963	3.2139	3.1842	3.19	3.1463	2.9981	3.1393	2.8491	3.12				3.0038					3.1662	3.257		3.1868	
K.LADDIPSNSPM*AINCEYGSFDNEHLVLPR.T +3													4.5386												
K.LSGNHTFDTTQSK.Y +2											2.9395		3.0926	3.7652	3.5752	3.4577	3.6999	4.305	3.2817	3.7272			4.3171		
K.M*GVIFGTGVNGAFYDVVSDIEK.L +2									2.5621				3.3496	3.8547		2.8634									
K.M*TSGYYLGELLR.L +2													3.843	3.7348	3.5919			2.9365					3.2561		
K.MGVIFGTGVNGAFYDVVSDIEK.L +2							2.9088	2.5824																	
K.MTSGYYLGELLR.L +2									3.2834		2.9391	2.7586			3.5398	3.7474	3.0819			3.0766					
K.TGHIAADGSVYNK.Y +2													3.3888	3.4913		3.2171	2.5938						3.1922		
K.YDVAVDEQSPR.P +2													3.1418									3.8342			
K.YDVAVDEQSPRPGQQAFEK.M +2									3.1203							2.9848		3.5803							
K.YDVAVDEQSPRPGQQAFEK.M +3														4.0831											
R.DIYGWTGDASK.D +2											3.165						3.1215	3.0054						3.2088	
R.DIYGWTGDASKDPTIVPAEDGSGAGAAVIAALSEK.R +3														5.0762											
R.IEDDPFENLEDTDDIFQK.D +2		5.8574	6.2544		6.0854	6.4186	6.0752	6.2203	6.3466	4.73	5.5263	5.1296	5.5227	5.9024	5.1867	5.8334	4.4874	4.5524	5.0688	5.6855	4.8629	3.0885		4.8195	
R.LAVCGIAAICQK.R +2									3.4011		2.8765	3.3255	3.8942	3.7294	3.6464	3.7358				3.7925	4.0625	3.4745	3.8023	2.9701	
R.LCELIGTR.A +2						2.9854	2.9308		2.8325	2.6154		2.7048		3.0968	2.7114							2.7111			
R.LVLLELNEK.G +2				2.7303										2.5753											
gi|6319279|ref|NP_009362.1|	62.8	68.4	67.2	67	66.6	56.6	62.4	74	74.2	50	52.8	65.4	76.4	79.4	70	70.2	57	55.4	60.8	66.2	45.4	38.2	44.2	44.8	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate, the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration; Cdc19p [Saccharomyces cerevisiae]
K.AGAGHSNTLQVSTV.- +1					2.8036	3.1523			2.8334	2.7859	2.3351	2.6829	3.2218	2.9133	3.091	3.3783	3.0312	2.6114		2.8758	2.4587	2.8464		2.4869	
K.AGAGHSNTLQVSTV.- +2	3.0583	3.1444	3.023	3.0473	3.1068	3.1726	3.2695	3.3141	3.1993	3.1702	2.9259	3.0528	2.8795	2.929		2.9526	2.8182		2.5664	3.0239		2.8934			
K.AGLNIVR.M +1		1.8845	1.9231					2.1469																	
K.AIIVLSTSGTTPR.L +1		2.3774			2.8109				2.4889				2.8154	3.1594	2.3244	3.062				1.9402	2.5538		2.3376		
K.AIIVLSTSGTTPR.L +2	3.9974	4.0914	4.3158	4.2769	4.0958	3.9711	4.0017	3.9841	3.8159	3.9919	4.0251	4.3055	3.7582	3.7288	4.0321	3.9002	3.788	3.714	3.6701	3.8859	3.8336	3.5544	3.0508	3.4913	
K.AKEFGILK.K +2														2.7217											
K.EPVSDWTDDVEAR.I +1					2.6353	2.1825		2.3342	2.0692		2.4562	2.0423	2.3849	1.97	2.5477	1.9905	2.2472		2.4175	2.4356					
K.EPVSDWTDDVEAR.I +2	4.2059	4.0328	3.9399	3.9055	4.006	3.9317	4.0307	4.0459	3.7213	3.9598	3.9032	3.9737	3.5574	3.382	3.8114	3.7958	3.6266	3.3957	3.1493		2.6121	2.5818	2.8425	3.1943	
K.GDTYVSIQGFK.A +1									2.0396																
K.GDTYVSIQGFK.A +2					3.6381	3.7694	3.743	3.6774	3.6157	3.4264	3.389	3.5027	3.3206	3.4563	3.3123	3.4173							3.5702	3.2861	
K.GNYPINAVTTM*AETAVIAEQAIAYLPNYDDM*R.N +3				3.9576									3.9318	4.4664											
K.GNYPINAVTTMAETAVIAEQAIAYLPNYDDM*R.N +3				4.6585	4.2496		3.7358	3.8637	3.746																
K.GVNLPGTDVDLPALSEKD.D +2	5.6313	5.6548	5.9159	5.5012	6.0183	5.8653	6.1262	5.8687	5.7374	5.6326	5.6917	5.7763	5.6113	5.3012	5.6106	5.5581	3.9688	5.5948	2.7497	4.8849	5.6377	5.0045	4.3208	4.7308	
K.GVNLPGTDVDLPALSEKDKEDLR.F +2																				2.6082					
K.IENQQGVNNFDEILK.V +2	5.5398	5.3088	5.3149	5.275	5.4048	5.3804	5.4078	5.4501	5.2311	5.3167	5.1561	5.1135	5.0645	5.2342	5.1492	5.2862	4.9195	4.9501	4.4848	5.1092	4.5577	3.2748		4.3084	
K.IMYVDYK.N +1	2.2892	2.3952	2.2485	2.4055	2.2102	2.3111	2.3	2.3719	2.2545	2.293	2.3585	2.3787	2.2904	2.363	2.1839	2.2109	2.2728	2.4822				2.1717	2.2944	2.236	
K.IMYVDYK.N +2	2.5922	2.5334	2.6447	2.7449	2.7407	2.7683	2.537	2.6204	2.679	2.6397	2.6774	2.7738		2.5333			2.7692				2.6384				
K.KGDTYVSIQGFK.A +1									3.5295				3.406	3.3861	3.0812	3.2022	3.3407	3.4838	3.2079	3.3665					
K.KGDTYVSIQGFK.A +2	3.8477	4.2159	4.1459	4.5349	3.9094	3.8754	3.5722	4.3062	4.2871	3.4565		4.1766	3.9664	3.9594	4.0758	4.2219	3.965	3.7632	4.0515	4.2216				2.8353	
K.KGDTYVSIQGFK.A +3													3.6683	4.0869											
K.NGVHM*VFASFIR.T +2	2.6493	3.2152							2.7128				2.5879	3.4163	2.7572	2.7236			3.3554						
K.NGVHMVFASFIR.T +2		2.6426												2.5329					2.6205	2.6175					
K.PTSTTETVAASAVAAVFEQK.A +2					6.6673		6.5854	6.2126	6.5683			5.9522	5.9222	6.1194	6.1693	6.4505	5.56		4.9319	4.6184	4.0792	5.3258	5.5011	5.6856	
K.PTSTTETVAASAVAAVFEQK.A +3					5.8782		5.7451	5.7804	5.5432			5.3686	5.641	6.0724	5.5156	5.2485	4.9349			4.3353	4.6318		4.5526		
K.PVICATQM*LESM*TYNPR.P +2										4.3397			5.1011	5.0149	4.3968						4.8454				
K.PVICATQM*LESM*TYNPR.P +3													4.4785	4.2815							3.5843				
K.PVICATQM*LESMTYNPR.P +2												2.9541		5.0931	4.7434	4.7788									
K.PVICATQM*LESMTYNPR.P +3														4.5654											
K.PVICATQMLESM*TYNPR.P +2												4.7371			4.1983			2.9612			5.1164		4.3155		
K.PVICATQMLESM*TYNPR.P +3													3.6205	4.0546											
K.PVICATQMLESMTYNPR.P +2					4.514			5.0215	5.5143			5.3793			5.5834	5.7839				4.1598			5.3447		
K.SEELYPGR.P +1												2.1239	2.2598												
K.SEELYPGRPLAIALDTK.G +2	4.2998	4.3455	4.3329	4.4983				2.765	4.4302			4.4089	4.2334	4.4768	4.1379	3.8662	3.5546		3.9146	3.7521					
K.SEELYPGRPLAIALDTK.G +3		3.9847	4.142	3.9114					3.8969			3.6356	3.7503	3.8545		3.6588			3.5082	4.0931					
K.SNLAGKPVICATQM*LESM*TYNPR.P +2													4.4783	4.5358	3.8821	3.2973									
K.SNLAGKPVICATQM*LESM*TYNPR.P +3													4.0555	3.856	4.0413										
K.SNLAGKPVICATQMLESM*TYNPR.P +3														4.1721											
K.SNLAGKPVICATQMLESMTYNPRPTR.A +3			3.8559																						
K.SVIDNAR.K +1	2.1604	2.0681	2.2145		2.2146	1.9903	2.1345	2.2114	2.1597		2.0939	2.0954		2.1194			2.278			2.1002			2.1036		
K.TNNPETLVALR.K +1							2.2312																		
K.TNNPETLVALR.K +2	3.621	3.5848	3.6198	3.5356	3.6302	3.6366	3.6881	3.6705	3.5417	3.6141	3.6083	3.5421	3.4247	3.3013	3.316	3.3558	3.2933	2.8018	2.9561		3.2894		3.4465	3.5082	
K.TNNPETLVALRK.A +2	3.9008	3.7953	3.8738	3.8664												3.2688	3.4206		3.5396				3.2461		
K.VTDGVM*VAR.G +2		3.2608								2.6998			3.2632	3.3274	2.9215			2.6718	2.9041		3.1128			2.8541	
K.VTDGVMVAR.G +1	1.877	1.9265	1.981			1.8376			2.1133											1.8948			2.3057		
K.VTDGVMVAR.G +2	3.3386	3.242	3.2473	3.2739	3.3578	3.1888	3.2075	3.2622	3.0897	2.9317	3.0501	2.9282	3.0568	3.1209	3.4142	2.8959		2.8764	2.9448	3.0544				2.7365	
K.YRPNCPIILVTR.C +2	4.0036	3.8927	3.9808										3.135	3.4272	3.6214	3.3615	3.5563	3.1681	3.6427						
K.YRPNCPIILVTR.C +3		4.0946	3.9739										4.2479	3.6398	3.988				3.9777	3.7296					
R.AEVSDVGNAILDGADCVM*LSGETAK.G +2				5.4956	6.1707	6.3618	6.5113	6.1847	6.1464	6.1912	5.7653	6.1615	6.2556	6.1807	6.0941	6.0179	5.7528	5.8517	5.8466	5.7121	5.8986	5.6453	6.1177	5.9587	
R.AEVSDVGNAILDGADCVM*LSGETAK.G +3		4.3102		5.2026	5.8344	6.1953	6.4116	6.4967	5.9203	6.3093	5.1447	6.4749	6.7384	7.0382	5.2357	6.6897		5.7123	6.9442	6.5622	6.1796				
R.AEVSDVGNAILDGADCVMLSGETAK.G +2	6.3087	6.1917	6.2759	6.338	6.3443	6.2312	6.2909	6.3052	6.4757	6.2944	6.5542	6.1117		6.3509	6.0631	5.9853	6.1349	5.9945	5.8706	5.3849	5.9508	5.7409	5.9692	5.8379	
R.AEVSDVGNAILDGADCVMLSGETAK.G +3	6.0126	5.7847	5.7883	6.1029	6.0532	5.8531	6.6362	5.9527	5.2711	5.3668	5.3966	5.0808		5.4542	5.7112	5.6014	5.4798	5.5586	4.0393	5.5741	4.7847	4.8862	4.7222	4.8218	
R.EVLGEQGK.D +1	2.168	2.2371	2.2333	2.2703	2.0183	2.231	2.1947	2.2741		1.9521		1.9829	1.9258	1.8903	2.3208										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.EVLGEQGK.D +2	2.6986	2.5998		2.5434												2.5087									
R.GDLGIEIPAPEVLAVQK.K +2	4.9042	4.7979	4.7204	4.6266	4.8013	4.8376	4.6682	4.8025	4.4643	4.7788	4.6523	4.5675	4.2767	3.8666	4.1428	4.4255	4.228	2.9487		3.9701	3.7384	2.8153	3.6182	3.8219	
R.GDLGIEIPAPEVLAVQK.K +3							4.2032			4.1156	3.9773	4.395	4.2518	4.6588	4.3361	3.5962			3.9591	3.7732			4.0228		
R.GVFPFVFEK.E +1	2.4047	2.8122	2.7041	2.8123	2.4116	2.4833	2.6734	2.6215	2.4821	1.9677	2.4464	2.5128	2.6975	2.8889	2.6978	2.6674	2.6207	1.8229		2.3957			2.3688		
R.GVFPFVFEK.E +2			2.5961		2.5264																				
R.IIYVDDGVLSFQVLEVVDDK.T +2		5.2414		6.6469		2.6963		2.6351	4.0512			3.7428	4.9645	6.118	5.5264	6.204			5.849	4.9132					
R.IIYVDDGVLSFQVLEVVDDK.T +3														4.846					3.8063						
R.KAGLNIVR.M +2						2.784					2.5789	2.7701						3.067			2.7756				
R.KSEELYPGR.P +2					2.8803			2.6733				2.7523	2.5662		2.7347	3.0643				2.5295					
R.KSEELYPGRPLAIALDTK.G +2		5.4506	5.4413	5.1133									5.36	4.9417	4.9055	4.5186	4.9549		5.1187	4.9663					
R.KSEELYPGRPLAIALDTK.G +3		4.4111	4.5856	4.2676										3.9038	3.8559					3.5646					
R.LTSLNVVAGSDLR.R +1					2.9962	3.1113	3.3326	2.4722	2.5116		2.1507		3.2544	3.357	3.0581	2.9442					3.0576		2.4123	2.4946	
R.LTSLNVVAGSDLR.R +2	5.0085	5.0629	5.0018	5.0807	4.9152	4.8773	4.9491	5.136	4.8363	4.9173	5.0273	4.7229	5.1792	4.9727	4.6174	4.9533	4.7891	4.9335	4.5384	3.1016	4.7104	4.4386	4.6277	4.8075	
R.LTSLNVVAGSDLRR.T +2	2.9591	2.9668	3.0095																2.6781	2.889					
R.M*NFSHGSYEYHK.S +2		3.4945	3.3435	4.0961	3.3387	3.2512	2.8275	3.0582	3.5151	3.5048	2.9812		3.84	3.5411	3.6075	3.7167	3.0879		3.8672	3.4522					
R.M*NFSHGSYEYHK.S +3													3.738												
R.MNFSHGSYEYHK.S +1																	2.0822	3.6953		2.9169					
R.MNFSHGSYEYHK.S +2	3.5138	4.0376	3.9927	4.1141									4.0136	3.8709	3.5131	3.9623	3.9147			3.2019			3.9686		
R.NCTPKPTSTTETVAASAVAAVFEQK.A +2	5.7842	5.4375	5.417	4.8513					3.2843				5.149	5.2223	4.9478	2.7669	2.9324		5.0856	5.8766					
R.NCTPKPTSTTETVAASAVAAVFEQK.A +3	4.4452	4.6018	4.2737	4.0228									4.0764	3.8316	4.0116				3.7331	3.641					
R.PLAIALDTK.G +1					2.6704	2.6573	2.7218	2.7458	2.6866	2.5768	2.6145	2.5832	2.6007	2.6219	2.6294	2.6271	2.5216	2.7558	2.2819	2.3859	2.4869	2.5427		2.342	
R.PLAIALDTK.G +2					3.2851	3.2865	3.3169	3.3229	3.2494	3.3166	3.3408	3.2842	3.1539	3.0855	3.1277	3.1194	2.6137							3.0716	
R.PLAIALDTKGPEIRTGTTTNDVDYPIPPNHEMIFTTDDK.Y +3							3.5782																		
R.PNCPIILVTR.C +2								3.9388	3.7712	3.3125	3.6657	3.716	3.8685	3.8156	3.9385									4.0221	
R.RTSIIGTIGPK.T +2		3.4625	3.4257										2.7772	2.6864	2.8819	2.9889			3.5163	3.3014					
R.TANDVLTIR.E +1	2.4717	2.58	2.4425	2.635	2.6554	2.4696	2.5883	2.7332	2.5148	2.3275	2.325	2.4793	2.3351	2.1702	2.205	2.4331		2.552	2.5927	2.0081	2.6427	2.6728		2.2547	
R.TANDVLTIR.E +2	3.1417	2.9524	3.0328	3.1509	3.1478	3.1414	3.1359	3.1021	3.1329	3.2201	3.0723	2.9747	2.8062	3.326	2.9862	2.8094	2.8521		3.0821	3.0527	2.9641	2.9659	2.8875		
R.TGTTTNDVDYPIPPNHEM*IFTTDDK.Y +2											3.4865		3.1536	3.8293	3.1433	3.4796			3.4097						
R.TGTTTNDVDYPIPPNHEM*IFTTDDK.Y +3		5.1195			4.6755	4.6085	3.5728	5.0917	4.4081		4.8787	4.2819	4.2089	4.6485	3.9245	4.8182	4.1708	4.2763	4.0559	4.731					
R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y +2		3.7862	4.0171						4.2307						2.8442	4.3788	4.2124	3.3601							
R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y +3	5.7285	5.8061	6.0229	4.7734	5.4088	5.1156	5.529	5.4661	5.1925			4.7656		3.6526	4.805	4.8611	4.8047	4.8118		4.482					
R.TSIIGTIGPK.T +1	2.0113	2.1336	2.1045	2.3247	2.1384	2.2444	2.162	2.2219	2.1728	2.1766	2.197	2.1007	2.3066			1.8965		2.0566			2.2506	2.2858	2.1516	2.0673	
R.TSIIGTIGPK.T +2	3.3657	3.281	3.4493	3.3351	3.5532	3.5611	3.5096	3.648	3.0779	3.4805	3.2276	3.3505	3.2895	3.1476	2.841	3.2453	3.088	3.3528	2.6757		2.8868	3.1376	3.2949	3.1242	
gi|6319307|ref|NP_009390.1|	14	10.2	14	12.7	19.8	19.3	19.8	19.8	22.1	19.8	22.3	22.1	24.6	27.7	24.6	19.8	16.8	16	10.2	10.2	11.9	18.8	16.2	18.3	Cystathionine gamma-lyase, catalyzes one of the two reactions involved in the transsulfuration pathway that yields cysteine from homocysteine with the intermediary formation of cystathionine; Cys3p [Saccharomyces cerevisiae]
K.ENVVAVNYPGLK.T +2					3.8333	4.2726	4.0092	3.9247	3.9634	2.9247	3.6185	3.544	4.0438	3.8763		3.9742		3.8601				4.078		3.4879	
K.IAEFLAADK.E +1						2.6677			2.6503			2.802										2.8106	2.5242	2.0737	
K.IAEFLAADK.E +2																					2.7902				
K.IAEFLAADKENVVAVNYPGLK.T +2													5.3309	5.9152											
K.IAEFLAADKENVVAVNYPGLK.T +3													3.9402	4.4293	4.8618										
K.LVWIETPTNPTLK.V +1									2.0417																
K.LVWIETPTNPTLK.V +2	4.0724	3.9733	4.1722	4.2505	4.0893	4.2231	4.0415	4.3094	3.9981	3.6455	3.8056	4.0406	4.1639	3.8341	3.9267	4.0578	3.1976	3.291	3.8903	3.9355		3.734	3.5976		
K.QSSPANPIGTYEYSR.S +2	3.783		4.1356		3.5385	3.6611	3.8933	3.8666	3.8135	3.3913	3.7435	3.4838	3.5423	3.4707	3.1859	3.4886	3.9239				3.6613	3.4244			
K.THPNYDVVLK.Q +1											2.0994														
K.THPNYDVVLK.Q +2				2.5406									2.5368	2.89	2.5194										
K.YINGHSDVVLGVLATNNKPLYER.L +3														3.6097											
R.DALGGGM*ISFR.I +2													3.6234			2.9254			3.3868	2.99					
R.DALGGGMISFR.I +2					4.3291		4.4765	4.2985	4.3599	3.9183	4.104	3.9136			4.1086	4.3278	4.0496	3.9782			4.1519	3.1601		3.7841	
R.EASGVFDDLVR.I +2	3.3252	3.4168	3.5696	3.5235	3.4602	3.585	3.6655	3.624	3.2821	3.5038	3.2189	3.0013	3.4297	3.5338	2.5669	3.0556	3.2249	3.0719			2.8536	3.7493	3.4047	3.1786	
R.ISVGIEDTDDLLEDIK.Q +2	5.0947	5.7663	5.8117	5.937	5.855	5.9895	5.8287	5.8689	5.5673	5.2745	5.95	5.9451	5.0952	5.709	5.7723	5.6888	4.7832	5.5329	4.0417	4.2502	4.3905	5.334	3.5372	4.5461	
gi|6319314|ref|NP_009396.1|	39.4	49.4	43.9	45	42.1	45.8	44.9	47.8	50.5	40.2	46.6	49.5	49.4	52.2	47.7	50.2	42.5	40.2	28.8	41.1	32.1	33.3	34.3	30.4	ATPase involved in protein folding and nuclear localization signal (NLS)-directed nuclear transport; member of heat shock protein 70 (HSP70) family; forms a chaperone complex with Ydj1p; localized to the nucleus, cytoplasm, and cell wall; Ssa1p [Saccharomyces cerevisiae]
K.AEETISWLDSNTTASK.E +2					5.923	5.553	5.8247	5.6438	5.5483	5.3656	5.5489	5.2744	4.2718	4.1453	5.5269	5.5043		2.7052			4.5566	5.3663	5.5155	4.6454	
K.AEETISWLDSNTTASKEEFDDK.L +2														4.1329		3.4529									
K.ATAGDTHLGGEDFDNR.L +2	4.9377	4.8789	4.8088	4.8479	4.9405	4.99	4.8401	5.0364	4.9026	4.6088	5.016	4.5105	4.6526	4.8013	3.9896	4.408					4.1281	3.6706	3.0906	3.8346	
K.AVGIDLGTTYSCVAHFANDR.V +2														4.7779											
K.AVGIDLGTTYSCVAHFANDR.V +3														3.8129											
K.DNNLLGK.F +1																				1.8274					
K.DNNLLGKFELSGIPPAPR.G +2																				3.5476					
K.ELQDIANPIM*SK.L +2					2.9532	3.5457			3.372			3.4522	3.9965	4.3102	3.9963	3.7835					3.1072				
K.ELQDIANPIMSK.L +1					2.0379	2.4058			2.7903																
K.ELQDIANPIMSK.L +2	4.0364	3.9605	4.0085	4.1369	4.1212	4.0737	4.2223	4.2304	3.7393	3.9688	3.84	3.8432	3.9382	3.7922	4.2106	3.8064	3.8619	3.6581			3.882	4.1445		4.085	
K.ETAESYLGAK.V +1		2.3081		2.343			2.2078	2.4185	2.5075		2.3759		2.4782	2.4361		2.6104	2.1904	2.2452	2.5624	2.5065					
K.ETAESYLGAK.V +2				2.5775				2.5528				2.526													
K.FELSGIPPAPR.G +1											2.2309										2.5392				
K.FELSGIPPAPR.G +2	3.6341	3.5119	3.5434	3.3402	3.4878	3.6945	3.6055	3.7462	3.4398	3.7985	3.4059	3.5806	3.4655	3.359	3.4755	3.3556	3.3157	3.349	3.3099	3.1183	3.3153	3.3887	3.3638		
K.KAEETISWLDSNTTASK.E +2									4.654			3.8444	5.6549	5.6989	5.6578	5.7	3.6977	5.4843		4.4543					
K.KAEETISWLDSNTTASK.E +3													4.2727												
K.KAEETISWLDSNTTASKEEFDDK.L +2																	4.3688			3.8755					
K.KAEETISWLDSNTTASKEEFDDK.L +3													4.185	4.6068			3.6085								
K.KAEETISWLDSNTTASKEEFDDKLK.E +2																				3.5901					
K.KAEETISWLDSNTTASKEEFDDKLK.E +3		4.5619																		4.0278					
K.LIDVDGKPQIQVEFK.G +2	4.8317	4.7688	4.5976	4.7397				4.6146	4.3385			4.1854	4.2126	4.9594	4.576	4.5554		4.3681	4.376	4.8067					
K.LIDVDGKPQIQVEFKGETK.N +2																	2.999		2.8471	3.3385					
K.LVTDYFNGK.E +1						2.378					2.5908	2.4373		2.3244	2.6042	2.5519	2.2338	2.1721	2.5806				2.4771		
K.LVTDYFNGK.E +2	3.1996	3.133	3.0982	3.0145	3.1917	3.3894	3.2912	3.5762	3.1629	2.9001	2.884	3.2394	2.9463	2.9503	3.0053	3.0148					3.1635	3.1176	2.5883		
K.LVTDYFNGKEPNR.S +2	2.6137			3.0027				3.5318	3.2458		3.3252	3.0369	3.1185	3.151	3.4737	3.1728	3.5439	3.2943	3.6193	3.2707					
K.M*KETAESYLGAK.V +2																				3.0491					
K.M*VAEAEK.F +1																						2.2691		1.9793	
K.MKETAESYLGAK.V +2											3.1775		3.8339	3.6299			3.7526	3.839		3.9247					
K.MVAEAEK.F +1					1.8514	1.8422	1.9611	1.8379	2.0003	1.8515	1.9182	1.9459	2.1449	1.9156	1.9109	2.151				1.888					
K.NFTPEQISSM*VLGK.M +2		3.1644			4.118	4.2308	4.3259	4.3887	4.1134	4.1871	4.0499	4.0114	3.6348	3.8795	3.8326	3.8464		3.1175		3.9758	4.2319	2.8	3.9145		
K.NFTPEQISSMVLGK.M +1									2.332																
K.NFTPEQISSMVLGK.M +2	4.3633	4.323	4.3763	4.2322	4.5861	4.5145	4.2221	4.4547	4.2125	3.6137	4.2472	4.2404		3.5837	3.718	3.6268	3.9291			3.0985			2.9616		
K.NQAAM*NPSNTVFDAK.R +2					4.6345	5.0825			4.9375	4.9858	4.9429	4.9429			5.4481		4.9102				4.9658		5.0458	4.8993	
K.NQAAMNPSNTVFDAK.R +2	4.7007	4.8769	4.7936		4.8953	5.0646	5.0653	5.1041	4.8024	4.8691	5.0528	4.8012				4.7034	2.5186					3.8419	4.6109	3.8372	
K.NQLESIAYSLK.N +1					2.9792		2.7346	2.8732		2.7009	2.5889		2.7263	2.9823	2.5723	2.848	2.7602	2.6027			2.7288	2.8305			
K.NQLESIAYSLK.N +2	3.7574	3.8288	3.757	3.9038	3.8385	3.9627	3.6629	3.8792	3.8784	3.735	3.8925	3.6253	3.8015	3.8619	3.5819	3.8395	3.236	3.2452			3.6558	3.6168	3.6304	3.5876	
K.NTISEAGDK.L +1																						2.0556			
K.NTISEAGDKLEQADK.D +2	4.618	4.7777	4.7745	4.9555	4.5648	4.8375	4.8343	5.0148	4.7596	4.6735	4.8347	4.836	4.7203	4.7254	4.7968	4.7826	4.709	4.7907			4.5455			2.8006	
K.NTISEAGDKLEQADKDTVTK.K +2									3.2467	3.2006	2.6802			5.6656	4.8828	4.9711		4.1184							
K.NTISEAGDKLEQADKDTVTK.K +3									4.5716		4.0088		3.5571	5.3013	3.9017								3.8207		
K.SQVDEIVLVGGSTR.I +1					2.9334				2.5646	2.78	2.9327				2.6397	3.2136	3.136		2.0024	2.8722	2.5428				
K.SQVDEIVLVGGSTR.I +2	5.0149	4.926	4.9019	5.2081	4.9598	5.0333	4.8988	5.0638	4.7175	4.9421	4.652	4.5151	4.4978	3.7206	4.7695	4.3494		4.3556		4.545	3.1241		3.7348		
K.TQDLLLLDVAPLSLGIETAGGVM*TK.L +2					5.5093	4.9859	6.0329	5.8566	5.9295		4.3691	4.9884	5.9854	6.0594	5.6898	5.8767		4.3441	2.7313	3.0904					
K.TQDLLLLDVAPLSLGIETAGGVM*TK.L +3				5.5141			4.0281	4.7043	5.2543			4.1508	6.2551	6.0831	5.5809	4.4807		4.0019							
K.TQDLLLLDVAPLSLGIETAGGVMTK.L +2		5.3026	6.9682	5.8455	6.2476	5.7776	6.8214	6.2015	6.1584		3.0636	6.2641		5.4426	4.8477	6.0096		5.2931		4.9606					
K.TQDLLLLDVAPLSLGIETAGGVMTK.L +3					5.4391		6.0515	5.7578	5.9714			5.1268	4.4043	5.4808	5.7123	4.9361		5.1529		5.913					
K.VNDAVVTVPAYFNDSQR.Q +2	4.544	4.4852	4.5262	4.258	4.6541	4.7556	4.866	4.7313	4.3843	4.4339	4.2324	5.0374	3.9853		3.8832	4.681	4.1733	3.844	3.6533	3.5695	4.4573	3.9049	4.3225	4.2396	
K.VNDAVVTVPAYFNDSQR.Q +3							4.06			3.6503			4.568			3.9924				3.7919					
R.ARFEELCADLFR.S +2	3.7337	4.2022	4.1129	3.9047													3.2032		3.5025	3.5926					
R.FEELCADLFR.S +1								1.9717	2.2357				1.986	2.3495	2.21	2.5758					1.9985				
R.FEELCADLFR.S +2	3.9117	3.8945	3.98	4.1421	4.0162	4.1778	3.8927	3.9922	3.9344	3.9238	3.9138	3.9746	3.8189	3.9631	3.7523	3.987	3.7032	3.9944	3.4827	3.9332	3.5951	3.8665	3.855	3.8992	
R.GVPQIEVTFDVDSNGILNVSAVEK.G +2						2.6518																			
R.IINEPTAAAIAYGLDK.K +2	5.4234	5.6456	5.4945	5.6147	5.9293	5.7907	5.8466	5.7708	5.6002	5.6482	5.6936	5.7626	5.6224	5.5621	5.3866	5.7659	5.2446	3.7723	5.4782	4.6525	5.4048	5.1952		5.6237	
R.IINEPTAAAIAYGLDK.K +3									4.8594			4.9217	4.8156	5.2729	4.8542	5.0129	3.9747	4.0145	4.5842		4.6019	4.6401	4.4467	4.3033	
R.IINEPTAAAIAYGLDKK.G +2									4.5132				4.4143	4.729	4.5121	3.8927									
R.LSKEDIEK.M +2		2.9827	2.9533	3.0767																					
R.LVNHFIQEFK.R +1													2.7051	2.5647	2.4839		2.4429								
R.LVNHFIQEFK.R +2	3.7066	3.9083	3.8425	3.6697					3.1897			3.3771	3.614	3.4229	3.5363	3.53	2.6731		3.6996	3.5617					
R.NFNDPEVQADM*K.H +2									3.1394	2.5939			3.8075			3.8205	3.4498	3.4706	3.8494	3.7386		3.5435	2.7817		
R.NFNDPEVQADMK.H +2	4.1767	4.0176	4.0503	4.41	4.1598	3.9182	4.1058	4.0408	4.0765	3.9091	3.7925	3.9384			4.0339	3.7714		4.1276						3.3227	
R.SINPDEAVAYGAAVQAAILTGDESSK.T +2	7.0462	7.1555	7.2395	6.854	7.1402	7.0638	7.2401	7.3066	6.897	7.1702	6.8542	6.9365	6.9135	6.7728	6.9581	6.3677	6.9728	6.6366	6.7451	5.8955	6.0024	4.2354	6.8256	6.9738	
R.SINPDEAVAYGAAVQAAILTGDESSK.T +3					4.0958	5.0377	5.493		4.8254	4.7861	3.6748	4.8825	6.019	5.5917	6.2107	4.6956	4.5	3.9234	5.2596	4.7382		3.6232	3.9519		
R.STLDPVEK.V +1				2.2056			2.1634	2.0676	2.1847	1.9368	2.1254	1.9009	2.1088	1.8603			2.1981								
R.TLSSSAQTSVEIDSLFEGIDFYTSITR.A +2														3.6213											
R.TTPSFVAFTDTER.L +2	3.9364	3.852	3.7996	3.9674	4.0102	4.1356	3.988	4.169	3.6972	3.8926	3.7052	3.5352	3.434	3.9506	3.5153	2.8935	2.8369	3.7105		3.7685	2.7462	3.4927	3.47	3.5507	
R.VDIIANDQGNR.T +1								2.7184					2.5191	2.6389		2.1157									
R.VDIIANDQGNR.T +2	4.3474	4.3646	4.1908	4.3819	4.5142	4.4756	4.2544	4.2539	4.1388	4.0966	4.1295	3.9715	3.8439	3.9825	3.2473	4.1288				4.2088					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6319315|ref|NP_009398.1|	34	48.1	68	39.8	18.9	18.9	18.9	13.6	30.6	18.9	13.6	23.3	47.6	48.1	52.9	35	42.7	28.2	58.7	52.9	21.4	12.6	12.6	13.6	Translation elongation factor 1 beta; stimulates nucleotide exchange to regenerate EF-1 alpha-GTP for the next elongation cycle; part of the EF-1 complex, which facilitates binding of aminoacyl-tRNA to the ribosomal A site; Efb1p [Saccharomyces cerevisiae]
K.ADEFDSFPAASAAAAEEEEDDDVDLFGSDDEEADAEAEKLK.A +3			6.3623																						
K.AFQSAYPEFSR.W +1					2.5898	2.3446	2.4755		2.7026		2.1067		2.547	2.4887	2.3798	2.5266	2.5826		2.1228	2.136				2.4471	
K.AFQSAYPEFSR.W +2	3.9685	4.0002	4.0115	3.8924	4.0064	4.0751	4.0144	4.1602	4.0446	3.8688	3.9316	4.1321		3.2757	3.4961	3.8111	3.6079	3.267		3.5043	2.82			3.6561	
K.AIEM*EGLTWGAHQFIPIGFGIK.K +3															3.6922				3.798						
K.AIEMEGLTWGAHQFIPIGFGIK.K +2																				2.6439					
K.KLQINCVVEDDK.V +2		4.6713	4.8675	4.4587										4.4352				4.1107	4.4537						
K.LQINCVVEDDK.V +2					3.65	3.4218	3.857			3.4027		3.5231		3.7264											
K.LQINCVVEDDKVSLDDLQQSIEEDEDHVQSTDIAAM*QK.L +3													5.286	6.2769											
K.PWDDETNLEEMVANVK.A +2																	4.1535								
K.QLNASLADK.S +1												1.8913				1.8401	2.4154				2.0211	1.9571	1.8997		
K.SIVTLDVKPWDDETNLEEM*VANVK.A +2													3.9889	3.7263	3.2714										
K.SIVTLDVKPWDDETNLEEM*VANVK.A +3				3.7181									4.766	5.0911					4.4752						
K.SIVTLDVKPWDDETNLEEMVANVK.A +3		4.6828	5.5913	5.1618																3.5598					
K.SYIEGTAVSQADVTVFK.A +2	4.7294	2.8433	4.7751		5.6164	5.3825	5.6624	5.1995	5.4002	3.8726	4.8942	5.3571	5.2004	5.0846	5.2995	5.3488	5.2266		4.5272	5.1282	4.6457	4.7554	5.5212	3.4517	
K.VSLDDLQQSIEEDEDHVQSTDIAAM*QK.L +3									5.2882				5.3848	4.7022	4.0628	3.604		4.2093	4.7891	3.8899					
K.VSLDDLQQSIEEDEDHVQSTDIAAMQK.L +2																	3.8897			2.8588					
K.VSLDDLQQSIEEDEDHVQSTDIAAMQK.L +3	5.8137	5.708	6.2263	4.7439					4.605							3.672									
R.IAAYNAK.K +1	1.9919																				1.8801				
R.WFNHIASK.A +1			2.4584										2.4659	2.511	2.5485	2.4856	2.299	2.4982		2.2578					
R.WFNHIASK.A +2	3.5178	3.5267	3.5015	3.3174					3.0067					2.9599	2.7738	3.2729	2.9044	2.9474	3.2741						
gi|6319395|ref|NP_009477.1|	3.8	10.4	10.2	9.5	18.1	16	18.9	24.3	30.6	15.5	21.5	24.5	32.6	32.6	28.5	36.5	20.9	20.1	22.5	32.8	19.3	17.4	19.7	11	Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A; Ils1p [Saccharomyces cerevisiae]
K.ALNSLFDALFTFVR.A +2									2.92				4.7988	4.6469	3.7016	4.5464				4.5135					
K.AVADWPVLGK.K +1														2.3175				1.8862		2.037					
K.AVADWPVLGK.K +2							2.9648		2.576	2.6615		2.8602	3.0018	3.181	2.9754	3.2812	3.1115	2.6699	3.4087	3.1852	2.5133		2.9568	2.9432	
K.CGLEATDDVLVEYELVK.D +2															3.4663	5.6462				2.5783					
K.DALPSVTSEQVR.E +2	3.5267	3.1016	3.016	3.3207				2.9372			3.3735	3.613				2.9504	3.364	2.9396		2.771					
K.DTIDFEAIVK.E +2												2.88	3.359	3.5603	3.1296	3.1849				2.938	2.8197		2.9344	2.68	
K.DVNDPAVTIGFNVIGQEK.T +2					4.1309	4.508	3.9296	4.2725	4.2379	2.7743	4.0391	2.8953	3.2027		3.9509	5.107	3.1264			4.8619		3.6109	2.7354	3.2253	
K.DVPDFEGVYVK.D +1										1.8685							2.4983				2.6389	2.2587			
K.DVPDFEGVYVK.D +2					2.7031	3.1246	2.8551	2.7664	2.7264		3.2741						2.5048				2.7993	2.7091			
K.ELEELTGVR.V +2				2.5238		2.8389					2.5882	2.6002		2.5375		2.6244	2.592					2.6866			
K.EYFDEAIETAVSR.M +2					3.6488	3.7193	4.3355	4.0548	4.3426	3.5511	3.7835	3.8163	4.6598	4.428	4.5564	4.7159		4.1572	4.1203	4.1249	4.1225		4.6165		
K.EYIPEAVLAK.Y +1											1.8751								1.9987				2.0534		
K.EYIPEAVLAK.Y +2																						2.7343			
K.FLDGQIALLK.K +1																					2.1845				
K.FLDGQIALLK.K +2							3.4007		3.2545		2.5881	3.061	3.3559	3.48	3.2632	3.0986	2.6487	2.9182					2.9423		
K.GENGVEDCLK.A +2												2.5053				2.8538									
K.KEYFDEAIETAVSR.M +2														3.8126						3.2688					
K.KLGITGKDDVFK.Y +2																				2.5392					
K.LEVAGIELVK.G +2					2.7629		2.7713					2.7276	2.7217	2.5583	2.7021										
K.LLNFIDELTNWYIR.F +2								3.6643	3.614				4.4448			3.8494				3.3706					
K.M*SNIDFQYDDSVK.S +2																				3.581					
K.MSNIDFQYDDSVK.S +2				4.3843	5.011	4.8053	4.8132	4.2596	4.4651		4.4874	3.7695	2.7008		2.9471	4.107						4.6356		4.5516	
K.NGVISEDSVLPNAIDDLGR.F +2		4.6266	5.4245		4.5977	5.133	4.452	4.4915	4.7287	4.0278	4.2712	3.969	5.0707	5.0562	4.7664	4.8331	3.8133		3.6242	4.4938	3.6536	3.9355	4.6338	3.9781	
K.NIVPQMLDSVM*K.S +2									2.7072					2.9105	2.8451										
K.NIVPQMLDSVMK.S +2																	2.7544								
K.NVIVSGIVLAADGR.K +2									4.7195	3.6606		4.3963	4.5776	4.934	4.5794	4.5136	3.9192	4.6146	3.0311		4.995	4.7595	3.6392	
K.NVIVSGIVLAADGRK.M +2	2.6515	3.4588	2.7303																						
K.NYIIEELNVR.D +2					3.4072			3.2492	3.4726	3.0767	3.1172		3.2775	3.4254	3.2559	3.2552	3.4537	2.6059	3.0784	3.326	3.1213	3.2745	3.2946	3.1905	
K.NYPDPSIVLNK.Y +2					2.5476			2.7403														2.6619			
K.RFANWIANAR.D +2																	3.1032								
K.SHWVPNTIK.E +2				2.7195																					
K.TDPIGDEEQSINDTIFK.L +2			5.6319		6.0667	6.2547	5.9827	6.0392	5.8832	5.6443	6.0151	5.8428	5.7749	5.5896	5.5984	6.0152	4.1883	2.8709	4.9156		5.3833		5.546	5.6328	
K.TLVILHSDESYLK.D +2				3.2406					3.9204				3.9658	3.8836	3.2628	4.3303									
K.TM*YPSFM*ESTWWAFK.Q +2													3.2154	4.2955					2.7831						
K.TM*YPSFMESTWWAFK.Q +2																				3.0036					
K.VLLPWWNSFK.F +2		2.7539																	2.6897						
K.VM*PYSTGLTTPLSNFEAQQNYK.D +2																		3.8517	3.7999	3.9234	3.7446				
K.VMPYSTGLTTPLSNFEAQQNYK.D +2									2.8765								4.7948	4.6206		3.8554					
K.YGADALR.L +1																							2.0098		
K.YGLENYNNECR.S +2						3.4528				3.428	3.5258							3.056					3.3157		
K.YLTNTGNLLLASQIR.H +2					4.3009		4.7121	4.5394	5.0583	3.7885	4.6364	4.6145	4.8821	4.9323	4.4864	4.4536				3.5291	4.2344	5.1274	4.9342		
R.AM*APFTPFLSESIYLR.L +2					3.2352		3.9024	3.6748	3.6996		3.2584	2.682	5.0036	4.8727	4.0825	4.2105			4.8573	3.6637					
R.AM*APFTPFLSESIYLR.L +3													4.559												
R.AMAPFTPFLSESIYLR.L +2																				2.6841					
R.DVVITSDEAK.Y +1																					2.9475	2.8918	2.9326		
R.DVVITSDEAK.Y +2							2.8386	2.7155				2.6053													
R.FANWIANAR.D +2					3.0599	3.1627		2.8683	3.2909		3.242			2.8952		3.0335		3.2823			3.2029		2.6384		
R.FGWDTHGVPIEHIIDK.K +3														4.216						3.7496					
R.GLPESAVQAGQETR.T +2									4.3543	4.5801	4.4191	4.4092	4.4741	4.6495		4.0616		4.7837	4.4239		4.4983	4.3887	4.5787		
R.LKEYIPEAVLAK.Y +2													2.5987												
R.LYLINSPVLK.A +2						3.1541								3.3247	3.2256	3.2056						3.148			
R.M*QSVIDLGR.N +2														3.0599							2.9053				
R.MQSVIDLGR.N +2											2.7164		3.114		2.7076	2.9827		3.3228							
R.SIVM*TYASDWR.K +2																2.7377									
R.SIVMTYASDWR.K +2												3.6918								3.939				4.0269	
R.SVHFLSYPVVK.K +2																2.533			2.963	3.1492					
R.SVHFLSYPVVKK.E +2																				2.9707					
R.TDQDVLIIM*DTNIYSELK.S +2					3.2075	2.6824	3.8608	3.1928	4.5979			5.0671	4.6747	2.744		2.8883		3.9409							
R.TDQDVLIIMDTNIYSELK.S +2						3.3596											2.8464		2.6847	3.6446					
R.VISDDYVTSDSGTGIVHNAPAFGEEDNAACLK.N +3		6.6118	7.0595	6.2546				6.3338	6.6383				6.6941	6.5454	5.473	5.0303	6.0766	4.0405	6.4488	4.9786					
R.VPANFISEGLDQTR.G +2	4.5564	4.2716	4.5545	4.6919	4.768	4.5003	4.5636	4.6112	4.4547	4.3064	3.9842	4.0887	4.5875	4.3083	3.6468	4.1552		4.64		4.8048	4.5584	2.8365	4.1059		
R.WIDFDNDYK.T +1																				1.9574					
R.WIDFDNDYK.T +2		2.8974				3.3813	2.9145	2.8509					2.6537	2.9613	2.5898	2.8309						2.8875			
R.YFILLESLIK.T +2													3.9711	3.5452					3.2848	3.1638				3.1164	
gi|6319396|ref|NP_009478.1|	8.5	8.5	8.5	12.3	11.7	8.2	11.7	11.7	11.9	8.2	11.7	13.4	11.9	15.1	11.9	11.9	6	5.7	9.7	10.6	11.7	8.2	11.7	10	ATPase involved in protein folding and the response to stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Ssa3p [Saccharomyces cerevisiae]
K.ATAGDTHLGGEDFDNR.L +2	4.9377	4.8789	4.8088	4.8479	4.9405	4.99	4.8401	5.0364	4.9026	4.6088	5.016	4.5105	4.6526	4.8013	3.9896	4.408				4.1281	3.6706	3.0906	3.8346		
K.DNNLLGK.F +1																				1.8274					
K.DNNLLGKFELSGIPPAPR.G +2																				3.5476					
K.FELSGIPPAPR.G +1											2.2309										2.5392				
K.FELSGIPPAPR.G +2	3.6341	3.5119	3.5434	3.3402	3.4878	3.6945	3.6055	3.7462	3.4398	3.7985	3.4059	3.5806	3.4655	3.359	3.4755	3.3556	3.3157	3.349	3.3099	3.1183	3.3153	3.3887	3.3638		
K.KSETFSTYADNQPGVLIQVFEGER.T +3														4.1328					4.1284						
K.SETFSTYADNQPGVLIQVFEGER.T +2							2.5989		5.4443		2.5746	3.9003		3.9062	5.0339	4.907				3.5238			2.548		
K.SETFSTYADNQPGVLIQVFEGER.T +3					3.854			4.193			4.507	3.8719	4.4903	4.7136	3.8132	4.108					4.7864			3.9086	
K.TQDLLLLDVAPLSLGIETAGGIM*TK.L +3				3.5054																					
R.ARFEELCADLFR.S +2	3.7337	4.2022	4.1129	3.9047													3.2032		3.5025	3.5926					
R.AVGIDLGTTYSCVAHFSNDR.V +2														4.6378											
R.FEELCADLFR.S +1								1.9717	2.2357				1.986	2.3495	2.21	2.5758					1.9985				
R.FEELCADLFR.S +2	3.9117	3.8945	3.98	4.1421	4.0162	4.1778	3.8927	3.9922	3.9344	3.9238	3.9138	3.9746	3.8189	3.9631	3.7523	3.987	3.7032	3.9944	3.4827	3.9332	3.5951	3.8665	3.855	3.8992	
R.IINEPTAAAIAYGLDK.K +2	5.4234	5.6456	5.4945	5.6147	5.9293	5.7907	5.8466	5.7708	5.6002	5.6482	5.6936	5.7626	5.6224	5.5621	5.3866	5.7659	5.2446	3.7723	5.4782	4.6525	5.4048	5.1952		5.6237	
R.IINEPTAAAIAYGLDK.K +3									4.8594			4.9217	4.8156	5.2729	4.8542	5.0129	3.9747	4.0145	4.5842		4.6019	4.6401	4.4467	4.3033	
R.IINEPTAAAIAYGLDKK.G +2									4.5132				4.4143	4.729	4.5121	3.8927									
R.STLEPVEKVLK.D +2												2.987													
gi|6319483|ref|NP_009565.1|	17.8	43.9	43.9	38	48.8	42.9	42.9	42.9	36.2	40.4	38.7	46.7	54	52.3	52.3	54.7	48.1	48.1	47	42.2	21.6	16	40.4	21.6	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase; Ipp1p [Saccharomyces cerevisiae]
K.AASDAIPPASPK.A +1																						2.2823	1.8956		
K.AASDAIPPASPK.A +2					2.8264	3.6971	3.5545	3.1432		3.5993	3.3156	2.9881	2.7093	3.1211	2.8985	3.5522	3.0965	2.8099	2.5927	3.049			2.6688		
K.ALGIM*ALLDEGETDWK.V +2					4.0704	5.5374	5.3808	4.9294	5.6014	3.9856	3.8366	5.4509	5.5989	5.6762	5.7168	5.6977	4.4846	5.338	5.2875	5.4374			5.1582		
K.ALGIM*ALLDEGETDWK.V +3																			3.6562						
K.ALGIMALLDEGETDWK.V +2		6.018	6.0075	5.77	5.7594		5.2448	5.2487	5.8229			5.7737	3.0934	5.6309	5.9696	5.1628	5.6855	4.9134		5.3633					
K.AVGDNDPIDVLEIGETIAYTGQVK.Q +2		6.2575	6.0937	2.608	5.729	5.1865	6.1343	6.2575	5.9792	3.1211	5.3523	5.9177	6.0371	5.9952	6.114	5.6674	5.6496	4.9134	4.8396	4.6037	3.38		5.5912	5.5574	
K.AVGDNDPIDVLEIGETIAYTGQVK.Q +3		5.3007	4.9282	5.3646	5.4743		5.5077	5.5114	5.4195		4.4382	5.3337	5.6184	5.3051	4.2225	4.9913	5.1758	3.6778	3.797	5.1899	3.9605		4.7681	4.9676	
K.DGKPVSAFHDIPLYADK.E +2													4.5808	4.7128	4.2189	4.0176				4.1788					
K.EETLNPIIQDTK.K +1													3.73											2.7181	
K.EETLNPIIQDTK.K +2	3.3398	3.6998			4.5857	4.5487	4.6225	4.538	4.5109	4.5191	4.4578	4.697	4.5376	4.4893	4.4142	4.5003		4.5014		2.9518	4.2239	4.2809	4.3329	3.5405	
K.EETLNPIIQDTKK.G +2												3.1584													
K.ENNIFNM*VVEIPR.W +2					4.1038	4.4169	4.2091	4.1669	4.1499	3.8917		4.064	4.1319	4.2929	4.0571	4.0901	3.1744	3.7708	3.5017	3.5602	3.8628		3.601		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ENNIFNMVVEIPR.W +2		4.232	4.597	4.5915	4.3178	2.7551	3.6981	4.1663	4.4624			4.1434			3.4459	3.1661	4.176	3.1618		3.843	3.0547		4.1384		
K.GIDLTNVTLPDTPTYSK.A +2	5.268	5.3971	5.3363	4.4233	5.2605	5.3548	5.248	5.1967	5.2287	4.8791	4.584	4.8263	4.9742	5.1895	4.8832	4.9451	4.6132	4.3063	3.8037					5.3223	
K.IPDGKPENQFAFSGEAK.N +2		4.5653	4.096	4.699	3.022							3.1841	4.9324	4.8201	4.1735	3.9746	4.5847	4.5343					3.7766		
K.LEITKEETLNPIIQDTK.K +2		6.0702	5.9088										5.2114				5.709	5.0778	5.2859	5.8311					
K.LEITKEETLNPIIQDTK.K +3																	4.0796								
K.LNDIEDVEK.Y +1												2.8584	2.852	2.6755	2.6706	2.8563	2.7757	2.8124	2.7422	2.9016		2.9103	2.6651	2.705	
K.LNDIEDVEK.Y +2	3.1495	2.9645	3.1999	3.117	3.1235	2.8054	3.0414	3.0763	3.0293	2.6265	2.6445	3.175	3.1273	3.0675	3.0542										
K.PVSAFHDIPLYADK.E +2																			3.6831	4.276					
K.VIAIDINDPLAPK.L +1																					2.353				
K.VIAIDINDPLAPK.L +2	4.6265	4.9368	4.9049	4.8849	4.6619	4.7746	4.6825	4.6385	4.5138	4.8219	4.6854	4.6589	4.7872	4.5552	4.4978	4.5164	4.2861	4.456	2.7424	4.1803		4.6362	2.8342		
K.WFFISGSV.- +1											2.4094														
R.ATNEWFR.I +1					1.8516	1.9827																			
R.ATNEWFR.I +2					2.5941		2.6751	2.5083								2.5769									
gi|6319505|ref|NP_009587.1|	27.3	42	36.5	36.5	36.5	32.6	21.3	32	44.5	25.4	28.2	35.1	48.9	43.6	41.7	47	27.3	33.7	35.4	39.8	4.7	10.5	21	22.4	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4ap [Saccharomyces cerevisiae]
K.AGHQTSAESWGTGR.A +1																		3.1939					2.174		
K.AGHQTSAESWGTGR.A +2		4.2667	4.0815	4.1614	3.0099				3.5153	3.1952	3.9861	3.3488	4.0781	4.0219	4.4901	4.3064	2.8097	3.7599				3.7987			
K.AVGAHSDLLK.V +1													2.4894	2.4379	2.3415								2.2577		
K.AVGAHSDLLK.V +2	3.287	3.4267	3.4115	3.7016	3.2837	3.4375	3.6305	2.9899	3.0393	3.0255	3.119	2.5813	3.4915	3.4875	3.3418	3.2584		2.5594		3.1		3.0412	3.2057	3.0693	
K.EAVAALK.A +1													1.9036	2.0236						2.2717				1.9362	
K.IPEIPLVVSTDLESIQK.T +2	5.4644	5.5417	5.656	5.2013	5.6257	5.4796	5.4649	5.5921	5.569	3.3357	5.3767	5.0367	5.1598	5.2441	5.2618	4.8757	4.3737		5.6491	4.6751	5.1877		5.3973	5.6538	
K.IPEIPLVVSTDLESIQK.T +3						4.4573	4.6407				3.6893		4.3684	4.5632	4.2186	4.0801		3.5186			4.6038		3.7006		
K.LDQVWGSETVASSK.V +1																								3.1327	
K.LDQVWGSETVASSK.V +2	5.0856	4.919	5.1516	5.3291	5.3142	5.1403	5.3726	5.1068	5.3664	4.978	5.0132	5.1046	5.246	5.1246	5.1401	5.1652	5.1285		4.7241	4.8035		4.977	5.3114	4.8426	
K.PAAVFTETLK.H +1																	2.2726	2.3084		2.0667			2.0942		
K.PAAVFTETLK.H +2	3.0223		2.3353	3.3746	3.2457	3.277	3.1252	3.1899	2.9829		2.6764	2.628	2.9265	3.0675	2.7681	2.9455		2.5141							
K.RQAYAVSEK.A +2		2.9321															2.6372	2.7328							
K.TGTKPAAVFTETLK.H +2		3.6183	3.4879	3.6005				2.7724	2.9366				3.7947	3.4653	3.4789	3.7164				2.5355					
K.VGYTLPSHIISTSDVTR.I +2	5.1722	5.3443	5.1573	5.338				4.6296	5.0493			4.5354	5.1698	5.2283	5.0187	5.2978		4.0377	4.6281	4.4189					
K.VGYTLPSHIISTSDVTR.I +3		4.3783							4.5838			3.6276	4.9616	4.8273	5.0812	4.5001			3.6159						
R.FVIWTEAAFTK.L +2		3.3219			3.6043	3.3468			3.3543				3.4275	3.4821	3.5527	3.2952				2.8288			3.6425		
R.GPLVVYAEDNGIVK.A +1					3.7548				2.7548																
R.GPLVVYAEDNGIVK.A +2			4.9187		4.8819	4.9906	4.8338	5.0183	4.8875	4.3424	4.8721	4.5742	4.9107	3.6211	5.0789	4.8409	5.2747	4.8347						3.8686	
R.IINSSEIQSAIR.P +2					4.5754	4.4958	4.4495		4.6428	4.4402	4.333	4.4629	4.3887	4.3165	4.5857	4.5964				4.0516					
R.IINSSEIQSAIRPAGQATQK.R +2	5.292	5.929	5.9946	5.7048					5.1578				5.6276	5.8791	5.0808	5.9359	6.0728	4.2142	4.3751	4.6497					
R.IINSSEIQSAIRPAGQATQK.R +3	3.781	4.8136	4.4079	4.3155					4.038				4.3618			4.0996	4.2001		4.0156	4.6254					
R.NVPGVETANVASLNLLQLAPGAHLGR.F +2																			3.3971						
R.QAYAVSEK.A +1													1.8501			1.9041									
R.RGPLVVYAEDNGIVK.A +2		4.2638	3.8355	3.7121									2.6164		3.8698	3.2588	4.2505		3.203	3.181					
R.RGPLVVYAEDNGIVK.A +3													3.8357	3.9309	4.2008	3.8109			4.185	3.7541					
R.SGQGAFGNMCR.G +2	3.4191	3.6126	3.4251	3.3628	3.6325	3.7281		3.5927	3.7541	3.1824	3.2443		3.627			3.4461		3.0243							
R.YATASAIAATAVASLVLAR.G +2					4.8034	5.2565		4.5746	4.5436			3.7948		2.7245	2.9944	4.9678			4.7837	4.5428				4.6713	
R.YATASAIAATAVASLVLAR.G +3						4.0344			3.6668				4.7372	5.0272	5.129	4.4909			3.6357	4.0106					
gi|6319559|ref|NP_009641.1|	20.1	25.9	25.4	24.9	23.8	19.6	23.8	23.8	29.1	19	19	29.1	34.4	29.6	24.3	33.3	25.4	23.8	21.2	19.6	13.8	19	28	9	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal; Rpl19ap [Saccharomyces cerevisiae]
K.ALNEEAEAR.R +1											2.7203														
K.ALNEEAEAR.R +2					3.081		2.6895	2.6844	2.6109	2.8717	2.6475	2.9663	3.0066	2.603		3.1474			3.2991			2.8705	2.6905		
K.RALVEHIIQAK.A +2		2.8747																2.9145	2.7015	2.7577					
K.RLAASVVGVGK.R +1																	2.2855								
K.RLAASVVGVGK.R +2	3.1806	3.267	3.343										2.8076				3.0929								
K.VWLDPNETSEIAQANSR.N +2	5.571	5.4626	5.4891	5.6992	5.5834	5.5678	5.6455	5.7145	5.213	5.475	5.481	5.2313	5.4887	5.4441	5.2107	5.6153	5.4158	4.4512		5.2679	5.9067	5.3891	4.8403	5.6605	
K.VWLDPNETSEIAQANSR.N +3													4.0996	3.9533											
R.ALVEHIIQAK.A +2		3.5014	3.194	3.5517		2.7124			3.6457			3.5618	3.6382	3.5054	3.3791	3.616	3.4604	3.1885							
R.DALLKEDA.- +1													2.0491			1.9647		2.2357					2.3999		
R.LAASVVGVGK.R +1						1.9595																			
R.LAASVVGVGK.R +2					3.6814	3.6335	3.6795	3.646	3.5912	3.4934	3.6308	3.5689	3.4725	3.6381	3.6299	3.7863						3.6253	3.1209		
R.LAASVVGVGKR.K +2	2.9087	3.4487	3.2534	3.0941									2.8643	2.7122			2.9437		2.9643						
R.LPSQVVWIR.R +2	3.6766	3.6379	3.6761	3.6783	3.6197		3.5379	3.6713	3.5995			3.3229	3.454	3.5716	3.6829	3.5068	3.7013	3.5229	2.787	3.5226	3.286		3.5822		
gi|6319673|ref|NP_009755.1|	34.8	33	38.6	33.8	35	24.5	26.7	38.6	43.3	22.2	28.5	38.6	44.2	47.1	44	37.9	26.7	24	32.9	36.1	22.6	16.2	30.3	26.2	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation; Pgi1p [Saccharomyces cerevisiae]
K.AEGATGGLVPHK.V +1						2.0532												2.0514							
K.AEGATGGLVPHK.V +2	3.5941	3.6157	3.6467	3.5718	3.6881	3.7433	3.6568	3.7863	3.4655	3.2566	3.5805	3.6482		3.1518	3.1206	2.8443			3.4953		3.4679	3.1377	3.3603	3.0378	
K.EANVTGLR.D +1									2.078		2.013														
K.EANVTGLR.D +2	2.6536		2.8509	2.6996		2.8918						2.5693	2.74	2.6468											
K.EFSEQVR.S +1									2.1667										2.0368						
K.ELDNSSTISTHDASTNGLINQFK.E +2	4.4326	4.9154	4.7341	4.7195				4.1915	4.6053				4.8452	4.8598	4.5693	4.5986	4.3635	4.3801	4.4165	3.6252					
K.ELDNSSTISTHDASTNGLINQFK.E +3	4.6687	4.6067	4.9033	5.1741	4.6886			4.8062	4.2025			3.5827	4.6033	4.2466	4.522	4.7175	3.8201	4.7075	4.0779	3.9852					
K.GEHINSTEDR.A +2											2.5909														
K.HFAALSTNETEVAK.F +1									3.2398		2.157		3.5537	3.2205	2.0176	2.6364	3.7549	3.3552		2.7535		3.1413			
K.HFAALSTNETEVAK.F +2	3.2196	4.9007	4.7992	4.7032	3.7531		4.7095	4.2552	4.205	4.6829	4.9228	4.8221	4.3625	4.7062	4.3014	4.589	4.0321	4.4918	4.4003	3.1038	4.225	3.5125	3.1557		
K.HFAALSTNETEVAK.F +3													3.8415												
K.ILFDYSKNLVNDEIIAALIELAK.E +3					3.5005		3.754						3.5171												
K.ITDVVNIGIGGSDLGPVM*VTEALK.H +2					5.0834		5.4419	5.522	5.2228	3.9722		4.7825	5.7663	5.6178	5.5781	5.7662					5.4372				
K.ITDVVNIGIGGSDLGPVM*VTEALK.H +3													5.4918	5.3861	4.9163										
K.ITDVVNIGIGGSDLGPVMVTEALK.H +2			4.3093		6.352	5.8666	6.2915	6.0654	6.1738		5.3535	5.8657		4.5599	5.6824	5.536							4.7877	4.0037	
K.ITDVVNIGIGGSDLGPVMVTEALK.H +3					4.883		4.8638		4.9273			3.8202			5.6722	4.0596									
K.KITDVVNIGIGGSDLGPVM*VTEALK.H +3														5.0816					3.5262						
K.LATELPAWSK.L +1						2.2596			2.2055				2.3621	2.4744	2.5082	2.2214	2.3366	2.3037	2.2916	2.188	2.2352		2.4204		
K.LATELPAWSK.L +2	3.3093	3.1766	3.1947	3.1884	3.2242	3.1628	3.16	3.0642	2.6244	3.0395	2.847	2.9291	3.027	3.1099	3.1247	2.9378		2.9038				3.1602	2.9969	3.1696	
K.LIPSDFILAAQSHNPIENK.L +2	4.236	4.6502		4.4626									4.0317	4.4071	3.1859				3.6891	3.5343					
K.M*LASNFFAQAEALM*VGK.D +2											2.7223	4.5033	5.8135	5.6113	5.3291										
K.M*LASNFFAQAEALM*VGK.D +3													4.9649												
K.M*LASNFFAQAEALM*VGKDEEQVK.A +2														4.0955											
K.M*LASNFFAQAEALM*VGKDEEQVK.A +3													3.9469	4.11											
K.M*LASNFFAQAEALMVGK.D +2									4.1272			2.8688		3.1189						3.0218					
K.MLASNFFAQAEALM*VGK.D +2																							3.2057		
K.MLASNFFAQAEALMVGK.D +2					5.5376			4.401	5.3962																
K.NLVNDEIIAALIELAK.E +2		6.2833	6.0671	6.2559	6.2439	6.382	6.2973	6.1732	6.1547			6.2606	6.4266	6.088	6.3507	6.2043			5.2989	6.1169			3.2566	3.8769	
K.NLVNDEIIAALIELAK.E +3				6.0709		5.4799							6.0739	6.1661	5.0797	5.8188			3.5418	5.4156					
K.NM*FGFESWVGGR.Y +2					3.3421	2.5049	4.084	4.2354	3.8759			4.2705	4.3533	4.3666	3.9132	4.0626			3.8989	4.168	2.9814	2.8916		2.662	
K.NMFGFESWVGGR.Y +2	2.8975	2.9488	4.227		4.3125		4.2583	3.1401	4.2408			2.8828			3.3781	4.1664	4.1225			4.1248			2.7654	2.5672	
K.PM*YVDGVNVAPEVDSVLK.H +2													4.5886	4.4739	3.1777		3.1759		4.6221	4.6468		3.5818			
K.PMYVDGVNVAPEVDSVLK.H +2	5.5742	5.5441	5.6556	5.6073					4.2405								4.8573	4.1514		4.1416				3.9696	
K.TFTNYDGSK.I +1							2.2559	2.084	2.3203	2.2839	2.1013	2.2825	2.4126	2.3048	2.3088	2.3733	2.2112	2.137	2.1776	2.0705	2.1451	2.0939	2.0415	2.3723	
K.TFTTAEITINANTAK.N +1													3.1754	2.9773		2.4181	3.2804			2.7631	2.6455	3.0644			
K.TFTTAEITINANTAK.N +2	5.6065	5.322	5.3179	5.47	5.5415	5.322	5.4975	5.5357	5.2772	5.3511	5.007	5.5003	5.3188	5.2265	5.3349	5.231	4.9163	5.2874				4.8196	5.3494	5.2117	
K.TGNDPSHIAK.H +2	3.3954		2.7923			2.95		3.0743		2.9316	2.8638	3.343		2.6661		2.814							2.9693		
K.VFSGNRPTTSILAQK.I +2	4.1207	4.3141	4.3031	4.2557	3.6236			4.0997	3.7957			3.5865	3.7868	3.7502	3.8723	3.6674	3.6441			3.8222					
K.VVDPETTLFLIASK.T +1									2.4475																
K.VVDPETTLFLIASK.T +2	5.0327	5.0404	5.0187	5.1233	5.0732	4.8044	4.912	4.9364	4.7716	4.0993	4.7175	4.9204	4.7869	4.6553	4.9676	4.2363	4.8389	4.577	3.7244	4.4776	3.7226		4.6941	4.2225	
K.VVDPETTLFLIASK.T +3													4.9705	4.9321	4.3984		3.7879	3.6279		3.8173					
R.ANKPM*YVDGVNVAPEVDSVLK.H +2									5.1822				4.6858	4.9107	4.5788	4.986	3.8557	3.3083	3.5688	3.0618					
R.ANKPM*YVDGVNVAPEVDSVLK.H +3									4.1212				4.7952	4.6185	4.5814	4.4111									
R.ANKPMYVDGVNVAPEVDSVLK.H +2									3.2085						5.0846	5.6201	5.2502			5.0404					
R.AVYHVALR.N +2	2.693		2.722	2.6024				2.7794	2.5206						2.7301										
R.FPAYLQQLSM*ESNGK.S +2		3.0343				3.2622	4.7228	4.5377	4.1535	4.7274	5.1164	4.4546	5.1518	4.987	4.5073	4.857		3.6729					4.1301		
R.FPAYLQQLSMESNGK.S +2	5.1086	5.3079	5.2323	5.1092	4.8751	5.3485	5.3862	5.7249	5.4008		5.3114	4.37		3.5814	4.524	4.8137	4.3692	4.755		4.3609	5.2056		4.9726	4.9721	
gi|6319806|ref|NP_009887.1|	6.7	16.7	16.3	11.9	18.4	16.5	21.6	23	25.7	21.6	23.6	29.7	36.4	34.1	34.7	35.8	33.5	20.9	34.9	34.9	27.6	16.1	27.4	18.2	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for the formation of disulfide bonds in secretory and cell-surface proteins, unscrambles non-native disulfide bonds; Pdi1p [Saccharomyces cerevisiae]
K.AAEEADADAELADEEDA|HDEL.- +2			6.8675		6.8994	6.8622	7.1225	7.0082	6.1504	6.6136	6.8333	6.456	6.5645	6.4777	6.5353	6.7265	5.0936	4.5511	6.5459		7.0111		6.7027	6.5903	
K.AAETLVEK.N +1								2.1442				1.9167				1.8356									
K.ADIADADVFEK.W +2					4.1607	4.1925	4.3126		4.1205	4.1735	4.026	3.7699	3.8151	3.5705	3.3617					3.9999			4.1484		
K.ALYEEAQEK.A +1																	2.1682					2.1835	2.5399		
K.ALYEEAQEK.A +2		2.7902									2.5863		2.5659			2.7846	3.0118								
K.DFLKGDASPIVK.S +2																		3.3643		3.4168					
K.EQFPLFAIHDM*TEDLK.Y +2													4.0099	4.1712	3.834	3.7807			2.7745	2.5948					
K.EQFPLFAIHDMTEDLK.Y +2		4.8484																							
K.HFNDYDFVSAENADDDFK.L +2													6.6263	6.5545	5.925	6.0901	5.8366		3.6341	6.019					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.HFNDYDFVSAENADDDFK.L +3														3.9034											
K.KADIADADVFEK.W +2											2.6557	3.7484	4.3892	4.5896	4.0778	3.8083	3.6501		3.1018			2.5295			
K.KSESVVYQGSR.S +2													3.4396	3.1459	2.8389	3.6934					2.8276	3.0647			
K.LSIYLPSAM*DEPVVYNGK.K +2									3.4088	4.0505	3.196	4.352	5.3711	3.2397	4.7466			4.9437	4.226	3.6891	4.5542	3.2948			
K.LSIYLPSAMDEPVVYNGK.K +2					5.0849	5.7346	5.5753	4.9196	5.4163		3.9054	4.3367				5.5894	4.4159			2.6293	2.5195		4.0674	4.7335	
K.NHDEIVNDPKK.D +2																		2.7262							
K.NSDVNNSIDYEGPR.T +2																					4.3629				
K.SESVVYQGSR.S +2							3.6048	3.5471	3.7826	3.1963	2.5451	3.8124	3.5315		3.2835	3.4846						3.674	3.0726	3.4746	
K.SQEIFENQDSSVFQLVGK.N +2	5.0375	5.495	5.5241	5.3382	6.4133	6.5511	6.574	6.5451	6.5916	5.8285	5.7952	5.9751	5.8881	6.287	5.669	6.3773	3.0462	5.3982	4.055	4.3523	5.6881		6.1451	6.2486	
K.YGLPQLSEEAFDELSDK.I +2	5.3708	5.4373	5.7087	4.9958	5.9285	5.7664	5.5941	5.6986	4.8965	5.064	4.9742	5.5186	5.0236	5.0858	5.3657	5.4114	5.2646	4.2874	3.7966	5.1824		4.4674	3.1754		
R.GLM*NFVSIDAR.K +2													2.9313		2.9227				3.0191	2.9579			2.636		
R.GLMNFVSIDAR.K +2			3.8081						3.577						3.2238	3.2018	3.1771			3.4542					
R.GVVIEGYPTIVLYPGGK.K +2		4.2606	4.9108	3.7909			4.3095	4.2395	4.5111	3.5729	3.3729	4.4592	4.0729	4.2881	3.3697	3.8082	2.9292		5.0554	3.4642	4.3972	4.147	3.8344	3.9003	
R.HAGNLNMK.E +2														2.7407											
R.LAPTYQELADTYANATSDVLIAK.L +2												3.2037					2.6142		3.1299	2.8784	5.5963				
R.SLDSLFDFIK.E +1									2.2107					2.7212											
R.SLDSLFDFIK.E +2		3.881		3.0395	3.5445			3.5218	3.785			3.7742	3.5682	3.8018	2.6945	3.7879	3.6506		3.7212	3.6709	3.1205		3.4339	3.4259	
R.TAEAIVQFM*IK.Q +2													4.1452												
R.TAEAIVQFMIK.Q +2													3.9033	3.9033	4.2611			3.518		4.3892	3.729				
gi|6319901|ref|NP_009982.1|	10.3	9.5	17.1	16.1	18.7	19.6	29	18.7	27.8	8.9	25.5	25.7	41.8	29.4	33.1	29.6	24.9	15	28.6	28.8	16.9	11.9	15.8	15.8	Threonine synthase, conserved protein that catalyzes formation of threonine from 0-phosphohomoserine; expression is regulated by the GCN4-mediated general amino acid control pathway; Thr4p [Saccharomyces cerevisiae]
K.AGEIVNNWFQELK.T +2	3.1925	4.61	4.5985	3.5678	4.8498	4.9506	4.8312	4.783	4.7936		4.8075	4.4126	4.5168	4.512	4.4918	4.37	3.3164	3.5581	3.5924	4.5263		2.7241	4.4605	3.6546	
K.DVALQFVGNLFEYFLQR.T +2							2.5908																		
K.DVSVFILYPTGR.I +2		3.9732							3.6219			3.0038	3.3249	3.7388	3.5743	3.8969	3.5551			3.0286					
K.FADAVNNALSGFSNYSFEK.D +2			4.8414		5.6778	5.5772	6.1099	5.8872	6.056	4.6505	6.0036	5.062	5.833	5.9472	6.1642	5.7847	5.1281		5.6678	5.326	4.5229		6.1139	4.8038	
K.FIERADVELVKNAIEEELAKM*KL.- +3													3.5591												
K.FVVPSGNFGDILAGYFAK.K +2					5.435	2.5697	4.9837	4.9459	4.301		4.0135	4.8781	5.0715	4.7266	4.2998	4.2189	2.6293		5.0282	4.1656					
K.FVVPSGNFGDILAGYFAK.K +3													3.568												
K.HNVGAVNSINWAR.I +2			3.6921	3.8637														2.9023		4.0569					
K.HYILDPHTAVGVCATER.L +2																			3.0991						
K.IYESSVNPK.H +1																					2.3705		2.163		
K.IYESSVNPK.H +2						2.6355								2.7683											
K.KIYESSVNPK.H +2		3.3074	3.4137	3.4048													3.0596	2.879							
K.LAIATNENDILDR.F +2					4.0803	4.2052	4.2722	4.1832	4.4049	3.7644	4.0659	3.8415	3.4241		2.9123	4.0139	3.6274		3.3778		3.9672	2.51		3.7597	
K.LSFQDLAFAIM*R.L +2													3.7585	3.8872	3.8238				3.376	3.2751					
K.LSFQDLAFAIMR.L +2																				3.5572					
K.NAIEEELAK.M +1											2.5968														
K.NAIEEELAK.M +2												2.6711				2.756									
K.QITVVGATSGDTGSAAIYGLR.G +2							5.7084		5.7955				3.8474	5.5503	4.994	5.2312			5.3816	5.2702	5.9803		5.7366	6.1215	
K.SIQYISLSTAHPAK.F +1																	2.4944								
K.SIQYISLSTAHPAK.F +2	3.6467	4.2956	4.5057	4.1742					4.1382				4.1637	3.7385	4.0567	3.914				4.1627					
K.VAATLSPAM*DILISSNFER.L +2													4.3049	4.8373	2.7213			3.5697	4.1057						
K.VAATLSPAM*DILISSNFER.L +3													4.5343	4.9044	4.3082										
K.VAATLSPAMDILISSNFER.L +2			2.6669	2.8881	5.1618		4.8287	4.7048	4.8395		3.3914	4.4401			3.0776	4.8111				3.2604			4.3316		
R.EYLANGDDLK.A +1																						2.2224			
R.LLWYLAR.E +2													2.5702					2.7215		2.5762					
R.LYIAQEEIPDADLK.D +2				3.29	5.7177	5.8922	5.5731	5.7082	5.2531	4.9277	5.0367	4.6068	5.4405	5.3245	5.0264	4.8191	3.5131				4.9844	4.9642			
R.LYIAQEEIPDADLKDLIK.R +2													2.9231												
R.SDEVTPLVQNVTGDK.E +2	4.7496					4.2548	4.9245				3.345	3.98	3.5834		3.9594		4.666	4.0103	4.4959					4.6241	
R.VSNEETSETIK.K +2	3.3638										3.4377		3.0911								2.7897	3.3419			
gi|6319972|ref|NP_010052.1|	27.7	37.5	32.6	33	46.3	45	47.6	47.6	45	38.5	45.4	42.9	54.2	52.9	52	53.2	38.5	40.6	36.1	41.3	36.2	30.3	27.2	40.3	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p; Ssb1p [Saccharomyces cerevisiae]
K.AADEAFAK.K +1	2.1976	2.0824			2.1284		2.0254	2.0834		2.0394	2.0921		2.2565		2.0918	1.982			2.2631						
K.AADEAFAK.K +2																								2.5434	
K.AVITVPAYFNDAQR.Q +2	3.3587	3.5878	3.6203	3.1916	3.4944	3.4651	3.7119	4.0111	3.67	3.6113	3.6369	3.8299	3.3093	2.9469	3.7182	3.4348	3.3524	2.726	2.8607	2.797	3.4662			3.5948	
K.AVITVPAYFNDAQR.Q +3													4.1432	4.8346											
K.DAGAISGLNVLR.I +2	4.5184	4.5009	4.6063	4.2411	4.525	4.5413	4.5117	4.5571	4.442	4.3237	4.7281	4.225	4.0967	3.3424	3.4711	3.4902	4.22	4.2902			4.0787	4.4851		3.9554	
K.ENTLLGEFDLK.N +1																	2.1771								
K.ENTLLGEFDLK.N +2	3.6473	3.4982	3.6141	3.6964	3.7878	3.6577	3.7308	3.7449	3.4559	3.1762	3.6023	3.5038	3.6152	3.8746	3.4883	3.6732	3.4903	3.6911	3.5346	3.3111	3.1781	2.7433	3.6062	3.3228	
K.IEAALSDALAALQIEDPSADELR.K +2					6.4978	6.4335	6.6614	6.6838	6.1125	3.5228	6.0246	6.2248	6.3103	6.344	6.2202	5.865	5.0357	5.1661	5.3031	5.4348	5.2485	5.0569	6.0642	3.9954	
K.IEAALSDALAALQIEDPSADELR.K +3						6.32	6.5678		6.9402		4.9412	6.2586	7.1136	6.8315	6.6654	6.3478				4.3052			4.8927		
K.IEAALSDALAALQIEDPSADELRK.A +2													4.4366	5.0039	3.4157										
K.IEAALSDALAALQIEDPSADELRK.A +3		5.4997											6.2106	5.7109											
K.LLSDFFDGK.Q +1			2.5096	2.7643	1.8621		2.5746		2.8313				2.7624	2.8128	2.4151	2.8621	2.3126	2.1811	2.4895	2.4065	2.5204		2.4343	2.2012	
K.LLSDFFDGK.Q +2	3.2865	3.3192	3.5158	3.3017	3.2629	3.1763	3.2403	3.3814	3.2132	3.0361	3.1862	3.4087	2.7344	3.2707	2.9927	3.0948	2.7596	3.1547	2.9174	2.9351	3.2583	3.2079	2.969	3.2182	
K.MVNQAEEFK.A +1																					2.1975				
K.MVNQAEEFK.A +2															2.6312										
K.NIPM*M*PAGEPVLEAIFEVDANGILK.V +3													5.077	5.0288	5.6084	4.5456									
K.NQAALNPR.N +2	2.5868							2.6135				2.5616				2.5532									
K.SINPDEAVAYGAAVQGAILTGQSTSDETK.D +2					5.131	5.9649	6.4495	5.8412	5.3913	3.7045	3.6668	4.9815	5.1875	5.3122	5.0147	5.6262	3.8434	4.1772	5.1749	4.5563	5.8644	5.7023		5.3646	
K.SINPDEAVAYGAAVQGAILTGQSTSDETK.D +3						5.306	3.9962	4.9458	4.8678			4.6657				4.6473	4.828		6.0335	5.3331					
K.SQIDEVVLVGGSTR.I +1									2.8944							2.0802					2.4232				
K.SQIDEVVLVGGSTR.I +2	4.6926	4.4898	4.6947	4.6177	4.9938	4.9957	4.4974	4.9091	4.826	3.8035	5.0666	4.5458	4.7945	4.9185	4.5898	4.4583	4.501	4.0617	3.8115	4.4997	3.5202	4.7942			
K.SSNITISNAVGR.L +1													2.131	2.0677		2.3158			1.9645					2.3118	
K.SSNITISNAVGR.L +2		3.5932	3.7528	3.3818	3.7036	3.6634	3.7389	3.7418	3.5864	3.5165	3.6764	3.6657		2.7959	3.5723	2.9788		3.0612					3.6051	3.4222	
K.STSGNTHLGGQDFDTNLLEHFK.A +2													5.1026	5.7758					2.8957	3.6503					
K.STSGNTHLGGQDFDTNLLEHFK.A +3		5.0336	4.6538	5.3474									5.1329	4.9423					3.7621						
K.TFSPQEISAM*VLTK.M +2					2.8519					3.9389			2.8183											2.6728	
K.TFSPQEISAMVLTK.M +2	4.2174	4.5585	4.7575	4.4008	4.5816	4.6346	4.4141	4.7281	4.3155			3.4711		3.4295	4.4289	4.217	3.0465	4.0258		4.0357			3.4453	2.5137	
K.TGLDISDDAR.A +1												2.149	2.3729	2.3162				2.1113	2.0299				1.8324		
K.TGLDISDDAR.A +2	3.9712	3.9442	3.9445	4.0446	3.5138	3.607	3.2919	3.6422	3.9332	3.8437	3.4212	4.0028	3.829		3.7764	3.8614									
K.VIDVDGNPVIEVQYLEETK.T +2	6.3646	6.328	6.4133	6.1663	6.2553	6.4708	6.417	6.3296	6.0205	5.8818	6.2355	6.1389	5.9864	6.1623	6.1115	6.1853	5.6365	4.2275	5.7076	5.7272	6.0307	5.1117	6.0352	6.1451	
K.VIDVDGNPVIEVQYLEETK.T +3										3.6436	5.2483	4.7873	5.1817	5.1414		5.5578		4.8736	5.3368	5.511	5.2582	5.1678			
R.ARFEDLNAALFK.S +2			4.3353	3.8977															3.1743	3.4313					
R.FDDESVQK.D +2							2.7723				2.5974														
R.FEDLNAALFK.S +1						2.6891	2.6507	2.3825	2.6309	1.951	2.5528		2.6064	2.6649	2.5788	2.9183	2.3391	2.7301	2.8884	2.5929	2.4835	2.4664		2.1085	
R.FEDLNAALFK.S +2		4.0267	4.0515	3.8603	3.9091	4.0854	3.9431	3.953	3.9715	3.98	3.9538	3.8245	3.5409	3.9321	3.8576	3.9226	3.9094	3.7097		4.0829		3.7063	4.0006	3.9788	
R.IINEPTAAAIAYGLGAGK.S +2	6.1727	6.442	6.496	6.6285	6.2994	6.2223	6.1647	6.4006	6.0186	6.2081	6.0919	6.0501	6.1641	6.1693	5.8955	6.4188		6.0783	5.2785			5.177	5.4861	5.8165	
R.IINEPTAAAIAYGLGAGK.S +3							5.243					5.2925	5.2875	5.3103	5.6143	5.2474			5.2506	5.3419	4.4464				
R.LESYVASIEQTVTDPVLSSK.L +2	5.8229	6.2455	6.5961	6.0955	6.2694	6.4092	6.3796	6.3048	6.1387	6.3332	6.2756	6.1948	6.2591	6.2119	6.2104	6.2263	6.0794	5.5888	5.5847	5.4573	4.7523	3.3243	5.7559	5.7697	
R.LESYVASIEQTVTDPVLSSK.L +3													4.0816		3.5478										
R.QRLESYVASIEQTVTDPVLSSK.L +3				4.7753																					
R.RFDDESVQK.D +2																3.1255									
R.TFTTCADNQTTVQFPVYQGER.V +2					2.8217	4.4517	4.1722	4.7473	4.6321		4.0143			4.4356	4.6462	4.8846	3.986	4.2744		4.4823	4.2985	4.8902	4.6282	4.3195	
R.TFTTCADNQTTVQFPVYQGER.V +3													5.5357												
R.TLSSVTQTTVEVDSLFDGEDFESSLTR.A +2					4.9525	4.5154	4.6153	4.8248	4.7523		4.2499	4.5507	4.3337	4.3657	3.9278	4.5732	3.184			3.8986				4.1087	
R.TLSSVTQTTVEVDSLFDGEDFESSLTR.A +3									4.7699			3.5021													
R.VTPSFVAFTPEER.L +1									1.9976																
R.VTPSFVAFTPEER.L +2	4.0387	4.0109	4.064	3.824	3.8416	4.1323	3.808	3.7622	3.7302	3.9068	4.0543	4.069	3.7106	3.8267	3.7933	3.6076	3.1517	3.4981			3.6241				
gi|6320016|ref|NP_010096.1|	6	9.7	10.5	8.5	13.6	17	16.2	15.4	21.8	13.1	15.5	24.9	32	33.9	27.4	30.1	23.2	14.2	19.3	28.7	17.8	2.9	11.8	13.4	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-SceI), which is a site-specific endonuclease; Tfp1p [Saccharomyces cerevisiae]
K.AIKEESQSIYIPR.G +2																	3.9653	4.3345		3.9599					
K.ATIQVYEETAGLTVGDPVLR.T +2												2.9705			3.7291	4.9568	3.9214			3.9295	2.8148				
K.AVANGANWSK.L +2									2.5748			2.5836													
K.AYFEWTIEAR.D +2													2.5385				2.5134			3.2599					
K.EDFLQQNGYSTYDAFCPIWK.T +2			4.8359		5.1648	5.2783	5.3724	4.8694	5.128	3.7011	4.1624	4.3554	5.2764	4.4293	5.4313	5.8017	3.7362	5.1063	4.8685	4.7416	3.5263		3.9819	5.31	
K.EDFLQQNGYSTYDAFCPIWK.T +3													4.5012		3.6851										
K.EESQSIYIPR.G +2							2.7173	3.0379	2.7196	2.5123	2.8739			2.6274	2.9408										
K.EILSNAEELEQVVQLVGK.S +2	5.4433	6.1763	5.9679	4.2097	6.0497	6.2603	5.9265	6.0761	5.5928		4.9247	6.0648	5.1312	6.1224	5.2793	5.5635	5.4304	3.0738	5.514	3.7586	3.3415		5.856	4.4578	
K.EILSNAEELEQVVQLVGK.S +3													5.0023	5.4789	5.563	4.7871			3.6248	3.8266			3.6569	4.4274	
K.FRPAPAAAFAR.E +2													3.1465	2.6392	3.3238	2.9045		2.845		2.9045					
K.FTCNATHELVVR.T +2				4.3302						2.9284			4.2889	4.3082	3.9728	4.0655		3.7416		4.1944	2.5958				
K.FYDSNYPEFPVLR.D +2		4.4808	4.7066	4.3359	4.6579	4.6795	4.7694	4.7361	4.5841	3.7265	4.0107	4.7486	4.6145	4.2028	3.9056	4.5909	2.9476	3.9812	2.5412	3.9425	3.9335		3.8494		
K.GTNVLM*ADGSIECIENIEVGNK.V +2																					2.5401				
K.GTNVLMADGSIECIENIEVGNK.V +2																4.8496	5.7421			4.0074	3.9633				
K.GVEYFEVITFEM*GQK.K +2															3.2651										
K.HFPSINTSVSYSK.Y +1																	2.4216								
K.HFPSINTSVSYSK.Y +2		3.3495	3.4153														3.6544			2.939					
K.ILEVEFDGK.K +1																	1.8964	2.6817		2.3712		2.0887			

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ILEVEFDGK.K +2									2.7476							2.5885			3.0823			2.8322			
K.ISYAIYM*SGGDVLLNVLSK.C +2													3.8616	5.385					2.8279						
K.ITLDVATLIK.E +2									2.9042			2.9372	3.0911	3.1221	3.1072	3.112	2.8265							2.9777	
K.LLSTMQER.F +2						3.063						2.814											2.9783		
K.LSADYPLLTGQR.V +2					3.9979	4.2118	3.7497	4.0974	4.0133	3.7874	3.7549	3.7124	3.788	4.08	3.7593	3.8213	3.6574				3.7862			3.4508	
K.NIPSFLSTDNIGTR.E +2	3.5172	4.1053	3.7058	3.8505	3.9086	4.0981	4.2451	3.8848	3.817	3.5518	3.3799	4.1579	3.7666	3.992	3.9065	3.5494	3.4284			3.2284			3.3173	3.7748	
K.NVSM*IADSSSR.W +2													2.7068												
K.NVSMIADSSSR.W +2														3.4264	2.8688					2.7108					
K.RTTLVANTSNMPVAAR.E +2																		3.7033		3.8427					
K.SALSDSDK.I +1																1.8219									
K.SALSDSDKITLDVATLIK.E +2													4.656	2.9495	3.9638										
K.SDFTLYHTWPVR.V +2													3.2053	3.1256		2.9012									
K.SYPISEGPER.A +2						2.9684			2.9387	2.5406	2.6935		3.0197	2.7535	3.1637	2.6422									
K.TVISQSLSK.Y +1													1.9879												
K.VGHDNLVGEVIR.I +2		3.7494											3.4634	3.8445	3.4566	3.5854	3.5423	2.9784	2.6545	2.5053			3.8748		
K.YTNVLNK.F +1													2.0494				2.0965		2.3477			2.2277	2.3491	2.483	
R.AFISYHDEAQK.A +2											3.6234	3.2868	3.0216		3.0724	3.4518		2.7014		3.4171	3.2137				
R.ANELVESYR.K +2						3.1058					3.1384	2.8717		2.7206											
R.DLSLLGSHVR.K +2													2.547	2.9764	2.6663										
R.EASIYTGITLAEYFR.D +2									4.2896			2.8978		3.9968	4.2285	3.927			3.4581						
R.ETFLAGLIDSDGYVTDEHGIK.A +2													5.1728	4.95					2.7696	3.2755					
R.GFYFELQELK.E +2													2.9685	3.1093	3.0895	3.5102									
R.GTITWIAPAGEYTLDEK.I +2	4.1391	4.5215	5.6243	3.0524	4.322	4.2082	4.8344	4.0047	4.4881	3.6274	4.4302	2.6766	4.6615	4.1076		4.3638			3.0342		2.5876		4.3888	2.7902	
R.LGEMPADQGFPAYLGAK.L +2						4.5127	5.0044	4.6615	4.6329	4.8038	4.7136	4.5608	4.4477	4.4549	4.6632	4.4819		2.9055	4.9642		2.9627			4.8809	
R.LGEMPADQGFPAYLGAK.L +2		5.1735	5.3832	5.0221	5.3153	5.1215	5.2988	5.2032	4.876	3.7334	4.4607	5.1145		4.1692	4.2179	4.7595	4.9058	2.6679		4.7048	3.679		5.2677		
R.NNLNTENPLWDAIVGLGFLK.D +2					4.8517	3.6287	3.5559	4.7867	5.1389			5.0173	4.938	4.8112	4.0152	4.7821				4.7331					
R.NNLNTENPLWDAIVGLGFLK.D +3													4.456	4.952	3.8607										
R.PAPAAAFAR.E +2						2.9251	3.0599	2.6561						2.8889											
R.SLGLVVSVNAEPAK.V +2												2.7782	3.9678	4.3569	4.6973	3.463					3.2746			3.7324	
R.TGKPLSVELGPGLM*ETIYDGIQR.P +3														3.5926											
R.TTLVANTSNM*PVAAR.E +2												3.8159	4.6588	4.1918		4.5015			4.3383		4.0362	4.6157		3.7306	
R.TTLVANTSNMPVAAR.E +2	4.9814				4.7292	5.1764		5.0092	4.9113	4.7036	4.6352	4.9262	4.9931			5.0162	5.0805				5.0409	4.4088		4.9666	
R.VLDALFPCVQGGTTCIPGAFGCGK.T +2							2.8939		2.9812			2.7366					2.6844		3.2293	3.3908					
gi|6320148|ref|NP_010228.1|	36.8	46	39.1	51.8	38.2	38.2	38.2	43.2	47.6	36	39.3	42.1	48.2	56.8	51.5	51.5	40.2	24.7	50.1	51.5	23.3	15.8	33.2	24.9	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannose from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure; Psa1p [Saccharomyces cerevisiae]
K.DFLSGTVLYLNSLAK.R +2	5.0789	5.2139	5.6336	5.7962	5.5306	5.5158	5.6718	5.5134	5.48	3.3489	5.0169	5.6354	5.6904	5.3595	5.2804	5.4004	4.9503	5.7555	5.8562	5.2518			4.3471		
K.DFLSGTVLYLNSLAK.R +3													4.8166	4.7412	4.4252		3.749			4.5489			3.9238		
K.DNSPFFVLNSDVICEYPFK.E +2	5.2694	5.3243	5.3455	5.3848	5.487	5.5941	5.4688	5.5987	5.1715	5.0287	5.5957	5.0727	5.0531	5.0032	4.8418	5.1566	4.9981	3.3899	4.987	4.8535	5.2734		4.1571	4.6842	
K.DNSPFFVLNSDVICEYPFK.E +3													5.0209	5.1883	4.1411				3.6349						
K.ETFPILVEEK.Q +1					2.3908																				
K.ETFPILVEEK.Q +2	3.0316	2.6962	2.7345	2.9425	2.8692	2.8562	2.897	2.8401	2.5939	2.916	2.6755		2.6174	2.5115		2.6105	2.5616		2.7016			2.7091	2.6352	2.5466	
K.EYGVNITFSVETEPLGTAGPLK.L +2				2.8789	3.7961	4.2461	5.0789	5.4471	5.3776		3.5562	4.5475		5.0455	4.3922	4.7371			2.6765	3.1047					
K.GLILVGGYGTR.L +1														2.0315						2.0366					
K.GLILVGGYGTR.L +2	3.8643	3.903	3.9042	3.9129	3.8246	3.8483	3.9	3.9099	3.6475	3.7369	3.6302	3.7852	3.8084	3.8965	3.8125	3.8684	3.6352	3.7225	2.5535	3.7933			3.7715		
K.IGPDVVIGPNVTIGDGVR.I +2	5.061	5.1871	5.2249	5.1165	5.2944	5.3708	5.1152	5.0327	4.8687	4.9658	4.8325	4.9898	4.9188	5.0399	4.7831	5.3162	4.7855	4.3879	5.0864	4.5687	4.67		4.5958	3.1546	
K.IGPDVVIGPNVTIGDGVR.I +3													4.0416	4.6812											
K.KDNSPFFVLNSDVICEYPFK.E +3														4.4623											
K.KLATGANIVGNALIDPTAK.I +2	4.6546	5.3852	5.2583										4.9469	5.218	4.5731				3.6618	3.6195					
K.LAEDVLKK.D +2		3.2034	3.2228	2.7027														2.9454							
K.LATGANIVGNALIDPTAK.I +2		4.7271	5.3872	5.0891	5.4367	5.5197	5.6359	5.5739	5.5029	5.4565	5.4955	5.107	5.6494	4.9839	5.08	5.375	4.962	5.5396			5.4951	2.626	4.5439	3.5155	
K.QLYSFDLEGFWM*DVGQPK.D +2								3.1124	3.836			3.7596	4.8295	5.1845	4.7209	4			2.5083	3.2557					
K.STIVGWNSTVGQWCR.L +2	5.1148	5.1083	5.4226	5.1272	5.3528	5.2438	5.2634	5.3048	5.3216	5.3382	5.2819	5.0804	5.3266	5.0329	5.0664	5.0335	3.5695			4.3724	3.5517	5.0716	4.9808	4.842	
K.YGVIVHDIATPNLIDR.F +2	5.137	4.9117	5.094	5.2219					4.9513			2.9211	4.7427	4.7235	4.582	4.2994	3.7903		4.7045	4.6121					
K.YGVIVHDIATPNLIDR.F +3	4.4671	4.8029	4.7086						3.9222				4.3658	4.33	3.7894	4.3028			4.2218	4.7201					
R.INAGLYILNPEVIDLIEMKPTSIEK.E +3		3.7527		4.0603																					
R.LEGVTVLGDDVEVK.D +2										3.4513	4.1428			4.2567	4.0357	4.4012					3.8172	3.783	4.1498		
R.LEGVTVLGDDVEVKDEIYINGGK.V +2													2.9477	3.0721	4.2894		4.0327		3.4522	5.1534					
R.LEGVTVLGDDVEVKDEIYINGGK.V +3													4.3804	5.1344	3.5681					4.7682					
R.PLTLTVPK.P +2														2.6809											
R.SVVLCNSTIK.N +1						1.9113			2.241				1.828	1.955	1.9503	2.0016			2.357	1.8887				2.1405	
R.SVVLCNSTIK.N +2	3.1292	2.949	3.0358	3.0288	3.0467	2.8995	3.0965	3.0662		3.0677				2.974	2.8394	2.8592									
gi|6320215|ref|NP_010295.1|	24.6	42	35.4	32.6	33.7	32.6	21.3	28.2	43.4	25.4	25.4	32.3	48.9	42.5	37.8	47	28.5	33.7	38.1	38.7	4.7	10.5	18.2	25.1	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Ap and has similarity to E. coli L4 and rat L4 ribosomal proteins; Rpl4bp [Saccharomyces cerevisiae]
K.AGHQTSAESWGTGR.A +1																		3.1939					2.174		
K.AGHQTSAESWGTGR.A +2		4.2667	4.0815	4.1614	3.0099				3.5153	3.1952	3.9861	3.3488	4.0781	4.0219	4.4901	4.3064	2.8097	3.7599		3.7987					
K.AVGAHSDLLK.V +1													2.4894	2.4379	2.3415								2.2577		
K.AVGAHSDLLK.V +2	3.287	3.4267	3.4115	3.7016	3.2837	3.4375	3.6305	2.9899	3.0393	3.0255	3.119	2.5813	3.4915	3.4875	3.3418	3.2584		2.5594		3.1		3.0412	3.2057	3.0693	
K.EAVAALK.A +1													1.9036	2.0236						2.2717				1.9362	
K.IPEIPLVVSTDLESIQK.T +2	5.4644	5.5417	5.656	5.2013	5.6257	5.4796	5.4649	5.5921	5.569	3.3357	5.3767	5.0367	5.1598	5.2441	5.2618	4.8757	4.3737		5.6491	4.6751	5.1877		5.3973	5.6538	
K.IPEIPLVVSTDLESIQK.T +3						4.4573	4.6407				3.6893		4.3684	4.5632	4.2186	4.0801		3.5186			4.6038		3.7006		
K.LDQVWGSETVASSK.V +1																								3.1327	
K.LDQVWGSETVASSK.V +2	5.0856	4.919	5.1516	5.3291	5.3142	5.1403	5.3726	5.1068	5.3664	4.978	5.0132	5.1046	5.246	5.1246	5.1401	5.1652	5.1285		4.7241	4.8035		4.977	5.3114	4.8426	
K.PAAVFAETLK.H +1														2.1688		2.2604	2.2611	2.6241	2.3289	2.2583				2.0122	
K.PAAVFAETLK.H +2			3.3286			2.774	3.0251		3.1695					2.6682		3.1419	2.8468	3.1233		3.1809					
K.RQAYAVSEK.A +2		2.9321															2.6372	2.7328							
K.TGTKPAAVFAETLK.H +2		3.8839											3.5882			3.3403	2.8594								
K.VGYTLPSHIISTSDVTR.I +2	5.1722	5.3443	5.1573	5.338				4.6296	5.0493			4.5354	5.1696	5.2283	5.0187	5.2978		4.0377	4.6281	4.4189					
K.VGYTLPSHIISTSDVTR.I +3		4.3783							4.5838			3.6276	4.9616	4.8273	5.0812	4.5001			3.6159						
R.FVIWTEAAFTK.L +2		3.3219			3.6043	3.3468			3.3543				3.4275	3.4821	3.5527	3.2952				2.8288			3.6425		
R.GPLVVYAEDNGIVK.A +1					3.7548				2.7548																
R.GPLVVYAEDNGIVK.A +2			4.9187		4.8819	4.9906	4.8338	5.0183	4.8875	4.3424	4.8721	4.5742	4.9107	3.6211	5.0789	4.8409	5.2747	4.8347						3.8686	
R.IINSSEIQSAIRPAGQATQK.R +2					4.5754	4.4958	4.4495		4.6428	4.4402	4.333	4.4629	4.3887	4.3165	4.5857	4.5964				4.0516					
R.IINSSEIQSAIRPAGQATQK.R +3	5.292	5.929	5.9946	5.7048					5.1578				5.6276	5.8791	5.0808	5.9359	6.0728	4.2142	4.3751	4.6497					
R.IINSSEIQSAIRPAGQATQK.R +3	3.781	4.8136	4.4079	4.3155					4.038				4.3618			4.0996	4.2001		4.0156	4.6254					
R.NVPGVETANVASLNLLQLAPGAHLGR.F +2																			3.3971						
R.QAYAVSEK.A +1													1.8501			1.9041									
R.RGPLVVYAEDNGIVK.A +2		4.2638	3.8355	3.7121									2.6164		3.8698	3.2588	4.2505		3.203	3.181					
R.RGPLVVYAEDNGIVK.A +3													3.8357	3.9309	4.2008	3.8109			4.185	3.7541					
R.SGQGAFGNMCR.G +2	3.4191	3.6126	3.4251	3.3628	3.6325	3.7281		3.5927	3.7541	3.1824	3.2443		3.627			3.4461		3.0243							
R.YATASAIAATAVASLVLAR.G +2					4.8034	5.2565		4.5746	4.5436			3.7948		2.7245	2.9944	4.9678			4.7837	4.5428				4.6713	
R.YATASAIAATAVASLVLAR.G +3						4.0344			3.6668				4.7372	5.0272	5.129	4.4909			3.6357	4.0106					
gi|6320226|ref|NP_010306.1|	17.3	28.8	26.6	18.2	25.1	25.3	21.4	24.7	35.9	16.2	25.8	27.5	42.2	40.5	42.9	40.7	35.5	16.5	26.6	46.8	8.4	13.4	19.3	11.3	Cytosolic seryl-tRNA synthetase, class II aminoacyl-tRNA synthetase that aminoacylates tRNA(Ser), displays tRNA-dependent amino acid recognition which enhances discrimination of the serine substrate, interacts with peroxin Pex21p; Ses1p [Saccharomyces cerevisiae]
-.M*LDINQFIEDK.G +2									3.4034			3.7023	4.2411	4.5994	4.3296	4.185				3.798				3.8439	
- MLDINQFIEDK.G +2		4.6837	4.5351		4.1596	4.3329	4.4276	4.0057	4.4326		3.8923	3.8982			3.6039	4.0166	3.2629				4.0753			3.2553	
K.DAWGVFR.V +1																1.9164									
K.ELVSCSNCTDYQSR.N +2	4.2674	3.6534		3.5797						3.7781		3.9161	4.2879		4.2078	4.2508			3.8217			4.2054			
K.GYIPLQAPVM*M*NK.E +2														2.9553											
K.GYIPLQAPVMMNK.E +2			3.9115		3.0522	3.1694			3.162			2.5693				3.6558	3.8711	3.0308		3.2965		3.7343	3.9929	3.1182	
K.IEQFVITEPEK.S +2	4.6623	4.5404		4.3516	4.5729	4.6259	4.5889	4.748	4.2746	4.2389	4.2373	4.3833	4.4096	4.2134	4.4981	4.2536		4.5197					4.5982		
K.IEQFVITEPEKSWEEFEK.M +2													4.5339			3.1735									
K.KYDLEAWFPYQK.E +2		4.8532												4.6672						4.2389					
K.KYVHCLNSTLAATQR.A +2																			2.58						
K.MISYSEEFYK.S +2					2.9624		3.1604	3.1943	3.3309	2.7379	2.8581	2.9311		3.4534	3.4802	3.2341		3.1665		3.2826					
K.NKEDASGLLAEK.E +2										3.3453					2.6429					3.7357					
K.PASLSHHEILLR.L +2											3.0199		3.8174	4.0458											
K.SWEEFEK.M +1																				1.885					
K.TAQLSEFDEELYK.V +2	4.2552	4.6696	4.6557	4.3243	4.7426	4.4378	4.6245	4.7749	4.5665	4.0232	4.0938	4.5643	4.5879	4.8051	4.5135	4.4742	4.2476	4.1215		3.9812	3.4725	4.0829	4.14	4.1988	
K.VFQVGNIVHPSVVVSNDEENNELVR.T +2																				2.5737					
K.VFQVGNIVHPSVVVSNDEENNELVR.T +3	7.3051	7.9331	8.3825						4.7891				6.9115	7.5272	5.6559		7.0503		6.1574	8.5612					
K.YDLEAWFPYQK.E +2					4.064																				
K.YIPGEPEFLPFVNELPK.N +2	2.7955	3.5381	3.6605	3.1592	3.9531	3.5778	3.2057	3.4243	3.8853		3.0873	3.542	3.1252	2.782	2.6434	3.9092	2.7859		2.7048	3.0621					
K.YIPGEPEFLPFVNELPK.N +3													3.6003		3.501										
K.YVHCLNSTLAATQR.A +2			4.63	4.9456					2.6502				4.6365	5.0622	5.031	4.5882	4.9266	4.2798	4.4705	4.7841					
R.ALCCILENYQTEDGLVVPEVLR.K +2						3.8381	4.193	3.6831	5.5016		2.751				4.5716	3.9981	2.93		3.9218	2.952			2.9471		
R.ALCCILENYQTEDGLVVPEVLR.K +3													4.0351												
R.IVGIVSGELNNAAAK.K +1																2.042					1.9918		2.2649		
R.IVGIVSGELNNAAAK.K +2		5.2991	5.5304		5.5599	5.5094	5.3871	5.3726	5.9869	5.4096	5.3382	5.3598	5.4966	5.1838	5.4509	5.591	5.458	5.6415	3.4821	5.4619				5.5686	
R.LDGYDPDR.G +2											2.5959	2.6579													

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.NASVEIVDEIISDYK.D +2		5.2118	5.2961	3.8999	5.0013	4.6672		4.7459	5.0429			2.8023	5.5293	4.2606	5.3637	5.7666	5.6952		4.8897	3.3316			4.5389		
R.NYGVFLNQALINYGLQFLAAK.G +2																				5.2501					
R.NYGVFLNQALINYGLQFLAAK.G +3																				3.6279					
R.TWKPEDLEAVGPIASVTGK.P +2													5.4605	5.4238	5.1512	3.0613	3.3808			3.4819					
gi|6320255|ref|NP_010335.1|	41.9	53.2	75.4	53.2	48.4	28.2	45.2	48.4	54.4	25.8	39.9	46.4	64.1	78.6	66.1	64.1	29.4	32.7	47.2	46.4	31.5	21.8	21.8	20.6	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availability; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region; Tpi1p [Saccharomyces cerevisiae]
K.ADVDGFLVGGASLKPEFVDIINSR.N +2		4.6983		4.95										5.3387	4.7646	5.2989			4.2898	4.8338					
K.ADVDGFLVGGASLKPEFVDIINSR.N +3	7.2498	7.7259	7.3783	7.0472									6.1076	6.9131	6.9459	6.7207			6.6152	6.5118					
K.ASGAFTGENSVDQIK.D +1								3.3209	2.0563		3.3878	3.0718	3.183	3.8155				2.6091	3.0869	3.6915	3.1139				
K.ASGAFTGENSVDQIK.D +2	5.0512	4.923	5.2031	5.0651	5.386	5.1914	5.1773	5.1645	4.8558	5.0188	4.7368	5.2643			4.8274	4.8753	4.8332		5.1774	4.733		3.8027	4.8076	4.9255	
K.ASGAFTGENSVDQIKDVGAK.W +2																					2.9613				
K.DKADVDGFLVGGASLKPEFVDIINSR.N +3														4.3319											
K.DWTNVVVAYEPVWAIGTGLAATPEDAQDIHASIR.K +3			4.7526											5.813	3.619										
K.FALGQGVGVILCIGETLEEK.K +2		5.1456	5.5981	4.2665	5.5759	5.7237	5.8097	5.4616	5.8308			5.6013	4.9479	5.207	5.3882	5.605			4.4482	5.4141					
K.FALGQGVGVILCIGETLEEK.K +3						5.9722	6.0457		6.2518			5.2548	5.5923	6.5248	5.7944	6.1115			5.8724	4.8377					
K.KPQVTVGAQNAYLK.A +1								3.7221	2.8653				3.17	2.7727	3.7355	3.6611	3.8653	3.8832	3.1973	4.2763		2.5311	3.6094		
K.KPQVTVGAQNAYLK.A +2	5.0242	4.9116	4.8257	3.5265	4.6256			4.7771	4.492	3.4914			4.3825	4.5042	4.2296	4.6999	4.5109	3.6869	4.2488	4.6134			3.5725		
K.PEFVDIINSR.N +2													3.071			3.5622					2.5815				
K.PQVTVGAQNAYLK.A +2							2.844				3.6331										3.4451			3.987	
K.TLDVVER.Q +1	2.3118	2.0601	2.1679	2.1698	1.9588			2.2736			1.8504	2.0285												1.8529	
K.WVILGHSER.R +1													2.0059		2.2196		2.0861	1.8809		2.1023					
K.WVILGHSER.R +2	3.6639	3.6954	3.5318	3.6251					3.1621			2.5484	3.4781	3.0756	3.229	3.2319	2.7336	2.6489	3.2805	3.149					
R.ILYGGSANGSNAVTFK.D +1									2.9349																
R.ILYGGSANGSNAVTFK.D +2	5.2846	5.54	5.3334	5.2531	5.3157	5.3283	5.4377	5.3615	5.0199	5.3966	5.422	4.7562	5.0699	5.1622	3.8615	4.7922	5.2424	3.7632	5.2355	5.178	4.9695	3.364	4.8543	5.1274	
R.LNTASIPENVEVVICPPATYLDYSVSLVK.K +2					2.9606		2.7713	2.8945	3.2636			3.0458	2.6078	2.6966		2.8559									
R.LNTASIPENVEVVICPPATYLDYSVSLVK.K +3			4.321		4.7191		4.8809	4.3657	4.6467		4.7806	4.5087				3.5036									
R.QLNAVLEEVK.D +1								2.7008						2.4816		2.5052		2.5056	2.5328						
R.QLNAVLEEVK.D +2	2.8186	2.8271	2.8345	2.7795	2.7985	2.7756	2.8953	2.849	3.0763	2.8809	2.8282	2.6943	2.6235	2.8493	2.8511	2.9248	2.5365	2.9802			2.6553				
R.SYFHEDDK.F +1																		2.2051		1.8929					
R.SYFHEDDK.F +2		2.559		2.5999																					
R.SYFHEDDKFIADK.T +2									3.8618				4.655	4.4816	4.7383	4.7028									
R.TFFVGGNFK.L +1	2.5601	2.4052	2.4776	2.5351	2.433	2.4454	2.4882	2.5402	2.4159	2.4024	2.4596	2.3698	2.4572	2.4995	2.3685	2.4837	2.37	2.312			2.3301	2.3625	2.1475		
R.TFFVGGNFK.L +2	3.1519	3.2612	2.9781	3.2334	2.937	2.995	2.9304	2.9583	2.8017	2.7763	2.7979	2.926	2.578	2.6656	2.8621	2.6511	2.7641	2.6307	2.8486	2.6515			2.7861		
gi|6320304|ref|NP_010384.1|	20.9	41.8	35.5	47.3	27.1	26	28.9	28.9	34.8	32.2	32.2	34.4	46.9	46.9	28.2	44.7	28.9	30.8	33.7	33	16.8	21.2	28.6	20.5	14-3-3 protein, minor isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sensitive signaling, and others; Bmh2p [Saccharomyces cerevisiae]
K.ATNSSLEAYK.T +1													2.2656				1.9433					2.2193			
K.ATNSSLEAYK.T +2													3.6146	2.865		3.2525		3.0137							
K.AVASSGQELSVEER.N +2				4.5451		3.7256	4.4627	4.3894	4.4718	3.879	2.9605	4.4738	4.7357	4.5177	4.5277	4.3814	4.359	4.5136	4.3607				4.4547		
K.DSTLIM*QLLR.D +2						3.6263	3.6525		3.8058	3.5632		3.4711	3.3129	3.6425	3.5566	3.4696	3.2088	3.9718	3.5704	3.5173	3.5335	3.2221	3.4943	3.3971	
K.DSTLIMQLLR.D +2	3.9135	3.8362	4.1182	4.0022	3.7464		3.6473	3.757	3.5034		3.2672	3.6763		3.7393	3.658	3.7443	4.0853			3.3513	3.3633	3.3506	3.3479	3.4392	
K.IETLTKLI +1									2.3666			2.2706	2.3615	2.3877	2.3999								1.9202		
K.ISDDILSVLDSHLIPSATTGESK.V +2		5.7717	4.6918	6.1942									5.8678	5.4652					3.7449	4.0448					
K.ISDDILSVLDSHLIPSATTGESK.V +3		5.4095	4.7257	5.1304									3.9338	4.535		4.094			3.8411						
K.QAFDDAIAELDTLSEESYK.D +2	5.8811	6.3478	6.1698	6.2983	6.1639	6.1032	6.3984	6.1978	6.0604	4.434	5.2703	5.7312	6.132	5.9446	6.0708	6.0539	3.9377	5.7208	4.4075	4.827	5.8535	5.6643	5.6865	6.04	
K.QAFDDAIAELDTLSEESYK.D +3													3.9136	4.7788	4.6566	4.1921		3.9177	4.4279	4.6885			4.0016		
K.SEHQVELIR.S +2				2.9449	2.8632	3.0389	2.9226			3.1619	3.0126	3.0049				3.009									
K.TASEIATTELPPTHPIR.L +2	3.8058	4.1584	4.2395	4.2424	3.7082			4.1662	4.3498	3.9781			4.2493	4.5733	4.1268	4.0259	4.0496	3.8131	3.6524	3.8068					
R.EDSVYLAK.L +1		2.1662		2.074			2.0452	2.1107			1.8677	1.9425	2.0647		1.9875								2.0953	2.0945	
R.IVSSIEQK.E +1						2.325					2.3656			1.8227				1.8826			2.0467	1.8635		2.3878	
R.IVSSIEQK.E +2					3.1095	2.8661	3.0778		2.5415			2.9268													
R.IVSSIEQKEESK.E +2																				3.2198					
R.IVSSIEQKEESKEK.S +2																		3.4524							
R.NLLSVAYK.N +1		1.8356	1.8213							1.938		2.2139													
R.SKIETELTK.I +2		2.7951	2.7144	2.6677											2.5264		2.6311		2.5415						
R.YEEMVENMK.A +1																				2.491	2.8549		2.9687		
R.YEEMVENMK.A +2		3.4018		3.4102					3.4729		3.4578		3.1251	3.2665		3.3018									
R.YLAEFSSGDAR.E +2	4.07	4.3025	4.0681	4.0089	4.1917	4.2359	4.3445	4.3555	3.2541	3.9556	3.831	3.7936	3.506	3.4117		3.98						3.5225	3.7484	4.3061	
gi|6320359|ref|NP_010439.1|	42	46.9	46.9	46.9	25.9	25.9	25.9	25.9	32.7	30.9	30.9	25.9	42	42	42	42	37	35.2	22.2	34.6	17.9	13	25.9	21	Cytoplasmic peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds the drug cyclosporin A; Cpr1p [Saccharomyces cerevisiae]
K.FPDENFKK.H +2		2.7331	2.7052	2.6091			2.7646			2.5242	2.5765			2.7606	2.7003			2.6316							
K.GFGYAGSPFHR.V +2	3.9368	4.0314	3.9524	3.9346					3.2219				3.6583	3.8186	3.8009	3.4716	3.4967			2.969					
K.HVVFGEVVDGYDIVK.K +2	4.8058	5.9337	5.7958	5.8593									5.4483	5.1854	4.4098	4.2793	4.3718	4.8433	4.5251	5.9895					
K.HVVFGEVVDGYDIVK.K +3													4.247	3.9032						3.6356					
K.HVVFGEVVDGYDIVKK.V +3																				3.8168					
K.KVESLGSPSGATK.A +1									1.856				2.698			3.0691									
K.KVESLGSPSGATK.A +2	4.4759	4.5532	4.513	4.5646	4.2355	4.2906	4.4169	4.2724	4.0448	4.3825	3.7088	4.113	4.0376	3.8945	4.3439	3.9476	4.0994	3.5149				4.0518	3.5779	3.2262	
K.LYNDIVPK.T +1	2.3123	2.3839	2.449	2.3136	2.3633	2.3984		2.2643	2.2404			2.3719	2.2062			2.3217				2.4968	2.2768	2.3511			
K.LYNDIVPK.T +2	3.4024		3.2806	3.4332	3.3222	3.1094		3.4418	3.3829	2.9122	2.8151	3.0069	3.2699			2.9498							2.9475		
K.VESLGSPSGATK.A +2					2.9289	3.0588	3.1442			2.6498	2.7556	2.961	2.8167									2.8428		3.0261	
R.VIPDFM*LQGGDFTAGNGTGGK.S +2					5.5637	4.6809	5.8187	5.4388	4.934	5.906	5.2667	5.9258	6.4785	5.8575	5.0127	5.7994	4.0833	5.5561	5.6922	4.3813	5.28		3.2846	3.0194	
R.VIPDFM*LQGGDFTAGNGTGGK.S +3													4.1921	3.7885											
R.VIPDFMLQGGDFTAGNGTGGK.S +2	7.1985	7.3892	7.1055	6.6014	6.9591	7.0216	7.0491	7.06	6.6142	5.3218	6.153	6.4003		4.9709	5.5874	6.5873	5.7773	2.8071		4.62	6.5529		6.2771	6.675	
R.VIPDFMLQGGDFTAGNGTGGK.S +3						3.5011	3.6636									4.3009	3.8188								
gi|6320362|ref|NP_010442.1|	12.9	17	14.8	9.6	17.8	20.3	17	24.7	20.8	22.7	26	21.6	32.9	35.9	33.2	27.4	24.9	25.8	19.2	27.4	18.6	15.3	12.3	16.7	Aspartic beta semi-aldehyde dehydrogenase, catalyzes the second step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom2p [Saccharomyces cerevisiae]
K.ECDIVFSGLDADYAGAIEK.E +2	2.8097	5.4474	5.1364		6.5361	6.3019	6.4642	6.4982	6.3109	5.2137	5.3041	6.3677		3.9858	3.7697	5.5259	4.7669	3.9819	5.886	5.0442	5.8415	6.6151	3.6588	3.1068	
K.ECDIVFSGLDADYAGAIEK.E +3															3.6018										
K.EFM*EAGIAIVSNAK.N +2												2.8817	4.4608	4.6416	4.4251	3.404				3.5387					
K.EFMEAGIAIVSNAK.N +2	2.9067				2.7911			3.9069						2.7099	3.0709				2.6159	2.9779					
K.EYVCDAYK.L +1																		2.5657	2.3468	2.2941					
K.IAGVLGATGSVGQR.F +2	4.5102	4.7021	4.948	4.9025	4.8786	4.8979	4.9023	4.7976	4.778	4.422	4.847	4.7939	4.6581	4.5458	4.8328	4.5562	4.5011	4.666			4.4389			4.0935	
K.ILAPLAEDK.T +1											2.1486		2.1107	2.0545	2.0949		1.8179			2.1546	2.0797				
K.ILAPLAEDK.T +2						2.691																			
K.KIAGVLGATGSVGQR.F +2																	3.3641								
K.KILAPLAEDK.T +2		2.9759	2.8963	3.1328														2.8385							
K.LGCHSAPK.Q +2		2.6844																							
K.NRPAPSVEQVK.T +2		2.7658	2.8849	2.809			2.6282	2.6394	2.6747		2.7614		2.5227	2.5128	2.5912	2.6507		2.7668	2.7399			2.8987			
K.QTDLLPESATDIIVSECK.S +2					5.1645	5.2826	5.3085	5.6037	5.4472	3.7107	4.0826	5.4226	5.5143	5.6458	5.2748	5.387	4.8509	2.5074	2.9626	5.3465	5.2171	5.1358	5.3061	5.177	
K.QTDLLPESATDIIVSECK.S +3														3.7204											
K.YVDAVNWK.Q +1																	2.6252				2.6514	2.4306	2.3567		
K.YVDAVNWK.Q +2										2.5879			2.7285										3.4331		
R.DSGYGVSVGR.I +1																				2.5679				2.1221	
R.DSGYGVSVGR.I +2										3.0987	3.3733			3.5447		3.6219				3.7266					
R.EQDVPLIVPVVNIPEHLDIVAQK.L +2													3.916	3.922	2.6528		2.9596			3.0746					
R.IREDPLLDFK.M +2													2.525												
R.VAVSDGHTECISLR.F +2						3.2789		4.493	4.456	3.5543	3.6918	3.3082	4.403	4.3552	4.0102	4.2841		4.3956							
gi|6320590|ref|NP_010670.1|	33.6	33.6	33.6	33.6	53.6	53.6	33.6	53.6	53.6	33.6	33.6	53.6	53.6	53.6	53.6	85.5	54.5	34.5	53.6	54.5	50	23.6	30	80.9	Ribosomal protein P2 beta, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm; Rpp2bp [Saccharomyces cerevisiae]
K.AVVESVGAEVDEAR.I +1											2.546							2.095			2.6146			2.4259	
K.AVVESVGAEVDEAR.I +2	4.875	4.7641	4.8818	4.8425	5.0005	4.8478	4.879	4.7758	4.8517	4.8276	4.7226	4.8839	4.5997	4.7915	3.8661	4.7241	4.7038		3.1157	4.1371	4.2352	4.9614		4.4858	
K.FATVPTGGASSAAAGAAGAAAGGDAAEEEK.E +2																					5.151			2.7997	
K.FATVPTGGASSAAAGAAGAAAGGDAAEEEKEEEAK.E +3																3.6592									
K.GSLEEIIAEGQK.K +1						2.9483			3.5465					3.8837	3.1155				2.5531						
K.GSLEEIIAEGQK.K +2	3.9049	3.8403	3.8357	3.9873	4.0431	3.7705	3.8473	4.0451	3.7	3.8394	3.874	3.5608	3.6957	3.4633	3.8163	3.2816	3.6607	3.212	3.4732	3.7148		3.4425		3.6518	
K.GSLEEIIAEGQKK.F +2																	3.8279	3.4226		3.6216					
K.YLAAYLLLVQGGNAAPSAADIK.A +2					4.7301	4.4315		4.2941	5.6098			3.2174	5.0286	4.7812	4.2217	5.5035	3.0937		3.6814	5.4772				2.6058	
K.YLAAYLLLVQGGNAAPSAADIK.A +3					3.7932	4.8763			5.7853			3.9537	6.3824	6.2397	5.496	5.8255			5.4838	5.504			4.0656		
R.INELLSSLEGK.G +1					3.2525	3.0145	3.1248	2.9219	3.1835		2.7596	2.5999	3.0503	3.2092	3.1168	3.0679	2.9655	2.82	3.0622	2.8863	3.13			2.7229	
R.INELLSSLEGK.G +2	4.3766	4.39	4.3744	4.44	4.4156	4.3879	4.408	4.387	4.3199	4.3625	4.3962	4.2977	4.2287	4.2322	4.3852	4.3569	4.3811	4.2599			4.1173		3.7891		
gi|6320655|ref|NP_010735.1|	38.2	47.1	44.9	44.9	45.6	45.6	45.6	52.9	46.3	45.6	45.6	45.6	54.4	54.4	47.1	53.7	47.1	53.7	54.4	39	39	36.8	45.6	18.4	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Ap and has similarity to rat S17 ribosomal protein; Rps17bp [Saccharomyces cerevisiae]
gi|6323617|ref|NP_013688.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Bp and has similarity to rat S17 ribosomal protein; Rps17ap [Saccharomyces cerevisiae]
K.DQYVPEVSALDLSR.S +2	4.837	4.7323	4.7353	4.6169	4.5541	4.7226	4.8648	4.8121	4.3197	4.6975	4.4894	4.5296	4.197	4.5412	4.0087	4.4487	4.7115	4.3102	4.2364	4.2103	4.1177	4.387	4.6628	2.7624	
K.IAGYTTHLM*K.R +2		3.1435		3.4846				2.9552					3.1146	2.7147					3.5214	3.1405					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.IAGYTTHLMK.R +1																		1.8273		2.0148					
K.IAGYTTHLMK.R +2	2.5038	3.1273	3.4451	3.3434												2.821				2.9414					
K.LPLSVINVSAQR.D +1									2.5368							2.2584				2.717					
K.LPLSVINVSAQR.D +2	4.2425	4.28	4.3258	4.4013	4.328	4.4616	4.4136	4.2495	4.2171	4.1208	4.3684	4.039	3.7395	4.0353	3.9962	4.1131	3.9663	3.9755	4.0107	4.0237	3.5701		4.0842		
K.LTLDFQTNK.R +1																			2.6174						
K.LTLDFQTNK.R +2			2.9372	2.9952	3.0699	3.1836	3.1455	2.9868	2.987	2.6646	2.8633	2.8999	2.7041	2.6167		3.0148	2.8438	3.0983				3.1536	2.9003		
K.LTLDFQTNKR.L +2													2.7596	2.6699	2.915										
K.RLCDEIATIQSK.R +2		2.8807															4.3416	4.1121	2.7993						
R.KDQYVPEVSALDLSR.S +2									4.3646				4.1057	4.0449	4.0725	3.8959	3.79		3.2457	4.6132					
R.KDQYVPEVSALDLSR.S +3													5.2696							4.2619					
R.LCDEIATIQSK.R +1																					2.0121		2.7133		
R.LCDEIATIQSK.R +2					4.203	4.5785	4.4286	4.1185	4.3911	4.4409	4.1342	4.1101	4.3241	4.0825	4.2717	4.3349			4.2624			4.4312		4.3321	
R.SNGVLNVDNQTSDLVK.S +2	4.7427	4.919	5.0562	4.9109	4.8523	4.6967	4.8905	4.7996	4.7781	4.5384	4.6331	4.7532	4.5743	4.6964	4.441	4.7535	3.9335	4.3094	4.6943	4.5938	3.9059	4.9738	4.7679		
gi|6320679|ref|NP_010759.1|	27.2	27.2	33.8	33.8	25.7	25.7	25.7	25.7	39	26.5	25.7	25.7	39	44.9	34.6	33.8	36.8	33.8	29.4	38.2	24.3	25.7	25.7	25.7	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein; Rpl27bp [Saccharomyces cerevisiae]
gi|6321798|ref|NP_011874.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Bp and has similarity to rat L27 ribosomal protein; Rpl27ap [Saccharomyces cerevisiae]
K.VVIVKPHDEGSK.S +2										3.7138				2.6769	4.0029				3.1394						
K.NQWFFSK.L +1									2.0952				1.8859					2.0107			1.9711				
K.SHPFGHALVAGIER.Y +1																				2.44					
K.SHPFGHALVAGIER.Y +2														4.1039						3.9726					
K.SVVSTETFEQPSQR.E +1																							1.8162		
K.SVVSTETFEQPSQR.E +2	5.4004	5.3192	5.3342	4.7767	5.4121	5.3522	5.3421	5.2357	5.0675	4.9436	4.8829	5.1551	5.3087	5.3636	5.3805	5.0447			5.0358		4.8484	5.0959	4.9664	4.8187	
K.SVVSTETFEQPSQREEAK.K +2																	3.8224	4.101	3.7887	5.053					
K.VVIVKPHDEGSK.S +1																		2.3695							
K.VVIVKPHDEGSK.S +2	3.4181	3.9602	4.0169	3.9906	3.8834	3.354	3.4283	3.7965	3.4726	3.5423	3.5653	3.6527	3.6511	3.9192	3.3635	3.7653	3.6898	3.4387	3.5752		2.6639	3.6451	3.4127	3.2267	
K.VVNYNHLLPTR.Y +2	3.441	3.8157	3.7386	3.5255					3.3181				3.5312	3.5487	3.5621	3.3588	3.1309			2.6284					
R.YTLDVEAFK.S +1					2.0509	2.4684	2.4188	2.1833	2.6197		2.066		2.4741	2.3849	2.3403	2.2326	2.6371	2.0503	2.3374	2.2295		1.9834			
R.YTLDVEAFK.S +2			2.7809	2.7596	2.804	2.7755	2.8115	2.8576	2.9353	2.6092	2.8175	2.6722	2.9919	2.6791		2.6279	2.7433	2.8565		2.5809		2.6923	2.6877	2.8206	
gi|6320882|ref|NP_010961.1|	13.1	17.8	26.3	24.3	19.6	21.2	17.1	19.6	32.1	16.7	18.9	21.6	34.5	36.7	32.3	29.2	17.6	19.6	13.4	27.4	15.1	15.4	10.5	14.3	S-adenosyl-L-homocysteine hydrolase, catabolizes S-adenosyl-L-homocysteine which is formed after donation of the activated methyl group of S-adenosyl-L-methionine (AdoMet) to an acceptor; Sah1p [Saccharomyces cerevisiae]
K.AYGDVQPLK.G +1											2.5019		2.4528	2.4769	2.3409		2.3787	2.3882			2.3124	2.2705	2.4371	2.2394	
K.AYGDVQPLK.G +2						3.1372			3.0012	2.9283	3.225	3.2253	3.0726												
K.ECINIKPQVDR.Y +2			2.5001		2.5399			2.5731	2.885			2.5651													
K.EIELAEHEM*PGLM*AIR.K +2													3.8854	4.0267											
K.EIELAEHEMPGLM*AIR.K +2									2.6764					3.2814	3.9616	3.886				3.4512					
K.EIELAEHEMPGLMAIR.K +2			4.856														4.658			4.1464					
K.FDNLYGCR.E +2					3.0001	3.1146	3.1383	3.032	3.0623	3.12	2.8667		3.0001									3.2874		3.2155	
K.FHLGNLGVR.L +1														2.3052											
K.FHLGNLGVR.L +2			2.6143																						
K.GETEEEYLWCIEQQLFAFK.D +2				5.2537	3.8971	3.4155	3.9898	5.0403	4.1918			3.8723	4.5705	3.6906	3.4975	4.034	3.6836	4.348		4.4288					
K.IADISLAAFGR.K +1								2.1533	2.3652						1.9658			1.9232	2.0053	1.93	2.0689				
K.IADISLAAFGR.K +2	4.2436	4.46	4.4307	4.6886	4.5212	4.46	4.4998	4.3591	4.662	4.4582	4.4446	4.4072	4.4512	4.6779	4.3879	4.7391	4.296	4.6121	4.3396	4.3667	4.3923	4.3285	4.5075	4.597	
K.LKVPAINVNDSVTK.S +2													3.0864	2.996	2.5024										
K.LNLILDDGGDLTTLVHEK.H +2													5.6724	5.4836	5.5129	4.3031				5.4722					
K.LNLILDDGGDLTTLVHEK.H +3													3.9675												
K.RATDVMLAGK.V +2			2.9909	3.0034																					
K.SKFDNLYGCR.E +2													2.8316	3.4104		2.5887				3.005		2.8368			
K.TGPFEVGVHVLPK.I +2	3.6695	3.8925	3.8488	3.6004					3.6068				3.2711	3.5123	3.3207			3.4119	3.4359	3.152					
K.VAVVAGYGDVGK.G +1											2.7805	3.0609	3.3497	3.4086	3.0577	2.994		3.1129	2.9823	2.8808	3.1032		3.5774	3.3443	
K.VAVVAGYGDVGK.G +2		3.8468	3.7155	4.642	4.0896	3.8979	4.4349	3.8564	3.9923	4.5764	3.8804	4.5787	4.4521	3.9043	3.8239	4.3391					4.3253	4.0281	3.6482	3.8652	
K.VPAINVNDSVTK.S +1											2.2083											1.9653			
K.VPAINVNDSVTK.S +2	4.0264	3.7355	3.931	4.0279	3.8255	4.1007	4.0723	3.8808	3.6919	3.5725	3.0473	3.7912	3.8037		3.7726	3.9467					3.6186	3.5603			
K.VQSEYLGIPEEGPFK.A +2	4.8926	4.5881	4.719	4.5895	4.7384	4.7473	4.395	4.8231	4.3446	4.4016	4.3343	4.0955	4.4419	4.4867	4.3972	4.7262	4.4439	3.8041	2.8436	4.1336	4.3505	3.6291	4.7798	4.444	
R.ATDVMLAGK.V +1									2.2146		2.1122		2.3534	2.0958	2.0345	2.1835					2.0891				
R.ESLVDGIK.R +1	1.8992	2.0268		2.1174						2.1623		2.0022													
R.HVILLANGR.L +1													2.2807				2.0179	2.3269	2.2158	2.2968					
R.HVILLANGR.L +2		3.0519	3.1575	2.6899		3.1448			2.9608		3.1049		3.0645	3.0271	3.1193	2.8732	2.996	2.6666	2.7939	2.8776				2.6986	
R.KAYGDVQPLK.G +2														2.8577											
gi|6320905|ref|NP_010984.1|	13.6	10	10	10	10	13.6	13.6	15.2	13.6	13.6	19.2	18.8	13.6	22.4	19.2	13.6	10	10	3.6	18.8	10	10	9.6	9.6	One of two redundant DL-glycerol-3-phosphatases (RHR2/GPP1 encodes the other) involved in glycerol biosynthesis; induced in response to hyperosmotic stress and oxidative stress, and during the diauxic transition; Hor2p [Saccharomyces cerevisiae]
K.FAPDFANEEYVNK.L +2								3.489				3.5879													
K.IIGIATTFDLDFLK.E +2														4.6935	4.3063					3.1019					
K.LCNALNALPK.E +2	3.7649	3.4967	3.6811	3.5156	3.8074	3.8095	3.7674	3.8075	3.5004	3.4855	3.8238	3.3629	3.3003	3.6001	3.5937	3.4514	3.0069	3.6387		2.9686	2.5448	2.9821			
K.VVVFEDAPAGIAAGK.A +1							2.791		3.5355				3.1675			3.1926				2.6006	3.8164				
K.VVVFEDAPAGIAAGK.A +2	4.7068	4.6805	4.6297	4.9628	4.8809	4.7285	4.6705	4.9685	4.653	4.8024	4.5123	4.6645	4.5359	4.5843	4.5203	4.4723	4.4766	4.6458		4.8665	3.6776	4.3194	4.6745	4.2433	
K.WAVATSGTR.D +1														2.3528	2.1359				1.9021				1.8435	1.8888	
K.WAVATSGTR.D +2	3.0522					3.0239	3.0717		2.9349	2.9203	3.1883	2.9321	2.5089	2.9052	2.8264	2.9322			2.7985						
K.WFEHLGIR.R +2														2.8699						2.6194					
R.NGLGYPINEQDPSK.S +2											2.8534														
gi|6320936|ref|NP_011015.1|	5.1	11.2	17.5	15	27.8	22.6	27.4	25.2	39.2	22.6	29.6	31.9	46.9	38.6	44.3	44.9	32.5	24.3	25.3	45	13.4	14.1	25.7	20.3	Cobalamin-independent methionine synthase, involved in amino acid biosynthesis; requires a minimum of two glutamates on the methyltetrahydrofolate substrate, similar to bacterial metE homologs; Met6p [Saccharomyces cerevisiae]
K.ALDADVVSIEFSK.K +2		3.6278		4.401	4.4683	4.3646	3.9593	4.4188	4.7571	4.0146	4.4308	3.9947	4.3804	4.418	4.2994	4.6548	3.9622	3.9156		3.8888	4.2636	4.8061	4.1235	4.5658	
K.ATEGYWNGK.I +1																		2.4496					2.4495		
K.AVDVTALEMPVK.W +2													3.5859						3.6368		2.844				
K.AVDVTALEMVK.W +1															2.7964			2.2853		2.7559					
K.AVDVTALEMVK.W +2					4.4695		4.1294		4.2681	3.3933		4.1029			4.0517	4.2937	4.0274	4.4405	3.061	4.4328	2.8529	4.3075	4.4741	4.5502	
K.AYTYFGEQSNLPK.I +2					4.0753	4.1603	4.5372	4.4594	4.1785	4.1856	4.2856	4.1589				4.013	4.3022	4.2622	4.255			3.8036	3.8077	3.2277	
K.DDANYIAEFK.N +1																	2.1125						2.4232		
K.DDANYIAEFK.N +2							3.9406		3.8397	3.7974	4.0354	3.4618	3.572	3.5995		3.5823				3.3626		4.1411	4.1446		
K.DSLDLEPLSLLEQLLPLYTEILSK.L +2				5.3114									4.1535		3.397	3.4049				4.6742					
K.ESVYAQSITSK.P +2											3.2096		3.3796		3.2405	3.0541				2.7098					
K.ESVYAQSITSKPVK.G +2											3.2993		2.6012				3.3992	3.1456	2.6115						
K.FWVNPDCGLK.T +2			3.1129		2.8011	2.5771	3.099	3.1916	2.8508		2.5895	2.7713				2.8685	3.0609								
K.GFFSFATQK.L +2												2.7972	3.3558	3.0595	3.1197	3.1655	3.3226	3.0622	2.506	3.3054	3.1406		2.5756	3.1643	
K.GLPVAALHVDFVR.A +2													4.0897	3.9518					3.3528	3.7443					
K.GM*LTGPITCLR.W +2										2.6268			3.3792	3.1076	2.794				3.5956						
K.GMLTGPITCLR.W +2	3.1579	3.3696	3.4108	3.4026					3.1923		2.5395			2.918		3.1101	3.0638								
K.GTISAEEYEK.F +2				2.8094																2.6168					
K.ITLATYFGTVVPNLDAIK.G +2			4.2506		4.3019	3.5163	4.3262	4.3585	4.2718		3.227	4.2445	3.0768	4.2679		4.9639			2.521	4.0048					
K.ITVDELFK.V +1														2.4875											
K.ITVDELFK.V +2														2.7337	2.7225	2.6859	2.768				2.6135	2.7208	2.5426		
K.KATEGYWNGK.I +2																				2.6112					
K.LASAGATEVQIDEPVLVLDLPANAQAAIK.K +2						3.079			3.5074					2.5813											
K.LASAGATEVQIDEPVLVLDLPANAQAAIK.K +3					6.9291	6.6316	7.5394	7.1778	5.6402	4.2689	4.9054	7.0092	5.5503	7.3371	6.7917	7.3965	3.8773			5.2398			4.1701	5.8515	
K.LDEVVVITK.N +1					2.4531	2.4724			2.3954									2.6006	2.381		2.1262		2.4278	2.1846	
K.LDEVVVITK.N +2					3.5251	3.6313	3.6132		3.67			3.2554	2.6572		3.0128			3.5801			3.2907			3.0463	
K.LNGQKPVDEFLEAK.E +2													2.6796				3.3115	3.6651		3.512					
K.NVSGQDVAAALEANAK.S +1									2.4892												2.0401				
K.NVSGQDVAAALEANAK.S +2	4.3343	4.9379	4.5506	4.6055	5.1583	5.2253	5.2663	5.1111	5.1054	4.5042	5.103	5.266	4.9715	4.9569	4.7694	4.7414	4.9566	4.3723	4.9801	4.5485	4.3072	5.1538	5.0846	4.9845	
K.NVSGQDVAAALEANAK.S +3																			3.6033						
K.QTLSVGIVDGR.N +2					2.8044		2.9941		3.0272		2.8249				2.7166	2.9961				2.628					
K.TQAM*QLALALR.D +2									4.0158			3.1315	3.9847	3.9365	3.3988				3.6597					3.6899	
K.TQAMQLALALR.D +2					4.5056				4.3134			4.1765	3.942	4.2101	4.2808	4.1706				4.1467	2.956			3.7544	
K.TQIHSHFCYSDLDPNHIK.A +3																				3.6493					
K.VFNLPLFPTTTIGSFPQTK.D +2		4.8955	5.1871		5.4226		5.2312	5.1635	4.9516	4.4678	3.9457	4.8869	4.6288	4.6897	4.2052	4.9494	4.3332	3.7745	2.8543	4.0448			3.6674	3.9786	
K.VFNLPLFPTTTIGSFPQTK.D +3													4.4454	3.5036											
K.VIQVDEPALR.E +2				3.0464	3.3573	3.1047	3.2769	3.4178	3.4911	3.2027	3.4614	3.3634	3.0521	3.3342	3.2977	2.9299	3.0253					3.4099	3.1549		
K.YDLSPIDTLFAM*GR.G +2					3.3111	4.4581	3.9783	3.7836	4.2034	4.4535	3.365	3.8385	4.0398	4.1419	3.5296	3.4023				3.605	4.146		2.5175	4.3438	
K.YDLSPIDTLFAMGR.G +2			4.6735		5.0012	4.7755	4.6003	4.6351	4.3279		2.8277	2.5099			3.3471	4.5	3.885						4.2139		
R.APEQFDEVVAAIGNK.Q +2		5.106	4.9896		5.0987	5.061	5.2781	4.9791	4.8986	4.7428	4.8659	4.6846	4.0121	5.2965	5.0773	4.7618	4.3073	5.0458		4.3883		4.6496	3.229		
R.DEVNDLEAAGIK.V +1																					2.6663		2.5556	1.9515	
R.DEVNDLEAAGIK.V +2						4.1129	4.3463	4.1485		3.8651	3.7055	3.8334	3.5791		3.3949		3.2729					4.4495			
R.FQEEIGLDVLVHGEPER.N +2													4.8645	4.8157	2.8747										
R.IPSKDEFIAK.I +2			2.9173	3.6458				2.9872	2.755					3.3187	3.0631	2.8672									
R.LSLTHM*VEAAK.Y +2													2.7868	3.3173											
R.LSLTHMVEAAK.Y +2									3.1468				3.5177	3.4904	3.2334	2.5563				3.2887					
R.PVLLGPVSYLFLGK.A +2					4.1489	3.8755		4.0864	3.8014			3.5432	3.4823	3.8524	3.9151	3.8982			3.7413	3.3442					
R.SAYYTWAAEAFR.V +2	3.4924	3.8221							3.4871		4.1589	3.7013	3.8645	3.9228	3.9316	3.1123		4.1376		2.5458					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.VATSGVANK.T +1															2.3707										
R.VVVATSSSLLHTPVDLNNETK.L +2			5.9218						5.7898				6.0042	5.7005	5.0492	5.6017	5.7063	5.3462	4.7534	4.6515					
R.VVVATSSSLLHTPVDLNNETK.L +3				4.6156									5.1355	5.3056	4.3384				3.7614	4.253					
R.WSFPRDDVDQK.T +2																		3.1441		2.783					
R.YVRPPIIVGDLSR.P +2									2.515				3.6813		3.459	3.0438			3.0714						
R.YVRPPIIVGDLSR.P +3													3.6353												
R.YVRPPIIVGDLSRPK.A +3														5.4183					3.8108						
gi|6320949|ref|NP_011028.1|	27.5	49	34.5	28	20	20	20	27.5	39	20	20	27.5	42	34	26.5	34.5	27	27.5	35	32.5	13.5	14	20	13.5	Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S8 ribosomal protein; Rps8bp [Saccharomyces cerevisiae]
K.AAIVQIDATPFR.Q +1									2.5807					1.9671											
K.AAIVQIDATPFR.Q +2	4.3029	4.1804	4.2674	4.2186	4.1974	4.1119	4.0707	4.1601	4.0469	3.7987	3.9472	3.965	4.0824	4.1039	4.0999	4.0323	3.4843	4.205	3.7563	4.0108	3.8049		3.3664	3.4093	
K.EEETVAK.S +1									2.0098																
K.IESSVESQFSAGR.L +2	4.5149	4.374	4.2983		4.7154	4.5966	4.5666	4.4608	4.5099	4.3724	4.6066	4.501	4.3462	4.501	4.632	4.3857	4.2251	4.46	3.7948			4.1021			
K.RKFELGR.Q +2																				2.6444					
R.CDGYILEGEELAFYLR.R +2		4.6137							3.1724				4.1208			3.3213			4.9129	3.5581					
R.IAGVVYHPSNNELVR.T +2	3.7085	3.8821	3.821	3.7688				3.8309	3.4422			3.2477	2.8795	2.6566				3.2205		3.1572					
R.IETGNFSWASEGISK.K +2	5.1	5.1775	5.0842	5.4436	5.3323	5.2804	5.3762	5.2787	4.8679	5.1997	4.9543	5.1025	4.9552	5.2194	5.0147	5.2647	5.1242	4.7174	4.0945	4.5805	4.6829	4.0846	4.9754	4.1536	
R.IETGNFSWASEGISKK.T +2																			4.2533						
R.LYACISSR.P +2																	2.9438								
R.LYACISSRPGQSGR.C +2		3.0204	2.8774	3.1077													2.6219								
R.QWFEAHYGQTLGK.K +2		2.8175											2.738	3.2699	3.2091	3.1514			3.0512				2.8746		
gi|6320950|ref|NP_011029.1|	6.1	9.8	6.1	6.1	10.4	10.4	10.4	10.4	12.9	10.4	12.8	12.8	10.6	16	12.9	12.9	9.7	11.7	9.8	11.8	9.3	6.9	5.8	8.7	Heat shock protein that is highly induced upon stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of the HSP70 family; cytoplasmic protein that concentrates in nuclei upon starvation; Ssa4p [Saccharomyces cerevisiae]
K.AVGIDLGTTYSCVAHFANDR.V +2														4.7779											
K.AVGIDLGTTYSCVAHFANDR.V +3														3.8129											
K.DAVVTVPAYFNDSQR.Q +2									3.1991		2.6776	2.7523		3.4942	2.9345	3.4998		2.966							
K.DNNLLGK.F +1																				1.8274					
K.DNNLLGKFELSGIPPAPR.G +2																				3.5476					
K.FELSGIPPAPR.G +1											2.2309										2.5392				
K.FELSGIPPAPR.G +2	3.6341	3.5119	3.5434	3.3402	3.4878	3.6945	3.6055	3.7462	3.4398	3.7985	3.4059	3.5806	3.4655	3.359	3.4755	3.3556	3.3157	3.349	3.3099	3.1183	3.3153	3.3887	3.3638		
K.KSEVFSTYADNQPGVLIQVFEGER.T +3		6.304																	4.554						
K.M*VAEAEK.F +1																						2.2691		1.9793	
K.MVAEAEK.F +1					1.8514	1.8422	1.9611	1.8379	2.0003	1.8515	1.9182	1.9459	2.1449	1.9156	1.9109	2.151				1.888					
K.SEVFSTYADNQPGVLIQVFEGER.T +2					6.25	6.0192	6.1546	6.1758	5.9719	4.6673	5.6704	5.6796	5.99	6.1021	5.8173	6.0481	5.5564	4.3329	5.1104	4.7417	4.3607			5.5962	
K.SEVFSTYADNQPGVLIQVFEGER.T +3					5.8799	5.5908	6.1017	5.6739	5.6902	3.596	5.5767	5.8745	6.1014	5.7486	6.0194	5.7555	4.0982		4.8371	3.8779					
R.ARFEELCADLFR.S +2	3.7337	4.2022	4.1129	3.9047													3.2032		3.5025	3.5926					
R.FEELCADLFR.S +1								1.9717	2.2357				1.986	2.3495	2.21	2.5758					1.9985				
R.FEELCADLFR.S +2	3.9117	3.8945	3.98	4.1421	4.0162	4.1778	3.8927	3.9922	3.9344	3.9238	3.9138	3.9746	3.8189	3.9631	3.7523	3.987	3.7032	3.9944	3.4827	3.9332	3.5951	3.8665	3.855	3.8992	
R.IINEPTAAAIAYGLDK.K +2	5.4234	5.6456	5.4945	5.6147	5.9293	5.7907	5.8466	5.7708	5.6002	5.6482	5.6936	5.7626	5.6224	5.5621	5.3866	5.7659	5.2446	3.7723	5.4782	4.6525	5.4048	5.1952		5.6237	
R.IINEPTAAAIAYGLDK.K +3									4.8594			4.9217	4.8156	5.2729	4.8542	5.0129	3.9747	4.0145	4.5842		4.6019	4.6401	4.4467	4.3033	
R.IINEPTAAAIAYGLDKK.S +2									4.5132				4.4143	4.729	4.5121	3.8927									
gi|6321013|ref|NP_011092.1|	6.9	15.3	9.9	15.8	20.6	20.6	18.4	22.5	32.8	13.7	18.5	24.3	42.1	32.9	37.1	36	16.8	22.2	24.4	23.1	18.9	15.4	10.7	12.5	Poly(A) binding protein, part of the 3'-end RNA-processing complex, mediates interactions between the 5' cap structure and the 3' mRNA poly(A) tail, involved in control of poly(A) tail length, interacts with translation factor eIF-4G; Pab1p [Saccharomyces cerevisiae]
K.AHYTNLVVK.N +1													2.0802					2.0588							
K.AHYTNLVVK.N +2		2.6169		2.6324																					
K.AIEQLNYTPIK.G +2					3.907	3.8769	3.627	3.6769	3.9957		3.8561	3.2215				3.4044		3.4855				3.4244			
K.ALYDTFSVFGDILSSK.I +2					4.5909	3.764	4.8317	5.0769	5.5189			4.3538	5.3771	5.0715	4.7722	4.8256		3.2853	3.4705	3.2097					
K.AVEALNDSELNGEK.L +2	3.9292	4.2862	3.3551	4.4562				3.1746	4.5155	3.8368	4.2745	3.0618	4.0447			4.2939									
K.EAIDALNGM*LLNGQEIYVAPHLSR.K +3													4.8085		3.7022				4.2499						
K.EASAAYESFK.K +1																						2.2862	2.7282	2.063	
K.EASAAYESFKK.E +2																						2.6299			
K.FGPIVSASLEK.D +1														2.3612	2.2656			1.9927		2.2042	2.0029		2.3115		
K.FGPIVSASLEK.D +2	3.4477	3.5614	3.4326	3.6322	3.6393	3.6964	3.7718	3.6164	3.526	3.4616	3.4609	3.1201	3.4993	3.4699	3.2706	3.506	3.3128	2.9653	3.2189		3.5483	3.1874		3.4206	
K.GFGFVCFSTPEEATK.A +2					4.1236		4.2936	3.0244	3.3188				4.046	4.3337	3.5962	3.5594		4.618	4.6862		4.0679				
K.GFGFVHFEEEGAAK.E +2													4.2205	4.1496	4.5151	4.3881				4.2596					
K.GFGFVNYEK.H +2															2.5636			2.6494							
K.LEEEFAPYGTITSAK.V +2						3.1703															3.2467				
K.M*AKYQGVNLFVKNLDDSVDDEKLEEEFAPYGTITSAK.V +3		3.788							3.8107				3.6025		3.6441										
K.NINSETTDEQFQELFAK.F +2		5.9692	5.7741	5.8928	6.014	5.9512	6.1669	6.0414	5.9101	5.5219	5.781	5.771	5.821	5.9494	5.5732	5.8716	5.6023	4.1118		3.9793	5.5056	5.7627	5.9612		
K.NLDDSVDDEKLEEEFAPYGTITSAK.V +2		4.928		3.8239					4.9479			3.3145	5.0849	4.7344	4.932	5.2223	4.4267	5.079	3.5566	4.5727					
K.NLDDSVDDEKLEEEFAPYGTITSAK.V +3									4.0654				4.315		3.5753	4.1833									
K.NLHPDIDNK.A +2														2.5079											
K.NQQIVAGKPLYVAIAQR.K +2													5.276	5.1239	4.7212	4.3414	3.9048		4.3585	4.4552					
K.NQQIVAGKPLYVAIAQR.K +3													4.6385	5.0901	5.0579	4.5199	4.5152		5.2381	4.5278					
K.PLYVAGQR.K +2								3.2291	3.3014		3.1883	3.295	3.1278	3.2657	3.0936	3.1988					3.492	3.276		3.159	
K.TAEQLENLNIQDDQK.Q +2	5.6388		5.2053	5.2388	5.3242	5.437	5.5496	3.5236	5.3276	5.1194	5.1918	5.4723	4.8124	4.4249		4.9358		4.0643		4.7899	3.2465	4.8291	3.2137	4.8656	
K.TSLGYAYVNFNDHEAGR.K +2									4.2776				4.5997	4.8747	4.3646	4.5171				2.5485					
K.TSLGYAYVNFNDHEAGRK.A +2																			3.3543	2.8853					
K.YQGVNLFVK.N +2					2.7945	2.7518	2.8193		2.6478				2.8785	2.8133	2.8653	2.5107							2.7557		
R.DSQLEETK.A +1											2.0019														
R.NANDNNQFYQQK.Q +2							4.1346	4.2103	4.1503	3.7232	3.9202	4.1406	3.9132		3.7405	4.295	3.5123				3.7791			4.1284	
R.NGPVYGVPPQGGFPR.N +2					2.712	2.7931			3.1313				2.9074	3.7734	3.299	3.6251	2.617		3.2547		3.2887	2.6257		2.8568	
R.SQLAQQIQAR.N +2					3.5531	4.0595		3.4702		4.0652	3.9822	3.7844	3.9506	3.6271	3.6963										
gi|6321025|ref|NP_011104.1|	26.6	47.9	41.6	48.7	24.3	21.7	30	33.3	43.8	33.3	33.3	35.6	52.4	52.4	31.8	58.1	43.8	30.7	38.2	56.9	22.5	21.7	33	30	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sensitive signaling, and others; Bmh1p [Saccharomyces cerevisiae]
K.ATNASLEAYK.T +1						2.1903			2.1081				2.3158	1.9332	2.1406		2.2097	2.2611	2.0299	2.2777		2.283	2.1643	2.3877	
K.ATNASLEAYK.T +2				2.9969		3.0316	3.0177	2.9312	3.1882	3.0025	3.2007	2.8441		2.9658	2.7529										
K.DSTLIMQLLR.D +2						3.6263	3.6525		3.8058	3.5632		3.4711	3.3129	3.6425	3.5566	3.4696	3.2088	3.9718	3.5704	3.5173	3.5335	3.2221	3.4943	3.3971	
K.DSTLIMQLLR.D +2	3.9135	3.8362	4.1182	4.0022	3.7464		3.6473	3.757	3.5034		3.2672	3.6763		3.7393	3.658	3.7443	4.0853			3.3513	3.3633	3.3506	3.3479	3.4392	
K.IETELTK.I +1									2.3666			2.2706	2.3615	2.3877	2.3999								1.9202		
K.ISDDILSVLDSHLIPSATTGESK.V +2		5.7717	4.6918	6.1942									5.8678	5.4652					3.7449	4.0448					
K.ISDDILSVLDSHLIPSATTGESK.V +3		5.4095	4.7257	5.1304									3.9338	4.535		4.094			3.8411						
K.QAFDDAIAELDTLSEESYK.D +2	5.8811	6.3478	6.1698	6.2983	6.1639	6.1032	6.3984	6.1978	6.0604	4.434	5.2703	5.7312	6.132	5.9446	6.0708	6.0539	3.9377	5.7208	4.4075	4.827	5.8535	5.6643	5.6865	6.04	
K.QAFDDAIAELDTLSEESYK.D +3													3.9136	4.7788	4.6566	4.1921		3.9177	4.4279	4.6885			4.0016		
K.SEHQVELICSYR.S +1																2.5994									
K.SEHQVELICSYR.S +2									3.2013				4.1779	4.2286	3.8159	3.9669	3.7116	4.2554		3.9244					
K.TASEIATTELPPTHPIR.L +2	3.8058	4.1584	4.2395	4.2424	3.7082			4.1662	4.3498	3.9781			4.2493	4.5733	4.1268	4.0259	4.0496	3.8131	3.6524	3.8068					
K.TVASSGQELSVEER.N +2	4.4583	4.5781	4.358	4.8315			4.5436	4.4663	4.4662	4.1975	4.1405	4.6423	4.837	4.2852		4.4208			4.0696		4.5041		4.567	4.5775	
R.DNLTLWTSDM*SESGQAEDQQQQQQHQQQQPPAAAEGEAPK.- +3																3.62									
R.DNLTLWTSDMSESGQAEDQQQQQQHQQQQPPAAAEGEAPK.- +3																4.3482	5.4983			3.73					
R.EDSVYLAK.L +1		2.1662		2.074			2.0452	2.1107			1.8677	1.9425	2.0647		1.9875								2.0953	2.0945	
R.IVSSIEQK.E +1						2.325					2.3656			1.8227				1.8826			2.0467	1.8635		2.3878	
R.IVSSIEQK.E +2					3.1095	2.8661	3.0778		2.5415			2.9268													
R.IVSSIEQKEESK.E +2																				3.2198					
R.IVSSIEQKEESKEK.S +2																		3.4524							
R.NLLSVAYK.N +1		1.8356	1.8213							1.938		2.2139													
R.SKIETELTK.I +2		2.7951	2.7144	2.6677											2.5264		2.6311		2.5415						
R.YEEMVENMK.T +1																				2.491	2.8549		2.9687		
R.YEEMVENMK.T +2		3.4018		3.4102					3.4729		3.4578		3.1251	3.2665		3.3018									
R.YLAEFSSGDAR.E +2	4.07	4.3025	4.0681	4.0089	4.1917	4.2359	4.3445	4.3555	3.2541	3.9556	3.831	3.7936	3.506	3.4117		3.98						3.5225	3.7484	4.3061	
gi|6321184|ref|NP_011261.1|	17.7	37.4	40.1	31.5	49.6	48.4	58	53.5	60.5	36.4	39.3	63.2	61.5	55.6	62.6	68.5	47.1	45.9	37.4	58.4	24.3	16.3	40.9	24.5	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokinase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of its own gene; Hxk2p [Saccharomyces cerevisiae]
K.AFIDEQFPQGISEPIPLGFTFSFPASQNK.I +3			4.3409		5.1913		4.9607	4.824	4.6782		3.5299	5.1487	4.2174		3.552	5.2608									
K.DIYGWTQTSLDDYPIK.I +2	4.7139	4.8223	4.8654	4.4626	4.965	4.8999	5.0042	4.8553	4.859	4.5245	4.6731	4.6803	4.5085	4.6561	3.6465	4.5103	4.3396		4.3649	3.775	4.2242	4.5401	4.6113	3.7199	
K.ELM*QQIENFEK.I +2									3.1667	3.3144			3.4853	3.3923	3.543	2.9479		3.342							
K.ELMQQIENFEK.I +2	4.0413	4.1211	4.1906	4.2563	4.2188	4.4388	4.1068	4.2947	4.1508	3.8258	3.8724	4.0702			4.0548	4.169	3.6213			3.6037		3.3165	3.988	4.133	
K.ESGDFLAIDLGGTNLR.V +2	5.4352	5.2616	5.4084	5.2655	5.2599	5.3339	5.2526	5.4891	5.0631	4.961	4.7414	5.0717	5.1148	4.9282	5.1045	5.145	4.401	5.173	4.3815	5.2849	4.5797		3.7448	4.9781	
K.FDKPFVM*DTSYPAR.I +2									3.102	3.2412		3.2592	3.8353	3.9291	2.6711	3.4047									
K.FDKPFVM*DTSYPAR.I +3													3.9669												
K.FDKPFVMDTSYPAR.I +2									4.6319				4.3139	4.4532	4.0019	4.2637	4.2301			2.5203					
K.GFDIPNIENHDVVPM*LQK.Q +2													3.3775	2.8856	3.5252		2.5032		3.3365	3.6371					
K.GFDIPNIENHDVVPMLQK.Q +2		3.6996																							
K.GGNIPM*IPGWVM*DFPTGK.E +2									3.8696			3.3609	3.7237	4.2983	3.7975	3.5679			3.3093						
K.GGNIPM*IPGWVMDFPTGK.E +2							2.8609	3.2742	2.948			3.0599								2.946					
K.GGNIPMIPGWVM*DFPTGK.E +2							2.7295		3.1278			2.5722													

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.HFISELEK.G +2		2.9288		2.8645						2.9966			3.0356	2.7557	2.615	2.9029	2.7431	2.5262							
K.IFTVPTETLQAVTK.H +2	4.1961	4.2972	4.1337	4.0031	4.1959	4.268	4.0692	4.2726	3.291	3.8242	4.0127	4.1325	3.4054	4.0184	3.8954	3.6044		2.3208	3.4187	3.8537			2.8939	3.9599	
K.IFTVPTETLQAVTK.H +3													3.8169	4.0459											
K.INEGILQR.W +1																					2.0241				
K.INEGILQR.W +2	3.149	3.069	3.0979	3.0963	3.2139	3.1842	3.19	3.1463	2.9981	3.1393	2.8491	3.12				3.0038					3.1662	3.257		3.1868	
K.IVPAEDGSGAGAAVIAALAQK.R +2	6.6954	6.4382	6.3384	5.6916	5.9624	6.1689	5.7909	5.8358	5.7963	5.6627	5.1764	4.5938	4.1918	4.9191	4.492	5.4401	4.4758	4.569	5.528	5.4299			4.6428		
K.IVPAEDGSGAGAAVIAALAQK.R +3		3.8771	3.6808	3.9494	3.5737	3.7984	3.811	3.6966	3.5979	3.5504	3.5995	3.9487		3.5843		3.5612			3.7898				3.7829		
K.KGGNIPMM*IPGWVM*DFPTGK.E +3														3.9874					3.7401						
K.M*GVIFGTGVNGAYYDVCSDIEK.L +2												2.878	5.2924	5.0577	4.5506			4.8782	4.7352	3.4352					
K.M*GVIFGTGVNGAYYDVCSDIEK.L +3													5.6322	5.0327	5.393										
K.M*SSGYYLGEILR.L +2							3.1552	3.5765	3.4876	3.7478	3.0981	3.5399	4.0504	3.9319	3.6011	3.9624		3.9249						3.5669	
K.MGVIFGTGVNGAYYDVCSDIEK.L +2					4.9628	4.7159	5.1866	4.4075	4.7317		2.6379	3.9621			4.2154	5.8588	4.1232			3.4859	2.7433		2.5103		
K.MGVIFGTGVNGAYYDVCSDIEK.L +3															4.192										
K.MSSGYYLGEILR.L +2		4.3153	4.2971	4.3375	4.2493	4.3235	3.9308	4.4275	3.9944		4.3107	4.2085		3.8573	4.1379	4.0084		4.3082		4.3278	2.9934	2.7076	3.6119	3.4604	
K.PFVMDTSYPAR.I +2		2.8004															3.7737	3.7264		3.8663					
K.TGHIAADGSVYNR.Y +1																						2.4583	2.1169		
K.TGHIAADGSVYNR.Y +2		3.9088	3.8449	3.4857		3.7662	3.5441	3.6083	3.5894	3.648	3.6152	3.556	3.4969	3.5725	3.5624	3.6885	3.4357	3.3108			3.5078	3.9019	2.7784	3.4072	
K.TGHIAADGSVYNRYPGFK.E +2																			4.2761	3.8492					
K.YDITIDEESPR.P +2																						3.0411			
K.YDITIDEESPRPGQQTFEK.M +2					4.1984			3.1394	4.153	3.4528		3.8068	4.6661	4.7106	4.6475	4.6285	4.6205	4.3142	3.8486	3.8722	3.6181				
K.YRLPDAMRTTQNPDELWEFIADSLK.A +3		4.0375	4.1901	3.9064	4.2554	3.9824	4.3708	4.0867	4.0368			3.9895	3.8396		3.7078	3.7618				3.8811					
R.IEEDPFENLEDTDDLFQNEFGINTTVQER.K +3						4.5135	5.2201					4.7606	4.8226			4.6035	3.6924	5.9354		4.5184			4.5997	3.7014	
R.LALMDMYK.Q +1					1.9838		2.2718		2.0714						2.1949	1.8532	2.3326	2.2623		2.2233		2.1491	1.8134		
R.LALMDMYK.Q +2														2.7196		2.6691	2.5319	2.9335					2.5263		
R.LSELIGAR.A +1								2.5477	2.451	1.8638						2.5586		2.4125							
R.LSELIGAR.A +2						2.8096				2.7094													2.5137		
R.LSVCGIAAICQK.R +2					3.7969	4.0451	3.8603		3.6622		3.5339	3.676	3.8628	3.9218	3.8868	3.9007		2.6068		3.762	3.513		4.0689		
R.NIPIEVVALINDTTGTLVASYYTDPETK.M +2					5.2604	5.1992	3.9589	5.4269	5.8599			4.8093		5.6549	5.6879	5.2159									
R.NIPIEVVALINDTTGTLVASYYTDPETK.M +3					4.9279	5.446	5.0741	4.6818	5.4711			4.5745				5.4932									
R.RLSELIGAR.A +2		3.3972	3.7662	3.5377													3.279			3.5168					
R.TFDTTQSK.Y +1																	1.8773								
R.TKYDITIDEESPRPGQQTFEK.M +2													5.0712			3.2901		4.3212	4.0943	4.1978					
R.TKYDITIDEESPRPGQQTFEK.M +3			4.1576										4.5204	3.9957					4.1202	3.6922					
R.TTQNPDELWEFIADSLK.A +2		5.6751	6.2242	5.8925	6.0149	5.7515	6.1691	6.0038	5.6226	3.0758	4.9404	5.6436	5.858	5.2067	5.4947	5.4423	5.1656	3.8869	2.7884	5.3206			3.5068		
R.TTQNPDELWEFIADSLK.A +3													4.6059	4.8663											
gi|6321291|ref|NP_011368.1|	24.1	19.4	25.7	25.7	29.3	29.3	33.5	29.3	38.7	29.3	33.5	45	45	52.9	52.9	52.9	29.3	20.4	27.2	42.4	29.3	29.3	27.2	29.3	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Bp and has similarity to E. coli L6 and rat L9 ribosomal proteins; Rpl9ap [Saccharomyces cerevisiae]
K.DEIVLSGNSVEDVSQNAADLQQICR.V +2					5.7371	6.157	6.2228	6.2139	5.9896	3.5899	5.3474	6.332	5.3167		5.8969	6.1457	3.5785			3.4148		5.5345	2.5141	2.5539	
K.DEIVLSGNSVEDVSQNAADLQQICR.V +3					6.3767	6.8545	7.2838	5.9875	6.1897		4.6248	5.8965	4.6326	5.3996	3.9284						4.257	5.3394	6.0605	6.1577	
K.FLDGIYVSHK.G +2		3.6561	3.5127	3.5725					3.0989			3.1473	3.2382	3.4608	3.5482	3.5799			3.3059	3.4668					
K.HIDVTFTK.V +1									2.6282		2.1789		2.4939						2.4594						
K.HIDVTFTK.V +2			2.7211	2.6743			2.5074		2.8207		2.9924	2.7369	2.8085	2.9175	2.7819	2.6469		2.9696	2.7543				2.8615		
K.SLVDNMITGVTK.G +2									2.5634																
K.SLVDNMITGVTK.G +1								2.1788	2.2151						2.215		2.0536	2.2623		2.0243					
K.SLVDNMITGVTK.G +2	4.2031	4.3266	4.2932	4.469	4.3135	4.483	4.4577	4.4975	4.2917	3.8899	4.2746	4.2577	3.8926	4.3202	4.3966	4.3294	4.0094	4.3163		3.973	3.9482	4.3051		4.4009	
K.YIQTEQQIEVPEGVTVSIK.S +2	4.9809		5.5278	5.3085	5.3764	5.6319	5.7822	5.618	5.6368	4.5377	5.1766	5.0504	5.4421	5.3553	4.8091	5.6929	5.0061	5.4087	5.1529	4.6119	5.5094	5.5657	5.5054	5.4619	
K.YIQTEQQIEVPEGVTVSIK.S +3												4.0578	4.9877	5.4	3.9661	3.5457		4.0097							
R.DGVTIEFSTNVK.D +2												3.2192	3.0001	3.5384	3.6615	2.661									
R.YVYAHFPINVNIVEK.D +2	2.6522	4.6396												4.5246	3.205	3.857			4.072	4.5594					
R.YVYAHFPINVNIVEK.D +3														4.6573											
gi|6321362|ref|NP_011439.1|	22.1	24.6	36.1	27.9	26.6	26.6	26.6	21.7	30.7	26.6	26.6	30.7	29.5	26.6	26.6	38.9	33.6	23	25.4	24.6	21.7	16.8	23	26.6	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7ap [Saccharomyces cerevisiae]
K.AAGSYYVEAQHK.L +1																							2.591		
K.AAGSYYVEAQHK.L +2		3.8738	3.57	3.5375	3.1801	3.4158	3.6313		3.2268	3.2969	3.8154	3.4759	3.5786	3.4568	3.3326	3.4609	3.6876	2.9719	3.1924			3.8077		2.8793	
K.HFIQGGSFGNR.E +2			2.5077													2.905									
K.HFIQGGSFGNREEFINK.L +3																				3.6852					
K.ILTPESQLK.K +1																2.6027	2.5264		2.3089						
K.LIEPYVAYGYPSYSTIR.Q +2	4.913	5.3207	5.0257	4.5716	4.9501	5.1284	4.9401	4.9585	4.5619	4.8746	4.6969	4.3685	4.7678	4.9944	4.8064	4.9605	4.9692	3.7186	5.1576	4.6376	4.9589	4.168	3.1086	4.5201	
K.LIEPYVAYGYPSYSTIR.Q +3													4.1781	4.9403	3.8784					4.0246					
K.LSNPSGGWGVPR.K +1																							2.0681		
K.LSNPSGGWGVPR.K +2	3.8335	3.6231	3.9498	3.6998	3.9097	3.9282	3.7514	3.84	3.6416	3.6901	3.6953	3.301	3.7405	3.7636	3.2283	3.341	3.2181	3.1045			3.7116	3.4992		3.7985	
K.QANNFLWPFK.L +2	2.8825	3.1564	3.0173	2.88					2.6042			2.545				2.636	2.6144								
K.QRVPLSDNAIIEANLGK.Y +2			3.56	2.9026																3.6659					
K.TAEQVAAER.A +1											2.1622										1.8878				
K.TAEQVAAER.A +2		3.3237	3.1319		3.4275	3.2194	3.4867	3.3872	3.034	2.8425		3.4681	3.4011	3.1698	3.3026	3.4609			3.3818	3.2338				3.0318	
R.KVLQLLR.L +2													2.8177				2.7707								
R.VPLSDNAIIEANLGK.Y +1									2.7518																
R.VPLSDNAIIEANLGK.Y +2	4.7891		5.0612	5.136	5.0607	5.2709	5.0061	5.2394	4.8277	5.1147	5.2399	4.7525	4.3118	5.1173	4.3726	5.081	4.901	4.6787	4.9356	4.9911	4.6557		4.463	4.7273	
R.VPLSDNAIIEANLGK.Y +3														3.5999											
gi|6321524|ref|NP_011601.1|	7.6	10.3	7.6	6	6.9	6.9	5	5	6.9	5	5	6.9	7.6	7.6	7.6	7.6	7.6	7.6	12.6	7.6	7.6	5	6	3.4	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, involved in amino acid catabolism; Pdc6p [Saccharomyces cerevisiae]
K.GSIDEQHPR.Y +2	2.9046	3.1288	3.0816		3.0065	3.0524	3.2641	2.909	2.9259	3.0037	2.8558	3.1236	3.1628	2.9151	3.2792	3.241	3.0159	2.9257	2.772	2.8313	2.5223	2.9344			
K.PYLFVLNNDGYTIEK.L +2	5.915	5.9623	6.0396	6.0737									4.4317	4.305	4.5703	3.9073	5.6122	4.912	5.6825	5.9215	4.8667		3.9902		
K.PYLFVLNNDGYTIEK.L +3																				3.6253					
R.M*SANISETTSMITDIATAPSEIDR.L +3																			3.5595						
R.WAGNANELNAAYAADGYAR.I +2	6.315	6.1705	6.1054	5.9478	6.3728	6.416	6.273	6.305	6.1477	5.9351	6.1191	6.1423	6.1272	6.4155	5.8346	6.1666	5.8904	5.3582	5.7069	6.1369	6.3886	6.026	5.9441	5.9111	
R.WAGNANELNAAYAADGYAR.I +3						3.6009		4.1013	3.8919		4.1817	4.2851	5.4039	5.2578	4.5669	4.3758	4.7695								
R.WGLKPYLFVLNNDGYTIEK.L +2																			4.9392						
R.WGLKPYLFVLNNDGYTIEK.L +3																			5.0728						
R.YGGVYVGTLSK.Q +2					2.9572	2.8565			2.9244			2.7836													
R.YGGVYVGTLSKQDVK.Q +2		3.2279																							
gi|6321563|ref|NP_011640.1|	8.6	12.2	8.6	11.4	9.1	10.8	15.4	17.3	14.9	15.2	14.9	15.4	31.1	36.4	27.6	24.5	18.9	10.8	11.2	29.7	11	10.3	8.2	15.6	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn2p [Saccharomyces cerevisiae]
K.ADWGCAEDPSGR.Y +2	3.8202	3.7717	3.7242	3.4991			3.3801	3.6992	3.816		3.5754	3.6515	2.9243			3.3413				3.6379		3.5283			
K.ADWGDDIPTTK.E +1																								2.2139	
K.ADWGDDIPTTK.E +2	3.0346	3.0301	3.2942	3.4273		3.0352	3.5642	3.324	3.2253	3.025	2.8798		3.3399	3.4838	3.0257							2.8795	3.1534		
K.AFDTTDEPDVKPYLPEEILWR.Q +2													4.1663	4.4032	4.7416		3.0738			3.8266					
K.AFDTTDEPDVKPYLPEEILWR.Q +3		5.7647												4.5658						4.3354					
K.ANADANEDNNVDEK.Q +2										4.4654			3.6158			3.0582									
K.DFLQLCM*NIDPNEK.M +2														4.4935											
K.DFLQLCMNIDPNEK.M +2							4.2495	3.2669				3.1579		3.1979	3.9568	4.2217	3.7749	3.2019		4.3439				3.945	
K.EQFSDGVGYSWIDGLR.D +2	4.8358	5.0362	5.1906		4.725	4.4314	4.6598	4.4996	3.9745	4.6162	4.7082	4.3399	2.8385	2.9664	2.9537	4.7981	4.9548	4.301	3.9693	2.6869	3.2808		2.6214	2.6603	
K.FDAWFPQK.T +2																			2.5069						
K.FQTFSDCEPIIPLYLEHDIDAPK.Y +3				4.099																					
K.HEDINFKPK.A +2														3.118						2.5626					
K.M*VLSGEGSDEIFGGYLYFAQAPSAAEFHTESVQR.V +3														5.9927											
K.NLHLADCLR.A +2				2.5113															2.526	2.5188					
K.RIPSTPVDYHAIR.H +3																			4.1078						
K.STM*AWGLEAR.V +2																					3.1738				
K.STMAWGLEAR.V +2						3.6017	3.8204	3.5177	3.6293	3.1416	3.8449	3.319	3.4923	3.7411	3.6132	3.7301	3.6608	3.6384		3.9405		3.7125	3.6433	3.6189	
R.AISDAMFANPK.A +2					3.2591			3.4412	3.0278	2.8598	3.266	3.1855		3.0999	2.8305	3.3897						3.0685		2.8148	
R.ASTPMFLLSR.K +2																	2.5764								
R.DPIGVVTLYM*GR.S +2													3.124								2.7868				
R.DPIGVVTLYMGR.S +2															3.9835		4.5191	3.0222		4.2394	4.2691			4.24	
R.GPDWSGNAVM*NSTIFVHER.L +3													4.0887												
R.IPSTPVDYHAIR.H +2													3.0252	3.138	2.6125	2.7954				2.892					
R.LHSFAIGLPNAPDLQAAR.K +2														5.4683					3.639	5.2312					
R.LHSFAIGLPNAPDLQAAR.K +3														3.5461						4.4739					
R.LM*AEVPYGVLLSGGLDSSLIAAIAAR.E +2														3.3566											
R.LM*AEVPYGVLLSGGLDSSLIAAIAAR.E +3													4.3793	5.8326	4.781	3.6335				4.6912					
R.SSQSPETVYFASELK.C +2					5.4296	5.7418	5.5816	5.7139	5.1256	4.5518	4.6917	4.709	4.661	5.5203	5.5765	5.432	5.2364				4.2993	4.471		5.1058	
R.YFTPDWLDEK.R +1									1.9003							2.4137	1.9628	2.1642			2.2496				
R.YFTPDWLDEK.R +2	3.2332	3.2755	3.2128	3.0686	3.1303	3.1192	3.1828	3.1394	2.8689	2.942	2.9165	2.8231	2.9446	2.6385	2.7018	2.696	2.5919	2.939		3.2126			2.9541		
gi|6321631|ref|NP_011708.1|	54.8	75.3	65.4	63	53.9	53.6	53.9	60.5	49.1	53.6	48.8	49.1	62.3	70.5	75.3	72.9	53.3	46.4	60.2	67.8	46.4	41.9	48.8	53	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh3p [Saccharomyces cerevisiae]
K.ELDTAQK.H +1		1.9741						1.8644					1.9637												
K.ETTYDEIKK.V +2	2.7119		2.5517		2.8331	2.7078	2.8038	2.6031		2.5497															

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.GVLGYTEDAVVSSDFLGDSHSSIFDASAGIQLSPK.F +3		6.1338												4.341	6.0136	5.2324				4.2084					
K.HIDAGAK.K +1		2.2897	2.3916			2.1017		2.144		2.3737	2.3856	2.2129	1.8986	2.2111	2.0744	2.488	1.9217		1.9074	2.0769				2.1721	
K.HIDAGAKK.V +2		2.9828	2.8112														2.8728			2.563					
K.HIIVDGK.K +1	2.2806	2.2953	2.2495	2.2799	2.2396	2.2724	2.3386	2.3012	2.3124	2.221	2.2116	2.3319	2.2623	2.225	2.2925	2.1975	2.2466	2.1291	2.1844	2.4106	2.2329	2.0001	2.2198	2.1048	
K.HIIVDGKK.I +1		2.2472															2.0532								
K.HIIVDGKK.I +2	2.9129	3.1109	3.1597	3.1413				2.7957			2.5158	2.8436	2.666			2.5133	2.8873	2.7588	2.9616	3.0379					
K.IATYQER.D +1																							1.8752	2.0082	
K.IATYQERDPANLPWGSSNVDIAIDSTGVFK.E +3	6.3397	7.0207	6.8823	5.1398										5.386				3.6755	6.0455	4.1867					
K.IVSNASCTTNCLAPLAK.V +2	5.0341	5.0041	4.9339	4.6853	5.0496	5.0632	5.17	5.0947	4.8518	5.136	4.9084	4.7847	4.8806	4.4531	4.5623	4.9988	4.8111	4.4749	4.3861	3.2605	4.7302	4.5466	4.8866	4.8148	
K.IVSNASCTTNCLAPLAK.V +3												4.5327	4.5355	4.8682		4.5436									
K.IATYQER.D +2	3.3834	3.2804	3.1392	3.2745	2.9524		2.8247	2.522	2.931				2.6148	2.9315	2.5145	2.7118	2.9071			2.8759			2.7921		
K.IATYQERDPANLPWGSSNVDIAIDSTGVFK.E +3			6.2297																						
K.KVVITAPSSTAPM*FVM*GVNEEK.Y +2									5.9754			2.617	6.1637	5.9977	6.0665	5.9082		5.4693	5.972	5.1097					
K.KVVITAPSSTAPM*FVM*GVNEEK.Y +3		4.9762	4.697	4.8549					4.6553			3.5598	5.1057	5.1918	5.0654	4.3268	4.9348		4.203	4.7426					
K.KVVITAPSSTAPM*FVMGVNEEK.Y +2		5.3243											5.4146						2.6909	5.2503					
K.KVVITAPSSTAPM*FVMGVNEEK.Y +3		3.551	4.1012	3.6158											4.144										
K.KVVITAPSSTAPMFVM*GVNEEK.Y +2														5.2974	5.5351	5.4872	5.2059	2.7164		4.8803					
K.KVVITAPSSTAPMFVM*GVNEEK.Y +3	4.1354	5.4078							3.5129					5.0604	4.7147		3.7426			5.5935					
K.KVVITAPSSTAPMFVMGVNEEK.Y +2	5.2306	5.9756	5.5464																	5.6584					
K.KVVITAPSSTAPMFVMGVNEEK.Y +3	4.6473	5.1412	4.5956	4.2176																4.9878					
K.LVSWYDNEYGYSTR.V +2	4.5244	4.4775	4.476	4.6428	4.5224	4.7032	4.3903	4.5002	4.5277	4.4392	4.5254	4.4773	4.4005	4.2486	4.4405	4.2696	4.2531	4.3764	4.3397	4.3227	4.1083	4.1068	4.3614	4.3342	
K.VINDAFGIEEGLM*TTVHSLTATQK.T +2		4.3967		4.6677									3.9404	4.7955	4.4876	4.544			5.0202	3.7518					
K.VINDAFGIEEGLM*TTVHSLTATQK.T +3		5.5842		5.7798									5.2192	5.1453	5.3421	5.0614			5.3389	4.9018					
K.VINDAFGIEEGLMTTVHSLTATQK.T +2		5.7693	5.3259	5.3704																4.3572					
K.VINDAFGIEEGLMTTVHSLTATQK.T +3	4.5458	6.0358	5.5863	5.5016																					
K.VLPELQGK.L +1				2.0535				2.016							1.996		1.8059					1.8721			
K.VVITAPSSTAPM*FVM*GVNEEK.Y +2	4.3782	5.0786	5.0407	4.7681	4.5426	4.9726	4.8001	5.2583	4.5093	4.8672	5.0125	4.7631	4.9286	4.9627	4.499	4.8573	4.4176	4.0375	5.1496	5.0261	4.5876	4.6738	4.1814	4.6145	
K.VVITAPSSTAPM*FVM*GVNEEK.Y +3		3.8141				4.0886	4.1068	4.6011	4.4416	4.2319	4.1558	4.3222	4.6475	4.335	4.3777	4.1158		4.0664		4.1767		3.822			
K.VVITAPSSTAPMFVMGVNEEK.Y +2	5.0565	5.1659	5.1874	5.1275	5.1306	5.2997	4.9958	5.3656	4.1912	5.1654	5.0238	4.9851	4.206		3.9196	3.9978		4.5797	4.8169	5.3888	4.4953	3.0402		3.8704	
K.VVITAPSSTAPMFVMGVNEEK.Y +3	4.1215	4.0046					4.1046			4.3819		3.5275	3.6093	4.6344	4.8549	3.8024				4.7593		4.2615			
K.VVITAPSSTAPMFVM*GVNEEK.Y +2	4.4511	5.0299	4.6095	4.6384	4.2292	4.3637	4.8827	5.0091	5.03	3.6012	3.8534	4.4686		4.6742	4.9366	4.5229	4.4874	3.6444	3.6765	3.7111	4.7268	4.4374	5.1199	4.9589	
K.VVITAPSSTAPMFVM*GVNEEK.Y +3		4.4127		4.9621	4.7407	4.7454	4.7003	5.1788	4.8925	4.7451	4.6345	4.6001		4.6549	4.8153	5.0067	4.7931	4.5005		4.0843		3.5181		4.5893	
K.VVITAPSSTAPMFVMGVNEEK.Y +2	5.8465	5.8365	5.7724	5.3213	5.7547	5.6336	5.7178	5.7421	5.3155	5.2777	5.6068	5.0572		4.6963	4.9081	5.3584	4.7866	3.974	4.046	4.4081	5.1412	4.8005	4.923	4.5234	
K.VVITAPSSTAPMFVMGVNEEK.Y +3	5.2702	5.3832	5.7061	5.2737	5.2829	5.2936	5.2902	5.5039	5.1344	4.5423	5.2618	4.9306		4.669	5.423	5.1553		4.619		4.9214	3.9006	4.0763	4.0635		
R.DPANLPWGSSNVDIAIDSTGVFK.E +2	6.2531	6.6795	6.5868	6.38	6.4095	6.3271	6.4528	6.4127	6.7137	6.0984	6.429	6.1784	6.5701	6.1832	6.2152	6.1413	6.1329	5.6928	5.374	6.1389	6.1199	3.9695	4.7921	5.8858	
R.DPANLPWGSSNVDIAIDSTGVFK.E +3		4.3107	5.9356	6.0095	6.1611	5.974	5.955	6.085	6.022	4.5148	5.7288	5.9962	5.8902	5.6953	5.6122	5.7812	4.6996	4.8316	5.3383	5.0658		5.1267	5.2785	5.4529	
R.IALSRPNVEVVALNDPFITNDYAAYM*FK.Y +3		8.118	6.0311	7.6966									6.8567	6.7122	6.9147	7.6842			8.1652	5.8972					
R.IALSRPNVEVVALNDPFITNDYAAYMFK.Y +3		7.7082	7.5146	6.5487															5.059	7.3889					
R.PNVEVVALNDPFITNDYAAYM*FK.Y +2					5.9972	5.8752	6.2206	6.1468	6.0865	5.9181	5.7424	5.8931	6.0908	5.9256	6.0166	6.117			5.1088	5.1924	5.2979			5.7433	
R.PNVEVVALNDPFITNDYAAYM*FK.Y +3				5.059	7.3046	6.6087	6.9642	7.0578	6.5579	6.3058	6.2759	6.707	6.8227	7.3846	6.9345	6.5399		4.2042	6.0054	5.6824			6.1527		
R.PNVEVVALNDPFITNDYAAYMFK.Y +2		5.4962	5.7011		5.9268	5.9045	5.7825	5.8958	5.7452	5.4027	5.283	5.8803		5.3879	5.5313	5.58	4.9771	3.3637		5.2365			4.8933		
R.PNVEVVALNDPFITNDYAAYMFK.Y +3		6.5205	6.8398	6.6477	7.004	6.5315	7.0697	6.7808	7.0012	6.0928	6.3054	6.4469	4.3435	4.802	6.4126	6.1399	5.0256	3.5335		6.5396				6.3286	
R.TASGNIIPSSTGAAK.A +1	3.5197	3.3582	3.5211		3.1769	3.2293	3.5021	3.279	3.3946	2.8535	2.9998	3.1171	3.3366	3.1662	3.2624	2.7976	2.9028	3.2802	3.1224	3.0539	2.3978	2.9054			3.1785
R.TASGNIIPSSTGAAK.A +2	4.2985	4.1316	4.2183	3.9346	4.3615	4.2909	4.41	4.3666	4.3393	3.9976	4.2161	3.8733	3.1787	3.9328		4.2441					3.9644	3.912	4.3301	3.4692	
R.VAINGFGR.I +2	2.6601	2.592	2.6338	2.5292	2.5508	2.6116	2.5603	2.6338		2.5602					2.5975	2.5466	2.5055							2.5162	
R.VPTVDVSVVDLTVK.L +1			3.7441					3.3452	3.8582			3.5243	3.3285	3.6905	3.463	3.2615	3.0996	1.8026		3.4942					
R.VPTVDVSVVDLTVK.L +2	4.713	4.8316	4.7901	4.9685	4.8753	4.9145	4.6912	4.823	4.7057	4.4205	4.9024	4.6229	4.7104	4.7069	4.7409	4.852	4.4896	4.6465	4.6663	4.5917	4.4193	3.6465	5.057	3.7581	
R.VVDLVEHVAK.A +1		2.373	2.3364	2.3509	2.6218		2.3823	2.6106	2.5481	1.8535	2.3683	2.1962	2.4979	2.3318	2.4185	2.5234	2.1966	2.5292	2.4041	2.642	2.504	2.4429	2.1068		
R.VVDLVEHVAK.A +2	3.6796	3.7311	3.6379	3.8208	3.669	3.566	3.6211	3.671	3.5699	3.5893	3.622	3.5334	3.5462	3.7376	3.5686	3.639	3.7711	3.5554	3.649	3.2974	3.7124	2.6821	3.3847	3.361	
R.VVDLVEHVAKA.- +1																	2.2498	2.4083	2.0531	2.1893					
R.VVDLVEHVAKA.- +2	4.2741	4.5105	4.4622	4.5326									3.3249				4.0484	3.9482	3.2899						
R.YAGEVSHDDK.H +1											2.3038			2.0956	2.1901					2.7044					
R.YAGEVSHDDK.H +2	3.278	3.4984	3.3495	3.4914	2.7798	3.0447	3.3102	3.0864	3.0089	3.1353	3.0713	2.7195	3.0967	2.9244	2.5906	2.9727			3.0972		2.9078	3.2038	3.1013	2.562	
R.YAGEVSHDDKHIIVDGK.K +2											3.1626		4.3221	4.3936											
gi|6321648|ref|NP_011725.1|	47.1	47.1	58.7	47.1	45.2	45.2	58.7	58.7	58.7	58.7	58.7	58.7	52.9	58.7	35.6	35.6	35.6	24	26	35.6	24	35.6	21.2	47.1	Cytoplasmic thioredoxin isoenzyme of the thioredoxin system which protects cells against both oxidative and reductive stress, forms LMA1 complex with Pbi2p, acts as a cofactor for Tsa1p, required for ER-Golgi transport and vacuole inheritance; Trx2p [Saccharomyces cerevisiae]
K.AEVSSMPTLIFYK.G +2						3.2901			3.6567	3.454	3.0469	3.5158	4.0969	4.2652	3.9764	3.8506				3.7936				3.211	
K.AEVSSMPTLIFYK.G +2	3.7892	4.1855	4.2007	4.132	4.1974	4.4143	4.143	4.1204	3.7663	3.7345	3.9487	3.6859	3.6875	4.2207	4.1101	4.1486	2.8207	3.9321		3.9226	3.8239	4.0479		3.2081	
K.FAEQYSDAAFYK.L +1						2.4164			3.2216		1.9594													2.872	
K.FAEQYSDAAFYK.L +2					4.4374	4.3718	4.6228	4.641	4.208	4.3802	4.3158	4.3124	4.2289	4.5551	4.273	4.3521		4.0154					4.439	4.1575	4.1957	
K.FAEQYSDAAFYKLDVDEVSDVAQK.A +3			5.5902																	4.5005					
K.LDVDEVSDVAQK.A +2	4.4835	4.7101		4.7172	4.7407	4.4945	4.7761	4.5678	4.5103	4.5496	4.772	4.4911	4.4212	4.514	4.4164	4.5895			4.3023		3.5628	3.229			
K.LVVVDFFATWCGPCK.M +2																			2.564						
K.MIAPMIEK.F +1													2.0356												
K.SASEYDSALASGDK.L +1																	1.8002							1.9693	
K.SASEYDSALASGDK.L +2	4.8307	4.8633	4.7984	4.4856			4.8919	4.6062	4.7461	3.9931	4.5619	4.5326		4.4887			4.1892							3.2819	
R.VVGANPAAIK.Q +1													1.9488												
R.VVGANPAAIK.Q +2	3.2534	3.1977	3.1434	3.2061	3.0875	3.1794	3.2082	3.1427	3.0458	3.0275	3.0522	2.7833		3.1645			3.0071						2.7588	2.7562	
gi|6321679|ref|NP_011756.1| - MQSQDSCYGVAFR.S +2	7.3	13.9	18	11.8	22.8	27.9	29.1	34.7	33.8	21.8	30.1	33.3	34.5	35.8	34.1	38.5	34.1	30	25.8	35.6	25.9	15.3	24.5	25.8	Alpha subunit of heteroocttameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk1p [Saccharomyces cerevisiae]
K.AVLEFTPETPSPLIGILENK.I +2	5.7145	5.7933	5.8428	5.7265	5.5066	5.6264	5.5105	5.7455	5.1919	2.9825	5.1304	5.4017	5.3751	5.5844	5.5856	5.4945	4.9679	2.8144	5.0923	4.4742	2.6387		4.8032	5.5001	
K.AVLEFTPETPSPLIGILENK.I +3												3.7368	6.1931	5.9126	5.7477	5.6399			5.4539						
K.DAFLEATSEDEIISR.A +2			5.1628		5.1114	5.4827	5.302	5.192	5.2853	3.7488	4.8228	5.2418	5.3347	5.3887	5.395	5.3221	5.482	5.3784	4.7577	5.3379	4.6208	5.2401	5.1694	5.0676	
K.DALIELGLDTK.V +1																		2.9832		2.4795	2.5486			2.0374	
K.DALIELGLDTK.V +2						2.2664	4.1265	4.0391	4.1365	3.247	3.0116	4.0755	4.1685	4.064	4.3422	4.0115	4.104	3.602	3.9015	4.0631	4.3696	4.3758	4.1742	4.1492	
K.DDGSELLPVSDR.L +2							4.509	4.4048	4.1362	3.8869	2.9375	4.0632	3.7126			2.7964				3.8601		3.2935		3.9651	
K.DPM*GNNITFSGLANATDSAPTSK.D +2											4.5279				5.8031	3.6486		5.171	5.9627	6.0543	6.0608		4.3973	4.9643	
K.DPMGNNITFSGLANATDSAPTSK.D +2					5.6088	6.3115	6.213	5.8422	5.8808		4.8601					5.9996	5.8982	4.8903		5.4307	6.4304		5.5155	5.5985	
K.EEVAPYK.N +1																2.087									
K.ELSWIDVENWHNLGGSEIGTNR.S +2														4.608						4.1282					
K.ELSWIDVENWHNLGGSEIGTNR.S +3																				3.7355					
K.GFEVHWAEYNK.I +1															2.0398										
K.GFEVHWAEYNK.I +2													3.5706		3.5936	3.126				4.0841					
K.HGENSLLSSGTSQDSLR.E +2								5.4023			3.4773		4.1406			3.6341	4.6383	4.8211	5.22	4.5794			5.2785		
K.HGENSLLSSGTSQDSLR.E +3														3.7836											
K.IAVMTSGGDSPGM*NAAVR.A +2																					5.2631	2.9012			
K.IAVMTSGGDSPGMNAAVR.A +2					5.8878	6.0229	6.0956	5.7536	5.9174	4.9545	5.8094	5.8065	5.8239	5.8142	5.9095	5.4934	5.7801	5.8578			5.9137	5.8548	5.9186	5.6063	
K.IGDILSGR.L +2					3.2797	3.2338	3.3121	3.1571	3.2459	3.2386	3.1016	3.3244	3.1023	3.1796	3.1458	3.0315		3.0432	2.8427	3.0435				3.1952	
K.KIDLASIR.E +2				2.8636																					
K.LDGLILGGFEGFR.S +2						4.6567		4.5934	4.8432			4.4063	5.288	4.6695	4.9456	5.1589			4.2993	3.412				4.0975	
K.LRAEVAALAAENK.- +2			3.9779	3.5244									3.6029				3.5848			3.7315					
K.LSDTLVFLK.D +1		2.4266							2.2451			2.4108	2.1223	2.4143	2.3767	2.191					2.3662		2.2356	2.401	
K.LSDTLVFLK.D +2		3.2253	3.4573									3.2098	3.0793	3.3234	3.2677	3.3971	3.2778	2.8674			3.2371	3.2616	3.2672		
K.LSEVDASGFR.I +1																			2.3919						
K.LSEVDASGFR.I +2					2.9408	2.9206				2.7475	2.8584	3.2331	3.0894		2.66			3.2644			3.3943	3.279			
K.NLSIVGLVGSIDNDMSGTDSTIGAYSALER.I +2							2.5024																		
K.PIANLWENETNVELR.K +2												4.1815				3.8456					3.6264				
K.PYAIMNGFSGLIQTGEVK.E +2																	2.6247			4.0443					
K.VPTVEHEDDSAAVICVNGSHVSFK.P +2																	2.8036								
K.VPTVEHEDDSAAVICVNGSHVSFK.P +3																			3.7477						
K.VTILGHVQR.G +2		3.072	3.0998	3.291												2.9037		3.0816		2.5332			2.7497		
R.AATLYCLSHGHK.P +2																				3.179					
R.AEVAALAAENK.- +1								2.9154					3.1026		2.9347	2.6653			2.4123		2.7857	3.19	3.0105		
R.AEVAALAAENK.- +2					4.5189	4.4534	4.3572	4.2106	4.3335	4.364	4.4589	4.2769	2.7108	4.3344	4.2686	3.6353				4.0997				3.7618	
R.AFVVEVMGR.H +2						3.1308			2.9205			3.1005	2.8804	3.0599	3.1051	3.0222					3.2335				
R.AFVVEVMGR.H +1													2.8378	2.6269	2.9608	2.7631		2.2896			2.6313				
R.AFVVEVMGR.H +2			3.6628				3.6418		3.3166		3.1506	3.3418	3.5733	3.768	3.8638	3.6637	3.4288	3.6995		3.4586	3.5595				
R.ASSDASDDLLR.Q +1																	1.808								
R.ASSDASDDLLR.Q +2	3.1316	3.2009		3.3298			2.9454	3.0016	2.8824	2.5019	2.8378	2.8013	3.3589			2.9672		3.4233							
R.DTEFIELYENFLSTTVK.D +2					5.2375	5.4126		4.541	5.2159			4.696	3.4638	4.1683	2.5158	5.2102							2.5545		
R.DTEFIELYENFLSTTVK.D +3													3.5344												
R.EVWLESFK.L +1		2.6177	2.9315			2.9321		2.6023	2.6406				2.7008	2.78	2.3434	2.6525			2.2921	2.4312		2.2124	2.0068	2.1383	
R.FTKEEVAPYK.N +2				2.3613														2.942							
R.GWLSEGGTLIGTAR.S +2	3.2364		4.7214	4.5067			4.8256	3.825	4.6595		4.3026	4.0017	4.1612		4.7842	3.7233	4.0851								
R.HEWPSLVDELVAEGR.F +2		3.5316	2.9124										3.5296	3.1586											
R.HEWPSLVDELVAEGR.F +3														4.1666											
R.ICEM*VDYIDATAK.S +2										4.2121										3.6575	3.7314	4.3001			
R.ICEMVDYIDATAK.S +2					5.1992	4.8721	4.999	4.6585	4.7372	3.7621	4.5106	4.3635		4.1643	3.5869	4.2628	3.8217	4.6195			4.8817		5.2172	4.6926	
R.IPQQEATNK.A +2																					2.8626	2.6042			

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.KGFEVHWAEYNK.I +2														3.7644											
R.LNIGIVHVGAPSAALNAATR.A +2															3.3344				2.5965						
R.LNIGIVHVGAPSAALNAATR.A +3														5.0712	4.3728				5.3003						
R.MPLVESVK.L +1							1.9084		2.1812		2.2322		1.9952		1.982	2.0372	1.9752				2.0955			2.3579	
R.MPLVESVK.L +2												2.5709	2.5055												
R.NEQASSVYSTQLLADIISEASK.G +2		6.3612	6.4011		6.1174	6.8482	6.6092	6.4568	5.87	3.3447	5.2407	6.025	6.3768	6.3586	6.0795	6.4837	4.628	3.7376	5.2815	5.9099			3.7147	5.1475	
R.NEQASSVYSTQLLADIISEASK.G +3									5.4044				5.2407	5.6343	5.5551	5.2722	3.5266		4.1605	5.0791	4.0611		3.9751		
R.NNTIIVAEGALDDQLNPVTANDVK.D +2						6.5115	5.8684	4.7927	6.0627	3.9588	5.3564	3.7135		6.1647	6.4936	6.2092	6.6165	6.5355	5.9625	5.3323	6.0703	6.2429	6.3433	4.7854	
R.NNTIIVAEGALDDQLNPVTANDVK.D +3													6.1777	6.3366	6.0729			5.2331		4.2906			3.5778		
R.QAAGNLISQGIDALVVCGGDGSLTGADLFR.H +2								2.8157												2.7766					
R.QAAGNLISQGIDALVVCGGDGSLTGADLFR.H +3												4.251								4.0074					
R.SIITNDEALFK.K +2					3.5277	3.7913	3.8134	3.6889	3.7198		3.4472	3.4005	3.7523	3.8838	3.7315	3.6693	3.3857	3.4898			3.4649	3.4271		3.2221	
R.SIITNDEALFKK.T +2																	2.963			3.0601					
R.SVASEDLGTIAYYFQK.N +2		5.6076	5.6683	5.5163	5.6109	5.6429	5.577	5.7838	4.9809		5.061	4.9384	5.1637	4.5762	4.8842	4.9819	4.036	2.5469	4.6169	5.0893	5.1269			4.7595	
R.SVASEDLGTIAYYFQK.N +3													4.1473	4.0449	3.8823										
R.TAIPGHVQQGGVPSSK.D +2	3.0498	3.2627	3.3078	3.221	3.0472			3.3913	3.0903	3.2417			3.0068	3.204		3.311	2.843	2.5551							
R.WLATLQGVDAVK.A +2	3.8941	3.7791	4.3503		4.186	3.9839	4.041	4.0107	4.0294	3.2285	4.2141	4.0233		3.4959	3.9914	2.9973	4.0183	4.0047	3.4916	2.8864	3.0459		3.5681	3.5192	
gi|6321693|ref|NP_011770.1|	36.8	42.1	42.1	49.2	38.4	34.8	38.4	38.4	40.5	23.3	40.5	38.4	51	63.2	61.1	55.6	43.5	42.1	40.7	47.4	23.3	20.6	14.9	34.1	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose; Eno1p [Saccharomyces cerevisiae]
K.AADALLLK.V +1	2.2961	2.2641	2.2447	2.2434	2.235	2.1675	2.255	2.2935	2.1937	2.2606	2.2005	2.3306	1.9997	2.1089			2.4108	2.1036				2.2458			
K.AADALLLK.V +2	3.5145	3.3259	3.4272	3.3027	3.2814	3.2905	3.3537	3.3206	3.1553	3.387	3.3377	3.1374	3.1036	3.1505	3.2266	2.7469	3.2206	3.247		3.4084	2.9966		3.2619	3.1288	
K.AAQDSFAAGWGVM*VSHR.S +2													4.0593	4.2778	3.7214					3.3931					
K.AAQDSFAAGWGVMVSHR.S +2																				5.0673					
K.DGKYDLDFK.N +1									2.3771				2.0087	2.4861			2.3945	2.3978	2.4049	2.4697					
K.DGKYDLDFK.N +2	2.824	2.8359	2.8705	2.7717							2.5683		2.6899	2.6605		2.5761				2.5308					
K.HLADLSK.S +1		2.6378											2.5236	2.4928	2.6444	2.585	2.6575								
K.IGLDCASSEFFK.D +1			3.4166		3.4151	3.2158	3.3938	3.3243	3.4127	3.2462	3.0793	2.6695	3.3417	3.2083	3.4047	3.3419	2.6311	2.6015	3.045	2.8788	3.1624	3.0473	2.7319	2.94	
K.IGLDCASSEFFK.D +2	4.1526	4.145	4.1259	4.3198	4.1308	4.1785	4.236	4.1881	4.1003	4.1125	4.114	4.1513	4.0829	4.1217	4.1063	4.0091	4.0543	3.934	4.1145	3.9551	3.857	2.5652	3.987	3.8502	
K.KAADALLLK.V +1								2.3569	2.4951		2.1721	2.1379	2.48	2.8033	2.496	2.6221					2.488	2.6709	2.5778		
K.KAADALLLK.V +2					3.1236		3.2928	3.3983	3.1952	3.486	3.1263	3.3382	3.0472	3.0336	3.0381	3.3174		2.8517			3.3237		2.8303		
K.LGANAILGVSLAASR.A +2		3.4574			4.2225		3.9409	4.4233	4.3826		3.192	3.9332	4.3297	4.7114	4.4839	4.5461			4.0175					3.5517	
K.NVNDVIAPAFVK.A +1						2.7536			2.8347		2.3363		2.8005			2.5537			2.6322	2.8363					
K.NVNDVIAPAFVK.A +2	4.1684	3.5973	4.0813	4.0193	4.3423	4.2182	4.3947	4.3635	4.2231	4.3123	4.2908	4.0942	3.678	4.0945	4.1982	4.0953	4.0096	3.7029		3.6939	4.423			3.5693	
K.RIATAIEK.K +2				2.503																					
K.RYGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A +3		6.6491	6.0429	6.9936																3.995					
K.TAGIQIVADDLTVTNPK.R +2	4.9024	5.3961	5.7621	5.8044	5.2235	5.584	6.0321	5.3832	5.3755	5.5208	5.9393	4.9916	4.1208	5.4329	5.5652	5.3339	5.1045	5.9944	5.4356	3.9984	4.9611	3.2685	5.4758	4.5708	
K.TAGIQIVADDLTVTNPK.R +3														4.1789											
K.TSPYVLPVPFLNVLNGGSHAGGALALQEFM*IAPTGAK.T +3														3.8355	4.54	4.2219									
K.VNQIGTLSESIK.A +1		2.4219	2.3533		2.4254	2.4919	2.3745	2.2321	2.2187	2.0745	2.2886	2.5126	2.2404		2.4156	2.3881	2.3105			2.3035					
K.VNQIGTLSESIK.A +2	3.8482	3.8513	3.7797	3.9342	3.8793	3.8405	3.8749	3.8912	3.8163	3.8339	3.846	3.8919	3.8651	3.6699	3.8331	3.9997	3.4311	3.1043		3.7894	3.2483	3.3102		3.7525	
K.WLTGPQLADLYHSLM*K.R +2														3.1869	2.5965					2.9825					
R.GNPTVEVELTTEK.G +1		2.4873	2.5622		2.79	2.745	2.6572	2.6466	2.9677		2.6187	2.7718	2.796	2.6679	2.8232	2.8053	2.7797	2.8175	2.7644	2.8917	2.478	2.6141			
R.GNPTVEVELTTEK.G +2	4.3764	4.4955	4.3096	4.3486	4.335	4.0803	3.8046	3.8746	4.1212	4.2465	4.0494	3.9527	4.2142	4.1658	3.8232	4.0557	3.9594	3.6861	4.1994	3.2817	3.7234	3.7686		3.596	
R.IEEELGDNAVFAGENFHHGDK.L +2													4.166	4.0743											
R.IEEELGDNAVFAGENFHHGDKL.- +2													4.7184	4.906			5.1327	2.6455	4.1395	4.834					
R.IEEELGDNAVFAGENFHHGDKL.- +3			3.724	4.5905									4.3657	4.6065	3.5008	3.7193			4.6688						
R.IGSEVYHNLK.S +1						2.4516			1.8249						2.3423	2.3364	2.2044	2.4164							
R.IGSEVYHNLK.S +2	4.0481	3.9568	4.0104	3.8664	3.9031	3.9696	4.0295	4.0296	3.6602	3.7877	3.8279	3.951	3.6593	3.9781	3.7265	3.823	3.9467	3.982	2.8747		3.7045	2.812	3.6645	3.5583	
R.SGETEDTFIADLVVGLR.T +2	6.6199	6.5835	6.8861	6.4084	6.5942	6.5817	6.6476	6.5879	6.4854	5.0753	6.3922	6.449	6.5028	6.1885	6.3796	6.3771	6.1182	4.5486	6.3628	6.4381	5.7119	4.3967	5.4924	5.1638	
R.SGETEDTFIADLVVGLR.T +3			3.8845	3.6546	3.9129	3.9121	4.3123	4.2508	4.1404		3.6806	4.2068	4.4362	4.2558	4.156	4.232			4.331						
R.SIVPSGASTGVHEALEM*R.D +2		5.1969	4.7774	5.7989	5.5995	5.4132	5.1208	5.3061	4.658		5.2313	4.883	5.4723	5.0274	4.8	5.4947	4.9341	4.2757	5.0768	5.1255					
R.SIVPSGASTGVHEALEMR.D +2	5.3661	5.439	5.4533	5.2833				5.1945	5.2119			4.803	4.8649	4.7999	4.7385	4.6842	3.6868	4.7686	4.0364	4.9801					
R.YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A +3	6.7325	6.8201	6.8161	6.4823	6.9334	6.5574	6.661	6.7298	6.7354		6.6229	6.183	5.6199	4.9649	5.7005	6.4249	5.379	4.7989	5.4375	5.7555				3.8318	
R.YPIVSIEDPFAEDDWEAWSHFFK.T +3				6.593																					
gi|6321754|ref|NP_011830.1|	21.1	30.5	30.1	25.8	33.6	28.5	30.9	39.5	37.9	25.8	26.6	44.9	50	50	53.9	47.7	27.7	31.6	24.2	53.9	12.1	8.6	14.1	25.8	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Bp and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits; Rpl8ap [Saccharomyces cerevisiae]
K.EAAAVAEGK.S +1												2.5178						1.8531	2.312	2.1837					
K.HWGGGILGNK.A +1															2.4924					3.2529					
K.HWGGGILGNK.A +2		2.748	2.7802														2.5666								
K.ILSIRLKVPPTIAQFQYTLDR.N +3					3.5082																				
K.KM*GVPYAIVK.G +2																				2.7158					
K.KVAPAPFGAK.S +1																	2.0084								
K.KVAPAPFGAK.S +2		2.5035																							
K.LVLIANDVDPIELVVFLPALCK.K +2					3.5303	3.2995	4.0279	3.1397	3.9437			4.6431	4.7261	4.5576	4.1735	4.9294				4.8859					
K.LVLIANDVDPIELVVFLPALCK.K +3													4.6567	4.0179	3.8394										
K.LVSTIDANFADK.Y +2					3.9883	4.1409	3.5805	3.5753	3.5851	3.4912	3.4287	3.0962	3.6069	4.0065	3.0238	4.1479	4.1164	3.6421		3.7756				2.9324	
K.LVSTIDANFADKYDEVKK.K +2									4.4604		3.2103	3.2266	4.7804	4.7651	5.0222	4.8532	4.0116			3.2191					
K.LVSTIDANFADKYDEVKK.H +2													4.5853	4.2174	3.1378		4.301	4.6775		3.7554					
K.NFGIGQAVQPK.R +2	3.2101	4.0308	3.8527	4.21	4.173	4.0284	3.8155	3.9586	3.7866	3.6557	3.7831	3.8961	3.842	3.881	3.7472	3.4892		3.7516						3.6648	
K.QDASPKPYAVK.Y +2		2.5818	2.8745					2.6556			2.9442		2.8645			2.7236									
K.SKQDASPKPYAVK.Y +2		3.5932	4.1878	4.2378				4.0673	3.578			2.5571	3.5289	3.7102	3.5738	4.054	3.518		4.151	2.8037	3.2465	3.3259	3.3686		
K.TSAVAALTEVR.A +1									2.1888				2.3187	2.1901	2.2389	2.2965		2.5558						1.8254	
K.TSAVAALTEVR.A +2	4.5129	4.712	4.5009	4.7157	4.5869	4.626	4.7133	4.5811	4.4248	4.6592	4.5581	4.5638		4.2737	4.5065	4.625	3.0935	4.3446						4.2684	
K.TSAVAALTEVRAEDEAALAK.L +2																				3.2681					
K.VPPTIAQFQYTLDR.N +2	4.746	4.7216	4.8295	4.8178	4.7767		4.6106	4.7979	4.6467	4.3717		4.8213	4.6126	5.0065	4.2455	4.3981		4.3227	3.0002	3.5746			4.5953	4.3665	
K.VPPTIAQFQYTLDR.N +3													5.1637	5.0968	4.8955	4.6155			4.1457						
K.YGLNHVVALIENK.K +2													4.5921		3.209					3.9832					
K.YGLNHVVALIENK.K +3														4.0543											
R.AEDEAALAK.L +1	2.3897		2.4177					2.4416		2.3983	2.4839	2.0942	2.5071	2.4214	2.1716	2.2513		2.5271	2.4052		2.3288		2.4248	2.3389	
R.AEDEAALAK.L +2											2.7037														
R.LGTLVNQK.T +1						1.9344										2.1394									
R.LGTLVNQK.T +2				2.6044																					
R.NPLTHSTPK.N +1		2.4353			2.7162	2.4267	2.6071	2.4341	2.3281				2.277	2.402	2.3944	2.208		2.6069				2.1696		1.8047	
R.NPLTHSTPK.N +2	3.3641	3.5803	3.4624	3.4102	3.4987	3.5944	3.2486	3.5518	3.4664	2.9903	3.2814	3.1439	2.9222	3.1049		2.6918	3.5264		3.0141	2.5734	2.9995				
R.NTAAETFK.L +1													2.3264	1.9864	2.0429	1.9443			1.8707						
gi|6321772|ref|NP_011848.1|	27.3	32.2	30.6	19.8	45.5	45.5	45.5	38	45.5	38	38	45.5	39.7	45.5	38	61.2	19	28.1	30.6	29.8	22.3	38	16.5	43	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins; Rps20p [Saccharomyces cerevisiae]
K.EKVEEQEQQQQQIIK.I +2		5.4667	5.4059		2.9196	3.0892	3.6919	5.1113	3.7558	4.2062	4.3986	4.4572	5.2883	5.4081	5.2399	5.6322	4.8548	4.0163	5.4179	5.373	3.1433	5.2724			
K.EKVEEQEQQQQQIIK.I +3														4.3723											
K.NAEQHNLVK.K +2	3.0617		2.6467		3.0656	3.2085	3.0225		2.7657			2.9612		3.0965		2.5544			3.0141						
K.QLENVSSNIVK.N +2	3.4117	2.8816		2.7431	3.2703	3.053	3.0669	2.8175	2.8872	2.9031	3.2035	3.1764		3.1333	3.1604	2.6253		3.0741		2.7355					
K.RYIDLEAPVQIVK.R +2	3.406	3.3564	4.0684	3.8055															2.6052	3.3658					
K.TWETYEM*R.I +2													2.8867	2.5277											
K.TWETYEMR.I +1																	2.2453	1.9272		2.1957					
K.TWETYEMR.I +2					3.0715	2.8602	3.0951	2.9997	3.0181	2.8458	2.8426	2.7898	2.8394	2.9898	2.8635	2.8419	2.9288	3.0831				3.1634	2.5617	2.6783	
K.VEEQEQQQQQIIK.I +2		5.0861	4.8147		5.3183	5.4651	5.3035	5.2674	5.0546	5.1953	5.1173	5.3104	5.184	5.2242	5.2323	5.3168		5.0708	5.2259	5.2202		2.8675		5.2332	
K.VKQLENVSSNIVK.N +2													2.8356												
R.ITQITIEPGVDVEVVVASN.- +2																2.7038								2.6953	
R.YIDLEAPVQIVK.R +1									3.0065				2.989			2.4862					2.1609				
R.YIDLEAPVQIVK.R +2	3.9503	4.009	3.9641	4.1261	4.0623	4.0649	4.2211	4.1506	3.9274	4.1754	4.2997	4.1421	3.9214	3.4049	3.9816	4.0626				3.8654	3.2315	3.7413	3.3526	3.8758	
gi|6321968|ref|NP_012044.1|	48.7	57.4	49.9	58.8	46.9	49.2	49.7	49.7	52.6	38.7	50.3	48.1	59.3	64.8	64.8	64.8	50.1	52.2	51	53.5	33.2	32	30.7	43.5	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose; Eno2p [Saccharomyces cerevisiae]
K.AADALLLK.V +1	2.2961	2.2641	2.2447	2.2434	2.235	2.1675	2.255	2.2935	2.1937	2.2606	2.2005	2.3306	1.9997	2.1089			2.4108	2.1036				2.2458			
K.AADALLLK.V +2	3.5145	3.3259	3.4272	3.3027	3.2814	3.2905	3.3537	3.3206	3.1553	3.387	3.3377	3.1374	3.1036	3.1505	3.2266	2.7469	3.2206	3.247		3.4084	2.9966		3.2619	3.1288	
K.AAQDSFAANWGVM*VSHR.S +2		4.7142							3.5661				5.1413	4.995	4.5621	3.3067	3.0224		3.4852	3.249					
K.AAQDSFAANWGVMVSHR.S +2		5.492												5.1456	4.1894			4.2473	5.0078	4.5789					
K.AVYAGENFHHGDK.L +1													2.6546	3.0093											
K.AVYAGENFHHGDK.L +2			4.2569	4.4865	4.336	3.6125		4.1553	4.4543	3.7081	4.0991	4.5101	4.4406	4.0507	4.1794	4.1257	3.8773	3.6432		4.4024		3.8342	3.4078		
K.AVYAGENFHHGDKL.- +1													3.1952	3.2056		2.4174	3.2435	3.1893		3.2222		2.4177			
K.AVYAGENFHHGDKL.- +2	4.6464	4.8846	4.626	4.5194	4.5616		4.5383	4.9505	4.3207	4.3865	4.589	4.4285	4.5918	4.4498	4.3067	4.4011	4.2242	4.407	4.4842	3.7817		3.3651	4.0855		
K.DGKYDLDFK.N +1									2.3771				2.0087	2.4861			2.3945	2.3978	2.4049	2.4697					
K.DGKYDLDFK.N +2	2.824	2.8359	2.8705	2.7717							2.5683		2.6899	2.6605		2.5761				2.5308					
K.DGKYDLDFKNPESDK.S +2										2.9478			5.1387	5.1394	3.9797	4.4717									
K.GVM*NAVNNVNNVIAAAFVK.A +2	5.9179	6.049	5.3457	5.7383	6.1282	5.9061	6.0342	6.0128	5.9439	4.4298	5.7583	5.8502	5.7025	5.6302	5.4808	5.5084	5.2561	5.1861	5.7988	5.8468	3.1967		2.6009	5.733	
K.GVM*NAVNNVNNVIAAAFVK.A +3					4.0886			4.1266	4.6539		4.497	5.1482	5.5576	6.0564	5.6636			4.0277	4.0027	4.9282					
K.GVMNAVNNVNNVIAAAFVK.A +2	5.683	5.8065	5.9109	5.3116	5.6343	5.6445	5.4795	5.6884	5.7236		3.4598	4.9287		4.5885	5.164	4.842	5.1863	4.8573	5.1509	5.4172	2.8759		2.7521	2.955	
K.GVMNAVNNVNNVIAAAFVK.A +3		5.7922	5.307	6.0258		3.6376	4.8561		4.0115									5.4951		5.7952					
K.IGLDCASSEFFK.D +1			3.4166		3.4151	3.2158	3.3938	3.3243	3.4127	3.2462	3.0793	2.6695	3.3417	3.2083	3.4047	3.3419	2.6311	2.6015	3.045	2.8788	3.1624	3.0473	2.7319	2.94	
K.IGLDCASSEFFK.D +2	4.1526	4.145	4.1259	4.3198	4.1308	4.1785	4.236	4.1881	4.1003	4.1125	4.114	4.1513	4.0829	4.1217	4.1063	4.0091	4.0543	3.934	4.1145	3.9551	3.857	2.5652	3.987	3.8502	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.KAADALLLK.V +1								2.3569	2.4951		2.1721	2.1379	2.48	2.8033	2.496	2.6221					2.488	2.6709	2.5778		
K.KAADALLLK.V +2					3.1236		3.2928	3.3983	3.1952	3.486	3.1263	3.3382	3.0472	3.0336	3.0381	3.3174		2.8517			3.3237		2.8303		
K.LGANAILGVSM*AAAR.A +2	4.5684	4.5534	4.579	4.6776	4.7343	4.6025	4.7257	4.7438	4.5746	4.6357	4.4831	4.5598	4.6077	4.4713	4.4437	4.5405	4.3158	4.2658	4.148	4.7779	3.683	4.4517	4.4143	4.6693	
K.LGANAILGVSM*AAAR.A +3										4.2257		4.7399	5.7173	5.5618	5.4797	5.6402		4.3652	4.9796						
K.LGANAILGVSMAAAR.A +1									2.005																
K.LGANAILGVSMAAAR.A +2	4.949	4.9629	5.0076	5.2043	4.9763	4.9993	5.3075	5.0722	5.1275	4.9075	4.5575	4.9315	4.6378	4.7797	4.626	4.6957	4.6406	4.9907	4.6625	4.7376	2.8364		4.6081	3.9582	
K.LGANAILGVSMAAAR.A +3													4.3865	4.6609				3.6671	4.6751	4.7258					
K.NVPLYQHLADLSK.S +2													2.6825												
K.RYGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A +3		6.6491	6.0429	6.9936																3.995					
K.TAGIQIVADDLTVTNPAR.I +2	6.5025	6.441	6.2723	6.2238	6.293	6.3046	6.2319	6.4187	6.2442	6.3141	6.168	6.0673	5.997	5.816	5.8072	6.1229	5.893	5.097	5.5695	5.3952	5.5396	5.2169	5.8857	5.9332	
K.TAGIQIVADDLTVTNPAR.I +3					4.4634	4.5368	4.8179	4.7591	4.6396	3.8247	4.4944	4.5623	4.9206	5.0072	4.7567	4.8901	3.5749	5.1218	4.1441	4.555				3.9319	
K.TFAEAMR.I +1	1.8066	2.0605	2.0871	2.0382	2.1214	2.0029	2.0892	1.9487		2.0513	2.0282														
K.TFAEAMR.I +2		2.5568								2.5484															
K.TSPYVLPVPFLNVLNGGSHAGGALALQEFM*IAPTGAK.T +3														3.8355	4.54	4.2219									
K.VNQIGTLSESIK.A +1		2.4219	2.3533		2.4254	2.4919	2.3745	2.2321	2.2187	2.0745	2.2886	2.5126	2.2404		2.4156	2.3881	2.3105			2.3035					
K.VNQIGTLSESIK.A +2	3.8482	3.8513	3.7797	3.9342	3.8793	3.8405	3.8749	3.8912	3.8163	3.8339	3.846	3.8919	3.8651	3.6699	3.8331	3.9997	3.4311	3.1043		3.7894	3.2483	3.3102		3.7525	
K.WLTGVELADM*YHSLM*K.R +2		4.5765											5.0628	4.9573	5.1153	2.972			4.8192	4.2339					
K.WLTGVELADM*YHSLMK.R +2																				3.6879					
K.WLTGVELADMYHSLM*K.R +2				4.6248															3.6965	5.4537					
K.WLTGVELADMYHSLMK.R +2		5.8214																		5.898					
K.YDLDFKNPESDK.S +1																							1.9353		
K.YDLDFKNPESDK.S +2						4.3486	4.2521	4.5711	3.8158	4.2227	4.439	3.9665	4.2186	4.2061	4.4041	4.2595					4.0245	3.8298	3.976	4.195	
R.GNPTVEVELTTEK.G +1		2.4873	2.5622		2.79	2.745	2.6572	2.6466	2.9677		2.6187	2.7718	2.796	2.6679	2.8232	2.8053	2.7797	2.8175	2.7644	2.8917	2.478	2.6141			
R.GNPTVEVELTTEK.G +2	4.3764	4.4955	4.3096	4.3486	4.335	4.0803	3.8046	3.8746	4.1212	4.2465	4.0494	3.9527	4.2142	4.1658	3.8232	4.0557	3.9594	3.6861	4.1994	3.2817	3.7234	3.7686		3.596	
R.IEEELGDK.A +1	2.5553	2.6396	2.6373	2.7123	2.6751	2.6871	2.5906	2.6749	2.6069	2.7668	2.5186	2.6095	2.5828	2.639	2.7818	2.5952		2.5037	2.5273	2.4591	2.3917	2.4922	2.5278	2.6203	
R.IEEELGDK.A +2	2.9465	3.1394	2.9864	3.0274	3.0925	3.0225	3.0521	2.9625	2.6856	2.6737	3.0022	2.922	2.8893			2.9098							2.8108		
R.IGSEVYHNLK.S +1						2.4516			1.8249						2.3423	2.3364	2.2044	2.4164							
R.IGSEVYHNLK.S +2	4.0481	3.9568	4.0104	3.8664	3.9031	3.9696	4.0295	4.0296	3.6602	3.7877	3.8279	3.951	3.6593	3.9781	3.7265	3.823	3.9467	3.982	2.8747		3.7045	2.812	3.6645	3.5583	
R.SGETEDTFIADLVVGLR.T +2	6.6199	6.5835	6.8861	6.4084	6.5942	6.5817	6.6476	6.5879	6.4854	5.0753	6.3922	6.449	6.5028	6.1885	6.3796	6.3771	6.1182	4.5486	6.3628	6.4381	5.7119	4.3967	5.4924	5.1638	
R.SGETEDTFIADLVVGLR.T +3			3.8845	3.6546	3.9129	3.9121	4.3123	4.2508	4.1404		3.6806	4.2068	4.4362	4.2558	4.156	4.232			4.331						
R.SIVPSGASTGVHEALEM*R.D +2		5.1969	4.7774	5.7989	5.5995	5.4132	5.1208	5.3061	4.658		5.2313	4.883	5.4723	5.0274	4.8	5.4947	4.9341	4.2757	5.0768	5.1255					
R.SIVPSGASTGVHEALEM*RDEDK.S +2																				3.3686					
R.SIVPSGASTGVHEALEMR.D +2	5.3661	5.439	5.4533	5.2833				5.1945	5.2119			4.803	4.8649	4.7999	4.7385	4.6842	3.6868	4.7686	4.0364	4.9801					
R.SIVPSGASTGVHEALEMRDEDK.S +2		5.3597	5.6952	4.9267													4.9655	3.5262	3.5876	3.6737					
R.YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A +3	6.7325	6.8201	6.8161	6.4823	6.9334	6.5574	6.661	6.7298	6.7354		6.6229	6.183	5.6199	4.9649	5.7005	6.4249	5.379	4.7989	5.4375	5.7555				3.8318	
R.YPIVSIEDPFAEDDWEAWSHFFK.T +3				6.593																					
gi|6321973|ref|NP_012049.1|	11.8	34.2	17	14.8	28.2	26.5	21.2	31.5	27.8	21.2	23.8	32.8	32	46	38.2	33	21.2	15	32.5	34.8	14.2	15.8	18.5	22.8	Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism; Oye2p [Saccharomyces cerevisiae]
K.ANNPQHSITK.D +2										2.8255	3.0155	3.3373	2.8567		3.075	2.9747		2.6822			2.8294				
K.ANNPQHSITKDEIK.Q +2								2.6262					3.2912					3.9117	3.5435						
K.DFKPQALGDTNLFKPIK.I +2														3.9577											
K.DFKPQALGDTNLFKPIK.I +3																				3.7714					
K.IGNNELLHR.A +1															1.805		1.8899								
K.IGNNELLHR.A +2		2.7909	2.8132	2.9777					2.7179			2.5599		2.8378	2.626	2.5505				2.8367					
K.KANNPQHSITK.D +2					2.5267	2.5667							2.609												
K.M*SAEGYIDYPTYEEALK.L +2								4.5954	4.326	4.8987	3.9587	5.0885	5.4542	5.1142	5.8859	3.1205			4.0349		5.3738	2.8961		4.5316	
K.MSAEGYIDYPTYEEALK.L +2		4.7526			4.7727	4.7038	5.0062	4.8739	4.8751	3.8622	4.4655	4.5396			4.445	4.773	4.415	2.7981		4.0146	4.6213	4.6518	4.4736	4.7273	
R.AGNFALHPEVVR.E +1															2.6531										
R.AGNFALHPEVVR.E +2		3.8674	3.6701	3.1441									3.4156	3.5197	3.7455	3.923	3.0126		3.5637	3.0532					
R.AQHPGNIPNR.D +2						2.537		2.7424				2.6352		2.5533	2.6493										
R.AQRPGTLIITEGTFPSPQSGGYDNAPGIWSEEQIK.E +3		5.2135												5.8951					3.609	5.5688					
R.DWAVEYYAQR.A +2				3.7133	3.9144	3.7576	3.8233	3.9518	3.868		3.7533	3.8779	2.9046	3.5432	3.5081	3.7569			3.3685			3.3452	2.9965	2.6962	
R.FFISNPDLVDR.L +2					3.7802	4.0252	3.8483	4.1182	3.4302	3.6963	4.0141	3.6165		3.5409	3.1941	3.7772	2.6413			3.2528	2.7754		3.3596	3.8043	
R.FFISNPDLVDRLEK.G +2																			3.4054						
R.FTLEVVDAVVDAIGPEK.V +2	4.2441	5.2449			5.1045	5.6905	5.0621	4.6918	5.1492			5.3349	5.7722	5.5838	5.1755	5.4775			5.1901	5.0036				4.2923	
R.FTLEVVDAVVDAIGPEK.V +3													4.1776	4.6916	3.5011					3.8175					
R.LAFVHLVEPR.V +2													3.7574	3.6208	3.6958	3.8107		3.2089		3.3351					
R.TDEYGGSIENR.A +2	3.4376	3.8521	3.8658	3.8039	3.883	3.8268	3.7611	3.8313	3.5054	3.8013	3.6162	3.5107	3.6348		3.1531				3.5053	3.273					
R.VTNPFLTEGEGEYNGGSNK.F +2	5.7363	6.1296	5.9362		6.2635	6.4115	6.3933	6.4854	5.9116	5.9985	6.0969	5.2599	5.8027	5.4265	4.821	5.4299	4.6927	4.6842			4.2045	6.0021	5.4826	5.4685	
R.YDSASDNVYM*NAEQEEK.A +2													4.8458				3.8393					5.2811	4.0808		
R.YDSASDNVYMNAEQEEK.A +2		5.526	5.7033	6.0631	5.7531			5.6634	5.777	5.047	5.3508	5.4968	5.8385	5.9119	5.5144	5.6921	4.4612					5.5184	4.7909	5.6289	
gi|6321977|ref|NP_012053.1|	17.2	25.2	22.9	28.2	32.9	38.7	36.2	30.1	44.6	28.2	33.7	42.9	67.9	56.9	56.4	54	33.3	33.7	36.6	51.3	9.6	8.2	19.8	21.9	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p [Saccharomyces cerevisiae]
K.AGAPVDALINQIVPLLEK.G +2	4.2833	5.3083	5.2071	5.2686	5.4464	5.2698	5.3742	5.4583	4.98		3.9264	4.9268	4.8815	4.3727	3.5836	4.7345	3.3224	2.8288	4.7196	3.4563				4.7063	
K.AGAPVDALINQIVPLLEK.G +3					3.8853		4.9746		4.543			3.7264	4.9978	4.9839	5.2544	4.1285			3.6315	3.8495					
K.AYREEPDLENLLFNK.F +2			4.5595										5.0738	4.6624	4.5349	4.4955	4.34		3.5387	4.3602					
K.AYREEPDLENLLFNK.F +3													4.8697												
K.DIHINWTGHGGNVSSSTYQA.- +2																				3.1479					
K.DREQFVDDLEQALYASK.I +2		4.8225	5.2787	4.9248									5.3769	5.1351	4.2397	3.9376	4.5403								
K.DREQFVDDLEQALYASK.I +3													3.6441												
K.EISDVFAK.W +1										1.8163															
K.FDDVDGKPLVEK.I +2		2.7944		3.5121	3.678	3.6703	3.3471	3.2893	3.1864	2.7189	3.2164	3.2491	3.7334	3.3387	2.9311	3.6888					2.8837		3.1623		
K.FFADAVTK.A +1						2.227			2.2967		2.2713	2.2753	2.3356	2.3432	2.2333	2.2573						2.3139	1.868		
K.FFADAVTK.A +2					2.7016	2.8893			2.8126																
K.GDIIIDGGNSHFPDSNR.R +2										3.2105		4.1669	4.052		3.642	3.7365	4.6952	4.2971		4.5586			3.6147		
K.GILFVGSGVSGGEEGAR.Y +2	5.4037		5.7655	5.7126	5.5014	5.7653	5.7674	5.8873	5.3974	5.2598	5.31	5.3734	5.9935	5.651	5.5467	5.6471	4.6063	5.208		5.5651			3.1038	5.4832	
K.IISYAQGFM*LIR.E +2												2.8464	3.5061	3.7227	3.589				3.5247	3.6749					
K.IISYAQGFMLIR.E +2																		2.8618		3.2087					
K.KGILFVGSGVSGGEEGAR.Y +2																	5.0864		3.2051						
K.LNNPAIALM*WR.G +2									3.5928			3.781	3.9412	2.8653	3.1977	3.8638			2.9342		2.9046				
K.LNNPAIALMWR.G +2	4.0715	4.1687	4.1168	3.7815			3.647		3.8021			3.5538			3.6317	3.9799	4.023			4.0501					
K.M*VHNGIEYGDM*QLICEAYDIM*K.R +3													3.7716												
K.NIFQSISAK.S +1		2.219				2.3656	2.2081	2.3108	2.4732					2.4102	2.155	2.2411			2.0334						
K.NIFQSISAK.S +2						2.7673		2.5786							2.6433										
K.SDGEPCCEWVGPAGAGHYVK.M +2									3.7822				4.6766	4.8807	4.2109	4.2188	4.3261	4.4511	4.9261	3.7813					
K.SIALATTYGIPTPAFSTALSFYDGYR.S +2					3.9226	2.7938	4.4075	4.251	4.1473		3.3764	3.9055	4.4613	3.6656	3.7071	4.017				3.0952					
K.SIIGATSIEDFISK.L +2	4.7669	4.5303	4.5169	4.5505	4.4428	4.4035	4.1173	4.4703	4.5014	3.7604	4.3789	4.2594	4.3724	4.4933	4.6235	4.6831	2.6757		3.3761	3.7218			2.6581	4.1458	
K.VDHFLANEAK.G +1						2.1847																3.0198			
K.VDHFLANEAK.G +2			2.661	2.77		2.7729	2.72			2.922	2.9254		2.6896	2.708					2.7215			2.772		2.8122	
K.WNNGVLDSFLVEITR.D +2				4.8432	2.9727	3.8943						4.0059	4.1161	4.2783	3.5769	3.1473			3.062	4.3414					
K.WTAINALDLGM*PVTLIGEAVFAR.C +2									3.6444				4.8947		3.881	5.0438				3.8025					
K.WTAINALDLGM*PVTLIGEAVFAR.C +3													5.1642	3.9301	4.9488										
K.WTAINALDLGMPVTLIGEAVFAR.C +2									2.8752											3.954					
K.WTAINALDLGMPVTLIGEAVFAR.C +3																				4.709					
R.DILKFDDVDGKPLVEK.I +2																				2.502					
R.DYFGAHTFR.V +2																	2.5044								
R.EAAATYGWK.L +1													2.1783					2.1324							
R.EEPDLENLLFNK.F +2			3.4903		3.804	3.7594	3.5679	3.7567	3.7072	3.6993	3.7212	3.4292	3.5919	3.5103	3.4306	3.4868	2.9002	2.5992				2.6684			
R.EQFVDDLEQALYASK.I +2					5.5237	5.3417	5.7119	5.5139	5.2372	4.454	4.1313	5.0646	4.6767	4.9563	4.9899	5.1921	4.528	4.4605					3.8398	5.1506	
R.LGGFTDKEISDVFAK.W +2													3.4849												
R.LPANLLQAQR.D +1									2.437				2.658												
R.LPANLLQAQR.D +2	4.3452	3.874	4.2481	4.0392	4.3221	4.3867	4.3324	4.3881	4.1876	4.4064	4.4047	3.9872	4.3978	2.7723	4.0825	4.1262	4.2567		3.7376		4.0721	3.9983		3.5819	
R.SERLPANLLQAQR.D +2																		3.1859							
R.SVFLGQITK.A +1						2.2048			2.5026				2.2168	2.4909					2.4849	2.3997					
R.SVFLGQITK.A +2						2.6334	2.7751		2.8259	2.8475	2.7124	2.78	2.6617	2.7859										2.8145	
R.VLPECASDNLPVDK.D +2	3.7976	3.7956		3.4958	4.1648	3.64	3.7055	3.6274	3.6752	3.899	3.477	3.6493	3.5019	3.5902	3.6006	3.8891	3.3132	3.5056			3.5632		2.8874	3.4111	
R.YGPSLM*PGGSEEAWPHIK.N +2													3.8524	3.6958	3.4336	3.2634			3.7744	3.2856					
R.YGPSLM*PGGSEEAWPHIK.N +3													3.5911												
R.YGPSLMPGGSEEAWPHIK.N +2		3.5537																3.099							
gi|6322002|ref|NP_012078.1|	13.2	13.2	13.2	13.2	23.9	20.6	31.3	28.2	32.3	14.5	16.3	32.3	41.5	36.6	29.8	39.9	23.7	27.2	30.3	25.7	7.6	9.4	17	18.6	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase; Bat1p [Saccharomyces cerevisiae]
K.ELVTAPLDGTILEGVTR.D +2	4.8841	5.0031	5.0215	4.5758	4.9772	5.049	4.9739	4.9083	4.9461	4.345	4.4925	4.2082	4.6472	5.0022	4.5021	5.1161	4.7735	3.9295	4.3629	3.8328	3.8028	3.2317	4.7007	3.9282	
K.ELVTAPLDGTILEGVTR.D +3														4.5548											
K.GLGVGTPSEALLYVITSPVGPYYK.T +2					4.8679	3.474	4.4907	4.892	5.115			4.6408	5.0998	4.1482	4.2323	4.4549	2.7596	4.0013	3.3887	4.5515					
K.GLGVGTPSEALLYVITSPVGPYYK.T +3													5.7678	4.887	4.3732			3.7644	4.9007	4.8485					
K.KELVTAPLDGTILEGVTR.D +2													3.2466												
K.KLGANYAPCILPQLQAAK.R +2																			2.7304						
K.LDPQEWDINER.Y +2								2.7588																	
K.LGANYAPCILPQLQAAK.R +2					3.7548		4.0414	4.0998	3.9	3.3305	3.7181	3.3294	3.4083	4.1016	3.0297	3.5679		3.1866	3.6086	3.8167			3.5065		
K.NITEVGTM*NVFFVFLNK.V +2						2.5504								3.3348		3.6154			3.2163						

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.NITEVGTMNVFFVFLNK.V +2																			2.8503						
K.QGELLEAFGSGTAAVVSPIK.E +2							4.9478	3.9219	5.9487		2.8073	4.9959	5.9881	5.5739	5.9634	5.8983	4.492		2.812	5.9138		5.4084	4.3312	4.772	
K.QGELLEAFGSGTAAVVSPIK.E +3															3.5112										
K.QVAQWIADIQYGR.V +2	3.222				3.3775		3.5603		4.2031			3.9655	4.1333	4.4606	3.7554	4.0926		4.0678	3.1696	4.2244					
R.DKLDPQEWDINER.Y +2													3.0613												
R.GYQQNLWLFGPEK.N +2									3.4391			3.4012	3.7748			3.1884		3.5217			3.7928			3.2735	
R.ICLPTFESEELIK.L +2		4.1637	3.8268	3.9742	4.0504	4.1498	4.4982	4.1865	3.3717	2.8486		2.7743	3.5684	3.4124	3.5029	4.0241	2.6993	3.7339					2.8077	3.64	
R.LEATDYATR.A +1													2.4712												
R.LEATDYATR.A +2	3.357	3.3029	3.3327	2.9595			2.9499	2.9195					3.1819				3.5532								
R.TPQNTITM*FRPDK.N +2													3.5161	3.4248	3.3861										
R.TPQNTITMFRPDK.N +2	3.199	3.882	3.5909	3.6905									3.3268		3.2523	3.4726									
R.YYTITEVATR.A +2					2.6882	3.17	3.0942		3.4501	3.0866	2.7571	2.9961	2.9527	3.3032		3.2845	2.8115	3.2085	3.0185	2.6102				3.0404	
gi|6322138|ref|NP_012213.1|	29	42.8	42.8	42.8	30.3	46.2	33.8	46.2	74.5	24.1	30.3	49	74.5	74.5	64.8	74.5	58.6	42.8	51	58.6	24.1	30.3	30.3	16.6	Mitochondrial protein involved in maintenance of the mitochondrial genome; Mmf1p [Saccharomyces cerevisiae]
K.AEQVFQNVK.N +1						2.3973			2.6044	2.3612	2.6922			2.6073	2.5541	2.5642	2.3641	2.7442	2.7056	2.6213		2.5987	2.6843		
K.AEQVFQNVK.N +2		3.1566	3.1944	3.1291	3.2694	3.2588	3.2065	3.2512		3.0435	3.1848	3.1484	2.9856				3.2029								
K.ANNFVYVSGQIPYTPDNK.P +2																		2.8644		2.9611					
K.ANNFVYVSGQIPYTPDNKPVQGSISEK.A +2									3.1805				2.7889							2.7344					
K.ANNFVYVSGQIPYTPDNKPVQGSISEK.A +3	5.0814	5.1972	5.135	4.0043					4.805			3.8158	4.0868	4.8938	5.1191	3.6218	5.244		4.3804	4.6542					
K.LAPPAAASYSQAM*K.A +1														2.148					2.4049						
K.LAPPAAASYSQAM*K.A +3													3.7693	4.0067											
K.LAPPAAASYSQAMK.A +1							2.5235		2.9125							2.2596	3.1942			2.5334					
K.NFAEFNSVYAK.H +1						3.0271			2.7551		2.0445		3.2536	3.0153			2.7585	2.3016			2.5792		2.8304		
K.NFAEFNSVYAK.H +2		4.575	4.5815	4.0639	4.8011	4.6271	4.6036	4.6675	4.5998	4.3458	4.6493	4.157			4.5584	4.1609	4.4321	3.8021		2.6874	4.3333	4.6091	4.4856		
K.NILAESNSSLDNIVK.V +2	5.6648	5.3734	5.5566	5.4769	5.8524	5.837	5.9536	5.9024	5.7054	5.8848	5.8129	5.4556	5.504	5.4867	5.3148	5.6043	5.4146	3.7958	3.5537	4.8924	2.7644	5.3453	5.8492	4.3244	
K.VNVFLADM*K.N +1																			2.7039						
K.VNVFLADM*K.N +2												2.7062	3.397	3.2345		3.3302								3.1407	
K.VNVFLADMK.N +1					2.5228	2.5489		2.1243	2.5137		2.4159		2.5623	2.5872	2.5585	2.4975	2.6547	2.5253		2.65	2.2165	2.4666	2.6587	2.5216	
K.VNVFLADMK.N +2					3.157						2.9327	2.9006	2.8679	3.2219		3.1252	3.4647	3.0771		3.2188			3.4339		
R.SCVGVASLPLNVDLEM*EVIAVEK.N +2								2.6128	2.7887				3.1817	5.1378		2.9242									
R.SCVGVASLPLNVDLEM*EVIAVEK.N +3													4.4659	4.5152											
R.SCVGVASLPLNVDLEMEVIAVEK.N +2						2.5581		3.0706	3.9642							3.311									
R.SCVGVASLPLNVDLEMEVIAVEK.N +3															3.836										
gi|6322271|ref|NP_012345.1|	19.2	19.2	19.2	25.4	25.4	19.2	19.2	19.2	19.2	19.2	19.2	19.2	36.2	36.2	19.2	25.4	18.5	19.2	30	30	19.2	19.2	19.2	18.5	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22ap [Saccharomyces cerevisiae]
gi|6323399|ref|NP_013471.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Ap and has similarity to E. coli S8 and rat S15a ribosomal proteins; Rps22bp [Saccharomyces cerevisiae]
K.HGYIGEFEYIDDHR.S +2													4.2862	4.3233					2.5115	4.6165					
K.HGYIGEFEYIDDHR.S +3													4.4265	5.0684					4.6666						
K.IVVQLNGR.L +1																	1.9079								
K.IVVQLNGR.L +2				2.7922	2.6868								2.6372	2.6329		2.8027	2.5813							2.7994	
K.WTANLLPAR.Q +1														2.2843											
K.WTANLLPAR.Q +2	3.534	3.7339	3.7376	3.6326	3.4929	3.6168	3.5624	3.5482	3.3905	3.3552	3.3911	3.2631	3.463	3.2726	3.4377	3.4859		3.6987	3.2774	3.5561	3.0275	3.1972	3.387		
R.SSVLADALNAINNAEK.T +2	6.0301	6.176	6.0543	6.1261	6.2318	6.0018	6.274	6.1594	5.6961	3.189	5.8041	5.6764	5.5323	5.1586	5.5598	5.5405	5.5663	5.124	5.4016	5.6381	3.8004	2.7963	5.5811	5.0538	
R.SSVLADALNAINNAEK.T +3													6.2158	6.2539	5.8795			4.8993	5.8092	4.9432				5.2616	
gi|6322409|ref|NP_012483.1|	22.3	39.2	30.7	38.3	34.6	33.7	34.6	41.3	41	36.1	36.7	36.7	51.8	53	53	44	41.6	23.8	55.4	53	23.8	32.8	25.6	37	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 1, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh1p [Saccharomyces cerevisiae]
K.DIEVVAVNDPFISNDYAAYM*VK.Y +2						4.8837	4.5904	4.1513	5.0055	3.3939	3.2126	4.7769	5.9761	5.5845	5.6665	4.7856	2.6971	5.104	4.7617	4.8065		3.1111	4.7989		
K.DIEVVAVNDPFISNDYAAYM*VK.Y +3													4.7881	5.0115	4.3498										
K.DIEVVAVNDPFISNDYAAYMVK.Y +2					6.4708	6.167	6.496	6.5069	6.066		4.5063	5.162			4.7357	6.3354	5.9986	4.5164		4.0162		5.1995	5.4536	6.062	
K.ELDTAQK.H +1		1.9741						1.8644					1.9637												
K.HIDAGAK.K +1		2.2897	2.3916			2.1017		2.144		2.3737	2.3856	2.2129	1.8986	2.2111	2.0744	2.488	1.9217		1.9074	2.0769				2.1721	
K.HIDAGAKK.V +2		2.9828	2.8112														2.8728			2.563					
K.HIIIDGVK.I +1													2.314	2.3602											
K.HIIIDGVK.I +2		2.8319		2.941						2.7209			2.5319						2.7258						
K.IATYQER.D +1																							1.8752	2.0082	
K.IATYQERDPANLPWGSLK.I +2	3.5393			3.5407													3.6344		3.1845	3.2787					
K.IDVAVDSTGVFK.E +1									1.9433							2.0515					2.5153			1.8612	
K.IDVAVDSTGVFK.E +2		4.3168	4.5105	4.3097	4.3035	4.7982	4.394	4.1587	4.2241	3.8987	4.346	4.3275	4.4615	4.4488	4.5858	4.3339	3.9168		2.9672	3.3511	3.5977	3.8386		4.2465	
K.IVSNASCTTNCLAPLAK.V +2	5.0341	5.0041	4.9339	4.6853	5.0496	5.0632	5.17	5.0947	4.8518	5.136	4.9084	4.7847	4.8806	4.4531	4.5623	4.9988	4.8111	4.4749	4.3861	3.2605	4.7302	4.5466	4.8866	4.8148	
K.IVSNASCTTNCLAPLAK.V +3												4.5327	4.5355	4.8682		4.5436									
K.KIVSNASCTTNCLAPLAK.V +2		5.3739	5.3239	5.1564														5.0473	5.0608	4.9802					
K.KIVSNASCTTNCLAPLAK.V +3																		3.6159		3.5814					
K.LISWYDNEYGYSAR.V +2		4.084	4.2286		3.939	3.9676	4.2952	4.3579	4.0335	4.0968	4.1015	3.6378	3.9989	4.0201	4.1832	4.0966	4.2071		4.1613	3.9984					
K.VINDAFGIEEGLM*TTVHSM*TATQK.T +2													4.462	4.3206	3.5246				3.0128	2.694					
K.VINDAFGIEEGLM*TTVHSM*TATQK.T +3				3.6223									4.0146	3.749	3.6744				4.6214						
K.VINDAFGIEEGLM*TTVHSMTATQK.T +2																				4.6033					
K.VINDAFGIEEGLM*TTVHSMTATQK.T +3				5.3006																					
K.VINDAFGIEEGLMTTVHSMTATQK.T +2																			3.7771	3.488					
K.VINDAFGIEEGLMTTVHSMTATQK.T +3		5.4821		4.8822									4.0422	4.4128	4.5782	4.5752			3.8333	3.6171					
K.VLPELQGK.L +1				2.0535				2.016							1.996		1.8059					1.8721			
K.VVITAPSSSAPM*FVVGVNHTK.Y +2									3.5187				3.9851	4.2607	3.6321				3.3876	3.5162					
R.DPANLPWGSLK.I +2			3.6083		3.5661	3.8624	3.8632	3.649	3.6678	3.6943	3.4203	3.4473		3.2063	3.2341	3.3933					2.5988	3.6444		3.3763	
R.IAINGFGR.I +2																								2.6515	
R.KDIEVVAVNDPFISNDYAAYM*VK.Y +3													4.4619	3.8345	4.3977										
R.TASGNIIPSSTGAAK.A +1	3.5197	3.3582	3.5211		3.1769	3.2293	3.5021	3.279	3.3946	2.8535	2.9998	3.1171	3.3366	3.1662	3.2624	2.7976	2.9028	3.2802	3.1224	3.0539	3.2978	2.9054		3.1785	
R.TASGNIIPSSTGAAK.A +2	4.2985	4.1316	4.2183	3.9346	4.3615	4.2909	4.41	4.3666	4.3393	3.9976	4.2161	3.8733	3.1787	3.9328		4.2441					3.9644	3.912	4.3301	3.4692	
R.VPTVDVSVVDLTVK.L +1			3.7441					3.3452	3.8582			3.5243	3.3285	3.6905	3.463	3.2615	3.0996	1.8026		3.4942					
R.VPTVDVSVVDLTVK.L +2	4.713	4.8316	4.7901	4.9685	4.8753	4.9145	4.6912	4.823	4.7057	4.4205	4.9024	4.6229	4.7104	4.7069	4.7409	4.852	4.4896	4.6465	4.6663	4.5917	4.4193	3.6465	5.057	3.7581	
R.VVDLIEYVAK.A +1													2.2323		2.2717		0.2095								
R.VVDLIEYVAK.A +2	3.7996	3.9252	3.944	4.0812	4.164		4.1497	3.9334	3.9198		4.015	3.6991	3.9901	4.0867	4.0347	4.1042	3.8258	4.0176	3.8316	3.8366	3.7332	3.9193	3.7332	4.043	
R.VVDLIEYVAKA.- +2																			2.593						
gi|6322434|ref|NP_012508.1|	7	7	7	7	13.8	10	16.8	16.8	20.3	12.8	12.8	23.1	27.1	26.8	18.5	18.5	15.5	11.3	11.5	18	15.8	11.5	12.5	12.8	Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr2p [Saccharomyces cerevisiae]
K.AAADALSDLEIK.D +2	2.7803	3.0351	3.247	2.7926	4.1682	4.2697	4.2202	4.2622	3.5922	4.3715	3.9209	3.8976	4.0144	4.3607	4.0499	3.8659	2.7941		3.0829					4.1843	
K.AAADALSDLEIKDSK.S +2																	3.2607	4.1127	3.5439	3.5516					
K.ESEFLFNAIHTIPEIGEK.A +2												4.4215	4.6672	3.3218						3.6653					
K.IVTEAVEIEQR.Y +2									3.8544	3.8999	3.9457	4.3989	4.1186	4.1382	3.9096	4.0201	3.3944					4.1539	3.108	4.2217	
K.QEAGAFTFNEDF.- +2							2.8933	2.9714		2.8828															
K.VENPFDFM*ENISLAGK.T +2						3.6762			4.1927	3.1481		3.6141	4.463	4.7377	4.2725	4.0392			3.622	3.6708	4.0851		4.3127	3.9416	
K.VENPFDFMENISLAGK.T +2	4.5317	4.9291	5.0428	3.294	4.3887	4.6395	4.8526	5.1572	4.7725		4.3881			3.9962	4.7143	4.9657	4.3045		4.1944						
R.AEASFWTAEEIDLSK.D +2					3.4278		3.8271	4.6642	3.6633			4.7459	2.7265	3.3534	3.9387	4.0391					4.8529	2.6771	5.0532		
R.GM*M*PGLTFSNELICR.D +2									2.5393				4.4177	4.0822				3.306	3.5013	3.0707					
R.GMMPGLTFSNELICR.D +2																				3.0185					
R.LLVAFGNK.K +1													2.1528	2.1104	1.8355	2.0985	2.2168	2.0064			2.129		1.9161		
R.LLVAFGNK.K +2												2.5146	2.5945	3.1802		2.7957				2.5317		3.0061	2.6033		
R.LLVAFGNKK.Y +2													2.6449												
R.TVLFPIK.Y +1																		1.8866							
R.WIQDADALFGER.L +2					4.0214	3.8137	4.0455	3.7188	3.7771		3.2985	3.8019	3.2586	4.1478	3.7143	4.0547	3.608				3.7374	3.1681		3.9822	
gi|6322468|ref|NP_012542.1|	42.8	53.9	47.3	52.1	42.2	44.3	42.2	48.8	39.8	44.3	41.6	39.5	51.8	56.3	60.8	49.1	44	37	47	53.3	37	39.5	37	41.6	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; tetramer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm and cell-wall; Tdh2p [Saccharomyces cerevisiae]
K.ELDTAQK.H +1		1.9741						1.8644					1.9637												
K.ETTYDEIKK.V +2	2.7119		2.5517		2.8331	2.7078	2.8038	2.6031		2.5497															
K.HIDAGAK.K +1		2.2897	2.3916			2.1017		2.144		2.3737	2.3856	2.2129	1.8986	2.2111	2.0744	2.488	1.9217		1.9074	2.0769				2.1721	
K.HIDAGAKK.V +2		2.9828	2.8112														2.8728			2.563					
K.HIIVDGHK.I +1		2.7165	2.5901						2.2425		2.2318		2.407	2.1939	2.2488		2.346	2.1915							
K.HIIVDGHK.I +2			2.8804	2.6805					2.7234						2.68		2.6547			2.6577					
K.IVSNASCTTNCLAPLAK.V +2	5.0341	5.0041	4.9339	4.6853	5.0496	5.0632	5.17	5.0947	4.8518	5.136	4.9084	4.7847	4.8806	4.4531	4.5623	4.9988	4.8111	4.4749	4.3861	3.2605	4.7302	4.5466	4.8866	4.8148	
K.IVSNASCTTNCLAPLAK.V +3												4.5327	4.5355	4.8682		4.5436									
K.KVVITAPSSTAPM*FVM*GVNEEK.Y +2									5.9754			2.617	6.1637	5.9977	6.0665	5.9082		5.4693	5.972	5.1097					
K.KVVITAPSSTAPM*FVM*GVNEEK.Y +3		4.9762	4.697	4.8549					4.6553			3.5598	5.1057	5.1918	5.0654	4.3268	4.9348		4.203	4.7426					
K.KVVITAPSSTAPM*FVMGVNEEK.Y +2		5.3243											5.4146						2.6909	5.2503					
K.KVVITAPSSTAPM*FVMGVNEEK.Y +3		3.551	4.1012	3.6158											4.144										
K.KVVITAPSSTAPMFVM*GVNEEK.Y +2														5.2974	5.5351	5.4872	5.2059	2.7164		4.8803					
K.KVVITAPSSTAPMFVM*GVNEEK.Y +3	4.1354	5.4078							3.5129					5.0604	4.7147		3.7426			5.5935					
K.KVVITAPSSTAPMFVMGVNEEK.Y +2	5.2306	5.9756	5.5464																	5.6584					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.KVVITAPSSTAPMFVMGVNEEK.Y +3	4.6473	5.1412	4.5956	4.2176																4.9878					
K.LVSWYDNEYGYSTR.V +2	4.5244	4.4775	4.476	4.6428	4.5224	4.7032	4.3903	4.5002	4.5277	4.4392	4.5254	4.4773	4.4005	4.2486	4.4405	4.2696	4.2531	4.3764	4.3397	4.3227	4.1083	4.1068	4.3614	4.3342	
K.NVEVVALNDPFISNDYSAYM*FK.Y +2		5.8229		5.2769	6.4074	6.6569	6.5965	6.6108	6.3046	6.6693	6.0157	6.1812	6.1766	6.4783	6.3988	6.3155	4.6733	6.1937	6.0661	6.4565	5.5064		5.9633	6.1898	
K.NVEVVALNDPFISNDYSAYM*FK.Y +3				4.8157	6.3796	6.6664	6.6318	6.5077	6.3163	6.5887	5.284	6.4165	6.998	6.29	5.9794	6.1292	4.5338		6.2315	5.4668	4.9322	5.1777	5.6337		
K.NVEVVALNDPFISNDYSAYMFK.Y +2	5.9691	6.0116	6.1058	6.0921	6.0624	6.1562	6.0804	5.9635	5.9772	4.8371	5.9321	5.6474			5.9335	5.9329	5.745	3.7651	4.3907	5.5342	3.1981		4.5942	4.7956	
K.NVEVVALNDPFISNDYSAYMFK.Y +3	6.6014	6.9631	6.7259	6.3938	6.8171	6.3007	6.6009	7.0808	6.2656		5.805	5.9467			6.5219	6.2462	5.139			5.4857	5.638				
K.VINDAFGIEEGLM*TTVHSM*TATQK.T +2													4.462	4.3206	3.5246				3.0128	2.694					
K.VINDAFGIEEGLM*TTVHSM*TATQK.T +3				3.6223									4.0146	3.749	3.6744				4.6214						
K.VINDAFGIEEGLM*TTVHSMTATQK.T +2																				4.6033					
K.VINDAFGIEEGLM*TTVHSMTATQK.T +3				5.3006																					
K.VINDAFGIEEGLMTTVHSMTATQK.T +2																			3.7771	3.488					
K.VINDAFGIEEGLMTTVHSMTATQK.T +3		5.4821		4.8822									4.0422	4.4128	4.5782	4.5752			3.8333	3.6171					
K.VLPELQGK.L +1				2.0535				2.016							1.996		1.8059					1.8721			
K.VVITAPSSTAPM*FVM*GVNEEK.Y +2	4.3782	5.0786	5.0407	4.7681	4.5426	4.9726	4.8001	5.2583	4.5093	4.8672	5.0125	4.7631	4.9286	4.9627	4.499	4.8573	4.4176	4.0375	5.1496	5.0261	4.5876	4.6738	4.1814	4.6145	
K.VVITAPSSTAPM*FVM*GVNEEK.Y +3		3.8141				4.0886	4.1068	4.6011	4.4416	4.2319	4.1558	4.3222	4.6475	4.335	4.3777	4.1158		4.0664		4.1767		3.822			
K.VVITAPSSTAPM*FVMGVNEEK.Y +2	5.0565	5.1659	5.1874	5.1275	5.1306	5.2997	4.9958	5.3656	4.1912	5.1654	5.0238	4.9851	4.206		3.9196	3.9978		4.5797	4.8169	5.3888	4.4953	3.0402		3.8704	
K.VVITAPSSTAPM*FVMGVNEEK.Y +3	4.1215	4.0046					4.1046			4.3819		3.5275	3.6093	4.6344	4.8549	3.8024				4.7593		4.2615			
K.VVITAPSSTAPMFVM*GVNEEK.Y +2	4.4511	5.0299	4.6095	4.6384	4.2292	4.3637	4.8827	5.0091	5.03	3.6012	3.8534	4.4686		4.6742	4.9366	4.5229	4.4874	3.6444	3.6765	3.7111	4.7268	4.4374	5.1199	4.9589	
K.VVITAPSSTAPMFVM*GVNEEK.Y +3		4.4127		4.9621	4.7407	4.7454	4.7003	5.1788	4.8925	4.7451	4.6345	4.6001		4.6549	4.8153	5.0067	4.7931	4.5005		4.0843		3.5181		4.5893	
K.VVITAPSSTAPMFVMGVNEEK.Y +2	5.8465	5.8365	5.7724	5.3213	5.7547	5.6336	5.7178	5.7421	5.3155	5.2777	5.6068	5.0572		4.6963	4.9081	5.3584	4.7866	3.974	4.046	4.4081	5.1412	4.8005	4.923	4.5234	
K.VVITAPSSTAPMFVMGVNEEK.Y +3	5.2702	5.3332	5.7061	5.2737	5.2829	5.2936	5.2902	5.5039	5.1344	4.5423	5.2618	4.9306		4.669	5.423	5.1553		4.619		4.9214	3.9006	4.0763	4.0635		
R.DPANLPWASLNIDIAIDSTGVFK.E +2														2.6193	2.5965					2.9711					
R.KNVEVVALNDPFISNDYSAYM*FK.Y +3													4.739	5.7651											
R.TASGNIIPSSTGAAK.A +1	3.5197	3.3582	3.5211		3.1769	3.2293	3.5021	3.279	3.3946	2.8535	2.9998	3.1171	3.3366	3.1662	3.2624	2.7976	2.9028	3.2802	3.1224	3.0539	3.2978	2.9054		3.1785	
R.TASGNIIPSSTGAAK.A +2	4.2985	4.1316	4.2183	3.9346	4.3615	4.2909	4.41	4.3666	4.3393	3.9976	4.2161	3.8733	3.1787	3.9328		4.2441					3.9644	3.912	4.3301	3.4692	
R.VAINGFGR.I +2	2.6601	2.592	2.6338	2.5292	2.5508	2.6116	2.5603	2.6338		2.5602					2.5975	2.5466	2.5055							2.5162	
R.VPTVDVSVVDLTVK.L +1			3.7441					3.3452	3.8582			3.5243	3.3285	3.6905	3.463	3.2615	3.0996	1.8026		3.3942					
R.VPTVDVSVVDLTVK.L +2	4.713	4.8316	4.7901	4.9685	4.8753	4.9145	4.6912	4.823	4.7057	4.4205	4.9024	4.6229	4.7104	4.7069	4.7409	4.852	4.4896	4.6465	4.6663	4.5917	4.4193	3.6465	5.057	3.7581	
R.VVDLVEHVAK.A +1		2.373	2.3354	2.3509	2.6218		2.3823	2.6106	2.5481	1.8535	2.3683	2.1962	2.4979	2.3318	2.4185	2.5234	2.1966	2.5292	2.4041	2.642	2.504	2.4429	2.1068		
R.VVDLVEHVAK.A +2	3.6796	3.7311	3.6379	3.8208	3.669	3.566	3.6211	3.671	3.5699	3.5893	3.622	3.5334	3.5462	3.7376	3.5686	3.639	3.7711	3.5554	3.649	3.2974	3.7124	2.6821	3.3847	3.361	
R.VVDLVEHVAKA.- +1																	2.2498	2.4083	2.0531	2.1893					
R.VVDLVEHVAKA.- +2	4.2741	4.5105	4.4622	4.5326									3.3249				4.0484	3.9482	3.2899						
R.YAGEVSHDDK.H +1											2.3038			2.0956	2.1901							2.7044			
R.YAGEVSHDDK.H +2	3.278	3.4984	3.3495	3.4914	2.7798	3.0447	3.3102	3.0864	3.0089	3.1353	3.0713	2.7195	3.0967	2.9244	2.5906	2.9727			3.0972		2.9078	3.2038	3.1013	2.562	
gi|6322505|ref|NP_012579.1|	21.6	28	25.7	18.2	26.8	30.1	38.7	36.4	40.5	27.1	34.3	32.1	40.1	36.1	42.2	34.1	29.8	32.1	28.7	28.9	32.4	18.7	22.3	20.6	Mitochondrial matrix ATPase that is a subunit of the presequence translocase-associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family; Ssc1p [Saccharomyces cerevisiae]
K.DAGLSTSDISEVLLVGGM*SR.M +2									4.7952	3.5239		4.0098	4.4731	4.7505	4.0159	5.1182		4.2881	3.1224	4.1975	4.6106			4.158	
K.DAGLSTSDISEVLLVGGM*SR.M +3													4.7013	4.0958											
K.DAGLSTSDISEVLLVGGMSR.M +2	5.3189	5.5635	5.6254		5.5792	5.8827	5.6999	5.4085	5.103		3.8027	4.3391			3.9307	5.1983	5.1506			4.6161				5.2431	
K.DAGQIVGLNVLR.V +2	4.1624	4.227	4.1268	4.2377	4.1645	4.2872	4.3027	4.1982	4.3112	4.0576	4.0792	4.2738	4.0108	4.0592	4.2145	3.8672	4.041	4.1115	3.9012	4.2045	3.7989	2.8282	4.2126	4.127	
K.DSSITVAGSSGLSENEIEQM*VNDAEK.F +2						3.5325										3.0667					4.0356				
K.DSSITVAGSSGLSENEIEQM*VNDAEK.F +3																			3.6831						
K.DSSITVAGSSGLSENEIEQMVNDAEK.F +2						5.0368	5.3148	5.095	5.3463		4.6465	4.7482				5.9586	5.1271	3.1747			4.3015	3.7884	4.5377		
K.DSSITVAGSSGLSENEIEQMVNDAEK.F +3	4.1744					5.315	5.3776	4.5527	5.0193		3.8313	4.2501			4.28	4.4998					3.7058				
K.ETAEAYLGK.P +1																	2.3007	2.192	2.1787				2.3069		
K.ETAEAYLGKPVK.N +1									2.1018																
K.ETAEAYLGKPVK.N +2								3.3194	3.3605	3.1844	3.2675	3.187	3.3976	2.861	3.0373	2.9256			3.2465	2.9856	3.1037				
K.HSNGDAWVEAR.G +2				3.0902																					
K.IELSSTVSTEINLPFITADASGPK.H +2						2.7453	4.519	4.2958	4.5535		3.011	2.9125		3.319	4.1248	3.9177									
K.IELSSTVSTEINLPFITADASGPK.H +3									5.5378				4.4132	5.4265	4.7995	4.1527									
K.IIENAEGSR.T +2											2.7207														
K.LIGNFTLAGIPPAPK.G +2		4.0723	4.1539		3.544		4.1575	4.0365	3.9358	4.003	4.0763	3.899	3.8319	3.9383	3.6784	3.5122			3.5085	3.8585					
K.MKETAEAYLGKPVK.N +2													3.2699	3.6876											
K.NAVVTVPAYFNDSQR.Q +2	3.9187	3.9026	3.9821		4.1041	4.1642	3.999	3.9169	3.6392	4.0506	3.8088	3.5729	3.6773	4.0392	3.9035	3.8203	3.7214			2.8272	3.2045	2.8786	3.2222	3.6695	
K.RQAVVNPENTLFATK.R +2		4.4836															4.617			4.5166					
K.SQIFSTAAAGQTSVEIR.V +2							4.1897		4.9869			4.0905	4.881	4.9827	5.4293			3.2839	2.7593	3.5159	5.7275				
K.STNGDTHLGGEDFDIYLLR.E +2		4.2848	4.9018	4.4787									5.43	3.11	3.4538	2.8198			3.2732	4.1099					
K.STNGDTHLGGEDFDIYLLR.E +3													3.7545												
K.TEELQTSSM*K.L +2																			2.6186			2.8035			
K.TEELQTSSMK.L +2		3.5274	3.1349		2.8972	3.3488	3.4637		3.063	3.0879				2.7234			3.269	3.3146					2.9414	3.7503	
K.TETGIDLENDR.M +1																					1.8299				
K.TETGIDLENDR.M +2	3.202	3.5333	3.11	3.52			3.8278	3.6573	3.5768	2.7083	3.5951	2.9569	3.2662		3.3976	3.4203				3.4345				3.1701	
K.VQGSVIGIDLGTTNSAVAIM*EGK.V +2															4.2308			4.6075			5.3067		3.7262		
K.VQGSVIGIDLGTTNSAVAIM*EGK.V +3													3.9122												
K.VQGSVIGIDLGTTNSAVAIMEGK.V +2					5.298		5.2414	5.414	5.58						5.1108		4.7269		3.7138	5.3599			3.8466		
K.VRDQITSLK.E +2		3.1744	2.9467	3.0062														3.1654	3.1589						
R.AQFETLTAPLVK.R +2	4.0742	3.9303	3.9708	4.2069	4.2163	4.0509	4.1592	4.1098	4.2593	3.7623	3.9275	4.11	3.9661	3.7286	4.2284	4.0797	3.8662	4.1307	3.893	3.2608	4.1048			3.9138	
R.FEDAEVQR.D +2								3.1401			3.1595			2.7177	2.8618	3.1644	2.8349				2.8274		3.1159	2.9884	
R.FKTETGIDLENDR.M +2										2.8098			4.0375	4.4389	4.2505	4.1502	4.3165	4.1423		2.6335					
R.GQTYSPAQIGGFVLNK.M +2	5.3018	5.3591	5.4037	5.5635	5.3106	5.444	5.3972	5.3495	5.3122	4.7047	4.7681	4.9638	5.0147	4.8629	5.1319	5.0484	4.5825	5.0017			4.4791	2.7813	5.3005	4.6427	
R.QAVVNPENTLFATK.R +2		3.5938			4.2821	4.1047	4.3532	4.1878	3.9343	3.8975	4.0738	3.772	4.0824	4.2818	3.7007	3.9406	3.2502	3.5276		4.3532	3.0182	3.7498	3.7254	3.5542	
R.RFEDAEVQR.D +2					2.7171	2.7713	3.0319	3.7096	3.572	2.8139	2.9351		3.323	3.1235	3.0189	3.4073								2.7927	
R.TTPSVVAFTK.E +1						1.8034							1.9849	1.8151							1.8218				
R.VQGGEEVNAEELK.T +1																						2.1714			
R.VQGGEEVNAEELK.T +2	4.1243	4.0582	4.1099	4.2707	3.8977	4.1193	3.9293	4.0461	3.0827	4.0379	3.7613		4.0521		4.0934			3.4369	4.1404			3.656	3.1913		
R.VVNEPTAAALAYGLEK.S +2	5.1943	5.4269	5.4853	5.4516	5.423	5.5385	5.4758	5.5689	5.0218	5.4704	5.2329	5.2216	5.2395	5.2778	5.4721	5.3251	3.4606	4.1509		4.9077	5.5559	5.7482		4.4199	
R.VVNEPTAAALAYGLEK.S +3													4.7755	4.8567	4.5331						4.1308	3.8658		4.3175	
gi|6322564|ref|NP_012638.1|	17.5	29.9	46.1	37.7	31.2	42.2	48.7	48.7	53.9	53.9	60.4	53.9	47.4	49.4	53.9	60.4	47.4	40.9	47.4	47.4	48.7	31.2	42.2	42.2	Cytosolic superoxide dismutase; some mutations are analogous to those that cause ALS (amyotrophic lateral sclerosis) in humans; Sod1p [Saccharomyces cerevisiae]
K.FEQASESEPTTVSYEIAGNSPNAER.G +2			5.3646		4.3413	4.6865	4.82	5.4661	5.1819	4.6008	4.8082	5.2185	5.2181	4.7122	5.2579	5.2462	5.2065	5.1224	4.9843	4.661	5.4054	5.0496		4.3841	
K.FEQASESEPTTVSYEIAGNSPNAER.G +3					5.3253	5.3591	5.9578	5.4377	5.2629	5.2607	4.6396	5.222	5.6434	4.9653	4.8916	5.1695				5.2891			4.2287	5.6972	
K.GDAGVSGVVK.F +1							1.8311					1.9809			1.8488	1.9467	1.9437				2.1039				
K.GDAGVSGVVK.F +2				3.7268			3.5711	3.6064	3.4518	3.1942	2.5809					3.6217			3.7765	3.2243	3.2321		2.9336		
K.LIGPTSVVGR.S +1						2.0605							2.1416	1.9719	1.8716										
K.LIGPTSVVGR.S +2	3.2548	3.0416	3.0448	3.0903	3.0045	3.2129	3.2213	3.2486	3.1484	2.9031	2.9499		2.86	2.7576		2.59					3.1717			2.9128	
K.TGNAGPRPACGVIGLTN.- +2	3.9582	4.0934	3.6144	3.9366		3.1795	3.5086	3.5098	3.2925	3.2775	3.3554	2.9466	3.2529		3.3089	3.6637	3.3477	3.9478	3.2097	3.4431	2.7378		3.3144	3.2946	
K.THGAPTDEVR.H +2		2.8226	2.6471								2.589	2.7024		2.6535		3.0166									
R.HVGDMGNVK.T +2		2.6036	2.7442																						
R.PACGVIGLTN.- +1							2.5438	2.2395	2.5037		2.2924		2.3097	2.4623	2.4943		2.161			2.2494		1.9061		2.4876	
R.SVVIHAGQDDLGK.G +1																						2.7865		2.004	
R.SVVIHAGQDDLGK.G +2					3.687	3.7885	3.9837	3.2401	3.6185	3.0135	3.7432	3.496	3.7942	3.788	3.597	3.6469					3.1403		3.4162		
R.SVVIHAGQDDLGKGDTEESLK.T +2									3.5064	2.6451	3.8546	2.6524	6.1193	6.1669	4.7774	6.2983	5.9242	5.8516	5.2603	6.3313					
R.SVVIHAGQDDLGKGDTEESLK.T +3				4.8545									5.0326	4.9652	4.6545	4.746		4.0996							
gi|6322565|ref|NP_012639.1|	9.1	17.6	15.6	21.8	22.4	30.3	22.4	26.5	40.9	11.5	30.3	35.3	26.8	30.9	37.1	37.1	17.9	13.8	29.7	40	13.8	16.5	31.8	20.3	Adenosine kinase, required for the utilization of S-adenosylmethionine (AdoMet); may be involved in recycling adenosine produced through the methyl cycle; Ado1p [Saccharomyces cerevisiae]
K.CAALITGHNR.S +2		3.2303	3.7749	3.6438	3.5033	3.3666	2.9501	2.9039	2.6133		3.0814	3.6531	3.3748	3.3022	3.1161	3.8279						2.9821		2.5715	
K.CAALITGHNRSLVTDLGAANFFTPDHLDK.H +3					4.1021	4.011	4.4154	4.0191	4.0054		3.7156	3.9567	3.9139	4.4336	3.6091	3.8659							3.5513		
K.ENDAILVDAK.S +1																				2.8924				2.81	
K.GTSTYPVKPLDSSK.I +2		3.3052	3.579	3.7568	3.5313	3.7886	3.5432	3.5578	3.849		3.2538	2.7636		3.3437	3.3527	3.2569	3.3035			3.3487				3.4893	
K.HWDLVEAAK.L +1																				2.1597					
K.IVDTNGAGDAFAGGFM*AGLTK.G +2															3.8992				4.1725		4.5611	3.9061			
K.IVDTNGAGDAFAGGFMAGLTK.G +2					4.1494	5.3797	3.8468	3.7135	5.6118		3.1349	3.6986			3.6923	5.3396	5.5411	3.4049		4.1205	2.6323	6.4064	4.1897	4.7288	
K.LVAGGAAQNTAR.G +2	3.1513		3.7737		3.1916	2.9762	3.5419	3.8092	2.7943	4.0606	3.5516	3.5026	2.8297	3.2153	2.71	3.8253	3.1232	2.7554	3.6138		3.1122	4.0672	4.0266		
K.M*AIFDELLQM*PETK.L +2										2.6629		3.0909	4.1772	4.2534	4.1263			3.9047		3.7535				2.7214	
K.M*AIFDELLQMPETK.L +2															3.1658	4.3176				3.9396			2.5028	2.797	
K.MAIFDELLQM*PETK.L +2												2.9776		3.8351	3.55	3.5777		3.8371		3.6684	3.1645		3.9613		
K.MAIFDELLQMPETK.L +2				3.8924		3.6986		4.0648	3.9508		3.6495					3.3444	3.2914			3.4236			2.6466		
K.SM*YQVQNDIGTGK.C +2																			4.1691						
K.SMYQVQNDIGTGK.C +2						4.7724			4.1975	3.8601	4.2047	4.1145								3.5606		4.8009	4.8089		
K.VIFTHGVEPTVVVSSK.G +2		5.1731	5.3893	4.5145					4.4252			4.0946	4.4592	4.3528	4.702	4.1594			4.2627	5.0619					
K.TVIFTHGVEPTVVVSSK.G +3													3.7253	3.9327	3.6297	3.7861									
R.GAAYVLGAGQVVYFGSVGK.D +2									4.038				3.8693	4.7926	3.0567	3.6919			4.0093	5.1778			3.0182		
R.SLVTDLGAANFFTPDHLDK.H +2	4.0094	3.089		5.6933									5.35	5.9956	4.8464				3.1494	4.1077					
gi|6322583|ref|NP_012657.1|	26.2	34.2	29.3	25.8	25.8	16	25.3	21.3	25.8	23.6	25.8	25.8	30.2	29.8	29.8	29.8	21.3	25.8	21.3	21.3	14.7	12.9	10.7	20	Protein component of the small (40S) ribosomal subunit, the least basic of the non-acidic ribosomal proteins; phosphorylated in vivo; essential for viability; has similarity to E. coli S7 and rat S5 ribosomal proteins; Rps5p [Saccharomyces cerevisiae]
K.AQCPIIER.L +2		2.5109	2.5361																						
K.DASLVDYVQVR.Q +1									2.6825																
K.DASLVDYVQVR.Q +2	4.0922	3.898	3.8983	3.9225	3.9928	3.9234	4.0475	4.0659	3.8378	3.8098	4.0073	3.8038	3.721	3.8305	3.7952	3.8587	3.917	3.8009	3.5809	3.8425	3.9392	3.6672	3.8396	3.9682	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.TIAETLAEELINAAK.G +2	4.9778	5.0233	4.9647	5.2993	5.0453	4.6113	5.0428	4.9887	4.8498		4.502	4.8607	5.0439	4.8872	5.0901	4.742	4.8226	4.8433	4.9481	4.9357				4.872	
K.TIAETLAEELINAAK.G +3									3.6245			4.53	4.4961	4.6725	4.5786	4.6914			4.0196	3.9234					
K.WSFEEVEVK.D +1					1.9989						2.3043		2.3908	2.248	2.1462	2.7426		2.5969	2.2946						
K.WSFEEVEVK.D +2	3.4821	3.371	3.3246	3.494	3.3498		3.5328	3.3449		3.2613	3.2574	3.0313	3.3075	3.1185	3.2735	3.1207	3.1498	3.1687	3.3225	2.9929	3.0776	3.1983		3.1302	
R.KAQCPIIER.L +2									3.4276					2.9905	3.1164	2.6007						3.3193			
R.LTNSLMMNGR.N +2					3.5725	3.5102			3.7603	3.1642	3.7917	3.2025	3.8582	3.1204	3.8077	3.8002								2.5434	
R.QAVDVSPLR.R +2							2.6518																		
R.QPIFVAHTAGR.Y +2	2.5789	2.7189																							
R.RQAVDVSPLR.R +2		3.058	3.0667	3.04						2.8564			2.8512					2.9817							
R.VNQAIALLTIGAR.E +2	4.8942	4.8772	5.1547	5.0143	5.2922		5.1622	5.2664	5.3448	4.7001	4.0301	5.1067	4.8936	5.0524	4.9328	4.7307	4.5621	4.047	4.4964	5.0791	4.0586		3.9511		
gi|6322599|ref|NP_012673.1|	9.2	16.7	11.4	23.7	30.4	40.7	39.8	33.1	50.7	14.5	29.2	48.7	45.7	58.2	51.5	57.7	11.7	6.7	37	25.3	16.4	9.5	28.7	26.2	Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase), dimeric enzyme that catalyzes the third step in the common pathway for methionine and threonine biosynthesis; enzyme has nucleotide-binding, dimerization and catalytic regions; Hom6p [Saccharomyces cerevisiae]
K.AALAASTTK.T +1													1.9683												
K.AALAASTTK.T +2						2.5274																			
K.AFSSDLATWK.A +1						1.8807	2.0043		2.3058		2.0664		2.0853	2.1164	2.1492	1.9974	2.0831	1.9036						2.1419	
K.AFSSDLATWK.A +2					3.4945	2.8898		2.5107	2.6141	3.0877		3.1852	3.0327		3.1738	2.9002	2.5453						3.0761		
K.DFSPLNVGSDWK.A +1															2.2684										
K.DFSPLNVGSDWK.A +2	4.0421	4.0253	4.1537	3.9365	4.1823	4.264	4.1683	4.1527	3.9311	3.6704	3.7691	3.8463	3.3473	3.6173	4.0256	4.2731	3.9258				4.2509	3.9092	3.9088	3.1457	
K.FVENGISIATPNK.K +2	3.5841											3.3762				3.6207						3.9121			
K.FVENGISIATPNKK.A +2			2.6703	3.3903									3.7849	3.4428				2.9778		3.4945					
K.GSDNVISIK.T +2											2.8363					2.5479									
K.IEGIFSGTLSYIFNEFSTSQANDVK.F +2					3.7011	4.4953	3.1753	4.9048	4.336			3.8077		4.6543	3.2053	3.4145									
K.LGYTEPDPR.D +2						2.8067			2.8247		2.7566											2.7014	3.121		
K.PVILVDNTSSAYIAGFYTK.F +2						5.1461			4.3049			2.519		4.0584	4.6038	3.2016									
K.RYTNPVVIQGAGAGAAVTAAGVLGDVIK.I +3																			3.8992						
K.SADEFLEK.L +1											2.0719														
K.SADEFLEK.L +2	2.6679																								
K.STITYNLVLLAEAER.S +2			2.8277		4.7422	4.5523	2.5106	3.3081	4.7137			4.076	5.1177	4.7714	4.9816	5.2229			3.5843	4.0325			3.6199	3.2238	
K.STITYNLVLLAEAER.S +3														5.2841											
K.TLPLDDLIAHLK.T +2		3.3512		3.0138									2.6171	3.1907	2.6408	3.1069			2.5837						
K.TSPKPVILVDNTSSAYIAGFYTK.F +2														3.1029											
K.TSPKPVILVDNTSSAYIAGFYTK.F +3														3.7357											
K.VVNVAVIGAGVVGSAFLDQLLAM*K.S +2							2.8104		2.9769			4.5376		7.2289	6.4319	5.3543			2.5939	4.7964					
K.VVNVAVIGAGVVGSAFLDQLLAM*K.S +3												3.8696	5.9046	6.6496	4.8832	6.6815				4.6769					
K.VVNVAVIGAGVVGSAFLDQLLAMK.S +3																				4.0199					
K.YDYSHPFASLK.G +2				3.338					3.3286				3.2519	3.1184	2.9438	3.2736			2.8144	2.7937					
R.DDLNGLDVAR.K +2		3.8176		3.5827			3.6637	3.7467	3.743	2.8921	2.7977	3.8356	3.6122	3.3315	3.4646	3.4372							2.8872	3.2648	
R.ISGVEVESPTSFPVQSLIPK.P +2					4.69	5.2408	5.0529	3.6968	4.9535	4.7935	4.6868	4.6013	5.0047	5.1824	5.0563	5.1627	2.8833		4.3264		3.2075		3.7537	4.5946	
R.ISGVEVESPTSFPVQSLIPKPLESVK.S +2														4.0286											
R.ISGVEVESPTSFPVQSLIPKPLESVK.S +3		5.2981		5.8679										4.3068											
R.YTNPVVIQGAGAGAAVTAAGVLGDVIK.I +2					6.3204	6.3025	6.6558	6.9537	6.6761		4.3972	6.0184	6.8864	6.963	6.9862	6.5066			3.5042		6.4476		3.9686	6.5418	
R.YTNPVVIQGAGAGAAVTAAGVLGDVIK.I +3					4.7829	4.8029	5.1679	5.1202	5.0371		3.9774	4.4257	5.4096	5.3173	4.9062	4.9612				3.7075					
gi|6322605|ref|NP_012679.1|	19.2	34.9	34.5	22.2	23	33	34.5	34.5	34.1	19.9	29.9	26.8	35.6	43.3	28.7	31.8	21.1	16.5	27.6	30.3	13	16.9	19.9	15.3	Protein component of the small (40S) ribosomal subunit; mutation affects 20S pre-rRNA processing; identical to Rps4Bp and has similarity to rat S4 ribosomal protein; Rps4ap [Saccharomyces cerevisiae]
K.DSLDNTFVTR.L +1													2.7377												
K.DSLDNTFVTR.L +2	3.641	3.7045	3.6801	3.784	3.5846	3.6835	3.6724	3.6819	3.5201	3.5455	3.6877	3.4366	3.6299	3.4568	3.5792	3.5867	3.1982					3.7244	3.514		
K.ERHDGGFDLVHIK.D +2																				3.4023					
K.ERHDGGFDLVHIK.D +3																				3.9959					
K.GVPYVVTHDGR.T +1									2.006																
K.GVPYVVTHDGR.T +2		2.9317	2.7695	2.8117		2.811	2.9913	2.9218	2.7408	2.7883	2.7616	3.0002	2.8438	2.7653		2.8851	2.5317	2.6905			2.7313	2.655			
K.IDLASGK.I +1						1.9994	1.9031	1.9147	1.933		2.0287														
K.KGVPYVVTHDGR.T +1																				2.2236					
K.KGVPYVVTHDGR.T +2		4.1552	4.3072											3.1039			3.4686		3.7127						
K.LSGCYAPR.P +2	3.0006	2.846	2.8743	2.7696	2.8708	2.752		2.8336	2.7147	2.8904	2.6524	2.598		2.8011		2.7102			3.1192						
K.LVYVTGGR.N +1			1.9733				1.823																		
K.LVYVTGGR.N +2						2.7579			2.5682			2.7559												2.699	
K.VRTDTTYPAGFM*DVITLDATNENFR.L +3																				4.1682					
R.ESLPLIVFLR.N +2		2.8548	3.3175	3.0712	3.2022	2.5975	2.8321	3.2134	2.9512		3.0791	2.6836	2.9271	2.8677	2.8359	2.6745	2.7415		2.7177	2.5994			3.3615		
R.HDGGFDLVHIK.D +2													2.5118	2.7277	3.1651										
R.HDGGFDLVHIK.D +3													4.0229	4.0719											
R.ITDEEASYK.L +1	2.4402						2.2253				2.2323		2.2511	2.5169	2.1661			2.258					2.4288	2.5483	
R.ITDEEASYK.L +2	3.4165	3.2314			3.2011	3.3686	3.326	3.053			2.8184		2.603		2.5285	3.0849									
R.LAAPHHWLLDK.L +2														2.9442											
R.LNNVFVIGEQGK.P +2			2.8176				3.7257	3.9967	4.0648				4.1873	3.4461	3.4457	3.5793									
R.LNNVFVIGEQGKPYISLPK.G +2		5.683	5.3669										5.1834	5.8172					5.2003	5.1417					
R.LNNVFVIGEQGKPYISLPK.G +3		3.8181		3.5511									3.6183	3.6083											
R.TDTTYPAGFM*DVITLDATNENFR.L +2					2.8607	3.3203	3.0266		4.6425	3.2669		3.38	5.3241	5.2547	4.5947	3.9075		3.6503	4.4379	2.9518		4.5966		2.9166	
R.TDTTYPAGFM*DVITLDATNENFR.L +3													4.7512	4.7176	4.069				4.3116						
R.TDTTYPAGFMDVITLDATNENFR.L +2	5.0245	5.1504	5.3853		5.5004	5.6597	5.6351	5.4195	5.4309	4.7511	4.9396	5.0664		3.8223	4.1944	4.5798	4.6855	5.099		3.6026	4.8543	3.8892	5.0814	5.2205	
R.TDTTYPAGFMDVITLDATNENFR.L +3					5.5451	5.5135	5.3008	4.9444	5.5549	3.7142		4.1494						5.0617			4.7751		4.3471		
gi|6322608|ref|NP_012682.1|	6.9	12	11.4	11.4	19.4	9.8	19.9	21.5	33.8	9.3	19.7	28.2	34	42.3	34.3	31.1	24.2	15.2	19.9	37.5	19.7	9.8	14.9	22.3	Cytosolic branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during stationary phase and repressed during logarithmic phase; Bat2p [Saccharomyces cerevisiae]
K.ELVTAPLDGTILEGVTR.D +2	4.8841	5.0031	5.0215	4.5758	4.9772	5.049	4.9739	4.9083	4.9461	4.345	4.4925	4.2082	4.6472	5.0022	4.5021	5.1161	4.7735	3.9295	4.3629	3.8328	3.8028	3.2317	4.7007	3.9282	
K.ELVTAPLDGTILEGVTR.D +3														4.5548											
K.ERLEPSEWTISER.Y +2																	3.4618	3.2429		2.8535					
K.EVAQWINGIQYGETEHGNWSR.V +2																				2.9712					
K.GEQINIPLLPGEQTGPLAK.E +2		4.052			3.5085		3.7594		3.5552		3.5837	3.1717	3.4715	3.4359	2.8487	3.8084	3.1892		3.9327	3.5011	4.1113		3.2977	4.1113	
K.KELVTAPLDGTILEGVTR.D +2													3.2466												
K.KLGANYAPCVLPQLQAASR.G +2																			3.8603	4.4911					
K.LGANYAPCVLPQLQAASR.G +2								3.6554	4.5749	3.4419	4.2085	3.2334	3.9063	3.8134	2.9377	4.4816	3.3398		3.5002		3.6426			3.5203	
K.LGANYAPCVLPQLQAASR.G +3													3.8739												
K.NGELLEAFGSGTAAIVSPIK.E +2					3.4916	4.2653	4.2318	4.4801	4.0566		3.1285	3.4641		3.875		4.3066			4.0811	4.9832	4.1376	3.5305	3.7039	4.1629	
K.SFTDHM*LTAEWTAEK.G +2													3.99	4.0729	2.7032										
R.ALLYVICCPVGPYYK.T +2									4.6505			4.3667	4.799	4.8554	4.9118	4.7685	3.976			4.7172					
R.ICLPTFDPEELITLIGK.L +2			3.9075	3.2251	4.417			4.4763	4.5497			3.7508	3.8531	3.4706	2.8243	4.6474		2.7085		3.8472					
R.LEATDYATR.A +1													2.4712												
R.LEATDYATR.A +2	3.357	3.3029	3.3327	2.9595			2.9499	2.9195					3.1819				3.5532								
R.LEPSEWTISER.Y +2									2.6388					2.5616	2.7395	2.9433									
R.PTLIGTTAGLGVSTPDR.A +2													2.6406	5.0845	4.1187										
R.YFTIGEVTER.S +2							2.7048		2.5633					2.9012				2.5405						3.0582	
gi|6322666|ref|NP_012739.1|	3.3	10.3	12	7.9	16.3	15.9	19.6	15.9	26.1	12.5	17.4	20.4	25.8	27.7	26.6	21.9	21.3	15.8	17.7	30.6	7.5	7.6	14.3	10.4	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities; Fas1p [Saccharomyces cerevisiae]
K.AHPNFPIALQWTGGR.G +3																				4.3177					
K.AIFPNTVDGDLLK.L +2		3.3384	3.5037	2.5264	3.2742	3.0761	3.3331	2.9308	2.8356	2.925	2.8189	2.8867	3.0005	3.3466	2.8891	3.2263	3.4228			3.038					
K.ALAGSEINWR.H +2	2.97				3.1883		3.7317			3.0768							3.2873	2.9804						2.9366	
K.ATHILDFGPGGASGLGVLTHR.N +3																				4.3858					
K.ATSSTDEESWFK.A +2	3.5575	3.4295	3.5169	3.5345	3.5639	3.6075	3.7319		3.2125	3.5156	3.5036	2.8339								3.777				3.0971	
K.CFGPIKVELPTK.E +2																			2.6546						
K.CIAACTGVPDDKWEQTYK.K +2													3.9005	4.5823			4.4102	4.5692		3.4118					
K.DIQIPVYDTFDGSDLR.V +2		4.7414	5.1195		4.9002	5.4239	5.3601	4.9905	5.3704	4.2875	4.4023	3.9218	4.9504	4.3698	4.1691	5.0389	4.851			4.1614	4.7268	3.2045	2.58	4.8162	
K.DSLWQSEHLEAVVDQDVQR.T +2																5.6542	5.485			4.8984					
K.DSLWQSEHLEAVVDQDVQR.T +3													3.9299							3.8025					
K.EFDETIFNLPK.N +2		3.8461	3.8223	3.5925	3.8505	3.9637	3.866	3.5667	3.8523	3.2101	3.7516	3.7065	3.592	3.9436	3.5574	3.4261					3.3947	3.4531	3.5871	3.5447	
K.EINEHSTSYTFR.S +2									3.5261							2.6758		2.8199							
K.ENIIQMEMIENR.T +2						3.6541	2.7333	3.835	3.139			2.9649				4.126	3.9837			2.9957					
K.EVYDFTHAVGNNCEDFVSRPDR.T +3													3.5334												
K.EWFQLDDEDFDLLNK.T +2		5.4259	5.5457	5.1667	5.7137	5.5547	5.7219	5.5268	5.618	3.716	4.1699	5.2524	5.4224	5.407	5.5622	5.5769	5.0465	4.271	5.2427	5.4383		3.0001	5.7457		
K.EYFQDVVDLTGSEPIK.E +2						5.1662	4.7825	4.2883	4.6316	3.5301	3.7217	4.2755	4.4775	4.8043	4.2643	4.8705			3.5361	3.8684	4.7275	4.8123	5.0372	4.5684	
K.FDYPPMPFDGFLFGSR.V +2							2.9593	2.5486	3.5648			3.2304		3.8026	4.0257										
K.FDYPPMPFDGFLFGSR.V +2					3.0419																				
K.FLGYVSSLVEPSK.V +2		3.1739			4.422	4.618	4.2306	4.7748	4.6775		3.7817	4.3313	4.7202	4.3488	4.3658	4.8401	4.167	4.7		4.1365	4.3837	4.7059	4.2058	4.2952	
K.FSAETLSELIR.T +2					4.0829	3.9562	4.1964	3.8963	4.0576	2.7505	3.9231	3.9193	4.1018	4.0828	4.1657	3.9748	3.6798	3.7477	3.8266	3.6033	3.3674		4.2126	3.6876	
K.GLLSATQFTQPALTLM*EK.A +2													4.5037	4.5882	4.3735			3.981	4.5428		4.0729				
K.GLLSATQFTQPALTLMEK.A +2			4.5083				3.4416	4.399	6.2452						4.0505		5.0509	2.6702	2.7135	4.691					
K.ILPEPTEGFAADDEPTTPAELVGK.F +2	4.7767	4.0293	4.3214		4.4712	4.7726	4.5843	4.7691	3.7121	3.8236	4.0064	3.9243	4.933	4.5082	4.0765	4.0213			4.0068			3.5723	4.2099	3.436	
K.ILPEPTEGFAADDEPTTPAELVGK.F +3													3.5026	3.6421											
K.IVDVVGTLSR.N +2						3.5139	3.4219	3.0939	3.0706	3.2846	3.0226	3.153	3.2465	3.534	3.6328		3.0341	3.1951							
K.KLLHQYYGDDESK.I +2																				3.7706					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.KPTGGIVTVR.S +2		2.8873	2.7739											3.087											
K.LLGFTPGELR.S +2			2.7246	2.6613	2.5724				2.9846			2.9356	3.3908	3.4308	3.2214	3.1374	3.153	2.9844	3.1461	3.5001					
K.LLHQYYGDDESK.I +2					3.2933		3.7993				3.9207		3.8933	3.8912	3.4073			3.5363							
K.LLQENDTTLVK.T +2					3.0068	3.3605	3.0789	3.4007	3.0726	3.0971	3.6266	3.59			2.8901	3.5674						3.0643			
K.LVHLSNGYK.M +1																	2.7012		2.7476	2.8991					
K.LWIDEPFNLDFDPR.D +2		3.3188	4.5752	4.6428	4.7531	4.5607	4.5121	4.6029	4.1922		4.2046	4.1599	4.7783	4.826	4.4124	4.2817	3.4573		2.9125	4.7573					
K.M*FVSNPIR.K +2														2.6011											
K.MFVSNPIR.K +2													3.0143	2.689	2.6943	3.0484				2.5341			3.1403		
K.MFVSNPIRK.V +2			2.7027	2.5266														2.523							
K.NANIFSSVK.C +1													1.9772		1.838										
K.NLVVSGPPQSLYGLNLTLR.K +2					5.5587		5.8053	5.2063	5.3402	3.3978	2.6393	4.5265	5.0707	5.7905	5.5177	2.9104		2.9751	3.2535	3.588				3.375	
K.NLVVSGPPQSLYGLNLTLR.K +3													5.4811						4.5022	4.0003					
K.NNVSFNAK.D +1																							2.0719		
K.NPNWLEEYHPK.L +2													3.2808	3.5337			3.4499			3.119					
K.PGSIDAISQVINIAK.A +2													3.2028		3.7568		2.5189	5.258		3.5432					
K.PLQVGDVVSTTAVIESVVNQPTGK.I +2									3.2084					3.7539						2.8482			4.9929		
K.PLQVGDVVSTTAVIESVVNQPTGK.I +3													4.3424	4.4345	3.7086										
K.PWFATVNGQAR.D +2																	3.1208	3.5313							
K.QEIFDVTSNGLK.K +2						3.1376			2.8713		2.6714	2.8382	3.1702				2.7957	3.3742		3.04					
K.QVEISLVNGAK.N +2																		2.6539							
K.RDYIISR.L +2																2.5831									
K.SIMDGIHDGHIK.K +2																				2.8578					
K.TLSLIQSYSLLDKPDEAIEK.V +2														2.7647					2.9876	4.6854					
K.TNSHLPAGK.Q +2	3.0131	3.126			2.884							2.5489													
K.TSIQHVGMINGR.K +2															3.0477			3.2094		2.5129			2.9578		
K.TVEPVYQM*HIK.T +2													2.6331						2.7645						
K.TVEPVYQMHIK.T +2																	2.8199	2.6076							
K.TVVTLSEPVQGELKPTVILK.L +2			4.5048						4.3696				4.6284	4.2537	4.3762				3.3583	3.2146					
K.VFKPSQGM*VVEISNGNTSSK.T +2																			3.9664						
K.VFKPSQGMVVEISNGNTSSK.T +2																	3.8704			2.9864					
K.VFNAYPAAR.E +1															2.2024			2.2718							
K.VFNAYPAAR.E +2					2.8545			3.2349	3.0793	3.2638	2.653											2.9564			
K.VFTQGLNILEWLENPSNTPDK.D +2												2.7339							3.771	4.4968					
K.VFTQGLNILEWLENPSNTPDK.D +3																				3.7356					
K.VNLENPIPIAVLDSYTPSTNEPYAR.V +2					4.1831	4.6077	4.646	4.1866	4.5637	3.36	3.3364	3.505				5.1611	3.2948		4.8932	3.2946					
K.VNLENPIPIAVLDSYTPSTNEPYAR.V +3															5.6479	4.0749									
K.YIPNLTAKPFQVTK.E +2																			2.8598						
R.ALDTVTNVLNFIK.L +2		4.5467		4.6198	4.3734	4.5524	4.4242	4.7828	4.1372		3.7515	3.9634	4.7034	4.798	4.9662	4.2292	3.9207		4.3585	3.3162			3.9833		
R.ALIENWAADSVSSR.V +2		4.6732	4.9722	4.9108	5.0003	4.8337	4.9087	4.858	4.9547	4.5918	4.7471	4.663	5.0493	4.7437	4.7956	4.8562	4.7861	4.3019		4.8761					
R.AVGEGNAQLVAIFGGQGNTDDYFEELR.D +2							3.643		3.0814																
R.DLATM*TYEEVAK.R +2						3.8641								3.6837				2.6276		2.8023	2.8645			2.7003	
R.DLATMTYEEVAK.R +2				3.6738	4.2291	4.1974	3.8308		4.0811		3.1867	2.9508			2.9823	3.1528	3.9312				3.597	3.4219	4.3931	3.7848	
R.DLYQTYHVLVGDLIK.F +2														3.7672											
R.DLYQTYHVLVGDLIK.F +3														3.9201											
R.ENYSAM*IFETIVDGK.L +2						2.5236			4.0151			4.4289	4.761	4.6973	4.4621	4.3401					4.3371		2.8554		
R.ENYSAMIFETIVDGK.L +2												3.3617			3.7887		4.3029			3.8545			2.7472		
R.GMTMQVAVPR.D +2																2.5728		2.7586							
R.GNYTDFENTFQK.T +2				3.4031	4.2834	4.0687	3.4437	3.9863	4.252	3.0301	4.3792			2.7792	2.9948	3.3603	3.8054	4.1049	4.0338			3.6669	4.1999	2.8721	
R.GYTCQFVDM*VLPNTALK.T +2									3.2919			3.4295	3.7521	3.7151	3.2369	3.5459				3.0077				2.9422	
R.GYTCQFVDMVLPNTALK.T +2											2.6934					3.4522	3.3558			3.6252			4.0591		
R.HASFLCSFITQDK.M +2	2.6363												4.2651	4.1276	3.5647					3.7144					
R.LNADFQKPWFATVNGQAR.D +2														4.6293	3.0976										
R.LNADFQKPWFATVNGQAR.D +3														5.2094											
R.LVELMFIR.S +2														2.572	3.1203	3.151				2.6656			2.9134		
R.NGKPVM*EVTSSFFYR.G +2													2.6708												
R.SNYGM*IAINPGR.V +2													3.4183	3.4899									3.7074		
R.SNYGMIAINPGR.V +2						3.3263	4.042		4.1836		3.9448	3.8832	4.0085	4.066	3.916	4.1628							3.5932	4.0891	
R.STNSWFDVTWR.T +2									2.5182							3.0184		3.6433	2.9206	3.2334	3.0686			2.631	
R.TCILHGPVAAQFTK.V +2		4.7816	4.6621						4.4307				4.4248	4.7726	4.4612	4.3822	4.1916		4.237	4.365					
R.TCILHGPVAAQFTK.V +3													3.6753	4.3476											
R.TM*DGKPVSLPLLYNFNPDNGFAPISEVM*EDR.N +3														5.0533											
R.VAASFSQEALQYVVER.V +2		4.3808	5.0243	4.8991	5.1821	5.0072	4.9241	5.2314	4.657	2.9401	4.7924	4.8833	4.9929	4.9231	4.8551	4.6766	3.3362	4.3858		4.898		3.0202	3.8431		
R.VAASFSQEALQYVVER.V +3													4.7522	4.44	4.4404				3.5468						
R.VIVAGTLDINPDDDYGRK.Q +2		3.0836	4.6511		5.5137	6.0358	5.8175	5.5116	5.7421		4.3639	4.8478	4.7435	5.2901	4.4904	5.447	3.8803		4.3946	5.1529	5.1542		4.8792	4.8894	
R.VLSGSISER.I +2																2.6772									
R.VSGDLNPIHVSR.H +2			2.6573	4.1676					3.7773	3.6597		3.7252	4.466	4.0733	4.1265	4.318	3.831	4.2393		4.0125	3.2459		4.0058		
gi|6322697|ref|NP_012770.1|	53.4	58.7	61.9	58.7	55.5	53	60.3	57.1	60.7	53.4	49.4	65.2	57.1	60.7	54.7	60.7	60.3	57.1	59.1	59.1	49.4	34	46.2	41.3	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglycerate during glycolysis and the reverse reaction during gluconeogenesis; Gpm1p [Saccharomyces cerevisiae]
K.HLEGISDADIAK.L +1						1.8892		3.6759	3.5064				3.395	3.5102	3.3836	3.3308		3.301	3.4582	3.5471			1.9711		
K.HLEGISDADIAK.L +2		4.0897	4.0666	4.0973		3.8115	3.0953	3.86	4.0486	3.8984	4.2287	4.0191	3.8083	3.7052	3.958	3.7455	3.5823	4.1959	3.0032		3.59	3.3391	3.5998	3.1055	
K.KVYPDVLYTSK.L +1													3.4499	3.3424	3.1738	3.3307	3.3939	3.4067	2.8767	3.3351					
K.KVYPDVLYTSK.L +2	4.1999	4.1292	4.436	4.2339				3.935	3.7004	3.719		3.253	3.6063	3.2123	3.6084	3.6043			2.6317	3.4134					
K.LNIPTGIPLVFELDENLK.P +2	3.9012	4.3257	4.2549	4.65	3.2192		3.3973	2.7303	3.183			3.1615	3.2089	2.7976		3.4934	4.0783	2.6672	2.6127	3.5273					
K.LNIPTGIPLVFELDENLK.P +3																		4.2127	4.607	4.5908					
K.NLFTGWVDVK.L +1							2.8045	2.9014				2.4713	2.9515	3.0605	2.8709		2.8156	2.9149	2.9081	2.1368					
K.NLFTGWVDVK.L +2	3.6576	3.7064	3.6714	3.7394	3.9215	3.5622	4.0342	3.6963	3.5552	2.9455	3.5834	3.9757	4.1499	3.5822	3.7466	3.5554	3.6338	3.3099	3.2883	3.4804	3.0699	2.6842	3.7051	3.1952	
K.PSKPSYYLDPEAAAAGAAAVANQGK.K +2	5.8654	5.8162	6.0312	4.7509											3.9943		5.2141		3.7854	4.5731					
K.PSKPSYYLDPEAAAAGAAAVANQGK.K +3	5.4087	5.3967	5.4831	5.0035															3.6763	4.4189					
K.PSKPSYYLDPEAAAAGAAAVANQGKK.- +2																				4.2469					
K.PSKPSYYLDPEAAAAGAAAVANQGKK.- +3		6.5181																		4.2394					
K.PSYYLDPEAAAAGAAAVANQGK.K +2					6.8446	6.6029	6.6246	6.5071	6.443	5.6042	6.3446	5.6645	6.3889	6.8356	6.5205	6.6867	6.3071	5.8368	6.601	5.9124	2.9082	5.5341	6.6183	6.4868	
K.PSYYLDPEAAAAGAAAVANQGK.K +3																			4.715						
K.PSYYLDPEAAAAGAAAVANQGKK.- +2																			3.9265	4.1421					
K.PSYYLDPEAAAAGAAAVANQGKK.- +3				4.5652																4.0572					
K.TVM*IAAHGNSLR.G +2	3.8615	3.856	3.7414	3.736	3.7287	3.3803	3.8227	3.798	3.4511	3.3718	3.545	3.713	3.7881	3.6879	3.5974	3.2196			3.153	3.0432			3.1861		
K.TVMIAAHGNSLR.G +1			2.9616								2.9821				2.6977					2.819					
K.TVMIAAHGNSLR.G +2	3.9311	3.8105	3.8828	3.8366	3.8014		3.823	3.9146	3.713	3.7079	3.6717	3.7161	3.6622	3.6852	3.5698	3.8775	3.7006	3.5745	3.6588	2.8945	3.52		3.604		
K.VYPDVLYTSK.L +1					2.4897	2.6243	2.1954	2.9053	2.6783	2.7926	2.6057	2.766	2.6601	2.6806	2.5816	2.7295		2.4085	2.1957	2.4049	2.606	2.496	2.5998	2.3804	
K.VYPDVLYTSK.L +2	2.5002			2.8124	2.8554	2.7988	3.0771	2.8401	2.8567	2.8538	2.8901	2.6072						2.5376							
K.YVDPNVLPETESLALVIDR.L +2	6.2875	6.4682	6.5467	6.2178	6.3021	6.188	6.3152	6.3634	5.9953	6.3298	6.3236	6.0919	6.028	6.0978	5.5334	5.8744	6.0331	5.3536	5.0917	5.663	5.5756	4.0985	4.3575	5.6482	
K.YVDPNVLPETESLALVIDR.L +3					4.4392	4.3326	4.6375	3.6579	4.614	4.0322	4.2633	4.7297	4.3125	4.6953	4.6773	4.3313			4.7056	3.5719	3.6808	4.3289	4.4565	4.0064	
R.AIQTANIALEK.A +1			2.5308		2.3778																				
R.AIQTANIALEK.A +2	3.8978	3.7212	3.8376	3.924	4.0013	3.8651	3.875	3.8419	3.8025	3.7139	3.7153	3.5737	3.7325	3.8008	3.7388	2.8929	3.8057	3.5551	3.1478	3.273	3.4481	3.7726	3.6464	3.5135	
R.HGQSEWNEK.N +2			3.1522		3.4231	3.1243	2.9061		3.1777	3.1219		3.2121		3.2485	3.3157	3.0758									
R.HYGDLQGK.D +2	3.3557	3.511	3.3751	3.4276	3.3119	3.1859	3.2882	2.8562	3.2043	2.6658	2.9119	2.9732	2.7672	2.6628	3.0226	3.333	2.9244	2.5951	3.2156	2.5806	3.1154				
R.LLPYWQDVIAK.D +2												2.6269													
R.RSFDVPPPPIDASSPFSQK.G +2																	2.5951		3.5431	3.0997					
R.RSFDVPPPPIDASSPFSQK.G +3																			3.8681						
R.SFDVPPPPIDASSPFSQK.G +2	3.856	3.7412	3.7104	3.5714	3.6461	3.7497	3.483	3.895	3.5753	3.1392	3.465	3.3619	2.8243	3.4168	2.9445	3.37	3.68	2.7836	2.902	2.989	2.7412		2.9994	2.6021	
R.SFDVPPPPIDASSPFSQK.G +3					3.5137		3.5024						3.7343	3.6101		3.776				3.5609				3.545	
R.SFDVPPPPIDASSPFSQKGDER.Y +2																	3.5161								
gi|6322790|ref|NP_012863.1|	44.6	50.4	49.6	40.9	35.9	23.7	31.8	35.9	40.7	31.8	31.8	36.2	58.5	54	53.8	46	37.9	42.6	54.3	58.2	20.6	20.9	27	15.6	Fructose 1,6-bisphosphate aldolase, required for glycolysis and gluconeogenesis; catalyzes conversion of fructose 1,6 bisphosphate to glyceraldehyde-3-P and dihydroxyacetone-P; locates to mitochondrial outer surface upon oxidative stress; Fba1p [Saccharomyces cerevisiae]
-.MGVEQILKRKTGVIVGEDVHNLFTYAK.E +3													3.8061												
K.DYIM*SPVGNPEGPEK.P +2																				4.343					
K.DYIM*SPVGNPEGPEKPNK.K +2				3.891					3.6479	3.9145			4.2262	3.95	3.9652	4.1025	3.8758	3.6774	3.996	3.2526					
K.DYIM*SPVGNPEGPEKPNKK.F +2					2.9812			4.3298		2.9794	2.8993		4.6601	4.4923	3.9631	4.6277		2.6471	5.0885	3.8002		3.5317			
K.DYIM*SPVGNPEGPEKPNKK.F +3		3.8647		3.6381			3.6514	3.929		3.728			3.9643	3.7662	3.7182										
K.DYIMSPVGNPEGPEK.P +2	4.6444	4.4309	4.5357	4.9345							4.24						4.5107	4.8045		4.5608		3.2853			
K.DYIMSPVGNPEGPEKPNK.K +2	4.754	4.6912	4.6381	4.5292			4.198		3.5751	3.985	4.0162	4.2882	4.3887	4.0964	4.146	4.4972	4.3285	4.1757		4.0807	3.3157				
K.DYIMSPVGNPEGPEKPNKK.F +2		4.9434	4.7793	4.0362				4.0588	2.8368				4.6632	4.5404	3.7649	4.6469	4.0027	4.3213		4.6423			3.0024		
K.EDLYTKPEQVYNVYK.A +2		4.3194			2.7893			4.3661	4.3218				4.4717	4.3628	4.2093	4.5191	3.7973	2.7686	3.8095	3.4296					
K.EHGEPLFSSHM*LDLSEETDEENISTCVK.Y +3		5.4063	5.4268	5.0121									3.519	4.7443	3.7668				3.5861	5.0488					
K.EHGEPLFSSHMLDLSEETDEENISTCVK.Y +3	5.393	6.0696	6.4902	5.217																5.062					
K.FAIPAINVTSSSTAVAALEAAR.D +2	6.8537	6.8756	6.8106	6.4763	7.1366	6.7768	6.8448	7.0465	6.8381	6.4597	6.5326	6.7366	6.2884	6.2423	6.4	6.3687	6.0228	6.0208	6.5394	6.5043			5.7888	6.1088	
K.FAIPAINVTSSSTAVAALEAAR.D +3					5.5678	5.2888	5.4543	5.5544	5.385	4.8539	4.5007	5.4073	5.2294	5.2639	5.045	5.0294	4.584	3.9076	5.2657	5.1111			4.7452	4.9881	
K.GAIAAAHYIR.S +1														1.8925				1.8667							
K.GAIAAAHYIR.S +2	3.6738	3.591	3.6414	3.6779	3.7016		3.7968	3.7234	3.6596	3.6722	3.4918	3.5883	3.5116	3.7271	3.6239	3.5632	3.3888	3.1583	3.3592	3.3886	3.3483	3.5491	3.4222		
K.GISNEGQNASIK.G +1																		1.8893							
K.GISNEGQNASIK.G +2	3.6512		3.5015		3.5268	3.5663	3.7815	3.2201	3.366	3.1462	3.4318	3.5059	3.1735	3.2029	2.7281	3.1018			2.9998		2.868	3.4188	3.6164		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.KDYIM*SPVGNPEGPEK.P +2																			3.9545						
K.KDYIM*SPVGNPEGPEKPNKK.F +3													4.3994												
K.KDYIMSPVGNPEGPEK.P +2																		4.8325							
K.KDYIMSPVGNPEGPEKPNK.K +2																				2.8942					
K.KDYIMSPVGNPEGPEKPNK.K +3														3.6005											
K.KDYIMSPVGNPEGPEKPNKK.F +3														3.6972											
K.KLLPWFDGM*LEADEAYFK.E +2																			2.5842						
K.LLPWFDGM*LEADEAYFK.E +2				4.3907	5.0134	4.4631	4.823	4.6622	4.7053	3.7094	4.5184	4.6193	4.0952	4.2875	4.1235	4.7411		3.0727	4.3592	3.9983					
K.LLPWFDGM*LEADEAYFK.E +3					4.683	5.03	5.3068	5.077	5.0646		5.1374	4.7948	4.7659	5.2103	5.1502	4.3295									
K.LLPWFDGMLEADEAYFK.E +2		4.3083	4.4369	4.2604	4.7844	4.583		3.4886				2.6373						2.5044							
K.LLPWFDGMLEADEAYFK.E +3																				3.9045					
K.PLFLVFHGGSGSTVQEFHTGIDNGVVK.V +3																				5.7763					
K.SPIILQTSNGGAAYFAGK.G +2	6.8457	6.8596	6.9717	6.6972	6.881	6.9524	6.7922	6.9444	6.5291	6.7128	6.7551	6.5716	6.5896	6.6499	6.5846	6.6522	6.294	6.5926	6.6236	6.3939	6.1747	6.4243	6.4528	6.305	
K.SPIILQTSNGGAAYFAGK.G +3													5.7092	5.8837	3.5321			4.1978							
K.TGVIVGEDVHNLFTYAK.E +2	5.8131	6.0052	5.9246	5.669					5.0593			4.9414	5.7912	5.804	5.642	5.3817	4.7669	2.9216	5.4654	5.5801					
K.TGVIVGEDVHNLFTYAK.E +3		3.6185																							
K.VNLDTDCQYAYLTGIR.D +2	5.7988	5.8772	5.7987	5.5847	5.837	5.8452	5.8304	5.8545	5.6978	5.7761	5.7627	5.8645	5.6229	5.5617	5.6262	5.6115	5.6118	4.0855	5.5902	5.799	5.1932	5.3011	5.5706	5.6113	
K.VNLDTDCQYAYLTGIR.D +3												3.7616	3.9344	3.8048		3.6557				4.159					
R.DYVLNKK.D +1													2.1476					2.315							
R.KTGVIVGEDVHNLFTYAK.E +2													2.6536												
R.SIAPAYGIPVVLHSDHCAK.K +2	3.6504	4.9844	4.9392										4.8764	4.5798	4.7463	4.3604	4.6216		3.6274	5.0484					
gi|6322912|ref|NP_012985.1|	5.6	16.7	11.1	10.9	30.9	28.1	30.1	29.9	43	25.8	29.9	34.7	50.4	47.8	47.6	46.1	28.1	29.1	19.7	39.2	20.3	12.4	19.2	23	Translation initiation factor eIF4A, identical to Tif2p; DEA(D/H)-box RNA helicase that couples ATPase activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker; interacts with eIF4G; Tif1p [Saccharomyces cerevisiae]
K.APQALM*LAPTR.E +2	3.7133	3.5532		3.6001		3.5002	3.6267		3.4127	3.4995	3.5429	3.1295	2.5336	3.5208	3.1983	3.2698		2.9054		3.3952	3.7192			3.6603	
K.APQALMLAPTR.E +1																				2.3301					
K.APQALMLAPTR.E +2	3.9176	3.967	4.0829	3.7231	4.0512	4.0117	3.8797	4.0964	3.712	4.3882	3.8407	3.1086	3.7331	3.4269	3.5898	3.7111	3.9338	3.7537			3.2448		3.9745	4.0154	
K.FDDMFELDENLLR.G +2					3.7542	4.0652	3.7574	3.8427	4.0327	4.2414	4.2113	3.8935	3.4858	3.4425		4.1183			3.8213	3.2736	4.205		3.1455		
K.FDDMELDENLLR.G +2		4.1678	4.372		4.4247	4.5869	4.4825	4.4124	4.4188		4.3321	4.0739			4.2186	4.2349		3.7361				4.1494		4.2076	
K.FTVSAIYSDLPQQER.D +2					3.7733	3.9473	3.019		3.4444	3.2014	3.8141	3.0719	4.4838	4.5127	4.0503	3.9558					3.1424			3.2354	
K.GVAINFVTNEDVGAM*R.E +2													4.342	4.8378	4.6562	3.6096		3.9202							
K.GVAINFVTNEDVGAM*R.E +3													4.8208	4.5719											
K.GVAINFVTNEDVGAMR.E +2							5.119		4.2693		4.3022	4.3804		5.1195	4.6987	4.8575		2.9916		4.9525		4.9183	5.3155	3.7901	
K.KDELTLEGIK.Q +2													2.5076					2.9949		3.0657					
K.M*FILDEADEM*LSSGFK.E +2										3.2117		3.9615	5.1645	5.3004	5.3301						6.1148		3.2931		
K.M*FILDEADEMLSSGFK.E +2					3.4245		5.1266	5.8689	5.2486		3.846	4.5404		2.8506	3.7229					5.2038			5.0142		
K.MFILDEADEM*LSSGFK.E +2		3.3599				4.2941	4.6582		3.4804			3.4609			4.8831	3.1855		4.0086		4.0058	5.3323				
K.MFILDEADEMLSSGFK.E +2					5.6608	4.017	5.7293	5.9892	5.8942			5.3842				5.9768	5.7035			5.1168			5.5544		
K.QFYVNVEEEEYK.Y +2					2.9458		2.9737	3.1486	3.2094				3.2905	3.8547	3.5049	3.6936		2.6232		2.7527					
K.TGTFSIAALQR.I +2	3.6247	3.7176	3.6574	3.4628	3.7192	3.8278	3.7187	3.9306	3.8323	3.6438	3.666	3.6916	3.9912	3.745	3.2553	3.8158				3.3538		3.7637	3.6292	3.4283	
K.VHACIGGTSFVEDAEGLR.D +2													5.8287	5.26	6.2248		4.4558								
K.VVM*ALAFHM*DIK.V +2													3.7315	3.5307	3.6079	3.3917		3.1962							
R.AIM*PIIEGHDVLAQAQSGTGK.T +2									5.0853				5.2652	5.304	4.4575	5.0528			4.9676	3.9469					
R.AIM*PIIEGHDVLAQAQSGTGK.T +3									4.6335				5.2188	4.8796	4.0025	3.7432									
R.AIMPIIEGHDVLAQAQSGTGK.T +2									4.0087						5.66	5.1508	5.8877			5.0107					
R.AIMPIIEGHDVLAQAQSGTGK.T +3															5.1535					4.711					
R.DAQIVVGTPGR.V +2				2.731		2.898		3.6471	2.793	2.775	2.6463	2.9655	3.6054		3.4276	3.3909									
R.ELALQIQK.V +1													2.5852												
R.GIDVQQVSLVINYDLPANK.E +2					3.7365	4.8839		4.2133	4.8569			3.0436		4.3412		3.8601	3.4387		3.6897	4.1267					
R.GIDVQQVSLVINYDLPANK.E +3														3.8764											
R.GVFGYGFEEPSAIQQR.A +2		5.1404			5.0289	4.631	5.2402	4.9124	4.5625	3.9953	5.1243	4.5142	5.3055	5.4421	5.0732	5.2467	4.6725	4.4116	3.5387	4.46	4.3878			5.1259	
R.ILISTDLLAR.G +2			3.6718	3.4313	3.43		3.7654	3.6241	3.6129	3.4823	3.1472	3.638	3.7143	3.7567	3.7474	3.7771	3.7326	3.375	3.4612	3.652	3.2909	3.6359	3.6477	3.4471	
R.KGVAINFVTNEDVGAMR.E +2																				3.166					
R.VFDNIQR.R +1															1.9135										
gi|6322978|ref|NP_013050.1|	38.5	55.9	38.5	38.5	55.9	55.9	55.9	72	72	49	55.9	72	55.9	72	46.2	72	62.2	29.4	54.5	46.2	46.2	39.2	55.9	51	Cofilin, promotes actin filament depolarization in a pH-dependent manner; binds both actin monomers and filaments and severs filaments , thought to be regulated by phosphorylation at SER4, ubiquitous and essential in eukaryotes; Cof1p [Saccharomyces cerevisiae]
K.ETSTDPSYDAFLEK.L +2	4.4437	4.3176	4.2476	4.146	4.1708	4.3383	4.4414	4.107	4.4641	4.0934	4.3209	3.8039	3.2315	3.9004		3.7813			3.8063		2.8109	4.1147	4.1467		
K.FILFGLNDAK.T +1									2.3159										2.3935	2.2775	2.2908				
K.FILFGLNDAK.T +2	3.0506	3.4579	3.4979	3.4971	3.4989	3.1828	3.5268	3.4561	3.4814		3.3353	3.5107	3.4841	3.5114	3.5018	3.3847	3.2067				2.7148		3.4183	3.0251	
K.IVFFTWSPDTAPVR.S +2	4.5415	4.644	4.7042	4.7	4.5389	4.0368	4.6286	4.4889	4.3132	3.7462	4.3756	4.0881	4.0307	4.2306	4.4037	4.4378	3.6069		4.3251	4.5675			3.9671	3.5606	
K.LPENDCLYAIYDFEYEINGNEGK.R +2								3.942	3.9329			2.5608		3.4451		2.6589	4.1041		2.692						
K.MVYASSK.D +1																								2.0038	
R.ALNGVSTDVQGTDFSEVSYDSVLER.V +2		5.2212			4.8256	4.91	5.5805	4.851	5.4026	2.7151	3.1085	4.2372	3.9458	5.3097	5.0912	5.533	5.494	5.6065		4.5237	5.1141	4.5471	4.8464	5.5426	
R.ALNGVSTDVQGTDFSEVSYDSVLER.V +3													5.4166	5.5293	4.967			5.7654			4.8721		4.319		
R.SGVAVADESLTAFNDLK.L +2	6.5374	6.7069	6.734	6.7966	6.8083	6.8992	6.6929	7.0352	6.095	6.2975	6.4433	6.0595	6.8462	6.4266	6.4105	6.5075	5.9196	6.5082	5.802	5.9664	6.5476	4.5236	2.7909	6.4071	
R.SGVAVADESLTAFNDLK.L +3														3.77											
gi|6322984|ref|NP_013055.1|	24.6	39.1	35.2	25.8	37.1	32	34.4	39.5	41.4	25.8	30.1	41.4	53.5	57	57.4	59.8	34.8	31.6	24.2	50.8	15.6	12.1	17.6	29.3	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Ap and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits; Rpl8bp [Saccharomyces cerevisiae]
K.EAAAIAEGK.S +1	2.9457	2.5353									2.5293		2.7464	2.1279	2.7399	2.548	2.2435	2.2112			2.3534	2.2525	2.3233	2.0996	
K.HWGGGILGNK.A +1															2.4924					3.2529					
K.HWGGGILGNK.A +2		2.748	2.7802														2.5666								
K.ILSIRLKVPPTIAQFQYTLDR.N +3					3.5082																				
K.KM*GVPYAIIK.G +2																				2.801					
K.KMGVPYAIIK.G +2																				2.5411					
K.KVAPAPFGAK.S +1																	2.0084								
K.KVAPAPFGAK.S +2		2.5035																							
K.LVLIANDVDPIELVVFLPALCK.K +2					3.5303	3.2995	4.0279	3.1397	3.9437			4.6431	4.7261	4.5576	4.1735	4.9294				4.8859					
K.LVLIANDVDPIELVVFLPALCK.K +3													4.6567	4.0179	3.8394										
K.LVSTIDANFADK.Y +2					3.9883	4.1409	3.5805	3.5753	3.5851	3.4912	3.4287	3.0962	3.6069	4.0065	3.0238	4.1479	4.1164	3.6421		3.7756				2.9324	
K.LVSTIDANFADKYDEVK.K +2									4.4604		3.2103	3.2266	4.7804	4.7651	5.0222	4.8532	4.0116			3.2191					
K.LVSTIDANFADKYDEVKK.H +2													4.5853	4.2174	3.1378		4.301	4.6775		3.7554					
K.M*GVPYAIIK.G +2																			3.0163						
K.MGVPYAIIK.G +2					2.7085	2.6924	2.6819		2.6837					2.7525		2.5285	2.5656								
K.NFGIGQAVQPK.R +2	3.2101	4.0308	3.8527	4.21	4.173	4.0284	3.8155	3.9586	3.7866	3.6557	3.7831	3.8961	3.842	3.881	3.7472	3.4892		3.7516						3.6648	
K.NPLTHSTPK.N +1		2.4353			2.7162	2.4267	2.6071	2.4341	2.3281				2.277	2.402	2.3944	2.208		2.6069				2.1696		1.8047	
K.NPLTHSTPK.N +2	3.3641	3.5803	3.4624	3.4102	3.4987	3.5944	3.2486	3.5518	3.4664	2.9903	3.2814	3.1439	2.9222	3.1049		2.6918	3.5264		3.0141	2.5734	2.9995				
K.QDASPKPYAVK.Y +2		2.5818	2.8745					2.6556			2.9442		2.8645			2.7236									
K.SKQDASPKPYAVK.Y +2		3.5932	4.1878	4.2378				4.0673	3.578			2.5571	3.5289	3.7102	3.5738	4.054	3.518		4.151	2.8037	3.2465	3.3259	3.3686		
K.TSAVAALTEVR.A +1									2.1888				2.3187	2.1901	2.2389	2.2965		2.5558						1.8254	
K.TSAVAALTEVR.A +2	4.5129	4.712	4.5009	4.7157	4.5869	4.626	4.7133	4.5811	4.4248	4.6592	4.5581	4.5638		4.2737	4.5065	4.625	3.0935	4.3446						4.2684	
K.TSAVAALTEVRAEDEAALAK.L +2																				3.2681					
K.VPPTIAQFQYTLDR.N +2	4.746	4.7216	4.8295	4.8178	4.7767		4.6106	4.7979	4.6467	4.3717		4.8213	4.6126	5.0065	4.2455	4.3981		4.3227	3.0002	3.5746			4.5953	4.3665	
K.VPPTIAQFQYTLDR.N +3													5.1637	5.0968	4.8955	4.6155			4.1457						
K.YGLNHVVSLIENK.K +2		4.4374	4.5482										4.4454	4.067	4.3811	4.0298				4.5693					
K.YGLNHVVSLIENK.K +3													4.1013	4.4565						4.1135					
K.YGLNHVVSLIENKK.A +3																				3.9488					
R.AEDEAALAK.L +1	2.3897		2.4177					2.4416		2.3983	2.4839	2.0942	2.5071	2.4214	2.1716	2.2513		2.5271	2.4052		2.3288		2.4248	2.3389	
R.AEDEAALAK.L +2											2.7037														
R.LGTLVNQK.T +1						1.9344										2.1394									
R.LGTLVNQK.T +2				2.6044																					
R.NTAAETFK.L +1													2.3264	1.9864	2.0429	1.9443			1.8707						
gi|6323004|ref|NP_013076.1|	39.6	53.4	48	51.5	45.9	49.6	48.7	51.6	55.6	43.2	47.7	53.4	54.6	60.6	52.7	52.4	42.7	43.7	35.2	47.3	35.8	31	33.2	32.1	ATP binding protein involved in protein folding and vacuolar import of proteins; member of heat shock protein 70 (HSP70) family; associated with the chaperonin-containing T-complex; present in the cytoplasm, vacuolar membrane and cell wall; Ssa2p [Saccharomyces cerevisiae]
K.AEETIAWLDSNTTATK.E +2					5.9254	6.1413	5.7559	5.5269	5.7449	5.1246	5.1121	3.9787	5.5616	5.4709	4.1513	5.6675					3.5568		5.4884	4.6436	
K.AEETIAWLDSNTTATKEEFDDQLK.E +2															3.3147	3.8386									
K.AEETIAWLDSNTTATKEEFDDQLK.E +3									4.541																
K.ATAGDTHLGGEDFDNR.L +2	4.9377	4.8789	4.8088	4.8479	4.9405	4.99	4.8401	5.0364	4.9026	4.6088	5.016	4.5105	4.6526	4.8013	3.9896	4.408					4.1281	3.6706	3.0906	3.8346	
K.AVGIDLGTTYSCVAHFSNDR.V +2														4.6378											
K.AVGIDLGTTYSCVAHFSNDRVDIIANDQGNR.T +3														4.3209											
K.DNNLLGK.F +1																				1.8274					
K.DNNLLGKFELSGIPPAPR.G +2																				3.5476					
K.EEFDDQLKELQEVANPIM*SK.L +2															3.9013										
K.ELQEVANPIM*SK.L +2						4.1004			4.0075		3.6424	4.042	4.1384		3.9615					3.3481		4.4062			
K.ELQEVANPIMSK.L +1									2.8484	2.2375							3.0306	2.2605		3.1061	2.3642		1.9015	2.282	
K.ELQEVANPIMSK.L +2	3.9025	3.8061	3.7662	4.013	4.0648	3.9141	4.0259	3.8876	3.8261	3.8999	3.5508		3.9685	3.7859				3.8838				3.7845		3.5885	
K.ETAESYLGAK.V +1		2.3081		2.343			2.2078	2.4185	2.5075		2.3759		2.4782	2.4361		2.6104	2.1904	2.2452	2.5624	2.5065					
K.ETAESYLGAK.V +2				2.5775				2.5528				2.526													
K.FELSGIPPAPR.G +1											2.2309										2.5392				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.FELSGIPPAPR.G +2	3.6341	3.5119	3.5434	3.3402	3.4878	3.6945	3.6055	3.7462	3.4398	3.7985	3.4059	3.5806	3.4655	3.359	3.4755	3.3556	3.3157	3.349	3.3099	3.1183	3.3153	3.3887	3.3638		
K.KAEETIAWLDSNTTATK.E +2									5.9419			2.8725	6.2422	6.0586	5.3662	6.1361	5.513	5.2711		5.2435					
K.KAEETIAWLDSNTTATK.E +3													5.0049	4.6678	3.5407										
K.KAEETIAWLDSNTTATKEEFDDQLK.E +2																				4.0572					
K.KAEETIAWLDSNTTATKEEFDDQLK.E +3		6.8656	6.504	6.8778										6.1302			5.12			6.5101					
K.KSEVFSTYADNQPGVLIQVFEGER.A +3		6.304																	4.554						
K.LIDVDGKPQIQVEFK.G +2	4.8317	4.7688	4.5976	4.7397				4.6146	4.3385			4.1854	4.2126	4.9594	4.576	4.5554		4.3681	4.376	4.8067					
L.IDVDGKPQIQVEFKGETK.N +2																	2.999		2.8471	3.3385					
K.LVTDYFNGK.E +1						2.378					2.5908	2.4373		2.3244	2.6042	2.5519	2.2338	2.1721	2.5806				2.4771		
K.LVTDYFNGK.E +2	3.1996	3.133	3.0982	3.0145	3.1917	3.3894	3.2912	3.5762	3.1629	2.9001	2.884	3.2394	2.9463	2.9503	3.0053	3.0148						3.1635	3.1176	2.5883	
K.LVTDYFNGKEPNR.S +2	2.6137			3.0027				3.5318	3.2458		3.3252	3.0369	3.1185	3.151	3.4737	3.1728	3.5439	3.2943	3.6193	3.2707					
K.M*KETAESYLGAK.V +2																				3.0491					
K.M*VAEAEK.F +1																						2.2691		1.9793	
K.MKETAESYLGAK.V +2											3.1775		3.8339	3.6299			3.7526	3.839		3.9247					
K.MVAEAEK.F +1					1.8514	1.8422	1.9611	1.8379	2.0003	1.8515	1.9182	1.9459	2.1449	1.9156	1.9109	2.151				1.888					
K.NFTPEQISSM*VLGK.M +2		3.1644			4.118	4.2308	4.3259	4.3887	4.1134	4.1871	4.0499	4.0114	3.6348	3.8795	3.8326	3.8464		3.1175		3.9758	4.2319	2.8	3.9145		
K.NFTPEQISSMVLGK.M +1									2.332																
K.NFTPEQISSMVLGK.M +2	4.3633	4.323	4.3763	4.2322	4.5861	4.5145	4.2221	4.4547	4.2125	3.6137	4.2472	4.2404		3.5837	3.718	3.6268	3.9291			3.0985			2.9616		
K.NQAAMNPANTVFDAK.R +2					4.7806	5.0354	4.5914	4.714	4.9782	4.8824	4.5814	4.9165	5.0423	5.0195	4.6179	4.9974	4.5323	3.5553	4.9545	4.8743	4.767	4.6312	4.7243	4.7414	
K.NQAAMNPANTVFDAK.R +1					3.2111				3.3446		1.9616						2.4311								
K.NQAAMNPANTVFDAK.R +2	5.1911	4.8099	4.9086	5.0956	4.8546	4.8519	4.908	5.2319	4.9332	4.4538	4.8101	4.4035	4.6591	4.7718	4.652	4.6246	4.6296	5.0383		4.7125		3.1947	4.6749	4.8906	
K.NQLESIAYSLK.N +1					2.9792		2.7346	2.8732		2.7009	2.5889		2.7263	2.9823	2.5723	2.848	2.7602	2.6027			2.7288	2.8305			
K.NQLESIAYSLK.N +2	3.7574	3.8288	3.757	3.9038	3.8385	3.9627	3.6629	3.8792	3.8784	3.735	3.8925	3.6253	3.8015	3.8619	3.5819	3.8395	3.236	3.2452			3.6558	3.6168	3.6304	3.5876	
K.NTISEAGDK.L +1																						2.0556			
K.NTISEAGDKLEQADK.D +2	4.618	4.7777	4.7745	4.9555	4.5648	4.8375	4.8343	5.0148	4.7596	4.6735	4.8347	4.836	4.7203	4.7254	4.7968	4.7826	4.709	4.7907			4.5455			2.8006	
K.NTISEAGDKLEQADKDAVTK.K +2															3.3054										
K.NTISEAGDKLEQADKDAVTK.K +3									3.8801				4.7383	4.5943	3.5908	4.3687									
K.SEVFSTYADNQPGVLIQVFEGER.A +2					6.25	6.0192	6.1546	6.1758	5.9719	4.6673	5.6704	5.6796	5.99	6.1021	5.8173	6.0481	5.5564	4.3329	5.1104	4.7417	4.3607			5.5962	
K.SEVFSTYADNQPGVLIQVFEGER.A +3					5.8799	5.5908	6.1017	5.6739	5.6902	3.596	5.5767	5.8745	6.1014	5.7486	6.0194	5.7555	4.0982		4.8371	3.8779					
K.SQVDEIVLVGGSTR.I +1					2.9334				2.5646	2.78	2.9327				2.6397	3.2136	3.136		2.0024	2.8722	2.5428				
K.SQVDEIVLVGGSTR.I +2	5.0149	4.926	4.9019	5.2081	4.9598	5.0333	4.8988	5.0638	4.7175	4.9421	4.652	4.5151	4.4978	3.7206	4.7695	4.3494		4.3556		4.545	3.1241		3.7348		
K.TQDLLLLDVAPLSLGIETAGGVM*TK.L +2					5.5093	4.9859	6.0329	5.8566	5.9295		4.3691	4.9884	5.9854	6.0594	5.6898	5.8767		4.3441	2.7313	3.0904					
K.TQDLLLLDVAPLSLGIETAGGVM*TK.L +3				5.5141			4.0281	4.7043	5.2543			4.1508	6.2551	6.0831	5.5809	4.4807		4.0019							
K.TQDLLLLDVAPLSLGIETAGGVMTK.L +2		5.3026	6.9682	5.8455	6.2476	5.7776	6.8214	6.2015	6.1584		3.0636	6.2641		5.4426	4.8477	6.0096		5.2931		4.9606					
K.TQDLLLLDVAPLSLGIETAGGVMTK.L +3					5.4391		6.0515	5.7578	5.9714			5.1268	4.4043	5.4808	5.7123	4.9361		5.1529		5.913					
K.VNDAVVTVPAYFNDSQR.Q +2	4.544	4.4852	4.5262	4.258	4.6541	4.7556	4.866	4.7313	4.3843	4.4339	4.2324	5.0374	3.9853		3.8832	4.681	4.1733	3.844	3.6533	3.5695	4.4573	3.9049	4.3225	4.2396	
K.VNDAVVTVPAYFNDSQR.Q +3							4.06			3.6503			4.568			3.9924				3.7919					
R.ARFEELCADLFR.S +2	3.7337	4.2022	4.1129	3.9047													3.2032		3.5025	3.5926					
R.FEELCADLFR.S +1								1.9717	2.2357				1.986	2.3495	2.21	2.5758					1.9985				
R.FEELCADLFR.S +2	3.9117	3.8945	3.98	4.1421	4.0162	4.1778	3.8927	3.9922	3.9344	3.9238	3.9138	3.9746	3.8189	3.9631	3.7523	3.987	3.7032	3.9944	3.4827	3.9332	3.5951	3.8665	3.855	3.8992	
R.GVPQIEVTFDVDSNGILNVSAVEK.G +2						2.6518																			
R.IINEPTAAAIAYGLDK.K +2	5.4234	5.6456	5.4945	5.6147	5.9293	5.7907	5.8466	5.7708	5.6002	5.6482	5.6936	5.7626	5.6224	5.5621	5.3866	5.7659	5.2446	3.7723	5.4782	4.6525	5.4048	5.1952		5.6237	
R.IINEPTAAAIAYGLDK.K +3									4.8594			4.9217	4.8156	5.2729	4.8542	5.0129	3.9747	4.0145	4.5842		4.6019	4.6401	4.4467	4.3033	
R.IINEPTAAAIAYGLDKK.G +2									4.5132				4.4143	4.729	4.5121	3.8927									
R.LSKEDIEK.M +2		2.9827	2.9533	3.0767																					
R.LVNHFIQEFK.R +1													2.7051	2.5647	2.4839		2.4429								
R.LVNHFIQEFK.R +2	3.7066	3.9083	3.8425	3.6697					3.1897			3.3771	3.614	3.4229	3.5363	3.53	2.6731		3.6996	3.5617					
R.NFNDPEVQGDM*K.H +2	3.6933												3.9044	3.2147	3.5174										
R.NFNDPEVQGDMK.H +1																						1.9798	2.2528	2.0743	
R.NFNDPEVQGDMK.H +2	4.2163	4.04	3.997	4.1679	4.0248	3.9803	4.1629	4.2266	3.9893	3.775		4.0398	3.9924		3.4927	3.9962							3.5969		
R.SINPDEAVAYGAAVQAAILTGDESSK.T +2	7.0462	7.1555	7.2395	6.854	7.1402	7.0638	7.2401	7.3066	6.897	7.1702	6.8542	6.9365	6.9135	6.7728	6.9581	6.3677	6.9728	6.6366	6.7451	5.8955	6.0024	4.2354	6.8256	6.9738	
R.SINPDEAVAYGAAVQAAILTGDESSK.T +3					4.0958	5.0377	5.493		4.8254	4.7861	3.6748	4.8825	6.019	5.5917	6.2107	4.6956	4.5	3.9234	5.2596	4.7382		3.6232	3.9519		
R.STLDPVEK.V +1				2.2056			2.1634	2.0676	2.1847	1.9368	2.1254	1.9009	2.1088	1.8603			2.1981								
R.TLSSSAQTSVEIDSLFEGIDFYTSITR.A +2														3.6213											
R.TTPSFVGFTDTER.L +1					2.016								2.7458	2.5133											
R.TTPSFVGFTDTER.L +2	3.4135	3.3396	3.304	3.2157	3.5522	3.6569	3.7096	3.5862	3.3871	3.3769	3.3161	3.3708	3.1696	2.9841	3.0375	3.2284		2.8118	2.6437	3.1668	2.5957	2.8757	3.1253		
R.VDIIANDQGNR.T +1								2.7184					2.5191	2.6389		2.1157									
R.VDIIANDQGNR.T +2	4.3474	4.3646	4.1908	4.3819	4.5142	4.4756	4.2544	4.2539	4.1388	4.0966	4.1295	3.9715	3.8439	3.9825	3.2473	4.1288				4.2088					
gi|6323072|ref|NP_013144.1|	46.6	58.3	58.3	46.6	45.6	45.6	45.6	58.3	58.3	58.3	58.3	58.3	54.4	46.6	36.9	48.5	58.3	48.5	35.9	12.6	36.9	24.3	58.3	45.6	Cytoplasmic thioredoxin isoenzyme of the thioredoxin system which protects cells against both oxidative and reductive stress, forms LMA1 complex with Pbi2p, acts as a cofactor for Tsa1p, required for ER-Golgi transport and vacuole inheritance; Trx1p [Saccharomyces cerevisiae]
K.FSEQYPQADFYK.L +2					4.4274	4.3101	4.4527	4.5895	4.4414	4.3086	4.2823	4.1824		4.4759	4.1041	4.3487		3.8833	2.6233		2.957		4.4763	3.0973	
K.FSEQYPQADFYKLDVDELGDVAQK.N +2																	3.954								
K.FSEQYPQADFYKLDVDELGDVAQK.N +3		4.5272	5.3589														4.68		4.2435						
K.LDVDELGDVAQK.N +1																				2.0639					
K.LDVDELGDVAQK.N +2	4.7011	4.6199	4.7674	4.8963	4.8589	4.9027	4.8815	4.8379	4.8522	4.8261	4.7349	4.7415	4.6178			4.2535		4.6506	4.3362			4.8644	4.8107	4.8781	
K.MIAPMIEK.F +1													2.0356												
K.NEVSAMPTLLLFK.N +2	2.6078	2.9159	3.1669	3.7318	2.7511	3.743	3.8078	3.5516	3.2504	3.7886	3.3215	4.124	3.8577	4.0039	3.9633	3.9703	2.7192	3.8759	3.4724	3.4089					
K.NEVSAMPTLLLFK.N +2		4.0968	4.1976	4.234	4.2077	4.0741	4.0053	4.1309	4.0354		3.8279	4.2244		4.1641	3.9724	3.7826	4.0143	3.4656	3.1399	3.945	3.9287	3.6415	4.0946	4.0642	
K.TASEFDSAIAQDK.L +1																							2.6721		
K.TASEFDSAIAQDK.L +2	4.4823	4.4528	4.4187	4.5195				4.1512	4.0137	4.204	3.4627	4.3323	4.4597	4.2047	4.2268	4.2733	4.215	3.7742			3.8626				
K.VVGANPAAIK.Q +1													1.9488												
K.VVGANPAAIK.Q +2	3.2534	3.1977	3.1434	3.2061	3.0875	3.1794	3.2082	3.1427	3.0458	3.0275	3.0522	2.7833		3.1645			3.0071						2.7588	2.7562	
gi|6323073|ref|NP_013145.1|	51.9	53.1	53.1	51.5	42.1	45.5	42.8	42.1	44	37.1	44.4	45.5	48.8	55.4	54.5	57.4	46.7	41.7	50.3	49.7	25.2	19.4	29.5	30.6	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism; Pdc1p [Saccharomyces cerevisiae]
K.AQYNEIQGWDHLSLLPTFGAK.D +2		5.2875		5.0654										5.1521	3.9481	3.2964			4.4117	4.4145					
K.AQYNEIQGWDHLSLLPTFGAK.D +3	4.3869	4.7063	4.2083	4.5179										4.773	4.0272				4.5111	4.0584					
K.EAVESADLILSVGALLSDFNTGSFSYSYK.T +2																3.4171									
K.EVIDTILALVK.D +1		2.692	2.6292	2.5925	2.4283			2.6663	2.4807				2.401	1.8741	2.585										
K.EVIDTILALVK.D +2	3.8074	3.9108	3.7275	3.9734	3.7378	3.7922	3.7469	3.7635	3.7702		3.7533	3.641	3.6347	3.6076	3.703	3.6397	3.6052	3.7702	3.5749	3.5781			3.7075	3.3546	
K.GSIDEQHPR.Y +2	2.9046	3.1288	3.0816		3.0065	3.0524	3.2641	2.909	2.9259	3.0037	2.8558	3.1236	3.1628	2.9151	3.2792	3.241	3.0159	2.9257	2.772	2.8313	2.5223	2.9344			
K.GYKPVAPAR.T +1					1.8411						2.1326	2.3872	2.4461	2.4245			2.1285	2.3115							
K.GYKPVAVPAR.T +2	3.1069	2.9353	3.043	3.1468	3.0421	2.5759	2.9127	3.1886	3.2846	3.1685	2.6514	3.348	3.0423	2.8853	2.8271	2.5766	2.8172				3.1643	2.8093			
K.IYEVEGM*RWAGNANELNAAYAADGYAR.I +3															3.6686	3.7443									
K.IYEVEGMR.W +1	2.4381	2.3254	1.8727	2.4253	1.9603	2.4837	2.1369	1.9746		2.2024	2.3487	1.9716		1.9356	2.3298	2.1718				2.2191			2.1435		
K.IYEVEGMR.W +2	2.8019		2.9874		2.9693	2.9713	3.0138	3.0576		3.071	2.6856	2.9796				2.9548									
K.KLIDLTQFPAFVTPM*GK.G +2																			5.0227	4.986					
K.KLIDLTQFPAFVTPM*GK.G +3																			4.4515						
K.LIDLTQFPAFVTPM*GK.G +2	5.1129	5.2774	5.2185	5.329	5.3233	4.8858	5.4004	5.1627	4.8496	5.197	4.6692	5.0351	5.0871	4.9342	4.8364	4.5817	4.5394	4.7907	3.6288	4.748			3.8151	4.6014	
K.LIDLTQFPAFVTPM*GK.G +3							5.295		5.4236	4.6967		5.3442	5.8248	5.7664	5.8149	5.5607			3.6032	4.3424			5.4578		
K.LIDLTQFPAFVTPMGK.G +2	5.4948	5.5726	5.5153	5.7933	5.5739	5.2705	5.6334	5.3679	5.4018	4.8595	5.3953	5.0752			4.8947	4.8733	5.0586	5.1974	3.3447	5.2917			3.2475	3.0137	
K.LIDLTQFPAFVTPMGK.G +3								4.3084	4.294	3.8793	4.5602	3.6732													
K.LLQTPIDM*SLKPNDAESEK.E +2		4.4763	4.1782	4.4154		3.8971			4.2616	3.6275	3.0491	4.0226	4.3602	3.9577	4.0515	3.5254	3.0526	3.9226	4.2936	4.2784				3.6381	
K.LLQTPIDM*SLKPNDAESEK.E +3				3.7644																					
K.LLQTPIDMSLK.P +2																	2.7334								
K.LLQTPIDMSLKPNDAESEK.E +2	5.3729	5.5896	5.7622	5.5381			5.1352		5.4329			4.835	5.1763	5.1872	4.973	4.9254	4.8331	3.7318	4.9309	5.0459					
K.LLQTPIDMSLKPNDAESEK.E +3	4.0577	3.8921	3.9899	4.0778																					
K.LLTTIADAAK.G +2	3.2128	3.043	3.2866	3.1541	3.1695	3.0913	3.1118	3.3297	2.9593	3.0541	2.9775	2.919	2.9541	2.8659	3.1954		2.874								
K.LTAATNAK.Q +1														1.9627	1.8513										
K.NIVEFHSDHM*K.I +1													2.2494	2.3938											
K.NIVEFHSDHM*K.I +2		3.9628	3.4792	4.0339	3.5939	3.4615	3.7155	3.7394	3.4865	3.8034		3.0615	4.2081	3.9015	3.6533	3.6391		3.6707	3.4181	4.0695		3.7296			
K.NIVEFHSDHMK.I +1														3.1767			2.7355	3.3261		2.7997					
K.NIVEFHSDHMK.I +2	3.725	3.8279	3.8703	3.9596		3.56			3.7868				3.873	3.868	3.8302	3.7975	3.7639	3.3609	3.1243	3.3903					
K.NPVILADACCSR.H +1					3.3247	3.5024	3.3136	3.1847	3.3996	2.7446	2.7996	2.8993	3.3079	3.3591	2.9012	3.3603	3.1777	2.1322		3.2385		3.0934	2.8363		
K.NPVILADACCSR.H +2	5.1473	5.0575	4.9793	5.0625	5.1644	5.1546	5.2217	5.3038	5.0898	5.1939	5.0393	5.0364	4.8888	4.7218	5.032	4.8936	3.955	4.3152	4.1721	4.8015	4.007	4.3559	3.274	5.0259	
K.PVAVPAR.T +1		2.1937	1.9896	2.0894															1.8858						
K.PYLFVLNNDGYTIEK.L +2	5.915	5.9623	6.0396	6.0737									4.4317	4.305	4.5703	3.9073	5.6122	4.912	5.6825	5.9215	4.8667		3.9902		
K.PYLFVLNNDGYTIEK.L +3																				3.6253					
K.QVNVVNTVFGLPGDFNLSLLDK.I +2	5.7171	5.862	5.9736	5.604	5.9983	5.2462	6.1479	5.7548	5.9471		5.1467	5.447	4.9662	5.3756	4.4907	5.5708	4.4377	3.9143	5.05	5.5963					
K.QVNVVNTVFGLPGDFNLSLLDK.I +3									3.5799			4.6062	4.8157	5.0689	4.3819				3.9769	5.1678					
R.M*IEIM*LPVFDAPQNLVEQAK.L +2		4.4018		6.1477	5.9319	5.7677	6.2753	6.2512	5.83	5.873	5.558	5.7819	6.0032	5.983	5.9465	6.2298	5.0489	5.5366	6.1334	5.9381	5.7364		3.0713	5.8508	
R.M*IEIM*LPVFDAPQNLVEQAK.L +3				3.5962					5.0251	4.5948		5.1105	5.0261	4.8659	5.0282	5.282			4.9296	5.3939			3.5145		
R.M*IEIMLPVFDAPQNLVEQAK.L +2		5.9529	5.8456	5.9822	6.0065	6.0087	5.9831	6.1083	5.516	4.9696	5.6846	5.6614			5.9024	5.8755	4.2629	3.1154	2.5562	5.479					
R.M*IEIMLPVFDAPQNLVEQAK.L +3		4.8051					5.1561		5.1998						5.3122	4.4718	4.1436			5.5892					
R.M*SANISETTAM*ITDIATAPAEIDR.C +2				4.2586	2.8719	4.3864	3.8418		3.7203	4.5918	2.9794	5.3847	5.264	5.1716	5.0554	4.42	3.2447	4.9226	4.2743	4.6448	4.1376			3.9791	
R.M*SANISETTAM*ITDIATAPAEIDR.C +3													4.8861												
R.M*SANISETTAMITDIATAPAEIDR.C +2					5.5861	5.8129	5.587	5.2037	5.5217	4.9105	4.9526	5.4611		5.5518	5.6527	5.9535	5.3986	3.3815	4.0253	5.4009	5.4894	5.4636	5.1342	5.6406	
R.M*SANISETTAMITDIATAPAEIDR.C +3							4.1679								3.9509										
R.MIEIM*LPVFDAPQNLVEQAK.L +2		5.845		5.7062	5.3495	5.3734	5.7515	5.8862	5.2964	4.3539	5.0832	5.282			4.796	5.3245	4.4237	4.6119		3.0649			5.3227	4.3092	
R.MIEIM*LPVFDAPQNLVEQAK.L +3									5.4734		3.748	5.401				5.1125									
R.MIEIMLPVFDAPQNLVEQAK.L +2	6.2894	6.4751	6.3433	6.2403	6.276	5.9244	6.31	6.1469	5.7502		5.1879	5.943			4.0627	5.9117	5.5828	5.17	3.9576	5.4735			4.2131		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.MIEIMLPVFDAPQNLVEQAK.L +3				5.5772	6.1564				6.8409							5.7082	5.1528	3.982					5.3728		
R.MSANISETTAM*ITDIATAPAEIDR.C +2					4.1866	5.4073	4.8538	4.2653	5.2666	3.3734	3.3986	4.6458		5.1316	4.9718	5.3085	4.7935	5.6138	5.2334	4.8494	4.8256	3.7471	4.6216	4.8293	
R.MSANISETTAM*ITDIATAPAEIDR.C +3														3.7927	4.0862										
R.MSANISETTAMITDIATAPAEIDR.C +2	6.0093	6.041	6.0509	5.7667	5.9771	5.9331	5.9151	5.9653	5.7326		5.4415	5.2868		4.5845	5.6084	5.8284	5.7207	4.3779	3.6835	5.6978			5.6709	4.4971	
R.MSANISETTAMITDIATAPAEIDR.C +3																	3.7434								
R.NATFPGVQM*K.F +1												1.9098													
R.NATFPGVQM*K.F +2			2.6376	2.6624			2.5006		2.5455										2.5534						
R.NATFPGVQMK.F +1	2.225	2.3053	2.2209		2.3813	2.265	2.3845		2.3303	2.1203	2.279	2.2597	2.4758	2.4804	2.279	2.5371	2.3185	2.3314		2.3383	2.2163	2.337		2.3398	
R.NATFPGVQMK.F +2	2.5678			2.6227	2.6843	2.675	2.7431	2.7366		2.826	2.6902	2.6678		2.5487				2.7235							
R.PVYLGLPANLVDLNVPAK.L +2	5.3154	4.6644	5.5097		6.5409	6.3206	6.4528	6.4794	5.9129	6.0127	5.4581	6.1357	6.0105	5.4587	5.708	5.7113	3.7099		4.8784	4.3242			5.519	4.0522	
R.PVYLGLPANLVDLNVPAK.L +3							4.5468		4.7205	3.9931		4.4235	5.03	4.7782	4.9516	4.6419							4.6227	3.5244	
R.TPANAAVPASTPLK.Q +1			2.9408		3.2011	3.1497	2.9419	3.0236	2.9485	2.8683	2.8701	2.8032	3.2787	3.1439	2.7366	2.9632		2.9018	2.9603	2.5902		2.75		2.1645	
R.TPANAAVPASTPLK.Q +2	4.0591	4.3108	4.1821	4.5064	4.198	4.2335	4.248	4.2289	3.8913	4.1199	4.1804	3.747	3.8703	2.8746	4.0064	3.8368	2.539				4.1		3.5562	4.1115	
R.TTYVTQRPVYLGLPANLVDLNVPAK.L +2		4.7387											3.4765	4.4998	4.6262	4.2053			2.8141	4.3847					
R.TTYVTQRPVYLGLPANLVDLNVPAK.L +3		6.1828	6.1807	5.8149									4.5249	5.5439	4.8299	5.6097			5.7176	6.026					
R.VATTGEWDK.L +1	2.1772	2.1398	2.128	2.363	2.2087	2.0851	2.1671	2.0471	2.0966	2.1565	2.0353	2.1531	2.1372	2.1212	2.2004	2.0338	2.1052	2.0928	2.0421	2.0664	2.2439		1.9514	2.2515	
R.VATTGEWDK.L +2	2.6655	2.7111	2.5596	2.5267	2.6207																				
R.VATTGEWDKLTQDK.S +2											4.2658		4.4439	4.6667		4.6709									
R.WAGNANELNAAYAADGYAR.I +2	6.315	6.1705	6.1054	5.9478	6.3728	6.416	6.273	6.305	6.1477	5.9351	6.1191	6.1423	6.1272	6.4155	5.8346	6.1666	5.8904	5.3582	5.7069	6.1369	6.3886	6.026	5.9441	5.9111	
R.WAGNANELNAAYAADGYAR.I +3						3.6009		4.1013	3.8919		4.1817	4.2851	5.4039	5.2578	4.5669	4.3758	4.7695								
R.WGLKPYLFVLNNDGYTIEK.L +2																			4.9392						
R.WGLKPYLFVLNNDGYTIEK.L +3																			5.0728						
R.YGGVYVGTLSK.P +2					2.9572	2.8565			2.9244			2.7836													
R.YGGVYVGTLSKPEVK.E +1									3.9804				3.5254	3.7955	3.5872	3.6565	3.723	3.5323	2.5216	3.4095					
R.YGGVYVGTLSKPEVK.E +2	4.8075	4.6359	4.6207	4.8237	4.5684	3.0475		4.5317	4.315		4.2126	4.5001	4.2736	4.4389	4.332	4.269	4.3526	3.903	3.7754	4.6946					
R.YGGVYVGTLSKPEVK.E +3		3.6249	3.5969	3.6076									3.7436	3.5856		3.7379	3.7626	3.5462							
gi|6323087|ref|NP_013159.1|	13	26	22.8	24.1	16	17.9	16	17.9	25.2	17.9	19.8	20.9	25.8	28.6	23	27.9	8.5	17.3	12.4	27.7	8.7	14.7	19.4	14.7	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm2p [Saccharomyces cerevisiae]
K.AFHVTPDK.W +1			2.3509										2.2757	2.3942	2.2774	2.2856		2.4255	2.5221	2.3429					
K.AKVDEGSDVLNTWK.K +2																		4.1663	4.2904	4.2262					
K.ALESEFK.N +1													1.8941			1.8245									
K.AVEFAQQVQQSLPK.D +2	4.8822	5.0291	4.8614		4.8824	4.8143	5.137	4.9731	4.8262	4.7094	4.6095	4.7797	4.7991	4.8026	4.6711	4.7067		3.6287	4.5422	3.518	3.6587	3.6028		4.3499	
K.EIYDWAGEYPLAV.- +1																								2.6178	
K.EIYDWAGEYPLAV.- +2				3.11																			2.9379		
K.ISAVSTYFESFPYR.V +2		4.6243	4.5444	4.5352	4.652	4.6668	4.6665	4.7099	4.6426	3.6708	4.3016	3.6824	4.4245	4.5258	3.6624	3.9027	3.9498	4.3957		4.6618			3.8188		
K.LITSHLVDTDPEVDSIIK.D +2									3.7207				4.4301	5.0283		4.1916									
K.LITSHLVDTDPEVDSIIKDEIER.Q +2														4.6529						3.6466					
K.LITSHLVDTDPEVDSIIKDEIER.Q +3		5.8985		4.3641										6.6778											
K.NAILYRPK.V +2		2.5873	2.6547																						
K.SALVPGGVR.I +1									1.947		2.0624		2.0449		1.8331										
K.VDEGSDVLNTWK.K +2	4.7952	4.543	4.5127	4.8788	4.8184	4.7141	4.7656	4.6765	4.6422	4.7962	4.7473	4.3015		4.5266	4.3195	4.3431		3.5853			4.2859	4.6835	4.5734		
K.VLVAGTSAYCR.L +2	4.0572	4.3143	4.1519	4.1186	4.0425	4.095	4.001	4.1278	3.9216	3.7581	4.0107	3.7656	4.0119	3.8844	3.9017	3.9094	3.9736					3.5609	3.9116	4.0183	
K.YSEGYPGAR.Y +2						2.7635		2.5218		2.7091	2.7258	2.5691	2.5249											2.7149	
R.IGAPAMTTR.G +2	3.0896	3.2416	3.2135	3.2107	2.9003	2.9918	2.9666	3.0955	2.72	3.0839	2.9777				3.1041	3.08				3.1797			3.0287		
R.LM*GLYLPDGGHLSHGYATENR.K +2														4.0022											
R.LVSNGTDSHM*VLVSLR.E +2									3.0595			3.4682	4.5119	4.323		3.7599		4.4835		2.7133					
R.LVSNGTDSHMVLVSLR.E +2		4.7743	4.6317	3.6678										4.7832	4.2559	4.43				4.4354					
R.VEYICEK.I +1												1.9855							2.0237	2.1507		2.1536	1.9306	2.0767	
R.VEYICEK.I +2																2.5966									
R.VNPETGIIDYDTLEK.N +2	5.205	5.1327	5.3212	4.4951	4.981	5.2132	4.9966	5.2133	4.3459	4.8674	4.7332	4.228	5.3396	5.012	4.16	5.0747	3.8569	4.4868	4.859	3.0666	5.0061	5.3279	4.5192	3.6931	
R.YYGGNEHIDR.M +2																				3.0184		2.5585	2.6616		
gi|6323138|ref|NP_013210.1|	40.9	52.8	52.8	44.3	52.8	62.5	32.4	44.3	62.5	40.9	47.7	52.8	46.6	51.1	41.5	41.5	41.5	46.6	46.6	56.2	29.5	14.8	45.5	26.1	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p; Ahp1p [Saccharomyces cerevisiae]
K.ETNPGTDVTVSSVESVLAHL.- +2	5.0793	5.4027	5.3468	5.3753	5.5292	5.5536	5.6937	5.7458	5.1409	3.114	5.0811	5.5539	5.0542	5.4558	4.5476	5.4673	4.3244	3.2617	3.9116	5.3515	5.2054		5.1597	5.5226	
K.ETNPGTDVTVSSVESVLAHL.- +3														3.6269											
K.EVDQVIVVTVDNPFANQAWAK.S +2		5.5952	6.7111	5.6913	6.4618	6.3594		6.3286	5.9712		4.0376	5.5772	5.9408	5.6952	5.6742	5.7644	6.2584	3.0191	5.3473	5.6219			4.9377		
K.EVDQVIVVTVDNPFANQAWAK.S +3													4.0855	4.5338						3.5333					
K.FASDPGCAFTK.S +1									1.9849																
K.FASDPGCAFTK.S +2	3.2042	3.3549	3.5205	3.2091	3.2602	3.4189	3.4377	3.4131	2.8933	2.9401	3.1135	2.9013													
K.FPAGDYK.F +1																							1.9372		
K.FQYIAISQSDADSESCK.M +2	6.7249	6.7225	6.6539	6.5183	6.7614	6.856	6.8821	6.8494	6.7356	6.5786	6.5838	6.5883	6.7941	6.4552	6.6529	6.5707	6.0995	5.2129	6.666	6.8609	6.1288	6.7243	6.8446	6.4699	
K.M*PQTVEWSK.L +1																			2.8284						
K.MPQTVEWSK.L +1									2.6735									2.6739		2.6375					
K.MPQTVEWSK.L +2	2.7616	2.7288	2.6854	2.6127	2.6837	2.7396	2.8183	2.7148	2.8871	2.674		2.7065	2.7924									2.7513		2.6941	
K.SIGFELAVGDGVYWSGR.W +2						2.8262			2.9854					3.6238						2.9804					
R.WAM*VVENGIVTYAAK.E +2									3.5277	3.3649	2.6667	4.9902	5.3521	4.9287	5.0442	4.6257		4.5443	4.3391	4.7511	5.259		3.6553		
R.WAMVVENGIVTYAAK.E +2	4.4018	4.8201	5.2507		5.2709	5.0346			5.1579			3.9095	3.2083	5.0604	3.699	4.0859	3.6816	3.1849		4.8921	3.614		2.8518		
gi|6323163|ref|NP_013235.1|	9.6	10.8	11.4	11.4	8.3	8.3	8.3	8.3	10.1	10.1	8.3	8.3	13.5	11.4	11.7	11.4	8.3	5.2	10.8	12.3	7.3	5.2	8.7	8.3	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, repressed by thiamine, involved in amino acid catabolism; Pdc5p [Saccharomyces cerevisiae]
K.DYKPVAVPAR.V +2			2.7051	2.7289					2.6304	2.8295			2.5246	2.6974		2.6689									
K.NPVILADACASR.H +2													3.1556		2.7577						4.2799		2.9051		
K.PVAVPAR.V +1		2.1937	1.9896	2.0894															1.8858						
K.PYIFVLNNNGYTIEK.L +2																				3.0269					
R.NATFPGVQM*K.F +1												1.9098													
R.NATFPGVQM*K.F +2			2.6376	2.6624			2.5006		2.5455										2.5534						
R.NATFPGVQMK.F +1	2.225	2.3053	2.2209		2.3813	2.265	2.3845		2.3303	2.1203	2.279	2.2597	2.4758	2.4804	2.279	2.5371	2.3185	2.3314		2.3383	2.2163	2.337		2.3398	
R.NATFPGVQMK.F +2	2.5678			2.6227	2.6843	2.675	2.7431	2.7366		2.826	2.6902	2.6678		2.5487				2.7235							
R.PVYLGLPANLVDLNVPAK.L +2	5.3154	4.6644	5.5097		6.5409	6.3206	6.4528	6.4794	5.9129	6.0127	5.4581	6.1357	6.0105	5.4587	5.708	5.7113	3.7099		4.8784	4.3242			5.519	4.0522	
R.PVYLGLPANLVDLNVPAK.L +3							4.5468		4.7205	3.9931		4.4235	5.03	4.7782	4.9516	4.6419							4.6227	3.5244	
R.TTYTTQRPVYLGLPANLVDLNVPAK.L +2		4.0044											4.5869	4.7454	2.5746	4.6559			3.8237	3.5266					
R.TTYTTQRPVYLGLPANLVDLNVPAK.L +3	5.0127	6.4467	5.2017	5.744									4.8209	5.8632	5.8225	5.5589			5.1257	5.1618					
R.WAGNANELNAAYAADGYAR.I +2	6.315	6.1705	6.1054	5.9478	6.3728	6.416	6.273	6.305	6.1477	5.9351	6.1191	6.1423	6.1272	6.4155	5.8346	6.1666	5.8904	5.3582	5.7069	6.1369	6.3886	6.026	5.9441	5.9111	
R.WAGNANELNAAYAADGYAR.I +3						3.6009		4.1013	3.8919		4.1817	4.2851	5.4039	5.2578	4.5669	4.3758	4.7695								
gi|6323288|ref|NP_013360.1|	16.6	27.8	27.6	30.6	33.7	29.5	33.4	34.1	40.9	30.1	37.8	37.1	45.8	41.3	47.6	40.7	40.6	30.2	21.7	38.1	23.3	22.6	29.4	33.7	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL; Hsp60p [Saccharomyces cerevisiae]
K.DRYDDALNATR.A +2					2.7599								3.5118	3.0747					2.9389				3.0545	2.7703	
K.EDTVILNGSSGPK.E +2	3.7477	3.5291		3.7957				3.6226	3.1695		3.7784	4.1123	3.5974		3.733	3.6474	3.4997					2.8241			
K.EITTSEEIAQVATISANGDSHVGK.L +2													2.6981		3.4268		4.3821	4.6234		4.3172					
K.GSIDITTTNSYEK.E +1																							2.7423		
K.GSIDITTTNSYEK.E +2		4.3804	4.3818	4.7633				4.0827	4.5513	3.0966	4.1917		3.5952	4.4595	3.9464			4.6273							
K.GVETLAEAVAATLGPK.G +2		4.6965	4.6612	4.6207	4.3886		4.5415	4.5501	4.8232		3.2367	4.4652	4.8369	4.2721	4.394	4.5728	4.0573		3.8349	4.5897			3.8589	2.8521	
K.GVETLAEAVAATLGPK.G +3													4.4726	4.8294	4.5985					3.9975			4.382		
K.ISSIQDILPALEISNQSR.R +2				3.6125	5.6285	5.6478	5.7611	5.9812	5.4779	4.8228	5.2843	4.9699	5.3231	5.133	4.9421	5.046	3.8848		5.0391	3.9587	2.8669		4.0783	3.1437	
K.ISSIQDILPALEISNQSR.R +3													5.2742		4.8816										
K.LGVDIIR.K +1																2.0343									
K.LIDEYGDDFAK.G +1																			2.4965	2.4844			2.3693	2.3233	
K.LIDEYGDDFAK.G +2			4.0603	4.1157	4.1903	3.8247	4.2026	3.1086	3.8527	3.74	4.2272			2.8258					3.7949		3.2505		3.1849	3.1433	
K.LLASAMEK.V +1																	1.9718	2.2944		2.0785		2.0901			
K.LLQEVASK.T +1									2.0359			1.9543	2.111	2.039	2.0161	1.9243	1.9136			2.1089					
K.LLQEVASK.T +2						2.7715																			
K.LSGGVAVIR.V +2					3.53		3.4008		3.4774	3.4024	2.9908		2.9896	3.4186	3.3905	3.5974		3.007					3.4186	3.0399	
K.NVAAGCNPM*DLR.R +2											2.589	2.9269	3.6734	3.4894		3.2329		3.1172							
K.NVAAGCNPMDLR.R +2					4.1485	3.9132	4.1333	3.8562	3.9378	3.8585	3.9649	3.624	3.854	3.8956	3.5398	4.0963	3.0106				3.9352	3.773	4.0179	3.3433	
K.PLLLLSEK.K +1															2.6708		2.5043	2.4457							
K.PLLLLSEK.K +2	3.1827	3.1908	3.0957	3.175									2.7288	2.9765			3.0417	3.0724		3.2221			2.7006		
K.QIIENAGEEGSVIIGK.L +2					5.2146	4.8108	4.7471	4.6677	4.6655		4.2126	3.8093	3.7806	4.7133	4.7124	3.8838	4.893	4.0085		3.3874		3.9766	5.1618	4.6194	
K.SEYTDM*LATGIIDPFK.V +2						4.1954	4.2533	4.0596	4.19	4.8533	4.7199	4.0543	4.5304	4.4045	4.5454	4.3927			5.0664	4.8243	4.9888			3.2055	
K.SEYTDMLATGIIDPFK.V +2	4.8877	5.2702	5.2568	5.2205	5.1621	5.0967	5.2617	5.3502	4.7759		4.8608	5.0424			4.6702	4.8522	4.6777	5.2008	2.5018	4.4317	3.5357			5.0541	
K.TNEAAGDGTTSATVLGR.A +2	4.8459	4.7099	4.7263	4.7689	4.5829		4.665	4.6409	5.0352	4.5239	4.8073	4.6465	4.5596	4.4832	4.4886	4.624	4.7442			4.8007		4.7309		4.4071	
K.VEFEKPLLLLSEK.K +2													4.5324	4.393	3.8398	2.6732									
K.VEFEKPLLLLSEK.K +3													3.8536	3.6868											
K.VIEFLSANK.K +1														2.2858											
K.VIEFLSANK.K +2												3.1439	3.37		3.4604	3.3004			3.3922	3.3381	2.6284				
K.VIEFLSANKK.E +2		3.0549	3.2671	3.3686					2.5847				2.948	2.5909	2.8402	2.8326	2.9147		2.9076	2.6492					
R.AAVEEGILPGGGTALVK.A +1								2.7588													1.8356				
R.AAVEEGILPGGGTALVK.A +2	3.7199	3.9469	3.7192	3.9127	3.9348	4.1452	4.0003	4.0746	3.8436	3.8272	3.7953	3.4567	3.8896	4.1605	3.911	3.7656	3.6533	3.6168	2.9205	4.1072	3.3794	3.4891	3.2395	3.8709	
R.GFISPYFITDPK.S +2		3.7226	3.7405	3.5549	3.8234	3.826			3.7	2.6945		3.2126	3.7771	3.5492	3.9885	3.6346	3.4778	3.8357		3.815	3.7066		2.6799	3.7428	
R.NVLIEQPFGPPK.I +1							1.8944																		
R.NVLIEQPFGPPK.I +2	4.1365	4.2266	3.9053	4.1453	4.0526	3.9534	4.0366	4.1438	4.0525	4.159	3.9385	3.929	3.9685	4.141	3.8045	4.1666	3.9474	3.7051	3.6365	3.7609		3.8714	4.0051	3.6587	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.TLEDELEVTEGM*R.F +2					4.4111	4.1657	3.9521	4.3247	4.4277	3.4653	3.9206	4.4345	4.3812	4.3695	4.2396	4.4183		4.3928	3.5825	4.1876	4.1855	3.622		3.7771	
R.TLEDELEVTEGMR.F +2		4.4626	4.8302		4.8758	5.0521	5.0339	4.8528	4.8418	3.9057	4.9016	4.7162		4.4572	4.6031	4.7892	4.2404	4.6388		4.3617	4.7842	3.9193		4.631	
R.VGGASEVEVGEK.K +2						3.6503	3.8701				3.4431	3.3458		2.8898	2.6484	3.3627				3.6458	3.6594				
R.VLDEVVVDNFDQK.L +1								2.065	2.552																
R.VLDEVVVDNFDQK.L +2	4.4018	4.614	4.5003	4.5476	4.6685	4.4804	4.6254	4.8692	4.4512	4.2164	4.5131	4.2954	4.3669		4.3164	4.4107	4.1325	4.1836			3.2899	4.6401	4.5954	4.5098	
R.YDDALNATR.A +1																							1.9334		
R.YDDALNATR.A +2						3.3017	3.4925	3.3211	3.3538	2.8123	3.4337	3.275	3.2216	3.2326	3.3053							3.6176			
gi|6323386|ref|NP_013458.1|	17	25.7	25.1	26	31.9	46.9	37	33.1	54.9	36.7	42.4	43.9	41.8	45.4	45.4	49.9	37.3	32.8	26.3	36.7	23.9	30.1	37.3	31.9	Transaldolase, enzyme in the non-oxidative pentose phosphate pathway; converts sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate to erythrose 4-phosphate and fructose 6-phosphate; Tal1p [Saccharomyces cerevisiae]
K.ASGTVVVADTGDFGSIAK.F +2		5.7375	5.8909	5.5747	5.6259	6.0936	5.7153	6.2005	5.5465	5.3851	5.7803	5.5212	5.9488	6.1857	5.9592	5.9982	5.5682	6.2975	4.0847	4.4592	5.1233	3.8356	5.5165	5.9179	
K.DYKGEADPGVISVK.K +2						3.9661	3.7074		3.0315	3.3045	3.798	3.4907	3.9273			3.7261	4.509	3.5803							
K.FQPQDSTTNPSLILAAAK.Q +2	4.8807	5.376	4.8817	4.8036	4.8994	4.7816	4.8705	4.9476	4.279	4.6407	4.4992	5.0125	3.708	4.2844	3.973	4.7161	4.1703	3.4708	4.2183	3.3304	4.6324	4.2828	4.6261	3.9061	
K.FRFDLNEDAM*ATEK.L +2													2.7295	2.6437											
K.FRFDLNEDAMATEK.L +2																	3.9945			3.6089					
K.FSADIVTLFDLIEK.K +2						5.6141		2.9825	5.1887			5.1677	5.5793	5.4941	5.4146	5.4484			3.8674	3.6099					
K.GEADPGVISVK.K +2									3.08		2.7014														
K.IASTWEGIQAAK.E +1																		2.2139		2.1266		2.0839			
K.IASTWEGIQAAK.E +2				4.3072	4.0278	4.1035	4.0882	4.1226	4.0229	4.0991	3.8659	4.0755	3.8958	4.0944	2.975	4.1949	3.7687	4.1258		3.4966	3.6219	3.9748	3.5874	3.7335	
K.ISYISDESK.F +1									2.5409																
K.ISYISDESK.F +2			3.1446					2.6097							2.7464					2.9719					
K.LIDVAVEYGK.K +1									2.4306						2.6495	2.7979	2.595	2.3169		2.03		2.6299	2.7045	2.6186	
K.LIDVAVEYGK.K +2									2.6292										2.6319		2.577			3.1478	
K.LIDVAVEYGKK.H +2																	3.0058	2.8192							
K.LM*NSTEPFPR.V +2										2.8816		2.8895				3.2904							2.741		
K.LMNSTEPFPR.V +2	3.6808	3.8765	3.8503	3.9439	3.9394	3.6896	3.9911		3.8407	3.3717	3.7378	3.6322		3.6738		3.5557	3.7965				3.2804	3.7942			
K.NLAGVDYLTISPALLDK.L +2	5.8964	6.3345	6.2255	6.1956	6.3514	6.3471	6.1601	6.2526	5.7445	5.5318	5.4963	5.8937	6.139	5.8111	6.277	5.7922	5.9205	6.079	6.0499	5.6324			5.5311	5.4311	
K.TIVMGASFR.S +1									1.8565					1.9811											
K.TIVMGASFR.S +2					2.8815	2.6215			2.9733			2.6846			3.0657	3.0111		2.8077					2.5612	2.7602	
K.TTEEQVENAVDR.L +1																							2.1795		
K.TTEEQVENAVDR.L +2	3.9387	4.0971	4.1745	4.2091		4.1042	4.0084	4.1369	3.2673	4.1511	4.1299	4.2268	3.892	4.0627	3.2778	3.4975					3.431			4.1973	
K.VANNSLEQLK.A +2						3.4147			3.1991	2.9951	3.4374		3.2452	3.3612	3.3008	3.2825				3.5874					
R.FDLNEDAM*ATEK.L +2													3.5797												
R.FDLNEDAMATEK.L +2					4.1357	4.3327	4.1917		4.4045	4.0016	4.3005	4.132	4.2332	4.1076	4.1632	4.0863	3.8604			3.8932					
R.LLVEFGK.E +1														2.1309											
R.LSFDTQATIEK.A +2		3.7408			3.6835	3.6625	3.621	3.4178	3.5738		3.7044	3.3827	3.5284	3.7475	3.6853	3.5625	3.6369	4.0809	3.5029	3.7342		3.2378	3.4076	3.2957	
R.VLDPVSAK.K +1									2.0676		1.9367												1.8998		
gi|6323387|ref|NP_013459.1|	15.4	41.3	32.4	44.3	34.9	39.7	34.7	40	43.8	23.5	39.7	37.2	41	56.5	43.3	40	36.7	32.4	55.2	49.1	27.1	23.5	30.9	31.9	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA; Ilv5p [Saccharomyces cerevisiae]
K.AAIEDGWVPGK.N +1									2.0092																
K.AAIEDGWVPGK.N +2	3.4803	3.1663	3.249	3.1517	3.4499	3.3524	3.5828	3.4991	3.3172	3.4256	3.4917		2.6692	2.8586		2.9267									
K.AQALAVAIGSGYVYQTTFER.E +2						6.403		6.3447	6.5221		2.5934	5.3167		6.1186	4.2428	5.5234			5.9965	6.1865			4.7623	2.8206	
K.AQALAVAIGSGYVYQTTFER.E +3														5.7617											
K.DLDVILVAPK.G +1					2.789			2.7632	3.2385					3.3095	3.3136	2.9735	2.513		2.4277				2.3914		
K.DLDVILVAPK.G +2								3.0025				3.3121	3.5716	3.5797	3.383	3.596		2.9112	3.254		3.1681	3.8928	3.7484	2.7983	
K.DLTHVEPPK.D +2						2.9012	2.9927				2.6173														
K.DLTHVEPPKDLDVILVAPK.G +2		4.7458		4.533									4.4754	4.6811	3.7543				3.0249	3.5588					
K.DLTHVEPPKDLDVILVAPK.G +3		5.9806		5.8889									5.278	5.6937			4.0017			5.4457					
K.NALKPVFQDLYESTK.N +2	4.2515	4.4082	4.472	3.9549					3.1129				4.4102	4.2143	2.6517				3.4063	4.1861					
K.NALKPVFQDLYESTK.N +3													3.5636												
K.NDTFALIGYGSQGYGQGLNLR.D +2		6.0889	6.1309	5.9505	6.2851	6.2173	6.2163	6.22	5.9911	6.052	5.8055	5.7668	6.0988	6.0968	5.9113	5.9275	5.5658	3.2706	5.9744	5.91	6.0097	4.2641	6.1034	6.016	
K.NDTFALIGYGSQGYGQGLNLR.D +3					5.2631		5.1071	3.9941	5.6431		3.7409	5.6852	6.1171	5.879	5.3346	5.889			5.9504	5.1708			5.1294		
K.NLFTVEDAIK.R +1					2.7157	2.8521	2.7888	2.7613	2.471			2.3329	2.4627	2.6277	2.5289	2.5686		2.5271	2.5394	2.2983			2.751	2.1695	
K.NLFTVEDAIK.R +2	2.7322	2.8511	2.8601	2.8042	2.9814	2.9565	2.9078	2.964	2.8571	2.9378	2.9327	2.6522		2.8237				2.9617							
K.PVFQDLYESTK.N +2																	3.1783								
K.QINFGGTVETVYER.A +2				3.4	3.9797	4.0256	4.3386	4.2277	4.181		2.8896	3.9312	4.138	4.2811	4.3993	4.1742		2.9975	4.4196	4.0387	3.9361			4.1929	
K.RSLEFNSQPDYR.E +2		3.0725	2.9314	3.4174													2.836	3.0356	2.7726						
K.TLYFSHGFSPVFK.D +2		4.3554	3.267											3.6869					4.1263	4.1923					
K.YGM*DYM*YDACSTTAR.R +2													4.6977												
K.YGM*DYMYDACSTTAR.R +2										4.8677			4.8893	4.7457			3.5915			4.6477	5.0461	4.7587		4.6621	
K.YGMDYM*YDACSTTAR.R +2											4.0905		3.8316					2.6243					3.4816		
K.YGMDYMYDACSTTAR.R +2		4.3397			4.7907	4.6233	4.7155	4.9338	4.8126	3.5843	4.1718	4.4811			4.4264	4.7619	4.4664	3.4907		4.1914		3.8335	3.8586	4.9046	
R.DNGLNVIGVR.K +2		4.4496	4.338	4.3699	4.0355	4.0046	4.3297	4.3253	4.1744		3.6212	3.588	4.1243	4.18	4.0972	4.2583	3.4161	4.0936	3.8186	4.0067	3.9038	3.9903		3.8449	
R.ENGHSPSEAFNETVEEATQSLYPLIGK.Y +3				4.0074										3.6869					3.6442						
R.EVNSDLYGER.G +1		2.3965							2.261			2.6325	2.4372		2.5139	1.9597	2.3478	2.6546	1.9961	2.4972		2.0977			
R.EVNSDLYGER.G +2	3.2192	3.2307	3.3487	3.3011	3.0948	2.9848	3.0855	3.0869	3.0198	2.9454	3.0604	3.0349	3.1914	3.1471	2.9447	3.0677	3.1306	3.3154		2.9229		3.0967	3.0778		
R.GALDWYPIFK.N +1									2.4862																
R.GALDWYPIFK.N +2		3.5696	3.4512	3.5752	3.4644	3.4493	3.3587	3.4672	3.2388		3.3626	3.3638	3.5655	3.5353	3.5243	3.5385	3.3048	3.376	3.5598	3.664	3.3318		3.375	3.424	
R.GINSSYAVWNDVTGK.A +2	5.1748	5.0209	5.3202	5.0963	5.1323	4.9836	5.0572	5.1788	4.691	4.744	4.8101	4.4443	4.523	4.8261	4.9087	4.2475	4.7692	4.888	3.235	3.0319	4.6693	4.7523	2.9542	4.4744	
R.GSYVM*NLLSDAAQSETWPAIK.P +2																			4.6176	2.973					
R.GSYVM*NLLSDAAQSETWPAIK.P +3																			3.8185						
R.GSYVMNLLSDAAQSETWPAIK.P +2																	2.6254			2.7262					
R.RGALDWYPIFK.N +2		2.5849												2.9592											
R.SLEFNSQPDYR.E +1																							1.8585		
R.SLEFNSQPDYR.E +2					3.9427	3.8459	3.9062	4.0261	3.9463	4.0861	3.6812	3.707	3.8987	3.7003	3.5965	3.7169			2.9815		3.4413	3.7379	3.9201		
gi|6323464|ref|NP_013536.1|	6.1	23.1	26	11.5	23.5	22.9	29.4	31.2	36.5	27	28.3	33.7	38	36.3	43	40	32.1	35.8	30.6	34	13.4	22.8	27	26.4	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed; Imd3p [Saccharomyces cerevisiae]
K.ERFGFSGFPVTEDGK.R +2																	2.8036								
K.ETFPDLEIIAGNVATR.E +2	5.2477	5.0377	5.4406	5.3772	5.806	5.8764	5.7099	5.4263	5.4056	4.8017	4.9435	4.9658	4.9706	5.4036	5.4283	4.9012	3.6754	5.3644	5.2525	3.3526			4.7486	4.8839	
K.ETFPDLEIIAGNVATR.E +3													4.1407	4.7163											
K.FIPYLYNGLQHSCQDIGYK.S +2																				3.3463					
K.LLIVDDNGNLVSM*LSR.T +2									3.2215	2.8478		4.5695	5.332	4.8244	4.8606			3.8512	5.2278	4.7011			3.2016		
K.LLIVDDNGNLVSMLSR.T +2	4.9092	5.2402	5.5671	5.3765	5.1388		5.1744	4.9498	4.9565			4.9671		3.2869	4.3414	2.8192	4.4053			4.4221			4.1665		
K.LM*GIVTSR.D +2																2.5652					2.6307				
K.LMGIVTSR.D +2									2.7027			2.6027	2.5655		2.6785						2.5033				
K.NPVTGAQGITLSEGNEILK.K +2		6.1584	6.1961		6.6906	6.1313	6.5625	6.0588	6.143	5.8717	5.3127	5.8825	6.8637	6.2463	5.8466	6.0527	5.5624	5.2941	6.0202	5.1802		6.7044	6.233	5.8445	
K.NPVTGAQGITLSEGNEILK.K +3													4.2899	4.7673											
K.NPVTGAQGITLSEGNEILKK.I +2									4.5582				5.0257	4.9282		5.4284			3.7879						
K.NPVTGAQGITLSEGNEILKK.I +3														3.9774											
K.NYENGFINNPIVISPTTTVGEAK.S +2		4.6099	5.8055		4.7503	5.297	4.88	4.8164	4.7772	3.8481	4.1399	4.3831	4.5934	5.5503	5.0538	4.7751	4.6763	4.0917	4.9272	4.7821	4.6626	3.0574	4.8267	4.48	
K.NYENGFINNPIVISPTTTVGEAK.S +3						4.5561		5.2067	3.7108		3.8598		4.6627	5.4392	4.0768		4.8462	4.6876				6.2168		4.7523	
K.QLLCGAAIGTIDADK.E +2															3.146		4.1345	4.5677				3.6928	3.4786	2.756	
K.QLLCGAAIGTIDADKER.L +2													3.7973	3.7478	3.4815										
R.DIQFVEDNSLLVQDVM*TK.N +2							5.2001		4.5524	3.6006	3.6839	4.015	3.634	3.9161	4.5558	4.8779		3.9191	3.7665	3.6691	5.0558		4.901	2.8836	
R.DIQFVEDNSLLVQDVM*TK.N +3														5.1713											
R.DIQFVEDNSLLVQDVMTK.N +2									4.2852							4.3566	4.5248								
R.EQAANLIAAGADGLR.I +1									2.5733																
R.EQAANLIAAGADGLR.I +2			4.5531	5.0645	4.672	4.7825	4.7581	4.7828	4.5999	4.7525	4.5345	4.6073	4.9458		4.2697	4.5431	4.3255	5.1225	4.3588			4.6913			
R.EQAANLIAAGADGLR.I +3														4.4129						4.2676					
R.FGFSGFPVTEDGK.R +2		4.0299	4.1478	4.2657		4.5322	4.0386	4.2372	4.4432		3.9482			4.2023	4.1966	4.4955	3.7621	3.9993		4.3449				3.7898	
R.FGFSGFPVTEDGKR.N +2									2.8806				3.3156		2.7508	3.525									
R.GGLTYNDFLVLPGLVDFPSSEVSLQTK.L +2								2.8343	3.2942			3.1225			3.0786	3.0181									
R.GMGSIDAMQK.T +2														2.6548											
R.LDGLSVQELM*DSK.T +2										3.3989		3.8118	3.9434	3.3642	3.8802				3.1848			3.9124			
R.LDGLSVQELMDSK.T +2		4.3853	4.4466		3.9856	4.3716	4.5122	4.2866	4.4231	3.3444	4.1088	4.0619		4.255	4.1319	4.1281	3.5995	3.9896		3.8896		3.9665	4.0854	4.2219	
R.TASAQLEGGVHNLHSYEK.R +2													4.9829	4.8521	3.1837	3.3026	4.7076	4.2446	2.6855	3.2225					
R.YFSESDSVLVAQGVSGAVVDK.G +2		5.9993	5.731		6.2921	5.919	6.0219	6.1313	6.2703	4.5902	4.9199	6.417	6.2792	6.0096	6.1684	6.2208		5.8755	3.5251	5.5607	3.9034	5.9741	3.6325	5.8171	
R.YFSESDSVLVAQGVSGAVVDK.G +3													3.8966	5.986				3.5647	3.9027			4.2958	3.8759		
gi|6323474|ref|NP_013546.1|	30.6	37.3	38	30.2	16.1	12.9	22.7	22.7	43.5	11.8	20.4	34.9	48.6	47.8	40	35.7	30.2	12.2	24.3	36.1	8.2	9	11.8	7.8	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Bp and has similarity to rat S3a ribosomal protein; Rps1ap [Saccharomyces cerevisiae]
K.APSTFENR.N +2	2.6367	2.5869	2.5835		2.5954	2.673	2.6269	2.5743																	
K.DIFPLQNIHVR.K +2	3.2583	3.7511	3.5785	3.3676									3.273	3.5094	3.334	3.2988			3.0101	3.1613					
K.EVQGSTLAQLTSK.L +1											2.5328										2.6292		2.1267		
K.EVQGSTLAQLTSK.L +2					4.4083	4.4238	4.3862	4.2771	4.2531	4.0977	3.8739		4.1171	4.322	4.0844		3.546	3.9192		4.4348		3.7656			
K.FDVGALM*ALHGEGSGEEK.G +2									3.7194			2.5221	3.9706		3.4001		3.2251								
K.FDVGALMALHGEGSGEEK.G +2	4.4116	4.6376	5.172											4.3868		2.5645	3.875								
K.KVTGFKDEVLETV.- +2													3.3421				3.3212								
K.LRVDEVQGK.N +2		2.8052	3.0528	2.903			2.743	2.913	2.864	2.6102	2.7261		2.728	2.869	2.7838	2.6597				2.6692			2.8821		
K.NLLTNFHGM*DFTTDK.L +2									4.3889			3.7493	4.5269	4.486	4.0846	4.144			4.5344	4.3308					
K.NLLTNFHGMDFTTDK.L +2	4.7953	4.9059	4.9058	4.3062										4.7324	2.982		4.0901			4.4302					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.RVVDPFTR.K +2		2.6729		2.5142															2.5225						
K.TSDDYVLR.I +2		3.1088		2.8695			3.2868	3.1204	3.3909	3.0881	3.4065	2.5708		3.0857						3.1024					
K.VTGFKDEVLETV.- +2					2.951	2.8751	2.9459	2.9982	2.9247		2.7091	2.6454	2.5226	2.7948		2.8123								2.5065	
R.HSYAQSSHIR.A +2		2.7289	2.8269						2.8889		2.6363	2.9456	2.9075	2.7888	3.0027					2.7131		2.6766			
R.IFAIAFTR.K +2	3.1685	3.1196	3.1906	3.3588	2.9713		2.972	2.9376	3.1746			2.8778	3.1179	3.0888	3.1721	3.0187			3.0496	2.7406	2.6666		3.0489	2.6342	
R.IFAIAFTRK.Q +2																			2.8235						
R.KVISEILTK.E +2													2.9961												
R.VDEVQGK.N +1											2.0092														
R.VVEVCLADLQGSEDHSFR.K +2	2.5678		4.4592	5.0973					5.6909			4.774	5.6893	6.043	5.8593	5.75	4.8417	5.6455	4.2441	4.4691					
R.VVEVCLADLQGSEDHSFR.K +3													3.6999												
R.VVEVCLADLQGSEDHSFRK.I +2																			2.9286						
gi|6323585|ref|NP_013656.1|	8.8	12.6	18.1	11.5	20	20.8	24	31.1	27.5	15.6	18.5	25	24	21.6	29.2	34.5	22.7	29.6	16.4	33	9.9	10.7	20	15.1	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, member of a four-gene family in S. cerevisiae, constitutively expressed; Imd4p [Saccharomyces cerevisiae]
K.DGLSVQELM*DSTTR.G +2																		3.6068		4.1748					
K.DGLSVQELMDSTTR.G +2	4.223		4.2086		4.8853	5.1205	5.0356	4.5501	4.7537	4.0228	4.7201	3.8487		4.1091	4.6129	4.5821				3.7706			4.1247	3.498	
K.ETFPDLEIIAGNVATR.E +2	5.2477	5.0377	5.4406	5.3772	5.806	5.8764	5.7099	5.4263	5.4056	4.8017	4.9435	4.9658	4.9706	5.4036	5.4283	4.9012	3.6754	5.3644	5.2525	3.3526			4.7486	4.8839	
K.ETFPDLEIIAGNVATR.E +3													4.1407	4.7163											
K.FGFSSDPVTIEDGK.C +2		4.0299	4.1478	4.2657		4.5322	4.0386	4.2372	4.4432		3.9482			4.2023	4.1966	4.4955	3.7621	3.9993				4.3449		3.7898	
K.LLIVDDNGNLVSM*LSR.A +2									3.2215	2.8478		4.5695	5.332	4.8244	4.8606			3.8512	5.2278	4.7011			3.2016		
K.LLIVDDNGNLVSMLSR.A +2	4.9092	5.2402	5.5671	5.3765	5.1388		5.1744	4.9498	4.9565			4.9671		3.2869	4.3414	2.8192	4.4053			4.4221			4.1665		
K.LVGLVTSR.D +1									1.948																
K.LVGLVTSR.D +2							2.9845		3.1892		3.1853	2.8226						2.904		3.2573	3.0845		2.7875	2.8589	
K.M*FENGFINSPIVISPTTTVGEVK.V +2									3.2508			3.3541	3.9259		4.4284	3.6128				3.8954	2.8224		3.4489		
K.M*FENGFINSPIVISPTTTVGEVK.V +3													4.0865												
K.MFENGFINSPIVISPTTTVGEVK.V +2					4.5033	3.8632	3.8784	3.4143	3.7759								3.5103			3.107					
K.NPVTGIK.G +1						1.8371												2.2556				1.847	2.1685	1.8359	
K.QLLCGAAIGTIEADK.E +2																				3.2076					
K.QLLCGAAIGTIEADKER.L +2													2.6835		3.2496										
R.DIQFLEDDSLVVSEVM*TK.N +2												3.6183													
R.DIQFLEDDSLVVSEVMTK.N +2								4.016	4.3403							4.148	4.5921								
R.EQAANLIAAGADGLR.I +1									2.5733																
R.EQAANLIAAGADGLR.I +2			4.5531	5.0645	4.672	4.7825	4.7581	4.7828	4.5999	4.7525	4.5345	4.6073	4.9458		4.2697	4.5431	4.3255	5.1225	4.3588			4.6913			
R.EQAANLIAAGADGLR.I +3														4.4129						4.2676					
R.GGLTYNDFLVLPGLVNFPSSAVSLQTK.L +2								3.0541										2.5527		2.899					
R.GGLTYNDFLVLPGLVNFPSSAVSLQTK.L +3																4.3821				4.1505					
R.GMGSIDAMQK.T +2											2.6548														
R.TASAQLEGGVHNLHSYEK.R +2													4.9829	4.8521	3.1837	3.3026	4.7076	4.2446	2.6855	3.2225					
R.YFSESDSVLVAQGVSGAVVDK.G +2		5.9993	5.731		6.2921	5.919	6.0219	6.1313	6.2703	4.5902	4.9199	6.417	6.2792	6.0096	6.1684	6.2208		5.8755	3.5251	5.5607	3.9034	5.9741	3.6325	5.8171	
R.YFSESDSVLVAQGVSGAVVDK.G +3													3.8966	5.986				3.5647	3.9027			4.2958	3.8759		
gi|6323613|ref|NP_013684.1|	39.8	36.2	36.2	29.1	23.5	19.9	27.6	35.7	41.3	23.5	19.9	33.2	58.2	53.6	57.1	46.9	29.6	19.9	52.6	52.6	27.6	23	16.3	24	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p, deletion results in mutator phenotype; Tsa1p [Saccharomyces cerevisiae]
K.EGGLGPINIPLLADTNHSLSR.D +2		4.6952											3.7071	4.1801	4.0965				3.2247						
K.EGGLGPINIPLLADTNHSLSR.D +3	3.6392	4.1587	4.1156										3.5028						3.5921						
K.EYFEAANK.- +1							2.5382					2.4036	2.4598	2.6839	2.3663	2.5802	2.4241		2.5049		2.1277	2.2941	2.4373	2.8089	
K.KTAVVDGVFDEVSLDK.Y +2													3.4369	4.6412		4.9392									
K.NGTVLPCNWTPGAATIKPTVEDSK.E +2								2.9592	2.9348				2.6374	2.8887	2.731	2.7184			2.8126	2.5406					
K.QAPTFKKTAVVDGVFDEVSLDK.Y +3										3.6195											3.5143				
K.TAVVDGVFDEVSLDK.Y +1								3.0197	2.6701																
K.TAVVDGVFDEVSLDK.Y +2	5.4277	5.3725	5.3845	5.587	5.4104	5.3923	5.4567	5.5603	5.1808	5.312	5.2438	5.024	5.1476	5.3829	4.9511	5.2572	4.7961	5.386	4.6253	5.2887	5.3118	4.7058		4.9197	
K.TAVVDGVFDEVSLDKYK.G +2													4.8174		3.2607	3.191									
R.DYGVLIEEEGVALR.G +1												1.8482				2.4907					2.057				
R.DYGVLIEEEGVALR.G +2	4.9603	5.3232	5.2154	5.2267	5.1914	5.1061	5.1582	5.2219	4.7888	5.1009	4.9893	5.2144	4.9072	5.0637	4.9934	4.9152	4.9695	4.7814	4.7281	5.1524	4.9087	4.9362	4.8158	5.1263	
R.GLFIIDPK.G +2													2.6074									2.7576			
R.HITINDLPVGR.N +1															2.8278		2.4321			2.0807					
R.HITINDLPVGR.N +2	2.9391	3.4465	3.4475	3.4197					3.1925			2.6822	3.3261	3.171	3.0585	3.1646	3.0179		3.3044	2.9363					
R.KEGGLGPINIPLLADTNHSLSR.D +2																				2.5404					
R.KEGGLGPINIPLLADTNHSLSR.D +3														5.8623						4.5313					
R.LVEAFQWTDK.N +1						2.3769	2.5665	2.6819	2.6885		2.3909		2.6681	2.6982	2.6982			2.1336	2.5242		2.537				
R.LVEAFQWTDK.N +2	4.0568	4.2319	4.1359	4.245	4.1219	4.1149	4.0788	4.2221	3.9837	4.0452	4.0099	4.1207	4.0349	4.0705	4.1522	4.0155	3.851	4.2072	3.3692	2.9589	3.86		3.8662	4.1022	
R.NVDEALR.L +1	1.9691			2.1897	2.0339		2.0376	1.9631	1.9947			1.9922			2.0421	2.0805				1.9923					
gi|6323615|ref|NP_013686.1|	29.5	43.8	54.1	42.5	42.5	42.5	47.9	47.9	47.9	34.2	42.5	47.9	47.9	53.4	45.9	40.4	38.4	43.2	27.4	38.4	28.8	34.2	18.5	13.7	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Ap and has similarity to E. coli S13 and rat S18 ribosomal proteins; Rps18bp [Saccharomyces cerevisiae]
K.DYHTLANNVESK.L +1						4.1832	3.975		3.5683		3.9832								3.6129	2.8616					
K.DYHTLANNVESK.L +2	3.2756	3.4306	3.4141	3.5084	3.5429	3.5996	3.557	3.284	3.1506	3.1349	3.4762	3.0052	3.3801	2.988		3.2438	3.4015	3.3251			2.7488	2.8364			
K.IPAWFLNR.Q +2	2.9858	2.9165	2.8977	2.9171			2.8435	2.7611	2.8901			2.9212	2.9729	2.9684	2.9298	2.9783	2.5649								
K.IVYALTTIK.G +1			1.8057		1.9134		1.9544	1.8978			1.8962					1.8438	1.938		1.8061						
K.IVYALTTIK.G +2		2.9808				3.4373	3.5429		3.447	3.5766	3.0161	3.0972	3.0094	3.1176	3.0263	3.3511	3.2265	2.8481		2.5967		3.1534	3.3903	3.4118	
K.KADVDLHK.R +2			3.2944														2.9285								
K.KADVDLHKR.A +2															2.6475										
K.RAGELTQEELER.I +2		4.4866	4.5206	4.1911														3.789	3.4701	4.6112					
R.AGELTQEELER.I +1												2.1752		2.9372		2.841					2.298	2.5496			
R.AGELTQEELER.I +2		3.6335	3.597	3.6775	3.7216	3.6626	3.6496	3.5696	3.3435	3.5434	3.3848	3.3966	3.9042	3.7136	3.5201	3.0882								3.5086	
R.IVQIM*QNPTHYK.I +2			4.0276	4.1569			2.9617		2.9375		3.5494	3.2184	4.0927	3.2152	4.0632	3.8515	3.5546			3.8507	3.2071				
R.IVQIMQNPTHYK.I +1																	2.7426			2.5879					
R.IVQIMQNPTHYK.I +2	4.6311	4.5273	4.4757	4.5065	3.2995	2.5667		2.7353	4.276		3.6229	3.9503	4.4837	4.2368	4.2781	4.3636	4.3936	4.3549							
R.LLNTNVDGNIK.I +1													2.2141	2.5339				2.4569		2.3648			2.5199		
R.LLNTNVDGNIK.I +2	3.4595	3.6215	3.3887	3.4063	3.3097	3.4682	3.2688	3.4631	3.6888	3.2707	3.0027	3.361	3.536	3.947	3.3565			2.9387				3.4751	3.6487		
R.QNDITDGKDYHTLANNVESK.L +3														3.9198											
R.YSNLVCK.K +1									2.1266	1.8906	2.2457	2.1571	2.0309	2.2476	2.1005	1.8757	2.1224	2.0789	2.5364		2.189	2.1194	2.3933		
R.YSNLVCK.K +2			2.8598	2.6174	2.9685	2.5332	2.8546	2.9144	2.6285			2.609			2.6625	2.5188	2.9979								
gi|6323763|ref|NP_013834.1|	30.1	54.5	28.5	22.3	27.9	31	21.9	27.9	30.7	21.9	30.7	28.5	28.5	50.2	27.9	28.5	28.2	17.2	35.4	36.1	15.4	14.7	25.7	11.3	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gcn4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RACK1; Asc1p [Saccharomyces cerevisiae]
K.AAEPHAVSLAWSADGQTLFAGYTDNVIR.V +3														4.9938											
K.ADDDSVTIISAGNDK.M +1												2.7693	3.186			2.729			2.9044	2.3969	2.2954	3.0235	2.4052		
K.ADDDSVTIISAGNDK.M +2	4.9861	5.1466	5.021	5.0849	5.2333	4.9957	5.2572	5.0445	4.6853	5.0045	4.7542	5.1464	4.6825		4.5149	5.0353	4.4923			4.5067	3.8851	3.9926			
K.AM*YTLSAQDEVFSLAFSPNR.Y +2					4.3337	5.8309		4.812	5.9086		3.8023	4.5485	5.8104	5.7597	4.493	5.328			4.9147	4.9315			4.9326		
K.AMYTLSAQDEVFSLAFSPNR.Y +2					4.0559	5.4488			5.4546			3.1752					3.6947		3.6512	4.4069					
K.ASMIISGSR.D +1						2.1543					2.0766	2.1928				2.5747	2.2283	2.0781				2.3588			
K.ASMIISGSR.D +2	3.2474					3.5165			3.066	3.1798	3.1258														
K.AWNLNQFQIEADFIGHNSNINTLTASPDGTLIASAGK.D +3		4.7151												5.0165											
K.DGEIM*LWNLAAK.K +2		4.4499		4.415	4.8373	4.7444	4.6542	4.7447	4.7704	4.6292	4.6505	4.7016	4.4575	4.3439	4.6587	4.6275	3.098	3.4227	3.1299	3.6908	4.5673	2.973	4.0502	4.7856	
K.DGEIMLWNLAAK.K +2	4.6931	4.7222	4.7866	4.8834	4.714	4.5964	4.6167	4.5361	4.445		4.7587	4.8072		4.0321	4.3996	4.5515	4.6175	4.2723		4.3964	4.3104	4.6107	4.9196	4.4449	
K.GQCLATLLGHNDWVSQVR.V +2	3.4513	2.5071												3.3251					3.763	3.5926					
K.GQCLATLGHNDWVSQVR.V +3		4.5111												4.0971					3.5104	4.8176					
K.KASM*IISGSR.D +2																						2.6859			
K.KASMIISGSR.D +2				3.214									3.226							2.5261					
K.SDVM*SVDIDK.K +2														3.0584											
K.SDVMSVDIDK.K +1			2.4222						2.5757		1.9821	2.5747	2.4113	2.3824		2.479	2.3735	2.4554			2.4869	2.4771			
K.SDVMSVDIDK.K +2	3.6091	3.6963	3.6688	3.656	3.5844		3.6665	3.5531	3.5366	3.2032	3.4686	3.3689	3.6634	3.5506	3.4368	3.5521	3.5379	3.3818			3.533				
K.SDVMSVDIDKK.A +2						3.0744	2.9802					3.2492	3.6271	3.3075		3.3122							2.6006		
K.VFSLDPQYLVDDLRPEFAGYSK.A +2														4.2427											
K.VFSLDPQYLVDDLRPEFAGYSK.A +3		3.5093	4.4419											3.771											
R.GTLEGHNGWVTSLATSAGQPNLLLSASR.D +3		4.8415																	3.9485	3.5043					
R.LWDVATGETYQR.F +1					2.5994	2.3682		2.5715	2.339							1.9682	1.9345		1.9018						
R.LWDVATGETYQR.F +2	4.6638	4.7102	4.6656	4.7029	4.7898	4.8553	4.803	4.87	4.7772	4.877	4.7432	4.5233	4.277		3.7911	4.579	4.0383	4.6225	2.9782				3.043	4.446	
R.VWQVM*TAN.- +1																			2.1255						
R.VWQVMTAN.- +1	2.0171	2.1254	2.1849		1.9496	1.9183	1.9553	2.2034	1.9951		1.8685				2.1543										
R.YWLAAATATGIK.V +1								3.1329	3.3349		3.2076		3.1583	3.4592	3.2373	3.3595	3.1424	2.782		2.2607				2.6805	
R.YWLAAATATGIK.V +2	4.5945	4.6113	4.5531	4.6109	4.5228	4.6332	4.5475	4.3609	4.4824	4.4891	4.2475	4.3531	4.2339	4.1831	4.0757	3.7975	4.2297	4.406		4.5109	4.4054		4.0795	4.1236	
gi|6323840|ref|NP_013911.1|	18.7	31.5	25.4	31.6	31.8	34.5	37.9	36.2	34.6	24.4	37.7	40.1	30.2	37.2	32.6	35	28.2	24	19.1	35.2	16	15.9	18.2	20.3	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold higher basal levels that HSP82 and induced 2-3 fold by heat shock; Hsc82p [Saccharomyces cerevisiae]
K.AELINNLGTIAK.S +2	4.0432	4.2019		4.2025	4.2215	4.3491	4.3092	4.4211	4.4279	4.3487	4.3029	4.4202	4.0731	4.1322	3.8046	4.1003	4.123	3.7757	4.0619			4.3854	4.2747		
K.DDQLEYLEEK.R +1																				2.6694	2.0052		3.0696		
K.DDQLEYLEEK.R +2					3.9919	4.3054	4.2314	4.2901	4.0201	3.7415	4.2516	4.1641	4.2009	4.1675		3.7868	4.0608								
K.DFELEETDEEK.A +1																		2.7669		2.3642	2.1694			2.6508	
K.DFELEETDEEK.A +2	4.2679	4.1262	4.1741	4.2588	3.6568	3.8922	4.0207	2.798	3.9775	4.1923	4.2022	4.0716			4.0799		3.7107	2.908				4.203	4.4807		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.DFELEETDEEKAER.E +2													3.9027	3.9719		4.6135	3.7605								
K.DILGDQVEK.V +1											2.3902	2.5391	2.4462	2.4537	2.2205		2.3645	2.873		2.3578		2.426			
K.DLTNLLFETALLTSGFSLEEPTSFASR.I +2					2.7408	3.7112		3.6383	3.2203			2.7442				5.0507				4.3066					
K.DLTNLLFETALLTSGFSLEEPTSFASR.I +3				4.9717																5.2167					
K.EVPIPEEEKKDEEK.K +2										3.0151															
K.GVVDSEDLPLNLSR.E +2	4.9569	4.9869	4.9765	5.2413	5.0117	5.0162	5.1	4.9963	4.9924	4.8136	4.8686	4.9007	5.1372	4.8706	4.8098	4.8612	4.7699	4.6334	5.0682	4.9082	4.4612	4.9733		4.7253	
K.KLIEAFNEIAEDSEQFDK.F +2		6.1543	5.9043																	4.6224					
K.KTFEISPK.S +2														2.7276											
K.LEEVDEEEEEEK.K +1																	2.3845	2.9055							
K.LEEVDEEEEEK.K +2	3.9382	4.1822	4.1791	4.0097								2.9286	4.1229				3.6064			3.0807	3.314				
K.LEEVDEEEEEKKPK.T +2							3.2014																		
K.LGVHEDTQNR.A +2			2.6643				2.5364				2.8392			2.7813		3.1111	2.5719								
K.LIEAFNEIAEDSEQFDK.F +2		4.6257	6.304		6.5814	6.5624	6.4051	6.1939	6.601	6.0052	6.2231	5.7661	5.6851	6.007	6.0622	5.9603	4.9734		5.2718	5.6703	4.7841	5.628	5.8805	4.0815	
K.LLDAPAAIR.T +1														2.2749	1.8926							1.8558		2.221	
K.LLDAPAAIR.T +2				2.9322	2.7483	2.715	2.9197	2.8291	2.6952	2.5774		2.5188		2.5779						2.8986					
K.NFEVLFLTDPIDEYAFTQLK.E +2		5.4699	5.9958	6.1048	6.0643	5.8953	6.2962	6.4731	6.1676		3.139	5.5551	6.1727	6.0953	5.9028	6.0303		4.2104		6.1757				2.562	
K.NFEVLFLTDPIDEYAFTQLK.E +3													5.7487	6.3567	5.9628	4.6483				4.783					
K.NIYYITGESLK.A +1								2.5389	3.4937				3.4773	3.5161						2.3424	3.6466				
K.NIYYITGESLK.A +2		4.0223	3.8354		4.2475	4.1593	4.1292	4.0708	4.2305	3.657	4.0268	4.0628	4.1356	4.1329	4.0437	4.0831	4.0426	3.713				3.5932	2.5354	4.159	
K.QLETEPDLFIR.I +2	3.6937	3.854	3.6595	3.8345	3.3823	3.6606	3.5924	3.3321	3.4057	3.3371	3.3463	3.448		3.1676	3.277	3.1654	3.2522	3.4948	3.6853	3.434			2.5534	2.8447	
K.RAPFDLFESK.K +2		2.7647		2.6526									2.9838		2.6248				3.105	3.0106					
K.SISNDWEDPLYVK.H +2	4.5727	4.5407	4.5376	4.2967	4.6035	4.6282	4.6987	4.5486	4.1775	4.4651	4.4211	3.859	3.6617	3.8796	4.0943	4.3068	4.4896	3.6931	4.2606		3.1158		3.909		
K.SPFLDALK.A +1	2.5865						2.5365		2.6878			2.3812													
K.SPFLDALK.A +2														2.6447											
K.SVDELTSLTDYVTR.M +2	5.1554	5.2413	5.2853	5.4009	5.2401	5.2247	5.1487	5.3767	4.8345	4.8466	5.0632	4.8872	4.9566	4.8041	4.431	4.8761	4.9299	5.0604	4.8442	4.3336	4.2908	4.895	4.2865	5.0648	
K.TFEISPK.S +1						2.0673	2.1739											2.2313							
K.TLVDITKDFELEETDEEK.A +2																	4.8536								
R.AILFIPK.R +2																2.5513									
R.APFDLFESK.K +1					2.6635	2.4933		2.2511	2.7161		2.302		2.6278	2.3219	2.5899	2.2626									
R.APFDLFESK.K +2					3.2541	3.3498	3.2478	3.3499	3.2311	2.7516	2.9706	2.8264		3.2297	3.1414	2.8385		2.8592	2.8206				2.9263	2.8067	
R.DSGIGMTK.A +1		2.2061					2.0614	2.1499			2.0401	1.9798	2.2247	2.0106	2.1999	2.1116		1.9348					1.811		
R.DSSMSSYMSSK.K +2	3.6914	3.2346		3.305			3.2113	2.8895				3.1873			3.2617					3.459					
R.ELISNASDALDK.I +2	3.8737	3.6922	3.7311	3.7809	3.4102	3.7027	3.8604	3.838	3.728	3.8382	3.5954	3.9178								3.6965					
R.HSEFVAYPIQLLVTK.E +2														4.5601					3.2443						
R.HSEFVAYPIQLLVTK.E +3														3.7742											
R.LFLKDDQLEYLEEK.R +2				4.504									4.9681	5.1591	4.8538	4.3935			3.1963	4.8866					
R.LISLGLNIDEDEETETAPEASTEAPVEEVPADTEMEEVD.- +3											3.5729														
R.NPSDITQEEYNAFYK.S +2	5.5717	5.8093	5.8222	5.5285	6.0636	6.1183	6.0564	6.0002	5.32	5.688	5.5978	5.5482	5.535	5.8194	5.728	5.8555	5.5586		5.4873	5.8308		5.8465		2.8778	
R.TGQFGWSANMFER.I +2									3.6207												2.9033				
R.TGQFGWSANMER.I +2		3.6859				4.236	4.231	4.1451	3.9947		3.1042	4.152	3.9137	3.7738	3.79	3.9436	3.6031			3.9626			3.2054	4.1127	
R.VFITDEAEDLIPEWLSFVK.G +2		4.6669	4.9123	4.9307	4.4797	3.8696	5.2259	4.7505	4.4711		3.4982	4.1175	2.6611	3.9469	2.9878	4.164	3.6577	2.6728		4.3984					
R.VFITDEAEDLIPEWLSFVK.G +3																3.7362									
gi|6323861|ref|NP_013932.1|	7.1	14.3	14.1	12.4	17.5	16.2	17.2	17.5	22.1	15.4	20.8	26.8	30.8	27.5	26.6	24.2	20.8	24.9	23.1	19.7	16.3	11.9	13.5	11.9	Beta subunit of heteroootameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes; Pfk2p [Saccharomyces cerevisiae]
K.AAIDFYTK.F +2																		2.6384							
K.AIAVM*TSGGDAPGM*NSNVR.A +2																			5.9753						
K.AIAVM*TSGGDAPGMNSNVR.A +2										3.6453				4.7201				4.4126		4.2533					
K.AIAVMTSGGDAPGM*NSNVR.A +2										4.2189										5.4918	5.4212	5.2513			
K.AIAVMTSGGDAPGMNSNVR.A +2	6.3451				5.5511	5.5128	6.356	6.1305	5.4421	6.5138	5.6009	5.5203			5.7398	6.4822	5.5053	5.0874		6.0172	5.8847		6.3971	4.9953	
K.AIDYVEATANSHSR.A +2									4.4103	4.4237	3.7921	3.873	4.3284		3.8807	4.4463	3.2596	3.2961			4.1548				
K.AVAEAIQAK.D +1											2.5123							2.4196		2.4103	3.3256			2.4148	
K.AVAEAIQAK.D +2					3.0614	3.2475	3.4661	3.042	2.8921	2.6989	2.576	2.9923	3.0026	2.8425		2.6409									
K.AVGFIKDNQAAIAEAR.A +2						3.2223												2.8549	3.0991						
K.DTLNAM*NAPLQGYPTELFPM*QLYTLDPLGNVVGVTSTK.N +3													4.1853		3.5088										
K.GSHVVYNSIR.Q +1													2.6171					2.5759							
K.GSHVVYNSIR.Q +2		2.9088	2.9227	2.8569	2.7336						2.5483	2.8583		2.6371	2.6712	3.0238		2.9355							
K.LAEVITAEADGR.F +1																					2.1042				
K.LAEVITAEADGR.F +2					4.2917	4.1763	4.0563	4.1637	4.4078	3.8939	3.5878	4.2004	4.1841	4.349	4.1077	3.8614	3.2617	4.0367	4.237		4.0382	4.0802	2.914	4.0899	
K.NAVSTKPTPPPAPEASAESGLSSK.V +2	3.4926	4.212						3.7421		2.8599			4.3002	3.84	3.9129	3.879	3.6629	2.6335	3.9361	3.8073	2.6894				
K.NAVSTKPTPPPAPEASAESGLSSK.V +3	4.9201	5.0413	4.9132	5.0917	3.9325	4.2435	4.1463	5.0004	3.6487	4.3323	4.1978	4.6604	5.1334	3.7982	4.628	4.1411	4.3082	3.5603		4.4535					
K.PAYPGHVQQGGLPSPIDR.T +2			4.657						3.5847				4.8646	4.374	4.3948	4.8327		4.2725	5.1642	4.1011					
K.PAYPGHVQQGGLPSPIDR.T +3		4.5959	4.9626						4.6445				4.4565	4.1887		4.5919	4.4364			4.4836					
K.TISDTAAVVGVK.G +1																	2.3054	2.1613		2.0947	2.4844		2.1325		
K.TISDTAAVVGVK.G +2						3.9761		4.2194	4.125	3.9409	3.7461	3.8724	4.291	3.4175	3.8974	3.9513						4.0698		2.9073	
K.TTDTYPSLPK.P +2						3.1292				2.623	2.6493	2.909													
K.TTDTYPSLPKPLNRPQK.A +2													2.6727	3.1284					2.6645						
K.VHSYTDLAYR.M +2													2.608				2.6713	2.6862							
K.VIHWQATR.L +1																		1.8889		1.9147					
K.VIHWQATR.L +2																				2.538					
R.AAEENFNADDK.T +1																		2.2015				1.9101			
R.AAEENFNADDK.T +2	3.5606	3.3486			3.0513		3.5889	3.0905			3.3536	2.9469	3.1249	2.8274		2.9625		2.7668	2.6055			3.3715			
R.AFVVEVM*GR.N +2						3.1308			2.9205			3.1005	2.8804	3.0599	3.1051	3.0222					3.2335				
R.AFVVEVMGR.N +1													2.8378	2.6269	2.9608	2.7631		2.2896			2.6313				
R.AFVVEVMGR.N +2			3.6628				3.6418		3.3166		3.1506	3.3418	3.5733	3.768	3.8638	3.6637	3.4288	3.6995		3.4586	3.5595				
R.AFVVM*EGYEGLVR.G +2										3.8783	3.3199	4.4603	4.41	4.444	4.3779	4.1686			3.7123	3.1996	4.5692	3.6555	3.38	4.0318	
R.AFVVMEGYEGLVR.G +2		3.0332	4.2844		4.0088		4.3948	4.4138	3.5507			3.1572		4.521	4.6679	3.9935				4.3954			3.9419	2.8784	
R.ARESYPAFR.I +2																			2.5166	3.2925					
R.DTEFIEHLNNFM*AINSADHNEPK.L +3														4.5847											
R.DTEFIEHLNNFMAINSADHNEPK.L +3				4.5519																					
R.FDAKPAYPGHVQQGGLPSPIDR.T +3													4.9582	4.7635	4.6134	3.8776	4.4463								
R.GWSAEGGTNIGTAR.C +2	3.7472	4.2493	4.4035	3.8818	4.6303				4.4224			4.4781			4.2298								4.5199	3.7449	
R.ILATLQGLEAVNAVLESTPDTPSPLIAVNENK.I +3												4.1342													
R.ITTLGHVQR.G +2		3.0555	2.8697	3.0951	2.8184	3.0534	2.8268	3.0707	2.8371		2.733	2.7454		3.0527	2.7759	2.9726	2.7151		3.0809	2.6719	2.8478				
R.KPLMESVK.L +2													2.6525												
R.LIADHLVGR.K +2		3.1069	3.2412	3.0301									2.6466	2.9188		2.7148	3.0112		2.7205						
R.QLYDYETEVSM*R.M +2													3.0392							3.302					
R.QLYDYETEVSMR.M +2							3.553	3.2776	3.4003		3.3679	3.0923			3.0563	3.5758	3.5901	3.2639		3.0841		3.3111	3.057		
R.SEWPSLIEELLK.T +2		3.234	3.8799	3.9332	3.8583		3.8297	3.9299	3.6169			3.5503	4.0603	4.0279	3.4615	4.1052	2.5577	2.577	3.992	3.315			3.5462		
R.SHATQSLVFNTSDILAVK.D +2													4.2652	6.0784					4.0231						
R.SHATQSLVFNTSDILAVK.D +3														4.2192											
R.SSPDENSTLLSNDSISLK.I +2				5.3687	5.6206	5.8123	5.7286	5.561	5.4536	5.1966	5.267	5.4749	5.545	5.6339	5.0733	5.4679	5.5374	5.1648	4.8736	5.4013	5.4985	5.3047	5.4558	5.297	
R.VTPEEADLGM*IAYYFQK.Y +2									4.1335	4.3766	3.3463	3.9755	4.3562	4.5175	4.2825	4.2512		4.0017	4.1011	4.3045	3.6966	4.003	3.544		
R.VTPEEADLGMIAYYFQK.Y +3													4.1353	3.8074	3.5192										
R.VTPEEADLGMIAYYFQK.Y +2		5.2515	5.0738		5.0964	4.6718	3.0059	5.5081	4.8944		4.1834	4.3748				4.8362	3.7613			4.6762			3.4964	3.2408	
gi|6324027|ref|NP_014097.1|	33.3	45.8	33.3	40.3	43.1	38.2	38.2	45.1	45.1	45.1	45.1	45.1	52.8	52.8	52.8	45.1	38.2	38.9	27.8	46.5	38.2	25.7	38.2	38.2	Protein component of the small (40S) ribosomal subunit, required for assembly and maturation of pre-40 S particles; mutations in human RPS19 are associated with Diamond Blackfan anemia; nearly identical to Rps19Ap; Rps19bp [Saccharomyces cerevisiae]
gi|6324451|ref|NP_014520.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	Protein component of the small (40S) ribosomal subunit, required for assembly and maturation of pre-40 S particles; mutations in human RPS19 are associated with Diamond Blackfan anemia; nearly identical to Rps19Bp; Rps19ap [Saccharomyces cerevisiae]
K.HIDASGSINR.K +2								2.6976				2.9085		2.7771		2.5792									
K.HIDASGSINRK.V +2	2.9238	3.1401	3.2996	3.2456									2.9344	3.1691	2.503		3.1499			3.118					
K.HIDASGSINRK.V +3			3.6415																						
K.IGIVEISPK.G +1		2.3309	2.2048	2.4958	2.2396	2.4084	2.5442		2.3959		2.1279	2.1844	2.4239	2.2234	2.7405				2.1899			2.4697	2.2837	2.5052	
K.IGIVEISPK.G +2	3.4221	3.5428	3.4809	3.3651	3.5169	3.44	3.45	3.3952	3.3624	3.3184	3.3253	3.2056	3.3349	3.3184	3.3708	3.5062	2.9912				3.372	3.4924	3.3182		
K.LEVPGYVDIVK.T +2	3.3395	3.4604	3.2198	3.3426	3.4457	3.4176	3.3956	3.5588	3.1871	3.3729	3.3176	3.4535	3.3964	3.3637	3.0732	3.3584		3.4384		3.1276	3.0499		3.1792	3.1607	
K.TSSGNEM*PPQDAEGWFYK.R +2					4.2873	4.4429	4.6688	4.5932	4.6583	4.9575	3.7078	4.4758	4.3038	4.3047	3.9867	3.3279				4.5441	4.0018		3.3543	3.4783	
K.TSSGNEMPPQDAEGWFYK.R +2		4.0442			4.572	4.4428	4.5431	4.3756	4.3971	3.9357	4.5084	4.4224		2.603	3.5901	4.4786	3.5945	2.6844		3.1692	4.0651	3.2025	3.0661	4.1023	
K.VLQALEK.I +1					2.3861																				
R.DVAAQDFINAYASFLQR.Q +2	6.2128	6.3322	6.1976	6.0389	6.1228	5.8744	6.0522	6.0514	5.8372	3.8477	6.2986	5.9379	5.7435	5.3352	5.2027	5.88	5.4056	2.7547	5.8223	5.2114	4.1749		5.5426	5.23	
R.DVAAQDFINAYASFLQR.Q +3					5.0413		5.2606	4.5961	4.7421		4.3791	4.9182	5.3574	5.2191	5.2187	4.5999	6.2039	4.2347	4.5225	5.2379	3.6221		4.4399	4.082	
R.IAAQTLEEDE.- +1				2.6813					2.2352	2.4852			2.5127	2.5042	2.6597			2.5601		2.6316		2.4636			
R.IAAQTLEEDE.- +2				3.7444						3.0906	2.6503		2.9955	2.8404						2.8333					
R.QGKLEVPGYVDIVK.T +2																			3.0434						
gi|6324120|ref|NP_014190.1|	27.7	37.5	32.6	33	46.3	45	47.6	47.6	45	41.9	45.4	46.3	54.2	52.9	52	53.2	38.5	40.6	41.6	43.4	34.1	30.3	29.4	40.3	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in the folding of newly-synthesized polypeptide chains; member of the HSP70 family; homolog of SSB1; Ssb2p [Saccharomyces cerevisiae]
K.AADEAFAK.K +1	2.1976	2.0824			2.1284		2.0254	2.0834		2.0394	2.0921		2.2565		2.0918	1.982			2.2631						
K.AADEAFAK.K +2																								2.5434	
K.AVITVPAYFNDAQR.Q +2	3.3587	3.5878	3.6203	3.1916	3.4944	3.4651	3.7119	4.0111	3.67	3.6113	3.6369	3.8299	3.3093	2.9469	3.7182	3.4348	3.3524	2.726	2.8607	2.797	3.4662			3.5948	
K.AVITVPAYFNDAQR.Q +3													4.1432	4.8346											
K.DAGAISGLNVLR.I +2	4.5184	4.5009	4.6063	4.2411	4.525	4.5413	4.5117	4.5571	4.442	4.3237	4.7281	4.225	4.0967	3.3424	3.4711	3.4902	4.22	4.2902			4.0787	4.4851		3.9554	
K.ENTLLGEFDLK.N +1																	2.1771								

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ENTLLGEFDLK.N +2	3.6473	3.4982	3.6141	3.6964	3.7878	3.6577	3.7308	3.7449	3.4559	3.1762	3.6023	3.5038	3.6152	3.8746	3.4883	3.6732	3.4903	3.6911	3.5346	3.3111	3.1781	2.7433	3.6062	3.3228	
K.IEAALSDALAALQIEDPSADELR.K +2					6.4978	6.4335	6.6614	6.6838	6.1125	3.5228	6.0246	6.2248	6.3103	6.344	6.2202	5.865	5.0357	5.1661	5.3031	5.4348	5.2485	5.0569	6.0642	3.9954	
K.IEAALSDALAALQIEDPSADELR.K +3						6.32	6.5678		6.9402		4.9412	6.2586	7.1136	6.8315	6.6654	6.3478				4.3052			4.8927		
K.IEAALSDALAALQIEDPSADELRK.A +2													4.4366	5.0039	3.4157										
K.IEAALSDALAALQIEDPSADELRK.A +3		5.4997											6.2106	5.7109											
K.LLSDFFDGK.Q +1			2.5096	2.7643	1.8621		2.5746		2.8313				2.7624	2.8128	2.4151	2.8621	2.3126	2.1811	2.4895	2.4065	2.5204		2.4343	2.2012	
K.LLSDFFDGK.Q +2	3.2865	3.3192	3.5158	3.3017	3.2629	3.1763	3.2403	3.3814	3.2132	3.0361	3.1862	3.4087	2.7344	3.2707	2.9927	3.0948	2.7596	3.1547	2.9174	2.9351	3.2583	3.2079	2.969	3.2182	
K.MVNQAEEFK.A +1																					2.1975				
K.MVNQAEEFK.A +2															2.6312										
K.NIPM*M*PAGEPVLEAIFEVDANGILK.V +3													5.077	5.0288	5.6084	4.5456									
K.NQAALNPR.N +2	2.5868							2.6135				2.5616				2.5532									
K.SINPDEAVAYGAAVQGAILTGQSTSDETK.D +2					5.131	5.9649	6.4495	5.8412	5.3913	3.7045	3.6668	4.9815	5.1875	5.3122	5.0147	5.6262	3.8434	4.1772	5.1749	4.4563	5.8644	5.7023		5.3646	
K.SINPDEAVAYGAAVQGAILTGQSTSDETK.D +3						5.306	3.9962	3.9458	4.8678			4.6657				4.6473	4.828		6.0335	5.3331					
K.SQIDEVVLVGGSTR.I +1									2.8944							2.0802					2.4232				
K.SQIDEVVLVGGSTR.I +2	4.6926	4.4898	4.6947	4.6177	4.9938	4.9957	4.4974	4.9091	4.826	3.8035	5.0666	4.5458	4.7945	4.9185	4.5898	4.4583	4.501	4.0617	3.8115	4.4997	3.5202	4.7942			
K.SSNITISNAVGR.L +1													2.131	2.0677		2.3158			1.9645					2.3118	
K.SSNITISNAVGR.L +2		3.5932	3.7528	3.3818	3.7036	3.6634	3.7389	3.7418	3.5864	3.5165	3.6764	3.6657		2.7959	3.5723	2.9788		3.0612					3.6051	3.4222	
K.STSGNTHLGGQDFDTNLLEHFK.A +2													5.1026	5.7758					2.8957	3.6503					
K.STSGNTHLGGQDFDTNLLEHFK.A +3		5.0336	4.6538	5.3474									5.1329	4.9423					3.7621						
K.TFSPQEISAM*VLTK.M +2					2.8519					3.9389			2.8183											2.6728	
K.TFSPQEISAMVLTK.M +2	4.2174	4.5585	4.7575	4.4008	4.5816	4.6346	4.4141	4.7281	4.3155			3.4711		3.4295	4.4289	4.217	3.0465	4.0258		4.0357			3.4453	2.5137	
K.TGLDISDDAR.A +1												2.149	2.3729	2.3162				2.1113	2.0299				1.8324		
K.TGLDISDDAR.A +2	3.9712	3.9442	3.9445	4.0446	3.5138	3.607	3.2919	3.6422	3.9332	3.8437	3.4212	4.0028	3.829		3.7764	3.8614									
K.VIDVDGNPVIEVQYLEETK.T +2	6.3646	6.328	6.4133	6.1663	6.2553	6.4708	6.417	6.3296	6.0205	5.8818	6.2355	6.1389	5.9864	6.1623	6.1115	6.1853	5.6365	4.2275	5.7076	5.7272	6.0307	5.1117	6.0352	6.1451	
K.VIDVDGNPVIEVQYLEETK.T +3										3.6436	5.2483	4.7873	5.1817	5.1414		5.5578		4.8736	5.3368	5.511	5.2582	5.1678			
R.ARFEDLNAALFK.S +2			4.3353	3.8977															3.1743	3.4313					
R.FDDESVQK.D +2							2.7723				2.5974														
R.FEDLNAALFK.S +1						2.6891	2.6507	2.3825	2.6309	1.951	2.5528		2.6064	2.6649	2.5788	2.9183	2.3391	2.7301	2.8884	2.5929	2.4835	2.4664		2.1085	
R.FEDLNAALFK.S +2		4.0267	4.0515	3.8603	3.9091	4.0854	3.9431	3.953	3.9715	3.98	3.9538	3.8245	3.5409	3.9321	3.8576	3.9226	3.9094	3.7097		4.0829		3.7063	4.0006	3.9788	
R.IINEPTAAAIAYGLGAGK.S +2	6.1727	6.442	6.496	6.6285	6.2994	6.2223	6.1647	6.4006	6.0186	6.2081	6.0919	6.0501	6.1641	6.1693	5.8955	6.4188		6.0783	5.2785			5.177	5.4861	5.8165	
R.IINEPTAAAIAYGLGAGK.S +3							5.243					5.2925	5.2875	5.3103	5.6143	5.2474			5.2506	5.3419	4.4464				
R.LESYVASIEQTVTDPVLSSK.L +2	5.8229	6.2455	6.5961	6.0955	6.2694	6.4092	6.3796	6.3048	6.1387	6.3332	6.2756	6.1948	6.2591	6.2119	6.2104	6.2263	6.0794	5.5888	5.5847	5.4573	4.7523	3.3243	5.7559	5.7697	
R.LESYVASIEQTVTDPVLSSK.L +3													4.0816		3.5478										
R.QRLESYVASIEQTVTDPVLSSK.L +3				4.7753																					
R.RFDDESVQK.D +2																3.1255									
R.TFTTVSDNQTTVQFPVYQGER.V +2					4.9204	5.5465	5.5884	5.6446	5.254	4.5038	4.8942	4.7031	4.9688	5.3754	5.3868	5.7153	5.5729	4.9567	5.5735	4.8709	5.3033	5.208	5.2833	4.2588	
R.TFTTVSDNQTTVQFPVYQGER.V +3													3.7437	5.6305									4.7093	4.0851	
R.TLSSVTQTTVEVDSLFDGEDFESSLTR.A +2					4.9525	4.5154	4.6153	4.8248	4.7523		4.2499	4.5507	4.3337	4.3657	3.9278	4.5732	3.184			3.8986				4.1087	
R.TLSSVTQTTVEVDSLFDGEDFESSLTR.A +3									4.7699			3.5021													
R.VTPSFVAFTPQER.L +2	4.5263	4.5324	4.3392	4.5284	4.5526	4.6127	4.1823	4.2586	3.8294	4.2568	3.8963	3.8138	3.6404	4.5265	4.0727	3.818	3.8993	3.0741	4.1811	3.6581			4.3659		
gi|6324151|ref|NP_014221.1|	43.8	47.1	37.9	47.9	50.8	38.8	41.7	42.5	41.2	36.2	35	45.8	63.8	51.7	50.4	49.6	25.4	30	46.2	56.2	21.7	21.7	21.2	43.3	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins; Rps3p [Saccharomyces cerevisiae]
K.ALPDAVTIIEPK.E +1						2.5911		2.4963	2.7817			2.4853	2.6707			3.0394			2.5736		2.6126				
K.ALPDAVTIIEPK.E +2	3.2946	3.3531	3.6333	3.3611	3.5927	3.5069	3.5443	3.5355	3.4014	3.4558	3.4043	3.1941	3.2688	3.4878	3.3007	3.3353	3.2366			3.2526				3.5346	
K.ALPDAVTIIEPKEEEPILAPSVK.D +2																			4.0492	4.8904					
K.ALPDAVTIIEPKEEEPILAPSVK.D +3			4.1327	4.1182															3.847						
K.DYRPAEETEAQAEPVEA.- +2	4.063	3.8905	3.8097	3.6718	3.7094	3.9859	3.8765	3.9037	3.8256	3.6426	3.6734	3.7073	3.5123	4.0222	3.6913	3.837		3.71	3.9997	3.688	3.5532	3.6925	3.6787	3.7618	
K.EEEPILAPSVK.D +1													2.6951			2.7022			2.0591		1.9834			2.54	
K.EEEPILAPSVK.D +2	2.653	2.558		2.5575	2.649			2.5726		2.512		2.6037	2.5801			2.5587									
K.FADGFLIHSGQPVNDFIDTATR.H +2				5.4249									4.4278	5.7464					3.3937	3.3729					
K.FADGFLIHSGQPVNDFIDTATR.H +3	3.5734	5.1393		5.2201									5.1409	5.4601	3.8313				4.3562	4.3156					
K.GCEVVVSGK.L +1							2.7343						2.651			2.4188	2.2933							2.5038	
K.GCEVVVSGK.L +2							3.0757																		
K.LLNGLAIR.R +2	2.996	3.0011	3.0301	3.2324	2.9723				2.8314		2.5248	2.7552	3.312	3.1449	3.1105	3.0736	2.62	2.9557	2.6783	2.8312				2.7134	
K.LVADGVFYAELNEFFTR.E +2					5.5475	5.7418	4.9185	5.0244	5.5406			5.1216	5.3588	5.3687	4.8753	5.5474			4.2165	5.2246					
K.LVADGVFYAELNEFFTR.E +3													5.0041	5.4693						4.1741					
K.YAPGTIVLYAER.V +1					2.1929				2.4968		1.8406		2.6652								2.2269				
K.YAPGTIVLYAER.V +2	4.0978	3.9263	4.2077	3.956	3.9812	4.0694	4.0927	4.1477	4.0574	3.7448	3.6827	3.9254	3.6871	3.8027	3.7944	3.8401	3.9633	3.6647		3.3223	3.7587	3.6163	3.1622	2.9942	
R.ELAEEGYSGVEVR.V +2	4.2272	4.4359	4.1455	4.4107	4.3579	4.2838	4.7272	4.4676	4.4869	4.5318	4.2788	4.5525	4.1532	4.2624	4.1571	4.2646		3.9305	2.5591	4.1813		2.8572		3.7427	
R.GLSAVAQAESM*K.F +2													3.9553	3.7616				3.0826					2.795		
R.GLSAVAQAESMK.F +1																		2.7349		2.8299			3.1776		
R.GLSAVAQAESMK.F +2					3.9719	4.3046				3.8561	4.1342													4.0001	
R.INELTLLVQK.R +2	4.2321	4.2882	4.3431	4.1758	4.318	4.195	4.1646	4.2847	4.2229	4.1101	4.1125	4.1061	3.8528	4.0817	4.1668	4.164	3.6886	3.2391					4.0722	4.0275	
R.RAAYGVVR.Y +2		2.6123	2.917																						
R.RINELTLLVQK.R +2														3.1947					3.0737	3.3546					
R.TQDVLGENGR.R +2				3.3402	3.4743		3.589	3.4482	3.1664			3.1574	3.2596		3.403	3.3714	2.5217					2.6344			
gi|6324233|ref|NP_014303.1|	12.1	28.9	23.7	21.6	27.4	27.4	27.4	27.4	31.6	31.6	31.6	35.8	30.5	35.8	44.2	31.6	30.5	31.6	20.5	18.4	23.7	23.7	35.3	27.4	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Ap; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins; Rps7bp [Saccharomyces cerevisiae]
K.ALVLFVPVPALSAYHK.V +2															3.4995										
K.DVQQIDYK.L +1	2.623	2.7619	2.7625						2.5432	2.6362	2.7758	2.8355	2.5202	2.6132	2.7965	2.3301	2.6842	2.7955	2.7301		2.728	2.7941	2.7008		
K.DVQQIDYK.L +2		3.096		3.0803												2.6614						2.7166			
K.ILSQAPSELELQVAK.T +2	4.3237	4.2603	3.9304	3.4567	4.7866	4.6729	4.3697	4.7129	4.4779	3.6313	2.6381	3.3715	4.1791	4.7678	4.9277	4.1934	3.6383	4.6528					4.6068	4.136	
K.LESFQAVYNK.L +1									1.9462							2.3687			2.2263		2.3601		2.1756		
K.LESFQAVYNK.L +2		3.1647		3.3237	3.4381	3.475	3.4443	3.4128	3.3241	3.3678	3.2795	3.2718		3.3195	3.0899			3.1128	3.2718		2.956	3.153		3.1702	
K.TFIDLESSSPELK.A +1																2.2726									
K.TFIDLESSSPELK.A +2					5.0762	5.1327	4.8684	5.0967	5.0414	4.8385	4.7769	4.5864	4.5622	4.7451	4.8826	4.7907	4.5923	4.9867	4.603	4.3541	4.8992	4.8865	4.8951	4.9089	
K.VLEDMVFPTEIVGK.R +2						3.6905	4.0175	4.2644	4.0099	3.98	3.6122	3.8989	4.4768	4.0764	4.0302	4.1346		2.6044		3.8033	4.182	3.4858	3.6258		
K.VLEDMVFPTEIVGK.R +2		4.2216	4.5578		4.2916	4.1252	4.6059	4.1689	3.7676			3.2988				4.1761	2.9508	4.0666		4.1661			3.7342	2.9952	
R.HVIFLAER.R +1													2.1701	2.15	1.8873		2.1652			2.2848					
R.HVIFLAER.R +2		2.6659	2.6198	2.6081										2.657					2.5003						
R.TLTAVHDK.V +2												2.8757													
R.YLVGGNK.I +1																							1.8608		
gi|6324260|ref|NP_014330.1|	20.7	18.2	18.2	6.1	17.2	19.2	26.3	20.7	26.8	17.2	22.7	17.2	17.2	13.6	17.2	21.7	17.2	14.1	18.2	18.7	13.6	13.6	14.1	17.2	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Ap, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16bp [Saccharomyces cerevisiae]
K.IFEGIPPPYDK.K +2						2.9537	2.821		2.6284		2.5955														
K.KVSSASAAASESDVAK.Q +2																		5.6068		2.8497			4.041		
K.LSTSVGWK.Y +1									1.833																
K.QLASFGY.- +1	2.0302							1.8998		1.8209															
K.RVVVPQALR.V +2		3.5344	3.496													2.8005			3.1436	3.2683					
K.VSSASAAASESDVAK.Q +1																2.5435						2.4347			
K.VSSASAAASESDVAK.Q +2	5.0194	4.6376	4.1124		4.9041	4.7812	4.7499	4.916	4.6479	3.3184	4.2924	4.6078	4.7951	4.9256	4.8477	4.8823	4.5935		3.1117		4.2342	3.9943		4.2086	
K.YEDVVAK.L +1	2.1947				2.1544		2.0546	2.1675	1.9968		2.1137	2.1408	2.0459		1.9833	1.9667	2.3721							2.0458	
R.AEALNISGEFFR.N +1																2.1934									
R.AEALNISGEFFR.N +2	4.5081	4.8588	4.8251	4.7172	4.658	4.8525	4.7451	4.7814	4.5601	4.3784	4.6288	4.4657	4.9407	4.852	3.7444	4.6299	4.4418	4.4221	4.0752	3.9323	4.7478	4.2886	4.4901	4.4399	
R.SAEYYAK.K +1							1.8527																		
gi|6324262|ref|NP_014332.1|	14.1	19.4	15.7	15.7	29.3	29.3	23.6	29.3	38.7	19.4	33.5	45	45	52.9	52.9	52.9	29.3	20.4	27.2	42.4	29.3	19.4	17.3	29.3	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Ap and has similarity to E. coli L6 and rat L9 ribosomal proteins; Rpl9bp [Saccharomyces cerevisiae]
K.DEIVLSGNSVEDVSQNAADLQQICR.V +2					5.7371	6.157	6.2228	6.2139	5.9896	3.5899	5.3474	6.332	5.3167		5.8969	6.1457	3.5785			3.4148		5.5345	2.5141	2.5539	
K.DEIVLSGNSVEDVSQNAADLQQICR.V +3					6.3767	6.8545	7.2838	5.9875	6.1897		4.6248	5.8965	4.6326	5.3996	3.9284						4.257	5.3394	6.0605	6.1577	
K.FLDGIYVSHK.G +2		3.6561	3.5127	3.5725					3.0989			3.1473	3.2382	3.4608	3.5482	3.5799			3.3059	3.4668					
K.HIDVTFTK.V +1									2.6282		2.1789		2.4939						2.4594						
K.HIDVTFTK.V +2			2.7211	2.6743			2.5074		2.8207		2.9924	2.7369	2.8085	2.9175	2.7819	2.6469		2.9696	2.7543				2.8615		
K.SLVDNM*ITGVTK.G +2									2.5634																
K.SLVDNMITGVTK.G +1								2.1788	2.2151						2.215		2.0536	2.2623		2.0243					
K.SLVDNMITGVTK.G +2	4.2031	4.3266	4.2932	4.469	4.3135	4.483	4.4577	4.4975	4.2917	3.8899	4.2746	4.2577	3.8926	4.3202	4.3966	4.3294	4.0094	4.3163		3.973	3.9482	4.3051		4.4009	
K.YIQTEQQIEIPEGVTVSIK.S +2					3.9085	3.1196		3.1802	5.4536		3.2292	3.4812	4.0248	4.354	4.5257	5.2032	4.2689	4.8388	5.1622	3.2813	4.5912			3.4238	
R.DGVTIEFSTNVK.D +2												3.2192	3.0001	3.5384	3.6615	2.661									
R.YVYAHFPINVNIVEK.D +2	2.6522	4.6396												4.5246	3.205	3.857			4.072	4.5594					
R.YVYAHFPINVNIVEK.D +3														4.6573											
gi|6324452|ref|NP_014521.1|	7.5	14.5	19.9	14.5	14.5	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	14.5	19.9	14.5	18.8	14.5	7.5	12.4	14.5	14.5	14.5	Protein component of the large (60S) ribosomal subunit, identical to Rpl18Bp and has similarity to rat L18 ribosomal protein; intron of RPL18A pre-mRNA forms stem-loop structures that are a target for Rnt1p cleavage leading to degradation; Rpl18ap [Saccharomyces cerevisiae]
K.AGGECITLDQLAVR.A +1								1.9715	2.0637																
K.AGGECITLDQLAVR.A +2	4.7689	4.8137	4.8416	4.8829	4.955	4.8411	4.7881	4.9538	4.8556	4.7473	4.8156	4.5954	4.8088	4.9235	4.7483	4.7647	4.8608	4.7549	4.9455	4.885		4.7475	4.7753	4.357	
K.GQNTLILR.G +2																		2.5672							
K.INRPPVSVSR.I +2			3.0821			2.6	2.785	3.0868	2.5878	2.9966	3.1086	2.9276	2.53	2.9823		2.9261					2.5467				
K.TVVVVGTVTDDAR.I +1																2.2008									
K.TVVVVGTVTDDAR.I +2		4.5373	4.6059	4.5902	4.9192	4.8918	4.9449	4.8397	4.7124	4.6184	4.8685	5.0596	4.7713	4.9809	4.669	4.9571	4.5458	4.5881	4.2752		4.1955	4.6713	4.8096	4.6188	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6324486|ref|NP_014555.1|	42.5	44	37.1	44	37.1	35.1	31	37.1	44	29.6	29.6	36.5	44	44	39.4	39.4	37.4	39.4	47.4	47.4	19.3	22.1	20.1	14.1	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the reduction of acetaldehyde to ethanol, the last step in the glycolytic pathway; Adh1p [Saccharomyces cerevisiae]
K.ANELLINVK.Y +1	2.1638	2.1167		2.1948	2.1911	2.1884	2.2227	2.3048	2.2712	2.0714	2.1579	2.1107		2.0959	2.3631	2.2452						2.3235			
K.ANELLINVK.Y +2	3.5208	3.5972	3.5239	3.6187	3.5563	3.5842	3.5568	3.5248	3.4093	3.6326	3.4422	3.5143	3.5041	3.4235	3.4347	3.5006	3.509	3.4859	3.1254	3.2428	3.4941	3.3043	3.5022	3.4095	
K.ATDGGAHGVINVSVSEAAIEASTR.Y +2		6.4333		2.5803		3.5137			6.5351			4.0071	5.9382	6.4923	6.083	5.2293	6.5496	5.2127	6.0456	5.7443					
K.ATDGGAHGVINVSVSEAAIEASTR.Y +3	3.938	4.0176											3.633	3.9626	3.7641										
K.CCSDVFNQVVK.S +1					3.0554	2.5496			2.6746				3.0348	3.08	2.7879	2.5638	2.847		2.6304	2.3422					
K.CCSDVFNQVVK.S +2	4.3009	4.2727	4.2285	4.2981	4.2131	4.2863	4.2813	4.3903	4.1288	4.288	4.104	4.1969	4.16	3.9067	3.6824	3.1683	2.6359	4.0971	3.8156	2.8265	3.3687	4.1221	2.6617		
K.DIVGAVLK.A +1	2.3609	2.2047	2.2296	2.4449	2.2589	2.3786	2.332	2.2584	2.2182	2.1786	2.3895		2.3202	2.0189											
K.GVIFYESHGK.L +1									2.4913				2.3993	2.445	2.3843	2.6432	2.2833	2.4265	2.1257						
K.GVIFYESHGK.L +2	3.0382	3.0361	2.8601	2.9368	2.9266		3.0229	2.8437	2.9653	2.7716	2.7541		2.9553	2.8672	2.767	3.0613	2.5856	2.8063		2.7415		2.8567			
K.LPLVGGHEGAGVVVGM*GENVK.G +2	6.3658	6.2137	6.1157					5.7963	6.3689			4.4066	6.291	5.8985	5.8965	5.7256			5.9649	4.7569					
K.LPLVGGHEGAGVVVGM*GENVK.G +3	5.9391	6.3418	6.0728	5.2889	4.5048			6.4612	5.9132			5.8265	5.9961	5.83	5.2374	5.8954		3.8994	5.8057	5.089					
K.LPLVGGHEGAGVVVGMGENVK.G +2	6.9714	7.051	6.696										3.8182	5.7562	6.0483		6.4201	5.1104	3.8982	5.4036					
K.LPLVGGHEGAGVVVGMGENVK.G +3	6.1031	6.076	5.8269	5.0411									5.0393	5.5345	5.6647	4.4405			4.9646	4.9574					
K.SANLM*AGHWVAISGAAGGLGSLAVQYAK.A +3																			4.2712	3.7117					
K.SANLMAGHWVAISGAAGGLGSLAVQYAK.A +3																				4.1726					
K.SISIVGSYVGNR.A +1					2.6582	2.4437		2.4908	2.4211		2.2259		2.231	2.3663	2.2471	2.3901	2.5733	1.9072	2.1197	1.9204		2.0213			
K.SISIVGSYVGNR.A +2	4.4232	4.4342	4.3855	4.47	4.4615	4.4706	4.4354	4.4566	4.3977	4.3894	4.3548	4.3173	4.2733	4.097	4.3867	4.3906	4.2559	4.1923	3.9316	4.1103	4.2189	4.3268	4.2353	4.4206	
K.VVGLSTLPEIYEK.M +1					3.0428	2.8578	2.9158	3.0419	3.2114		2.8673	2.7872	2.6936	2.5921	2.8318	2.8191	1.8657		2.5215	2.6029	2.8292	2.6698	2.7779	2.1227	
K.VVGLSTLPEIYEK.M +2	4.3061	4.3905	4.3675	4.5308	4.2799	4.4542	4.2205	4.3039	4.0214	4.2319	4.2206	4.2068	4.3494	3.9931	4.2698	4.1979	4.0944	4.301		3.1958	2.7966	4.1461	3.6684	3.5116	
R.ANGTTVLVGM*PAGAK.C +1																			2.1689						
R.ANGTTVLVGM*PAGAK.C +2	5.0626	4.9142	4.3199	4.7829	4.5438	3.784	4.4479	4.7167	4.413	4.3186	4.4986	4.907	3.3475	4.0954	4.8388	4.0644	2.9244	3.3438		4.1363	4.7424		3.6695		
R.ANGTTVLVGMPAGAK.C +1					2.3174	2.2396			2.4592		2.47		2.5839	2.4438	2.164	2.3878	2.3801	2.4443		2.2048				2.2569	
R.ANGTTVLVGMPAGAK.C +2	5.2318	5.0184	5.3599	5.1189	5.0862	5.256	5.1652	5.1853	4.5119	5.1615	4.9334	4.7001	4.8444	4.258	4.8189	4.6787	4.7496	4.9481			4.4865	3.4399	3.9784	4.8573	
R.EALDFFAR.G +1	1.8907	2.113	2.2321	2.0615	1.8049	1.9516	2.1824	1.9483	2.0127		1.8218		1.9828	1.8793											
R.EALDFFAR.G +2										2.539															
R.VLGIDGGEGK.E +1					2.3073	2.2484	2.318	2.3368	2.0457	2.3787	2.057	2.3053	2.4005	2.432	2.4331	2.05			2.1981				2.4165		
R.VLGIDGGEGK.E +2	2.7054				2.921	2.8442	2.8792	2.8127		2.8449	2.7986	2.969	2.5464			2.7329									
R.VLGIDGGEGKEELFR.S +2		4.594	4.4018	4.4188	2.9504	3.1922	2.9215	4.4239	4.1868			4.0131	4.3008	4.3033	4.1002	4.195	3.9103	3.6156	4.0588	4.5257					
R.YVVDTSK.- +1	2.4713	2.4816	2.4242	2.4586	2.4179	2.4486	2.4358	2.3307	2.3471	2.2966	2.1268	2.4336	2.3763	2.2757	2.5312	2.1846		2.063	2.4094	2.4214	2.3548	2.0289			
gi|6324534|ref|NP_014603.1|	39.6	52.8	52.8	52.8	52.8	39.6	52.8	52.8	52.8	21.7	79.2	52.8	41.5	52.8	52.8	52.8	41.5	41.5	52.8	41.5	54.7	34.9	79.2	52.8	Ribosomal protein P2 alpha, a component of the ribosomal stalk, which is involved in the interaction between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the cytoplasm; Rpp2ap [Saccharomyces cerevisiae]
K.AILESVGIEIEDEK.V +2		4.7724	4.9615	5.1249	4.8735		5.1111	5.1016	4.9684		3.9917	5.0149	4.9821	4.3545	4.9891	5.2615	4.1977	4.9189	3.9993	3.6497		4.2674	4.0485	4.6522	
K.LAAVPAAGPASAGGAAAASGDAAAEEEK.E +2																					5.7677		3.3764		
K.LAAVPAAGPASAGGAAAASGDAAAEEEK.E +3											3.8126										4.5914				
K.SVDELITEGNEK.L +1																			2.7621				3.1312		
K.SVDELITEGNEK.L +2	4.3408	4.228	4.2152	4.3209	4.2215	4.1839	4.4195	4.3392	4.3183	4.0668	4.3932	3.6023		4.1188	4.1105	4.3509						4.4595		2.9676	
K.VSSVLSALEGK.S +1						2.2885	2.3522	2.517	2.3639				2.2651	2.3877	2.291	2.1073	2.0521		2.5727			2.0154	1.9077	1.8552	
K.VSSVLSALEGK.S +2	3.6804	3.7523	3.7279	3.7489	3.6682	3.764	3.6074	3.716	3.6586	3.7576	3.6714	3.7692	3.6376	3.4735	3.1206	3.6703	3.6366	3.0085	3.4067	2.8398	3.6128			3.6187	
K.YLAAYLLNAAGNTPDATK.I +2	4.8297	5.5376	5.4641	4.3435	5.8582	4.5845	5.6455	5.5112	5.1146		4.3669	5.1153	4.9897	5.2442	4.9538	4.9686	4.9967	3.3533	4.2632	5.207	4.8807		5.2258	4.7917	
K.YLAAYLLNAAGNTPDATK.I +3													4.7479	4.9752	4.1599				3.6002	3.5226					
gi|6324601|ref|NP_014670.1|	3.9	7.8	7.8	4.4	11.9	10	11.9	11.9	27.5	18.7	16	17.5	27.3	27.5	27.2	23.4	21.2	17.1	23.3	21.1	15.8	10	14.3	11.2	Hsp90 cochaperone, interacts with the Ssa group of the cytosolic Hsp70 chaperones; activates the ATPase activity of Ssa1p; homolog of mammalian Hop protein; Sti1p [Saccharomyces cerevisiae]
K.AEAAYVNPEK.A +2									3.6197	2.9594	2.9602						2.7885								
K.AIEVSETPNHVLYSNR.S +2									4.0997	3.3503			4.6469	5.0167	4.4354	4.478	4.6875		5.0581	4.9635					
K.ALELDASNK.A +1																			2.3182						
K.ALELDASNK.A +2												2.9688	2.7108		3.0222	2.767									
K.DAEVNNGSSAR.E +2								3.2647	2.7991	3.6066	2.9882	3.4102			2.9521	2.6961								3.052	
K.ESEPM*EVDEDDSKIEADK.E +2																			2.6899						
K.EYASALETLDAAR.T +2			4.8391	4.6752	5.0483	4.832	5.1237	4.8484	4.5412	4.6806	4.7462	4.4115	4.0486	4.6915	4.4598	4.4664	4.6151	4.3337		4.6872	4.5844	4.8192	4.6014	4.9343	
K.FSDALNDANECVK.I +2		3.5596		3.8669		4.7047	4.6359		4.7636	4.3534	4.5038	4.3595	4.445	4.5534	4.2772	4.7813			3.1853		4.2675	3.4277	4.51		
K.GEYETAISTLNDAVEQGR.E +2		4.7745	4.8279		5.7825	5.8417	5.7978	5.7338	5.6892	4.9918	5.3074	5.3973	5.3017	5.2402	5.0385	5.6784	5.0656	5.0943		5.6098	5.4195	4.6175	5.2758	4.4649	
K.IQTLIAAGIIR.T +2					3.7631		4.1615		4.1177			3.6689	4.0296	4.1905	4.0427	4.0956	2.5583	3.6603		3.4271				3.1045	
K.KAEAEAYVNPEK.A +2													3.4925	3.2478				4.1738	4.3122				2.5101		
K.KIQTLIAAGIIR.T +2																			2.8585	3.4403					
K.LM*SFPEAIADCNK.A +2										2.7636			4.0734	3.1279				3.9607			3.2456				
K.LMSFPEAIADCNK.A +2					3.8146			4.0532	4.4296	3.3008	3.533	3.8349	3.034	3.3867	4.374	4.059	3.8672	4.0576			2.7677		3.7909	3.7315	
K.QNPQAIGQDLFTDPR.L +2		3.7106	3.9922		3.2496	3.689	3.6996	3.6955	3.3738	2.9265	3.0568	3.259	3.5148	3.5149	3.2078	3.492	3.8383	3.7948	3.1107		3.4642	3.3056	3.7666		
K.TIEYYQK.S +1																				2.2879					
K.TSEMMKDPQLVAK.L +2																					2.5593				
R.EIDQLYYK.A +1																	1.9961				2.779				
R.FQPGTSNETPEETYQR.A +2	2.9966																			3.1353					
R.IGNAYHK.L +2	2.5744																								
R.KATAQIAVK.E +2														3.3119											
R.LGAAHLGLGDLDEAESNYK.K +2									3.2919				5.7198	5.8815	4.5282	4.8461	4.866	4.752							
R.LGAAHLGLGDLDEAESNYK.K +3													4.0797	4.3064											
R.LGAAHLGLGDLDEAESNYKK.A +2																	4.2315		3.749	4.4019					
R.LGAAHLGLGDLDEAESNYKK.A +3														5.1248											
R.QAQPDLGLTQLFADPNLIENLK.K +2									3.9551						3.2832				4.4696	3.2986					
R.QAQPDLGLTQLFADPNLIENLK.K +3													5.2917	4.8681	5.5637					3.6777					
gi|6324670|ref|NP_014739.1|	17.4	31.6	26.3	46.3	33.2	33.2	37.4	37.4	37.4	21.1	22.6	45.8	25.8	45.8	35.3	50	26.3	22.6	29.5	20	21.1	22.6	20.5	16.8	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Bp; interacts with Kti11p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins; Rps7ap [Saccharomyces cerevisiae]
K.AELRPLQFK.S +2		2.6528	2.5072	2.5002													2.535								
K.ALAIFVPVPSLAGFHK.V +2															4.0375	3.5363			3.1175	3.4998					
K.DVQQIDYK.L +1	2.623	2.7619	2.7625						2.5432	2.6362	2.7758	2.8355	2.5202	2.6132	2.7965	2.3301	2.6842	2.7955	2.7301		2.728	2.7941	2.7008		
K.DVQQIDYK.L +2		3.096		3.0803														2.6614				2.7166			
K.ILEDLVFPTEIVGK.R +2	4.9333	4.8292	4.8629	4.8582	4.8025	4.7769	4.7544	4.7184	4.7952	4.6621	4.689	4.5406	4.8245	4.2846	4.6068	4.6513	3.6145	3.2499	4.5425	4.6766	3.6281	4.2286	4.0252	4.0368	
K.ILSQAPTELELQVAQAFVELENSSPELK.A +2					5.796	3.7608		5.0792	5.2087			3.9343		4.2303		3.4773									
K.ILSQAPTELELQVAQAFVELENSSPELK.A +3				3.8637	6.6995	5.5052	6.8116	6.724	5.1122			6.1752				5.5624									
K.LESFQAVYNK.L +1									1.9462							2.3687			2.2263		2.3601		2.1756		
K.LESFQAVYNK.L +2		3.1647		3.3237	3.4381	3.475	3.4443	3.4128	3.3241	3.3678	3.2795	3.2718		3.3195	3.0899			3.1128	3.2718		2.956	3.153		3.1702	
K.QIVFEIPSETH.- +2	3.3336	3.4223	3.3383	3.3035	3.3222	3.4902	3.5017	3.2604	3.1535		3.3584	3.278	3.0809	3.3822	3.2691	3.1557	3.4004	3.4423				2.991			
R.EIDVAGGK.K +1							2.4276	2.2881		2.287		2.0916	2.0113	2.3667		2.4719					2.0296			2.2338	
R.HVIFLAER.R +1													2.1701	2.15	1.8873		2.1652			2.2848					
R.HVIFLAER.R +2		2.6659	2.6198	2.6081										2.657					2.5003						
R.TLTAVHDK.I +2												2.8757													
R.YLVGGNK.I +1																							1.8608		
gi|6324707|ref|NP_014776.1|	9.7	29.7	32.7	26.7	36.7	30.4	36.8	38.1	43	22.2	38.2	39	41.3	45.2	41	45.1	32.2	29.7	18.5	39.1	15.4	18.9	28.6	23	Elongation factor 2 (EF-2), also encoded by EFT2; catalyzes ribosomal translocation during protein synthesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated by diphtheria toxin; Eft1p [Saccharomyces cerevisiae]
K.ADLM*LYVSK.M +2													3.1827	3.5022											
K.ADLMLYVSK.M +1																	2.0548	2.3627		2.1971			2.1547		
K.ADLMLYVSK.M +2					3.3913	3.1988			3.3377			3.288	3.2472	3.5892	3.4347	3.4244					3.0922	3.4443	3.8681	2.9725	
K.AEPIDEEVSLAIENGIINPR.D +2		4.8776	5.4966	5.0428	4.8201	6.0865	5.7926	5.7346	5.1205	3.9173	5.4163	5.3817	5.5207	5.4108	5.6367	5.6832	5.7347			4.2486	3.9841		4.7697	5.7664	
K.AEPIDEEVSLAIENGIINPR.D +3													4.0871	4.3152	4.6554	3.9396	3.9462							3.7123	
K.AGEIVLAAR.K +1								2.3744	2.3472					2.7367		2.5341									
K.AGEIVLAAR.K +2				3.6401	3.7308		3.6038	3.5405	2.7289			3.1778													
K.AVQYLHEIK.D +2			3.2744	3.3891				3.0312		2.9571	2.8965	2.6738			3.1784	3.0402	3.0229	3.1804		3.163					
K.AYLPVNESFGFTGELR.Q +2		4.6399	4.6093		4.808	4.6938	4.8793	4.9395	4.6599	3.9044	3.9981	4.6404	4.575	4.7499	4.3672	4.5165	3.4052		3.2159	3.969		4.2616	4.3432		
K.DEIPVLLEK.L +1																	2.1566							2.131	
K.DSVVAAFQWATK.E +1									2.1968																
K.DSVVAAFQWATK.E +2					2.6965						2.5906	4.2118	4.7278	4.4978	4.6446	4.8414				4.647			4.3939		
K.DTDAEGKPLER.A +2																						3.0407	2.9674		
K.EDLYQTFAR.T +2	2.94	2.8308	3.0552	2.978	3.0231	3.0382	2.8577	2.9702	2.8375	2.9562	2.8761	2.8562	2.8477	2.862				2.5998		2.788	2.7448		2.9067	2.887	
K.EEVPGWQEYYDK.L +2					3.2765	3.6925	3.9497	3.1138	3.4487	3.1754	3.2752	2.6497	3.0372	3.0803	2.8269							3.3791	3.6871		
K.EEVPGWQEYYDKL.- +2		2.8878	3.6621		3.6407	3.6812	3.6616	3.6606	3.5106	3.6126	3.4419	3.6217	3.476	3.7266	3.553	3.6575	3.4906	3.6652		3.527	3.4211	3.6596	3.4813	3.3137	
K.EGPIFGEEMR.S +2		2.7353		2.7279	2.8884	2.8684	2.9735	2.8514	2.7292	2.7729	2.562	2.6174						2.9901		2.5952		2.7595	3.0422		
K.FSVSPVVQVAVEVK.N +2					4.7186	3.0113	4.6651	4.596	4.4693				3.9176	4.5288	4.0521	4.2055			2.8921	4.0009					
K.IQEPVFLVEIQCPEQAVGGIYSVLNK.K +2					4.6598	2.7518	4.4557	4.3173	4.0727			3.765	3.6426	3.8154	2.9991	4.0164									
K.IQEPVFLVEIQCPEQAVGGIYSVLNK.K +3		6.2431	7.0597		6.4052	4.8683	7.0211	6.6613	6.5357		5.0381	6.131	3.5942			5.6008	4.2474		3.6173	6.8322					
K.IWCFGPDGNGPNLVIDQTK.A +2		5.8859	5.6808	5.1624	5.4614	5.2828	5.5634	5.6319	5.4259	4.8919	5.4593	5.1999	5.3012	5.2159	5.0491	5.2541	4.7525	5.0638	4.7659	4.9132	3.192		4.9262	5.0945	
K.IWCFGPDGNGPNLVIDQTK.A +3															3.5941										
K.KDEIPVLLEK.L +2													3.3291	3.0043		3.1423		3.2875		3.2156					
K.LEIVLKGDEK.D +2																		2.5707		2.5511					
K.PVVVINK.V +1					1.9599		2.1119	2.2178				2.092	2.0436		2.1022	2.0977									
K.PVVVINKVDR.A +2														2.5751											
K.STAISLYSEM*SDEDVK.E +2										3.8265	3.7711	3.5861	4.666					4.5654							

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.STAISLYSEMSDEDVK.E +2			4.8831		5.3106	5.3335	5.0889	4.9423	5.3908	3.3779	4.5053	5.0388	4.5202	5.1955	4.7269	4.8579	5.2846	3.5906		5.5313	5.3712	5.0321	5.2402	5.177	
K.STLTDSLVQR.A +1													2.4162												
K.STLTDSLVQR.A +2					3.7065	3.4909	3.5551	3.476	3.7186	3.566	3.3063	3.3322	3.4465	3.3874	3.1863		3.1839	3.4629				3.424	3.3937	3.4363	
K.TGTLTTSETAHNM*K.V +2														3.1941		2.728									
K.TGTLTTSETAHNMK.V +2		3.8811	4.0689	4.0863							3.7726		3.9982	3.7529	3.7839	3.8294	3.7507	3.9322				4.0067	3.4275	3.1872	
R.AEQLYEGPADDANCIAIK.N +2	6.2773	6.4989	6.2988	5.9558	6.3451	6.3987	6.3121	6.4396	6.1023	6.298	6.2041	6.0491	6.0607	6.5937	6.3167	6.2489	5.8375	4.0285		6.5088	6.3168	5.9844	6.2738	6.2253	
R.AFNM*FILDPIFR.L +2							3.3473	2.7917	3.5059		2.5333	2.6005	3.9415	3.4065	3.8041	3.6619			2.7773					2.6651	
R.AFNMFILDPIFR.L +2	3.6617	2.6782		3.6633														2.9359		3.7576					
R.AGIISAAK.A +1	1.9177						2.0437				1.9308	1.8526													
R.ALLELQVSK.E +2					3.2226	3.282	3.3355	3.4616	3.3024		3.139	3.3329	3.5083	3.1707	3.351	3.2511	2.7936	3.0847		3.0826		3.1886	3.2473	3.1884	
R.ATYAGFLLADPK.I +2		4.1646	4.2282	3.9969	4.3334	4.2423	4.3217	4.4082	4.3936	3.6173	3.8518	4.1835	3.9671	4.2385	4.1292	4.3084	3.8235	3.7395		3.9663	3.37		4.0702	4.4441	
R.ETVESESSQTALSK.S +2	4.7455	4.5857	4.703	4.6684	4.7175	4.6665	4.7742	4.564	4.2842	4.8557	4.8103	4.5402	4.5866	4.4591	4.7137	4.4892	4.2358								
R.FVEPIDDCPAGNIIGLVGIDQFLLK.T +2		3.6864	4.3753	3.6372	4.4634		3.9772	4.1938	4.1653			4.2678	4.7748	4.3652	4.5777	4.5291	3.3825	2.6993	3.1317	3.4082					
R.FVEPIDDCPAGNIIGLVGIDQFLLK.T +3					5.7565		5.5886	4.5857	5.5811		3.7432	4.8806	4.9419			5.6595	4.4888		3.7798	5.5933					
R.GGGQIIPTMR.R +2											3.1112														
R.GQVVSEEQRPGTPLFTVK.A +2		4.9807	5.1539	5.2563					3.7902			3.3121	5.1498	5.2369	4.364	5.34	4.9519	3.6931	3.859	4.0141					
R.GQVVSEEQRPGTPLFTVK.A +3													3.5831												
R.IKPVVVINK.V +1													1.9995												
R.IM*ADDYGWDVTDAR.K +2						4.9862		4.8902	5.5193	5.3451	4.5225	4.6243	5.2066	5.2506	4.9989	5.3624			3.5368		5.1368	5.0219	4.1303	4.8886	
R.IM*ADDYGWDVTDARK.I +2																		3.6464							
R.IMADDYGWDVTDAR.K +2	4.6805	4.7879	5.1248	5.1976	5.0599	4.7314	4.997	4.7566	4.9934	3.6961	4.87	4.875			3.8809	4.877	4.9433	4.8226		4.1518		4.9967	5.0346	3.5129	
R.IMADDYGWDVTDARK.I +2																		3.8077		3.0092					
R.IQGPNYVPGK.K +2			2.5742		2.5422	2.5868	2.5937	2.6876																	
R.IQGPNYVPGKKDDLFIK.A +2																				2.9857					
R.KIWCFGPDGNGPNLVIDQTK.A +2																				2.6401					
R.KIWCFGPDGNGPNLVIDQTK.A +3														3.6609											
R.LFTAIM*NFK.K +2															2.5439	2.9064									
R.LFTAIMNFK.K +1									2.2336						2.4507	2.7365									
R.LFTAIMNFK.K +2							2.7504																		
R.LWGDSFFNPK.T +2		3.6487	3.0872	3.3416	3.4261	3.5139	3.5843	3.5008	3.3017		3.2915	3.4282	3.3585	3.5143	3.3876	3.6423				3.4363			3.2407	3.3798	
R.NM*SVIAHVDHGK.S +2				3.4895				2.5265	2.562			2.5765	3.7304	3.4989	3.7037	3.4784		3.0394				3.5886	3.4153		
R.NMSVIAHVDHGK.S +2			3.9614	3.6672									3.3526		3.3497			2.8164	3.06						
R.QATGGQAFPQM*VFDHWSTLGSDPLDPTSK.A +3														3.6495											
R.TVESVNVVSTYADEVLGDVQVYPAR.G +2									3.2104							2.525									
R.VFAGTVK.S +1	1.8242				1.8902	1.8041		1.9334		1.8046	1.8712		1.8035		2.0874	1.8364						1.9781	1.9033		
gi|6324804|ref|NP_014873.1|	7.3	11.9	7.1	11.4	17.4	11.4	29.5	22	35	19	26.3	31.8	40.5	51.9	38	38	34.3	14.9	25.2	33.4	20.6	15.6	14.4	7.1	Transcriptional repressor involved in regulation of meiosis and silencing; contains WD repeats; Wtm1p [Saccharomyces cerevisiae]
K.DFSLAISDFGISNDTETIVK.S +2							4.5974		4.3453		2.5323	4.8199	5.0872	5.5924	4.6129	5.4514	4.7643		4.4075	5.4441	5.4779		3.5345	3.5192	
K.DYGDAFEGIENTSLSPK.F +2					4.8372	5.1894	5.2064	4.8841	5.0372	4.1685	3.9845	3.5976		4.2094		5.082	4.2398			3.509	4.3624	3.269			
K.FVYQGETVSK.M +2						3.2317			3.2998	2.8108	2.9462	3.1093	2.9902		3.0213	3.0458				2.6701					
K.IIDNAGKPGEILR.T +2				3.8017			3.0419			2.8695		2.9955	3.8061	3.7519	3.4566	3.5094				3.171	2.6952				
K.LTSFDCSQVSNNLFVTGFSTGIIK.L +2							5.0398	4.76	4.9			3.883			3.837		3.8699		3.5701	3.028					
K.LTSFDCSQVSNNLFVTGFSTGIIK.L +3					5.1856		5.4729	5.3743	5.5786			4.8047	5.4683	5.4527	4.6864	3.7222			4.3174	4.4448					
K.NGSLAWFK.E +2				2.6444															2.5001						
K.PIWVLGEPK.N +1																		2.59	2.3169						
K.PIWVLGEPK.N +2			3.3897														3.1768		3.6173	3.6519					
K.PIWVLGEPKNGKLTSFDCSQVSNNLFVTGFSTGIIK.L +3							3.6441																		
K.SLTFSNVVVPDK.K +2		3.1763			3.4793		3.527	3.1293	3.0077		2.9623	2.9061	3.1396	3.1837	3.2474		3.195	3.0064			3.2613		3.287		
K.SLTFSNVVVPDKK.N +2													3.696	3.6037	3.0185	3.4918									
K.SQSNGDEEDSILK.I +2				4.0194							3.2632							4.0029							
K.SSTPSTYEHISSLRPK.F +2				3.4578									3.9868	3.8803	3.4503	3.9513				2.6384					
K.TGETTLLSMSK.N +2					3.7466	3.8794	3.7749	3.6066	3.7012	3.5789	3.6783	3.4225	3.4284				3.6827	3.015				3.5782	3.1392	3.9272	
K.YNPDDTIAPPQDATEESQTK.S +2	4.0523	4.0254					3.8046	3.8052	3.4854	3.6209	4.071	4.3612	4.2918	3.6466	3.727	3.7077	3.9041	3.7877	3.5984	4.5412	3.7774	3.8758			
R.AAEAATTDLTYR.Q +2	3.8684	4.0572			3.9413	3.5545		3.9351	4.2295	3.614	4.262	4.0643	3.6652	3.0563	3.9466	4.2364	3.9802			3.6454		4.0546			
R.FFDNHIFASCSDDNILR.F +2													5.0321	4.8163	4.3635		5.048		2.6233	4.6422					
R.FFDNHIFASCSDDNILR.F +3														4.1239	4.2836										
R.NTAAWHPVIENLVGTVDDDSLVSIYKPYTEESE.- +3														4.2527											
R.PGDLPEKDFSLAISDFGISNDTETIVK.S +3														5.1578											
R.TSDKPWVLGEPK.N +2									2.7139				3.5512	3.4452	3.1218	2.9404			3.256						
R.TVHVPGTTVTHTVR.F +2			3.2521						2.5983					3.0404											
R.VDNVLHQR.K +2		2.6415	2.9667										2.8383	3.2566	2.6426	3.3606	2.75		3.0798		2.6059	2.9739	2.951		
gi|6324923|ref|NP_014992.1|	2	2.2	2.2	2	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	4	6.5	4	4	3.8	3.8	6.5	8.9	3.8	3.8	2	3.8	Pyruvate kinase that appears to be modulated by phosphorylation; PYK2 transcription is repressed by glucose, and Pyk2p may be active under low glycolytic flux; Pyk2p [Saccharomyces cerevisiae]
K.AIVVLSTTGNTAR.L +2																				3.3151					
R.AEVSDVGNAVLDGADCVM*LSGETAK.G +3																				3.5172					
R.PLAIALDTK.G +1					2.6704	2.6573	2.7218	2.7458	2.6866	2.5768	2.6145	2.5832	2.6007	2.6219	2.6294	2.6271	2.5216	2.7558	2.2819	2.3859	2.4869	2.5427		2.342	
R.PLAIALDTK.G +2					3.2851	3.2865	3.3169	3.3229	3.2494	3.3166	3.3408	3.2842	3.1539	3.0855	3.1277	3.1194	2.6137							3.0716	
R.RTSIIGTIGPK.T +2		3.4625	3.4257										2.7772	2.6864	2.8819	2.9889			3.5163	3.3014					
R.TSIIGTIGPK.T +1	2.0113	2.1336	2.1045	2.3247	2.1384	2.2444	2.162	2.2219	2.1728	2.1766	2.197	2.1007	2.3066			1.8965		2.0566			2.2506	2.2858	2.1516	2.0673	
R.TSIIGTIGPK.T +2	3.3657	3.281	3.4493	3.3351	3.5532	3.5611	3.5096	3.648	3.0779	3.4805	3.2276	3.3505	3.2895	3.1476	2.841	3.2453	3.088	3.3528	2.6757		2.8868	3.1376	3.2949	3.1242	
R.VQAVNSGYIASHK.G +2														2.8754											
gi|6324945|ref|NP_015014.1|	22.4	15.4	35.7	22.4	27.3	42.7	42.7	27.3	46.9	28.7	35.7	39.9	46.9	39.9	39.9	39.9	28.7	23.1	42	35.7	36.4	15.4	23.1	14	Protein component of the small (40S) ribosomal subunit; has similarity to rat ribosomal protein S12; Rps12p [Saccharomyces cerevisiae]
K.LVEGLANDPENK.V +1																	3.2123	3.1647	3.1825	3.3598	2.7755	2.7027			
K.LVEGLANDPENK.V +2	4.29	4.4868	3.9452	4.1421		4.1585	4.3103			3.7983	3.9263		3.8748		3.1954	3.365	4.1295						2.8694		
K.LVEGLANDPENKVPLIK.V +2									4.9374			3.0024	4.9274	5.122	4.8261	4.7147									
K.NWGAETDELSM*IM*EHFSQQ.- +2									4.5398	3.8326		3.3778	4.9595	5.4283	5.4078	4.7538			3.7447	2.7596	3.2089				
K.NWGAETDELSM*IMEHFSQQ.- +2					6.0051	5.0941	5.2058	5.8567	5.0525		2.6167	5.1395		5.1565	5.7612	5.0672			2.5661	4.6489					
K.NWGAETDELSMIMEHFSQQ.- +2			6.6879														4.9571								
K.QLGEWAGLGK.I +1													2.0373												
K.QLGEWAGLGK.I +2			2.5441			2.635	2.7223		2.5438																
K.VVGASVVVVK.N +1	1.8935			2.0222	1.9649	1.955	2.1469	2.2695	1.949		2.2298	2.0907	2.2913	2.0599	2.103				1.9089		2.0263		1.9319	1.9633	
K.VVGASVVVVK.N +2					2.9599	2.8622	2.9925	3.0883	3.2938		2.7907	3.3404				3.1228				3.1277		3.1376			
R.GEALLVVLVSSVTEANIIK.L +2																			4.1354						
R.GEALLVVLVSSVTEANIIK.L +3																			3.6176						
R.KVVGASVVVVK.N +1													2.2842		2.4357	2.2101									
R.KVVGASVVVVK.N +2									2.8482			2.8251	2.6952	3.3255	3.3074	3.4256		2.5944			3.6913		3.7738		
R.TALVHDGLAR.G +1						2.4223	2.658		2.2034				2.6313	2.6031	2.2556	2.5571				2.2932			1.8016	2.6447	
R.TALVHDGLAR.G +2	2.7176	2.9902	2.8395	2.9784	3.0062	3.1687	3.0226	2.7432	2.7454	2.8527	2.8279	2.6803		2.94	2.5856	2.6395	2.9241	2.7558			2.7178			2.7555	
gi|6324951|ref|NP_015020.1|	11.9	14.1	26.2	13.4	29.1	37.2	38.1	33.3	50	34.4	36.3	48	50	51.8	45.2	50	37.9	40.1	18.7	43.8	39.9	32.2	32.6	39.4	NADP(+)-dependent glutamate dehydrogenase, synthesizes glutamate from ammonia and alpha-ketoglutarate; rate of alpha-ketoglutarate utilization differs from Gdh3p; expression regulated by nitrogen and carbon sources; Gdh1p [Saccharomyces cerevisiae]
K.AANLGGVAVSGLEM*AQNSQR.I +2										5.714	4.7513		6.1086	6.0548	6.1002	5.4759	4.6512	5.5806		6.0024	5.7718	5.4604		4.9132	
K.AANLGGVAVSGLEMAQNSQR.I +2		5.7322	6.397	5.3791	6.536	6.4616	6.2634	6.4821	6.4627	4.9425	4.8826	6.0594		5.7348	6.0752	6.1066	6.1261	3.9939		5.3788	6.3836	6.0467	6.2249	6.0844	
K.AANLGGVAVSGLEMAQNSQR.I +3															4.4922			4.3146							
K.ALVAQGVK.F +1						2.1677								1.8227			1.9311								
K.FIAEGSNM*GSTPEAIAVFETAR.S +2						3.7336	4.2206		5.2266	4.2381		4.0571	5.4456	5.7215	5.3332	5.1921		5.3033	5.3553	4.5512		3.7478	4.5147		
K.FIAEGSNMGSTPEAIAVFETAR.S +2						5.6489			5.207		4.1516					5.1373	5.8628	4.3425		4.2007	4.4325		5.465	4.6273	
K.FLGFEQIFK.N +1																			2.1345	1.9111					
K.FLGFEQIFK.N +2									2.6711				3.2213	3.3691	3.3336	3.1166									
K.GANIASFIK.V +2	2.7628		2.8563															2.6708							
K.GCIISETGITSEQVADISSAK.V +2						6.2396	6.8684	6.2927	6.6712		5.191	6.0844	6.0235	6.5545	6.2723	6.766	6.4321	5.6816	6.0745	6.002	6.2701	5.8262	6.6377	5.9716	
K.GCIISETGITSEQVADISSAK.V +3													3.6371												
K.GEQEVAQGYR.V +2													2.8446			2.8213									
K.NSLTGLDM*GGGK.G +2																					2.7261				
K.NSLTGLDMGGGK.G +2					3.1399	3.13			3.401	3.1074	3.1326	3.0902	2.9786	3.3179		3.4391				2.8126	2.51	3.1364			
K.NSWEGVLTGK.G +1									2.1311				2.2565	2.2432	2.6346	2.077		2.018		2.2452		2.0933	2.3519	1.9917	
K.NSWEGVLTGK.G +2						2.9108	3.2282	2.9176	3.1502	2.6717		3.3315				2.9705	2.5001	2.9387					3.12		
K.SLEQIVNEYSTFSENK.V +2			2.5676		5.5926	5.6798	5.5625	5.7361	5.5379	4.5939	5.037	5.3086	5.3492	5.6712	4.5732	5.3838	3.0667	4.9088	4.9819	5.1637	3.8088	3.6068	5.2226	4.8915	
K.VDIALPCATQNEVSGEEAK.A +2	4.5115	4.8219	4.4941		5.5379	5.3314	5.6864	5.439	5.4671	4.9814	5.5016	5.0399	5.2618	5.4171	5.4435	5.1895	4.2274			4.6913	5.1252	5.3007	4.6863		
K.VIELGGTVVSLSDSK.G +2		3.0445	3.2989	3.7174	4.8341	5.0589	5.4837	5.0884	5.2552	3.8391	5.1585	4.9747	5.3956	5.4867	5.3646	5.4658	4.8353	4.5996		3.0822	4.9759			4.7775	
K.VLPIVSVPER.I +1													2.3087		2.4715					1.9488					
K.VLPIVSVPER.I +2	2.9843	2.9543	2.7797		2.7532	3.1442	2.6319	2.8223	3.1997	2.6732	2.9537	2.6351	2.7411	2.9948	2.7863	2.7668	2.6323								
K.VSDAMFDQGDVF.- +1																		2.252							
K.VSDAMFDQGDVF.- +2				3.0141																					
R.EIGYLFGAYR.S +2					3.1325		3.1749	3.3302	3.4282			3.348	3.4361	3.3642	3.4015	3.3817		2.9506		3.3802	2.9486	3.4439	3.3324	3.1787	
R.ICYAFMR.E +2																				2.5384					
R.IM*INCFNECIDYAK.K +2													4.4516	4.5181	4.5743	4.2799		3.4253		3.8989	4.2146		3.8238	3.7373	
R.IMINCFNECIDYAK.K +2			3.2853	2.9511	3.9012		3.8481	3.6865	3.8635		3.4803	3.3582			2.5137	3.7219	4.4007	3.6848							
R.PWTHVQK.V +2															2.7684										
R.STATGPSEAVWYGPPK.A +2	4.9505		4.832		5.2957	5.1538	5.2667	5.1022	5.2218	4.9097	5.1325	4.9436	4.9986	4.9388	4.9163	4.8428		4.1684		4.4995	4.6661	4.535	4.8768	4.5456	
R.VTISGSGNVAQYAALK.V +2									5.0584	3.4267		2.9526	4.4456	4.9046	4.5202	4.8798					4.741			4.8046	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.VTWENDKGEQEVAQGYR.V +2									5.2552			2.7562	5.3018	5.5396		4.8514	5.178	4.8689	3.6156	4.8733					
R.VTWENDKGEQEVAQGYR.V +3													3.9571												
gi|6325016|ref|NP_015084.1|	17.1	27.2	21.2	26.1	27.8	30.5	35.7	33	33.9	24.3	30.7	36.5	30.5	35.7	31.2	34.3	28.6	23.4	16.9	31.2	14.4	15.8	18.1	20.2	Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hsf1p; docks with the mitochondrial import receptor Tom70p for preprotein delivery; interacts with co-chaperones Cns1p, Cpr6p, Cpr7p, and Sti1p; Hsp82p [Saccharomyces cerevisiae]
K.AELINNLGTIAK.S +2	4.0432	4.2019		4.2025	4.2215	4.3491	4.3092	4.4211	4.4279	4.3487	4.3029	4.4202	4.0731	4.1322	3.8046	4.1003	4.123	3.7757	4.0619			4.3854	4.2747		
K.DDQLEYLEEK.R +1																				2.6694	2.0052		3.0696		
K.DDQLEYLEEK.R +2					3.9919	4.3054	4.2314	4.2901	4.0201	3.7415	4.2516	4.1641	4.2009	4.1675		3.7868	4.0608								
K.DFELEETDEEK.A +1																		2.7669		2.3642	2.1694			2.6508	
K.DFELEETDEEK.A +2	4.2679	4.1262	4.1741	4.2588	3.6568	3.8922	4.0207	2.798	3.9775	4.1923	4.2022	4.0716			4.0799		3.7107	2.908				4.203	4.4807		
K.DFELEETDEEKAER.E +2													3.9027	3.9719		4.6135	3.7605								
K.EILGDQVEK.V +1																				2.7117					
K.EVPIPEEEKKDEEK.K +2										3.0151															
K.GVVDSEDLPLNLSR.E +2	4.9569	4.9869	4.9765	5.2413	5.0117	5.0162	5.1	4.9963	4.9924	4.8136	4.8686	4.9007	5.1372	4.8706	4.8098	4.8612	4.7699	4.6334	5.0682	4.9082	4.4612	4.9733		4.7253	
K.KLIEAFNEIAEDSEQFEK.F +2																	3.194								
K.KTFEISPK.S +2														2.7276											
K.LGVHEDTQNR.A +2			2.6643				2.5364				2.8392			2.7813		3.1111	2.5719								
K.LIEAFNEIAEDSEQFEK.F +2					5.0984	6.1085	5.8046		4.6034	4.2836	4.2426	5.1702	5.8126	5.6402	5.1284	6.1769	4.8272	4.4029	5.1745		5.9854	4.8996	4.4728	5.4245	
K.LLDAPAAIR.T +1														2.2749	1.8926							1.8558		2.221	
K.LLDAPAAIR.T +2				2.9322	2.7483	2.715	2.9197	2.8291	2.6952	2.5774		2.5188		2.5779						2.8986					
K.LLYETALLTSGFSLDEPTSFASR.I +2								3.1205	4.8147			3.3334				3.7807	2.6149			3.5519					
K.LLYETALLTSGFSLDEPTSFASR.I +3													5.0778												
K.NFEVLFLTDPIDEYAFTQLK.E +2		5.4699	5.9958	6.1048	6.0643	5.8953	6.2962	6.4731	6.1676		3.139	5.5551	6.1727	6.0953	5.9028	6.0303		4.2104		6.1757				2.562	
K.NFEVLFLTDPIDEYAFTQLK.E +3													5.7487	6.3567	5.9628	4.6483				4.783					
K.NIYYITGESLK.A +1								2.5389	3.4937				3.4773	3.5161						2.3424	3.6466				
K.NIYYITGESLK.A +2		4.0223	3.8354		4.2475	4.1593	4.1292	4.0708	4.2305	3.657	4.0268	4.0628	4.1356	4.1329	4.0437	4.0831	4.0426	3.713				3.5932	2.5354	4.159	
K.QLETEPDLFIR.I +2	3.6937	3.854	3.6595	3.8345	3.3823	3.6606	3.5924	3.3321	3.4057	3.3371	3.3463	3.448		3.1676	3.277	3.1654	3.2522	3.4948	3.6853	3.434			2.5534	2.8447	
K.RAPFDLFESK.K +2		2.7647		2.6526									2.9838		2.6248				3.105	3.0106					
K.SISNDWEDPLYVK.H +2	4.5727	4.5407	4.5376	4.2967	4.6035	4.6282	4.6987	4.5486	4.1775	4.4651	4.4211	3.859	3.6617	3.8796	4.0943	4.3068	4.4896	3.6931	4.2606		3.1158		3.909		
K.SPFLDALK.A +1	2.5865						2.5365		2.6878			2.3812													
K.SPFLDALK.A +2														2.6447											
K.SVDELTSLTDYVTR.M +2	5.1554	5.2413	5.2853	5.4009	5.2401	5.2247	5.1487	5.3767	4.8345	4.8466	5.0632	4.8872	4.9566	4.8041	4.431	4.8761	4.9299	5.0604	4.8442	4.3336	4.2908	4.895	4.2865	5.0648	
K.TFEISPK.S +1						2.0673	2.1739											2.2313							
K.TLVDITKDFELEETDEEK.A +2																	4.8536								
R.AILFIPK.R +2																2.5513									
R.APFDLFESK.K +1					2.6635	2.4933		2.2511	2.7161		2.302		2.6278	2.3219	2.5899	2.2626									
R.APFDLFESK.K +2					3.2541	3.3498	3.2478	3.3499	3.2311	2.7516	2.9706	2.8264		3.2297	3.1414	2.8385		2.8592	2.8206				2.9263	2.8067	
R.DSGIGMTK.A +1		2.2061					2.0614	2.1499			2.0401	1.9798	2.2247	2.0106	2.1999	2.1116		1.9348					1.811		
R.DSSMSSYMSSK.K +2	3.6914	3.2346		3.305			3.2113	2.8895				3.1873			3.2617					3.459					
R.ELISNASDALDK.I +2	3.8737	3.6922	3.7311	3.7809	3.4102	3.7027	3.8604	3.838	3.728	3.8382	3.5954	3.9178								3.6965					
R.HSEFVAYPIQLVVTK.E +2														4.9095						4.5524					
R.HSEFVAYPIQLVVTK.E +3														4.2642											
R.LFLKDDQLEYLEEK.R +2				4.504									4.9681	5.1591	4.8538	4.3935			3.1963	4.8866					
R.NPSDITQEEYNAFYK.S +2	5.5717	5.8093	5.8222	5.5285	6.0636	6.1183	6.0564	6.0002	5.32	5.688	5.5978	5.5482	5.535	5.8194	5.728	5.8555	5.5586		5.4873	5.8308		5.8465		2.8778	
R.TGQFGWSANM*ER.I +2									3.6207												2.9033				
R.TGQFGWSANMER.I +2		3.6859				4.236	4.231	4.1451	3.9947		3.1042	4.152	3.9137	3.7738	3.79	3.9436	3.6031			3.9626			3.2054	4.1127	
R.VFITDEAEDLIPEWLSFVK.G +2		4.6669	4.9123	4.9307	4.4797	3.8696	5.2259	4.7505	4.4711		3.4982	4.1175	2.6611	3.9469	2.9878	4.164	3.6577	2.6728		4.3984					
R.VFITDEAEDLIPEWLSFVK.G +3																3.7362									
gi|6325025|ref|NP_015093.1|	3.4	3.5	7.7	4.1	12.7	14.7	17.6	19.5	27.2	11.5	18.5	22.7	34.9	35.8	27.9	30.9	27.3	20.7	16.8	29.6	14.3	8.1	16.4	15	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities; Fas2p [Saccharomyces cerevisiae]
K.AAEEAGVTDVK.V +1																		2.0508						2.005	
K.AAEEAGVTDVK.V +2	4.0088						4.0263	3.1956			3.2322	3.7703	3.5171	2.772	3.711	3.7671				2.8594					
K.AISAQADKQDISSSTR.V +2													4.7861										3.7773		
K.ATSNTLEEFEHGR.T +2													3.7116	3.4034		3.5096	3.4342	3.4955							
K.AVSIETALEHK.V +2														2.814			2.6628	2.7943							
K.DSYINANTIETAK.M +2	4.4626							4.2218		4.2545		3.9024	4.3421			4.1099	4.5151		4.4744			4.2992			
K.DWVENELEALKLAEEIPSEDQNEFLLER.T +3						3.7914	4.3735	3.8794	3.7425	3.2925	3.3873	3.1637	2.8627	3.9983	4.012	3.8047		2.6331			3.9222	3.4013	3.4123	3.2501	
K.DWVENELEALKLEAEEIPSEDQNEFLLER.T +3				5.9057																					
K.EEPAKEEAPAPTPAASAPAPAAAAPAPVAAAAPAAAAAEIADEPVK.A +3									6.687				5.9804	5.9256	6.3028	6.8026	5.9809	6.0149		5.6221					
K.EFGTTPEKPEETPLEELAETFQDTFSGALGK.Q +3				5.8228																					
K.EHAPYTDELEEDVYLDPLAR.V +2													4.4667		3.5833	5.0656	2.6292			5.5501					
K.EHAPYTDELEEDVYLDPLAR.V +3													4.0141												
K.EIDPSQTTQLAGM*DVEDALDK.D +2									3.104	3.1602		3.7413		4.2417	4.2734	4.3304		2.9935	4.6516	3.0411	2.9717				
K.EIDPSQTTQLAGMDVEDALDK.D +2			5.6614			5.2278	5.1021	5.4844	5.2748		3.7854	3.84					3.8259	3.7169							
K.EIYYTPDPSELAAK.E +2					4.178	3.6871	3.6674	3.8421	3.7575	3.5349	3.3799	3.2615	3.2746	3.5843	3.5238	3.8187		2.6813						3.1608	
K.ELVETSEVR.K +2							2.7357									2.7599	2.5474								
K.EM*AFNLLGLLTPEVVELCQK.S +2					2.8578		3.1024	3.7844	4.4802			4.1091	3.7187	4.3309	2.9317	3.0175			2.8749	3.1911					
K.EM*AFNLLGLLTPEVVELCQK.S +3													5.2278	5.9083	4.0707					3.8839					
K.EM*IQEVIVEEDLEPFEASK.E +2							3.1887		2.8473		3.9872	5.003	5.7282	5.8355	5.2896	4.9226		4.4442	4.6861		5.1151			4.3605	
K.EM*IQEVIVEEDLEPFEASK.E +3													4.4774												
K.EMAFNLLGLLTPEVVELCQK.S +2																		2.6891							
K.EMIQEVIVEEDLEPFEASK.E +2			4.9224		3.0421			2.7028	4.2631			3.5077				5.1543	5.1521	3.2308		3.3804			3.4903		
K.ESQPTIEEDLTR.V +2	3.296	3.6747	3.3008				3.5405	2.8307	2.7049		3.2357	3.1565	2.7384		2.8513	2.8328	2.9739								
K.FFHNGMIYNK.L +1																				2.0688					
K.FFHNGMIYNK.L +2																				2.6438					
K.FM*EYHISNTDETK.G +2																2.7357									
K.FM*EYHISNTDETKGENYQLVK.T +3													4.6848	3.6894				3.6588							
K.FMEYHISNTDETKGENYQLVK.T +3																				3.8586					
K.GAAGAWMMNGALQILNSGIIPGNR.N +2																				3.5719					
K.GGQAIVVHPDYLYGAITEDR.Y +2													4.5815	4.2423	3.7886										
K.GSIGAEVLQGLLQGGAK.V +2									5.5971			5.3191	5.7154	5.0942	5.9563	5.6019	4.7148		5.1491	4.8376					
K.GSTLIVVPPNQGSK.Q +2					2.8267				2.9893		2.8579	2.8712	3.7729		2.8259		3.3775		4.0093	3.2355				3.0727	
K.ILEQFEYVLYPSK.T +2		2.8862			3.7073			3.9766	3.1801		3.3179	3.4987	3.9694	3.6623	3.6444	3.7963	3.5733	3.5175	2.984	3.6854	2.731	4.0659	3.5897	4.3927	
K.LEAEEIPSEDQNEFLLER.T +2					5.4936	5.6966	5.7581	5.3791	5.2721	4.8772	4.4742	4.3245	5.0106	5.457	3.6664	5.4304	3.7311		5.0223		4.2888	4.9193	4.9425	2.7791	
K.LSLETLFNR.W +2							3.0472	3.1761				3.0268	3.0194	3.3375	3.2243	3.1785	2.9489	2.9003	2.728	2.6232	3.1443		3.1504	2.8714	
K.LSQYVQEM*ALGGPITK.E +2													5.7455	5.2857							5.095			3.8108	
K.LSQYVQEMALGGPITK.E +2			3.9354		5.4011	5.3951		5.6475	5.2664	4.6929		2.93	2.9685	4.7763	4.7483	3.5595	4.893	4.7303			5.0429		4.4928	5.208	
K.M*GVPIYGIVAM*AATATDK.I +2													2.5634	3.3969							3.4447				
K.M*PGGFTITVAR.K +2													2.9683	2.8901					3.0524		2.5186			2.8667	
K.MGVPIYGIVAMAATATDK.I +2							3.534																		
K.MPGGFTITVAR.K +2									3.4706			3.1921	3.3626	3.4311	3.1984	3.2672	3.4181	2.7409		3.2205	2.9822		3.1279		
K.NAPAVELHGNAK.K +2		2.8183									2.9179		3.4296	2.673		2.8011	2.714								
K.NESATINEMMK.H +2											3.4372														
K.NGNITYSEEPR.E +2					2.6499					2.8211		3.3754				2.5419							2.5735		
K.NKYESYDAALSLHR.E +2																				2.6796					
K.QDVEAIEFIYDTEK.N +2													3.4439	4.1816			2.7281			3.9307					
K.QIAPAELEGLLDLER.V +2						3.846	4.1783		4.1358		3.794	3.7903	3.825	2.6141		2.8942	4.3856		2.7882	4.8811			2.6242		
K.QIAPAELEGLLDLER.V +3																			3.8227						
K.QVLDVDPVYK.D +2						2.9198								2.8138		2.7297				2.9829					
K.QVTDYYQSIYAK.Y +2					3.3254	3.3902	3.7835	2.7619	3.2465	3.3129	3.3477		2.744	3.631		2.7283	3.7451		3.2328	2.6722	2.9909	3.3897	3.3428	3.4665	
K.SPVM*ADLNGGLQFVPELK.E +2												2.9134	4.656	3.2101											
K.SPVMADLNGGLQFVPELK.E +2				3.458		2.6162	3.5362	2.9153									2.8661			3.9873			3.0551	3.0243	
K.TLGEQLIENCK.Q +2					4.0319	4.0869	3.8524	3.9249	4.094	3.3745		3.1569	3.9635	4.0193	4.0558	4.1135				3.7745	3.8543		4.2085	3.9352	
K.TPVGACATSVESVDIGVETILSGK.A +2						4.1574			3.5079					2.5411					2.9042						
K.TPVGACATSVESVDIGVETILSGK.A +3									4.8135					4.3048											
K.VDIFEIPETGEYSVK.L +2			4.0288		4.0902	4.1892	4.1985	4.3439	4.0829	3.6139	3.5022		3.9009	4.0565	4.1829	4.1782	3.2222	3.8792	2.7686	4.0053	4.0087	3.7697	3.5581		
K.VSISHDDLQAVAVAVSTK.K +2									4.9258				6.1384	5.1175	5.6261	4.1015									
K.VSISHDDLQAVAVAVSTK.K +3													3.7907		3.8471										
K.VSISHDDLQAVAVAVSTKK.- +2																				4.7629					
K.VVNGNSADAAYAQVEIQPR.A +2								3.6538	4.5076		2.9769					4.5711	4.9579	4.8815		4.1285	5.2659		4.6801	4.8663	
K.YESYDAALSLHR.E +2												2.8358		3.5425	2.7359	3.3788		3.7305		3.132			3.8369		
K.YETSILEHSGIR.L +2			2.8526						2.9745				3.4114	3.4984	3.5297	3.5618	3.0404			3.4448					
K.YVHVSEVGNCSGSGM*GGVSALR.G +2																				3.009					
K.YVHVSEVGNCSGSGM*GGVSALR.G +3													5.9455	5.4508											
K.YVHVSEVGNCSGSGMGGVSALR.G +2																	6.1715	5.8406		4.8267					
K.YVHVSEVGNCSGSGMGGVSALR.G +3									3.9495					4.6848	3.6581	4.858	4.4872			3.9074					
K.YVLITGAGK.G +1														2.6884	2.2884		2.3506		2.2193			2.7044			
R.AAQQQWGNDFYK.R +2					3.9585		4.0439	4.0502	4.168	4.039	3.5155	3.8503	3.9915			3.7347		4.1031							
R.ANIQLDFPELKPYK.Q +2															4.2988				3.5967	4.0062					
R.AVSITSFGFGQK.G +2			3.5394		3.4208	3.4627	3.7341	3.5126	3.9376	3.494	3.5272	3.7076	3.72	3.6798	3.6489	3.6904	3.5491		3.0037		3.476		3.2484	2.8982	
R.EIHNEAESQLR.A +2														2.7772				3.1256							

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.EILCYSK.D +1																				1.8295					
R.EVVSEAINIM*NR.S +2													3.9566						3.9052						
R.EVVSEAINIMNR.S +2												3.803		4.3478	3.8914					4.2766	4.2647	4.7047	4.6196	4.3332	
R.GALATYGLTIDDLGVASFHGTSTK.A +3														4.1416											
R.GTGLM*SANNIIAEGIEK.M +2								2.9768					4.0469	4.2083	4.0107					4.2986	3.4009			3.211	
R.GTGLMSANNIIAEGIEK.M +2											3.7808	3.4851			3.19	4.7237	4.5578	4.4234		3.7336	4.5561	4.294	4.7838	4.1464	
R.IMLTNILR.M +2												2.7108			2.8098		2.663	2.6796		2.6125	2.6815			2.6041	
R.KAVSIETALEHK.V +2													3.0635	4.1584											
R.LIEPELFNGYNPEK.K +2					3.3592	3.2504	3.727	3.3095	3.9717		3.465	3.4151											3.3427		
R.LVAGQIPTGWNAK.T +2	3.3329	3.8259	3.9548			3.7407	4.0331	3.5358	3.5186	3.6928	3.4602	3.2898	3.9804	3.6923	3.8717	3.7833	3.1753					3.3842	2.6589		
R.QDGVLLVALSNEPAAR.L +2						3.5978			4.7944		3.2416	4.3103	5.1484	4.6837	4.9293	3.3515	4.213	4.7186	4.7565	2.5948					
R.QLSSLFLDGLEK.A +2									2.6871				2.672	3.3354											
R.SEGNPVIGVFQK.F +2					3.8413	3.7854	3.9612	4.0329	3.9459	3.8125	3.927	3.4613				3.5253	3.7831	3.9546			3.4781			3.5775	
R.TFDSSWNWAK.Q +2							3.473	3.4671		2.9147	3.2671						3.6271					3.4483			
R.TREIHNEAESQLR.A +2																				2.9518					
R.VIVVTGFAEVGPWGSAR.T +2									3.5195				5.0563	4.904	4.4363				3.9177	3.2809					
R.VVEIGPSPTLAGM*AQR.T +2										3.4525	3.3841		4.5861	4.7732	4.0734	3.5703			2.8675		3.2488				
R.VVEIGPSPTLAGMAQR.T +2	4.3585	4.6727	4.302		4.8373	4.6753	4.565	4.702	4.2155	4.0817	4.6955	3.9236		3.7761	4.5211		3.1088			3.7355			2.7138	3.9711	
R.VVEIGPSPTLAGMAQR.T +3														4.1591											
R.WIETQDVFLK.D +2			3.6719		3.3708	3.597	3.4151	3.2822	3.3109		2.7275	3.0761	3.0672	3.4878	3.404	3.6003		3.1654				3.3594		3.7453	
R.YNEYVAK.V +1													2.0677												
gi|6325058|ref|NP_015126.1|	22.1	20.9	32.4	27.9	23	23	23	18	27	26.6	23	30.7	29.5	23	23	35.2	33.6	23	25.4	20.9	18	20.5	23	23	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Ap and has similarity to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2); Rpl7bp [Saccharomyces cerevisiae]
K.AAGSYYVEAQHK.L +1																							2.591		
K.AAGSYYVEAQHK.L +2		3.8738	3.57	3.5375	3.1801	3.4158	3.6313		3.2268	3.2969	3.8154	3.4759	3.5786	3.4568	3.3326	3.4609	3.6876	2.9719	3.1924			3.8077		2.8793	
K.HFIQGGSFGNR.E +2			2.5077													2.905									
K.HFIQGGSFGNREEFINK.L +3																				3.6852					
K.ILTPESQLK.K +1																2.6027	2.5264		2.3089						
K.LIEPYVAYGYPSYSTIR.Q +2	4.913	5.3207	5.0257	4.5716	4.9501	5.1284	4.9401	4.9585	4.5619	4.8746	4.6969	4.3685	4.7678	4.9944	4.8064	4.9605	4.9692	3.7186	5.1576	4.6376	4.9589	4.168	3.1086	4.5201	
K.LIEPYVAYGYPSYSTIR.Q +3													4.1781	4.9403	3.8784					4.0246					
K.LSNPSGGWGVPR.K +1																							2.0681		
K.LSNPSGGWGVPR.K +2	3.8335	3.6231	3.9498	3.6998	3.9097	3.9282	3.7514	3.84	3.6416	3.6901	3.6953	3.301	3.7405	3.7636	3.2283	3.341	3.2181	3.1045			3.7116	3.4992		3.7985	
K.QANNFLWPFK.L +2	2.8825	3.1564	3.0173	2.88					2.6042			2.545				2.636	2.6144								
K.QRVPLSDNAIIEANLGK.Y +2			3.56	2.9026																3.6659					
K.TAEQIAAER.A +2										2.996		3.0272	3.1621						2.8261			2.5536			
R.KVLQLLR.L +2													2.8177				2.7707								
R.VPLSDNAIIEANLGK.Y +1									2.7518																
R.VPLSDNAIIEANLGK.Y +2	4.7891		5.0612	5.136	5.0607	5.2709	5.0061	5.2394	4.8277	5.1147	5.2399	4.7525	4.3118	5.1173	4.3726	5.081	4.901	4.6787	4.9356	4.9911	4.6557		4.463	4.7273	
R.VPLSDNAIIEANLGK.Y +3														3.5999											
gi|6325167|ref|NP_015235.1|	10.2	18.2	11.4	23.3	20.3	23.7	15.3	27.1	29.2	27.1	27.1	22	24.2	29.7	34.3	34.3	22.5	23.7	20.8	19.1	8.9	21.6	11.9	18.2	Protein component of the small (40S) ribosomal subunit; identical to Rps6Bp and has similarity to rat S6 ribosomal protein; Rps6ap [Saccharomyces cerevisiae]
K.GEELEGLTDTTVPK.R +2						3.7152				2.7726	3.5565				3.5992	2.7267						4.1489			
K.KGEQELEGLTDTTVPK.R +2		3.5938		3.8517		5.0746		4.6037	4.8538	4.1765	4.697	4.104	5.2085	4.8014	4.7682	4.9288	4.74	4.7905	4.866	3.9277			3.7327	2.8721	
K.LNISYPVNGSQK.T +2	3.8491			3.1688	3.275	3.2113		3.6692		3.5202	3.3628				3.6582	3.7336		3.2552		3.5971					
K.RIGQEVDGEAVGDEFK.G +2						2.5828								4.3908			4.1537	4.695	2.621						
K.TFEIDDEHR.I +2					2.611		2.667	2.8255	2.8481	3.0368	3.062	2.712	2.5546	2.7104	2.7974	2.7788	2.6269				2.5607	2.814			
R.EAAAEYAQLLAK.R +1							2.6958		2.7783					2.8312											
R.EAAAEYAQLLAK.R +2	3.876	3.8846	3.8313	3.9115	4.1469	4.0116	4.1021	4.1216	4.0716	4.0389	4.1597	3.6359		3.9883	3.6756	4.0343	3.7433	3.1918			3.6573	4.3834	4.0486	3.8443	
R.GAIVGPDLAVLALVIVK.K +2									3.1801				5.3379	5.6006	5.5932	5.6437			4.7109	4.8102					
R.IGQEVDGEAVGDEFK.G +1																								2.2236	
R.IGQEVDGEAVGDEFK.G +2		5.3394	4.9976	5.6118	5.266	5.3846	5.4762	5.3382	5.373	5.1145	5.138	5.1613	5.0953	5.3497	5.1927	5.1605						5.0283			
gi|6325196|ref|NP_015264.1|	26.2	47.6	45	44.4	42.6	52.6	51.4	55.6	67.6	54.8	51.2	55.4	70.4	73.4	64.2	71.4	44.4	42.4	55	58.4	23	16.4	32.4	24.2	Cytosolic aldehyde dehydrogenase, activated by Mg2+ and utilizes NADP+ as the preferred coenzyme; required for conversion of acetaldehyde to acetate; constitutively expressed; locates to the mitochondrial outer surface upon oxidative stress; Ald6p [Saccharomyces cerevisiae]
K.AGTVWINTYNDFDSR.V +2	4.0182	4.6201	4.6219	4.6885	4.3023	4.7352	4.4051	4.5818	4.5693	4.0664	4.5594	4.2866	4.6034	4.6844	4.5733	4.6121	4.1032	4.5681	3.3385	4.7428	3.8885	4.3722	3.3785	4.5345	
K.ANFGATNRQ.Q +2	3.3236	3.2723	3.2171	3.3397	3.327	3.3539	3.3265	3.2575	3.2229	3.1827	2.9485	3.4037	3.2028	3.1387	3.1376	3.1175	3.2151				3.1267			3.1533	
K.EEIFGPVVTVAK.F +1					2.2544	3.0738			3.0208			2.7872		3.3228	2.8038	2.48				1.9323					
K.EEIFGPVVTVAK.F +2	3.6223	3.7689	3.6614	3.3802	3.6203	3.9038	3.9179	3.7859	3.6142	3.5953	3.6375	3.6402	3.7242	3.5854	3.3209	3.557		3.8498			3.6636	3.1534	3.4827	3.8096	
K.GYFIRPTVFYDVNEDM*R.I +2													2.5409		2.6778										
K.GYFIRPTVFYDVNEDM*R.I +3																			3.6617						
K.GYFIRPTVFYDVNEDMR.I +2																				3.0116					
K.IAPALAM*GNVCILK.P +2													4.3278	4.29	2.6136	4.2744									
K.ILTGGEK.V +1																		1.85							
K.ITLELGGK.S +1					2.2325				2.2906																
K.ITLPNGLTYEQPTGLFINNK.F +2	5.4571	5.6529	5.7227	5.2746	5.4938	5.3724	5.268	5.3418	5.5058	4.742	4.9727	4.9491	5.1015	5.2226	5.418	5.1501	4.8909		3.2128	3.458	3.2922		4.271	4.9672	
K.ITLPNGLTYEQPTGLFINNK.F +3											3.5276	4.1097	4.4643	4.5004	4.9476										
K.KITLELGGK.S +1																			2.6382	2.8607					
K.KITLELGGK.S +2		2.8394	2.8643	2.8894																					
K.KTLPNLVNGIFK.N +2		3.9313																	3.6368						
K.KVGIPAGVVNIVPGPGR.T +2		3.7251																	4.558	4.1481					
K.LADELESQIDLVSSIEALDNGK.T +2		6.7398	6.4928	6.0797	6.5745	6.275	6.448	6.4658	6.3735	3.6822	5.4754	6.2465	6.2528	6.1023	6.0791	6.4465	6.0908	6.4716	5.4925	5.8581	4.1033		4.7177	4.7513	
K.LADELESQIDLVSSIEALDNGK.T +3						4.5195	4.5218						5.2343	4.1314	4.6876	5.0077	5.0321			4.0933				3.7305	
K.LAFTGSTEVGK.S +1													1.9788		2.1241	2.0272	1.8772	1.9293			2.1087		2.0368		
K.LAFTGSTEVGK.S +2			3.226	3.3274	3.19	3.1691	3.2599	3.2917	3.1158	3.4373	3.7823	3.0732		2.6713	3.0508	2.8895						3.1507	3.1458	3.0599	
K.LHFDTAEPVK.I +1						1.9921		3.0405					3.1738	3.2183				2.282	3.0028	2.6775					
K.LHFDTAEPVK.I +2		2.6864	3.0908	2.7164				2.6853	2.6504	2.8369				2.6797		2.7408	3.1075								
K.NAGQICSSGSR.I +2									2.8698	3.1039	3.0068	3.1186		3.032											
K.PAAVTPLNALYFASLCK.K +2	4.4635				3.7115			3.8937	4.4683						4.9032	3.6541		3.8178	2.5397	4.4768					
K.PAAVTPLNALYFASLCK.K +3													4.8488	5.3509	5.1216					4.4726					
K.SAHLVFDDANIK.K +1																	2.8675	2.5549		3.1046					
K.SAHLVFDDANIK.K +2		3.5531	3.6452	3.6754				3.0959		2.7121			3.8558	3.7023	3.5837	3.6692	3.362			3.6264					
K.SAHLVFDDANIKK.T +2						2.5122			3.2633				3.8968	3.9569	2.9875	3.6493				3.3865					
K.SAHLVFDDANIKK.T +3													4.2392	3.9613											
K.SVAVDSSESNLK.K +1									2.2133				2.6086	2.8242	2.6218	2.8667	2.0022								
K.SVAVDSSESNLK.K +2	4.2196	4.1813	4.1308	4.2816	4.1441	4.2522	4.1341	4.1859	4.2559	4.1541	3.9237	4.2028	4.1055	3.9885	4.1783	4.0726				4.0859					
K.SVAVDSSESNLKK.I +2											3.1029		3.1638		2.8508	3.2023							2.5792		
K.TLEEGVEM*ANSSEFGLGSGIETESLSTGLK.V +2							3.2985		3.6053										3.7227			4.3604			
K.TLEEGVEM*ANSSEFGLGSGIETESLSTGLK.V +3						4.1149						5.063	4.6343	4.1905					3.9008						
K.TLEEGVEMANSSEFGLGSGIETESLSTGLK.V +2						4.3139	3.0023	3.2132	4.0603											2.5114					
K.TLEEGVEMANSSEFGLGSGIETESLSTGLK.V +3						5.6477	4.6256		4.3619							5.9076							5.3306		
K.TLPNLVNGIFK.N +1									2.7866																
K.TLPNLVNGIFK.N +2	2.8684	2.8912	2.9517	2.983	3.0534	2.7742	3.2968	3.0419				2.9638	3.1782	2.6724	2.9323	2.8515									
K.TYPVEDPSTENTVCEVSSATTEDVEYAIECADR.A +3						5.8472	5.5455		5.4405	3.9214	5.3674	5.4718	7.8683	6.234	6.7873	5.9171	4.2678	5.922	4.9692	3.9559					
K.VGIPAGVVNIVPGPGR.T +2	3.9459	4.2594	4.0719	4.063	4.3666		4.0773	4.3122	2.8747	4.3605	3.5012	2.7653	3.9615	3.7501	3.5147	3.466			3.4779	3.5023					
R.AFHDTEWATQDPR.E +2		4.7262	4.7511	4.637				4.5483	2.686	3.8105	3.4125	2.8494	4.9548	4.8921	4.346	4.9535	4.4459	4.7189	3.9756	3.8988		3.405	3.9209		
R.DAAAYADKV +1							2.7478	2.6018	2.7523	2.5302	2.6915	2.4665	2.7569	2.5681	2.5709	2.5771		2.6737	2.0007	2.4221			2.7298	2.6556	
R.EM*GEEVYHAYTEVK.A +2										3.3686			3.9465	3.9938	2.7219	3.1953		3.6383		3.0979					
R.EMGEEVYHAYTEVK.A +2		4.1803	4.0474						2.8106				3.9472	4.2799	4.2714	4.1198	3.9029			4.1454					
R.GDVTIAINCLR.D +1									2.2172																
R.GDVTIAINCLR.D +2		4.1169		4.1469	4.3052	4.1518	4.1131	4.1688	4.1586	3.8669	4.1706	4.0425	4.2718	4.2384	4.1102	4.0617	4.2151	4.1231		3.4848	3.1808		4.1654	4.1787	
R.IVKEEIFGPVVTVAK.F +2		4.7356	4.1831	4.7763									3.5818	4.4869	3.0534	4.1418	4.6901		4.6512	4.1693					
R.IVKEEIFGPVVTVAK.F +3																	3.924								
R.IYVQEGIYDELLAAFK.A +2		5.8631	6.2484	6.1846	6.1994	6.0499	6.2365	6.1595	6.2178		3.8516	5.8495	6.1926	5.7431	4.8905	6.1285	3.7732	3.7716	4.4926	6.2049					
R.IYVQEGIYDELLAAFK.A +3														4.576											
R.KLAFTGSTEVGK.S +1																1.8701									
R.KLAFTGSTEVGK.S +2		4.0943	4.1012	3.9446							3.1944	2.7168	3.0952				3.8697					2.8377			
R.PTVFYDVNEDM*R.I +2										3.0219			3.3355	3.99		2.9398								3.2616	
R.PTVFYDVNEDMR.I +2						3.5296	3.2716			2.7736	3.7751			3.0779		2.5904								3.2055	
R.QQFDTIM*NYIDIGK.K +2										3.1795		3.3606	3.4781	3.5643	3.158	3.3128			3.2937		3.3789				
R.QQFDTIMNYIDIGK.K +2					3.7842	3.1493		3.7772	3.6983		3.0458	3.3642		2.9304	3.8964	3.8628									
R.QQFDTIMNYIDIGKK.E +2													3.1663	2.5174											
R.TVGAALTNDPR.I +2	4.16	4.0152	4.0575	3.6875	3.7199	3.758	3.7664	3.9967	2.5266	3.944	3.6593	3.5284		3.5632	3.296	3.281		2.737							
R.VPFGGVK.Q +1	2.0465	2.0072	1.9992	2.0311	2.0685		1.9234	2.0045		2.0004	1.9877		1.927	1.9321	1.9452	2.0421	1.8898		1.8077				1.8958		
gi|6325331|ref|NP_015399.1|	6.9	10.3	13.5	10.7	19.3	20.7	19.7	30.9	32.5	11.8	18.2	23.7	29.7	20.7	28.8	30.6	17.9	17.4	15	27.1	8.5	4.3	12.9	7.8	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids; Tkl1p [Saccharomyces cerevisiae]
K.EALDFQPPSSGSGNYSGR.Y +2					4.8718	4.7058	4.6824	4.492	3.9556	4.0667	4.41	4.5304	4.5213	4.4794	4.2235	4.6482	3.9877	3.4917	3.9398		2.9179	4.2457	4.1957	4.2651	
K.FFGFTPEGVAER.A +2	3.7916	4.1623	4.0021	4.1011	3.7912	3.8897	4.0717	3.8717	3.7598	3.5584	3.8369	3.6353	3.694	3.9569	3.8806	4.0561	3.7004	3.5289	3.1344				3.9701		
K.FGFNPDK.S +1																							1.9153		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.FPELGAELAR.R +2						2.5513								2.8522	3.1904	2.9971	3.6094	2.7425	2.7341	3.3859					
K.ITIDGATSISFDEDVAK.R +2					2.8504	4.0797	5.0221	4.3881	2.7484			2.875	3.4882	2.8625	3.3294	5.3725		4.7043		2.7241					
K.KFPELGAELAR.R +2		2.612											2.6492			2.6839									
K.LGNLIAIYDDNK.I +1									2.6739												1.9135				
K.LGNLIAIYDDNK.I +2			3.9711		4.3445	4.426	4.3131	4.0934	4.057	3.5478	4.2161	3.8364	4.4879	4.29	4.1762	4.5701	4.3448	4.0126	3.821	4.2075	3.9997			4.0803	
K.LSETVLEDVYNQLPELIGGSADLTPSNLTR.W +3								3.731	4.054			5.0307				4.4116									
K.PYGGTFLNFVSYAAGAVR.L +2															3.1163				5.7536	5.8279					
K.PYGGTFLNFVSYAAGAVR.L +3																			4.0798	4.7075					
K.SFVPPQEVYDHYQK.T +2				3.7424					3.9781				4.0764	3.9707	3.4903	3.8061	3.8012	4.0177		3.4724					
K.TILKPGVEANNK.W +2	2.8661	3.4011	3.4235	3.6035	3.2481	3.2316	3.0715	2.9722	2.9532		3.3957	3.2004	2.8946	3.3916	2.899	3.0173	2.9355				2.5747				
K.YAHQSFGIDR.F +1															2.213		2.517	2.442							
K.YAHQSFGIDR.F +2		2.8612	2.9898	2.9568						2.8436	2.6793		2.98		2.5062	2.7944									
R.EHAM*GAIM*NGISAFGANYK.P +2																			3.3405						
R.EHAMGAIMNGISAFGANYK.P +2																				3.4049					
R.ILAVDTVSK.A +1						2.3931					2.0002									2.2568					
R.ILAVDTVSK.A +2					2.6837																				
R.LSGQLPANWESK.L +2					3.622	3.9288	4.0817	3.4112	3.2604	3.1605	3.2794	3.5897		3.8585	3.452	3.5355							3.2571		
R.LSVLPDNVPIM*SVEVLATTCWGK.Y +3													3.9375												
R.LSVLPDNVPIMSVEVLATTCWGK.Y +2								3.4278	2.5533																
R.M*NPTNPDWINR.D +2													3.1865									3.3227	3.0196		
R.MNPTNPDWINR.D +2	3.2871				3.3194	3.1673	2.8421	3.0568	3.0649		3.0509	2.7237	3.3807		3.2273	2.5544	2.841							2.841	
R.PADGNEVSAAYK.N +2							3.0264	2.9103					2.9388			2.684									
R.QNLPQLEGSSIESASK.G +2					4.561	4.3431	4.493	4.4062	4.254	4.2792	4.1686	4.4485	4.2181		4.586	4.4973		4.0183		2.9136	4.4293		3.8552		
R.RLSGQLPANWESK.L +2		3.9781	4.0797	3.7316									3.5039	3.6743	2.5309				3.614	3.8022					
R.SLPNIQVWR.P +2									2.5247			2.8535				2.5939		2.51							
R.SLPNIQVWRPADGNEVSAAYK.N +2			4.8637										4.7566	4.6331	4.5505	3.1388	5.2262			3.5391					
R.VVSLPDFFTFDK.Q +2	3.2102	3.6696	3.6897	3.4329	3.4619	3.4699	3.7374	3.6361	3.135		3.0657	3.3675	2.9402	3.5739	3.12	3.2478				2.7817			3.0965	2.7067	
R.WKEALDFQPPSSGSGNYSGR.Y +2																	4.1317								
R.YEAYGWEVLYVENGNEDLAGIAK.A +2								2.9256	4.4567											2.708					
gi|6325403|ref|NP_015471.1|	6.1	17.5	8	7.3	19.9	25.3	27.4	25.3	36	18.9	21	25.5	22.7	29.9	30.1	32.3	21.7	16.3	14.7	30.8	19.4	11.4	7.9	11.5	Asparagine synthetase, isozyme of Asn2p; catalyzes the synthesis of L-asparagine from L-aspartate in the asparagine biosynthetic pathway; Asn1p [Saccharomyces cerevisiae]
K.ADWGCAEDPSGR.Y +2	3.8202	3.7717	3.7242	3.4991			3.3801	3.6992	3.816		3.5754	3.6515	2.9243			3.3413				3.6379		3.5283			
K.AEWGSDIPTTK.E +1																				2.4237	2.5904			2.0845	
K.AEWGSDIPTTK.E +2		2.8336	2.8255	2.6715		2.8356	3.1494	3.0675	3.1038	3.3491	2.9245			2.8459		3.4183			3.4351			3.1078			
K.AFDTTGEPDAKPYLPEEILWR.Q +2													3.7581	4.1403	3.4236		3.7438			3.3023					
K.AFDTTGEPDAKPYLPEEILWR.Q +3													4.792	5.235	4.0007		4.3513			3.7572					
K.ATNDVEPSTYDSK.A +2	4.2616	4.361	4.1182		4.4005	4.3097	4.2612	4.4595	4.2281	2.9463	3.9553	4.1243	4.3482	4.2585	4.3074	3.8706			2.8268				4.0852	4.1938	
K.DTAEAVISDEM*FASPK.A +2										3.7501								3.9528			3.88				
K.DTAEAVISDEMFASPK.A +2		3.4806			5.2967	5.0803	4.7462	4.7321	4.8055		3.9944	4.2781		4.2861	4.707	4.6726	4.5885	4.3672		4.6314	3.4733	4.9324		4.6447	
K.EQFSDGVGYSWIDGLK.D +2		4.3266			4.7128	4.7577	4.6565	4.9483	4.7971	4.0782	4.5757	4.3268	4.881	4.8049	4.7722	5.0181			3.4019	4.2906	2.9022	4.13		3.0952	
K.FDALFPQK.T +1																				1.8834	2.0456				
K.FDALFPQK.T +2					3.082	3.1153	3.2266	3.3157	3.2454	3.0819	2.9228	3.2347	3.0346		3.1785	3.0709	3.1495	3.0565							
K.M*VLSGEGSDEIFGGYLYFAQAPSAAEFHTESVQR.V +3														5.9927											
K.NLHLADCLR.A +2				2.5113															2.526	2.5188					
K.NSTIFVHER.L +2		2.7634							2.7517																
K.RIPSTPIDYMAIR.H +2		4.0028																							
K.STM*AWGLEAR.V +2																					3.1738				
K.STMAWGLEAR.V +2						3.6017	3.8204	3.5177	3.6293	3.1416	3.8449	3.319	3.4923	3.7411	3.6132	3.7301	3.6608	3.6384		3.9405		3.7125	3.6433	3.6189	
K.YLDGM*FAWTLYDAK.Q +2													4.4196	3.6078	3.9189	3.3275					3.6667				
K.YLDGMFAWTLYDAK.Q +2					2.648			2.5327	3.7186								4.0162	2.6723		4.7274					
R.ASTPMFLLSR.K +2																	2.5764								
R.DPIGITTLYM*GR.S +2										3.2955	3.2793	2.9971						3.7207			2.6628				
R.DPIGITTLYMGR.S +2						3.8161	4.1518		4.6865		3.2629	2.9858			3.8472		3.8373	3.461							
R.EECADYEFGTLSDCEPIIPM*YLK.H +2						2.5495	2.9072	3.4418	3.2226			3.2453				3.4647		3.6666	3.9511	3.1029					
R.EECADYEFGTLSDCEPIIPMYLK.H +2					2.6398	3.3181			3.1245								3.8857	2.9996		3.0284					
R.EFLQLCMNIDPNEK.M +2					3.2514		4.2435		4.0917			3.38			3.7191	4.481				3.747	3.2803				
R.IPSTPIDYM*AIR.H +2									2.6849	3.0185						2.6976			2.7291						
R.IPSTPIDYMAIR.H +2							3.5455	3.4302	3.2067		2.9269	3.0593			3.2165	3.0913				2.5649			2.9707		
R.LM*AEVPYGVLLSGGLDSSLIASIAAR.E +2						2.5044			2.5832							2.7855									
R.LM*AEVPYGVLLSGGLDSSLIASIAAR.E +3													4.7023	5.0268	4.1959										
R.YFTPDWLDEK.R +1									1.9003							2.4137	1.9628	2.1642			2.2496				
R.YFTPDWLDEK.R +2	3.2332	3.2755	3.2128	3.0686	3.1303	3.1192	3.1828	3.1394	2.8689	2.942	2.9165	2.8231	2.9446	2.6385	2.7018	2.696	2.5919	2.939		3.2126			2.9541		
gi|86558907|ref|NP_012211.2|	24.8	34	42.8	42.4	43.2	43.6	46.8	40.4	46.8	29.6	44	44	52	52.8	54.8	52	28.4	40	33.2	48.4	20.8	26	29.2	20.8	Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress; Rhr2p [Saccharomyces cerevisiae]
K.FAPDFADEEYVNK.L +2					4.2152	4.3295	4.382	4.4485	4.0437	4.3139	3.9827	3.6363	4.0365	4.2837	3.5104	3.4362						4.1347	4.1395		
K.FAPDFADEEYVNKLEGEIPEK.Y +2		5.4539	5.5005	4.8848					5.1559				4.845	4.7482	5.2885	4.9576	5.0492		4.7821	5.4471					
K.IKRPEYFITANDVK.Q +2														3.6852											
K.IVGIATTFDLDFLK.E +2	3.9668	4.2819	3.8008	4.5877	4.8408	4.704	4.778	4.8256	4.5255		3.7761	4.5012	4.8521	4.8724	4.4548	4.5972		4.2268	4.5004	4.2842				2.8112	
K.LCNALNALPK.E +2	3.7649	3.4967	3.6811	3.5156	3.8074	3.8095	3.7674	3.8075	3.5004	3.4855	3.8238	3.3629	3.3003	3.6001	3.5937	3.4514	3.0069	3.6387		2.9686	2.5448	2.9821			
K.LEGEIPEK.Y +1																2.5835									
K.RPEYFITANDVK.Q +2		3.9593	4.3415	3.9398		2.7876			2.532				3.0525	4.1688	3.5924	3.8625	3.7709	3.0781	3.4929	4.1611					
K.VVVFEDAPAGIAAGK.A +1							2.791		3.5355				3.1675			3.1926				2.6006	3.8164				
K.VVVFEDAPAGIAAGK.A +2	4.7068	4.6805	4.6297	4.9628	4.8809	4.7285	4.6705	4.9685	4.653	4.8024	4.5123	4.6645	4.5359	4.5843	4.5203	4.4723	4.4766	4.6458		4.8665	3.6776	4.3194	4.6745	4.2433	
K.WAVATSGTR.D +1														2.3528	2.1359				1.9021				1.8435	1.8888	
K.WAVATSGTR.D +2	3.0522					3.0239	3.0717		2.9349	2.9203	3.1883	2.9321	2.5089	2.9052	2.8264	2.9322			2.7985						
K.YGEHSIEVPGAVK.L +1											2.819						3.4997					2.6502			
K.YGEHSIEVPGAVK.L +2		4.1816	4.2998	3.8564	4.2884		4.0785	3.8268		4.1095	4.2843	4.1257	4.3055	4.1748	4.0832	4.1639	4.0747	4.1165	3.8712	4.2596	3.9603				
R.NGLGFPINEQDPSK.S +2	3.2259			2.9049	4.0704	3.7452	3.323	4.3486	3.0771	3.8291	3.5481	3.5569	3.4814	3.7691	2.8409	3.0078		2.9736	3.3023	3.3593	3.0161	2.8172	3.0118	3.8675	
R.TYDAIAK.F +1				1.8725	1.9674		1.8717								1.9461										
R.VGEYNAETDEVELIFDDYLYAK.D +2			6.1795		5.7039	3.4528	5.9164	5.328	5.5708		4.3145	4.8776	6.0203	6.2269	5.8516	5.9871		5.3653		5.3578			4.1103		
R.VGEYNAETDEVELIFDDYLYAK.D +3													5.0628	4.4366	3.6415	4.1927									
gi|9755341|ref|NP_013863.2|	35	40.6	40.6	46.2	40.6	30.8	25.2	46.2	40.6	40.6	25.2	35	40.6	40.6	46.2	46.2	18.9	35	39.9	35	35	20.3	28.7	18.9	Protein component of the small (40S) ribosomal subunit; identical to Rps16Bp and has similarity to E. coli S9 and rat S16 ribosomal proteins; Rps16ap [Saccharomyces cerevisiae]
K.GLVAYHQK.Y +2		2.789	2.9429	3.0325				2.754		2.6258					2.603	2.5344			2.6843						
K.SATAVAHVK.A +2	2.9283	3.0639	2.9661	3.1623	2.8782	2.9198	2.9464	2.9315	2.8224	2.717	2.7403	2.7997	2.7693	2.6359	2.7817	2.7962		2.5729		2.7515	2.7258	2.8306			
K.VNGSPITLVEPEILR.F +2	5.0605	5.1015	5.1561	4.9685	4.8036	5.161	5.0856	5.0651	4.3443	4.6229	4.9145	4.6731	4.5315	4.6083	4.8052	4.6147	3.4533	4.1966	3.4972	3.8504	4.0556		3.8633	2.6736	
K.VYEPLLLVGLDK.F +1									2.5781						2.4778		2.3832	2.1621	2.0989	2.1819	2.6217				
K.VYEPLLLVGLDK.F +2	4.412	4.6475	4.4836	4.6378	4.46	4.4525	4.4206	4.4043	4.1859	4.1083	4.2297	4.2659	4.1894	4.2446	4.2055	4.3953	4.2442	4.2604	3.985	4.1461	3.7578	4.0998	3.9075	4.1323	
R.TLLIADSR.R +1				2.159	2.1735	2.3045		2.1425	2.5351				2.5692	2.0932	2.191	2.2675			2.0882			2.4511			
R.VTGGGHVSQVYAIR.Q +1									2.4689						2.1955			2.63		3.3322	1.8376				
R.VTGGGHVSQVYAIR.Q +2	4.1406	4.3521	4.3248	4.4961	3.5443			4.4135	3.9931	4.0011		2.8493	4.1921	4.2837	4.4183	4.1676			4.2418	3.1121	3.9767		3.0557		
111	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|14318474|ref|NP_116609.1|		10.2	15.7	11.4	20.5	20.5	21.3	20.5	26	11	26.8	22.4	19.3	23.2	24.8	25.2	26.8	13.8	11.8	26	16.1	15	17.3	11.8	Phosphomannomutase, involved in synthesis of GDP-mannose and dolichol-phosphate-mannose; required for folding and glycosylation of secretory proteins in the ER lumen; Sec53p [Saccharomyces cerevisiae]
K.CCIGFVGGSDLSK.Q +2					4.3079	3.7597	3.8763	4.1562	4.1168	3.4097	4.2606	4.0135					3.5109								
K.EKPETLVLFDVDGTLTPAR.L +2														5.0855	3.267					3.055					
K.ELASQSFINWLGEEK.Y +2		4.8326	4.9379	4.7736	4.3536	4.7353	4.4959	4.978	4.4088		4.5395	4.2982	4.8789	4.6128	4.3113	4.3918	4.1834		3.0862		4.83		4.4933	3.8176	
K.ELASQSFINWLGEEK.Y +3																			3.6798						
K.LAVFILR.Y +1																				1.8805					
K.TM*VGGNDYEIFVDER.T +2										4.6402		3.6613						2.8608	3.7773						
K.TMVGGNDYEIFVDER.T +2					4.9891	4.8628	4.3066	4.6904	4.7946		4.1053	4.1001			4.4823	4.7929	5.0143	4.6555		4.1093	3.4224	4.9047	4.4859	4.4977	
K.TYCLQHVEK.D +2													2.7528												
R.NGM*INVSPIGR.N +2													2.5921	3.863											
R.NGMINVSPIGR.N +2		3.4238	3.4361				2.8845				2.7534			3.2821		3.2542	3.2902	2.9283		2.7987	2.8103				
R.TIGHSVQSPDDTVK.I +2			4.3088	4.6481					3.0158		3.515	2.5502	4.2665	4.3792	4.0793	4.5968	4.3088			4.1598		3.1527	4.4752		
R.YLSEIDLPK.R +2					3.1421	2.6236		3.0065	2.8233							2.983		3.0368				3.0993			
gi|6319603|ref|NP_009685.1|		22.2	16.6	7.7	27.3	30.6	40.2	40.6	54.7	30.4	38.5	46.4	50.9	53.2	40	46.4	27.5	18.6	28.4	38.5	22.2	8.5	26.5	24.6	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also detected in the cytoplasm; Vma2p [Saccharomyces cerevisiae]
K.AVEQGFNVKPR.L +2		2.9185	3.0085						3.206			2.8961	2.9069	2.7421	2.9684	3.1798	2.7036		2.8126	3.2194	2.733				
K.AVVGEEALSIEDK.L +1									2.7729																
K.AVVGEEALSIEDK.L +2					3.5284	3.8148	3.4222	3.4451	3.3215	4.2939	4.1252	3.6858	4.1287	4.0772	4.2079	4.0437				3.3999			4.4241		
K.DHGDVSNQLYAK.Y +2		3.5882							3.5566		3.3588	3.3633	3.9016		3.1422	3.8117			3.5377						
K.GIYPPINVLPSLSR.L +2		2.9076		2.6002			2.8365	3.3496	2.6332	2.6274		3.0552		2.8574										2.9035	
K.ILDEFYDR.A +2						2.7845		2.6159	2.7521		2.6035														
K.IPIFSASGLPHNEIAAQICR.Q +2														5.9734					4.3318						
K.KAVEQGFNVKPR.L +2													2.8078												

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.KTTVEFTGESLR.I +2													2.8164	2.8467						3.2772					
K.LSLEFLEK.F +2									2.5407			2.7849	2.5894			2.6686	2.5466		3.0528				2.771	2.5757	
K.QDFEENGSLER.T +2		3.2266	3.126					3.4548				3.4726	3.54			3.8146		3.7758							
K.SAIGEGMTR.K +2																	2.7251								
K.TFITQGAYEDR.T +2				3.4385	3.735	3.5178	3.3757	3.5051	3.1854	3.5847	3.5066	3.45		3.4645	3.5853	3.6062									
K.TTVEFTGESLR.I +2					3.8942	3.6297	3.7781	3.8754	3.7033	3.672	3.7009	2.9012			3.0118	3.641					3.6537		4.0803		
K.VFAEDYLDINGSPINPYAR.I +2		4.1778			4.873	4.6059	4.6799	4.334	4.6015	3.6548	3.6366	4.4803	4.4289	4.2994	3.6225	4.6155	3.9756		4.2644	4.3525	4.5355	3.1241	4.751	3.9302	
R.AIVQVFEGTSGIDVK.K +2							4.7594				2.8323	4.0761	4.0456	4.6691	4.2966	4.4794		4.5039	4.3516	3.6606					
R.DDADEDEEDPDTR.S +2													3.1137												
R.GYPGYM*YTDLSTIYER.A +2						3.118	3.2139		3.1297	2.5271		3.4817	4.4204	4.3648	4.5553	4.1183		3.5871		2.9877	3.4154		2.5964	3.0227	
R.GYPGYMYTDLSTIYER.A +2			5.2505			4.4256			4.3832		2.7381	2.6925				5.3246	2.964	3.8878		4.5911	5.155			4.2662	
R.HVLTILTDM*SSYADALR.E +2													4.8322	5.8552											
R.HVLTILTDM*SSYADALR.E +3														4.9606											
R.IFDGSGRPIDNGPK.V +2								3.0924	2.963							2.9915				2.9597					
R.IPVSEDM*LGR.I +2																					2.8867				
R.IPVSEDMLGR.I +2					3.2064	3.1852	3.3823	3.2366	2.9614	3.2056	3.1172						2.5353	3.4533			2.8121	3.4155			
R.IYPEEMISTGVSAIDTMNSIAR.G +2						4.5699	3.7756	4.2208	4.2088		2.762	2.7561			3.653	3.8378	4.2305			3.7554			3.0349	3.0374	
R.IYPEEMISTGVSAIDTMNSIAR.G +3																				3.6728					
R.KDHGDVSNQLYAK.Y +2													3.5821	3.6121											
R.LALTTAEYLAYQTER.H +2					4.4571		4.6688	4.7046	4.4505	3.6487		4.1766	4.7169	4.7997	4.4535	4.4349		4.4994	4.4271	4.0559	4.4658				
R.LNYNTVSGVNGPLVILEK.V +2		5.0525	5.333		5.0446	5.4626	5.4601	3.7152	5.1773	4.6172	4.9977	5.4639	5.3937	4.9788	5.3538	5.3192	4.7311		5.1003	4.8975	5.367		4.7247	5.689	
R.LNYNTVSGVNGPLVILEK.V +3													3.9945	4.279											
R.NGSITQIPILTM*PNDDITHPIPDLTGYITEGQIFVDR.Q +3									3.6899				3.9704	4.5891											
R.TSLFLNLANDPTIER.I +2		4.5802	4.6811	4.4483	4.8404	4.9222	4.6645	4.9288	4.8002	4.2616	4.8273	4.662	4.3698	4.6168	4.4176	4.8172			3.6924	4.2461	4.9526		4.357	4.1465	
R.TVFESLDQAWSLLR.I +2					4.6773		4.7526	5.0689	4.997		3.3197	4.5792	5.0442	5.2019	4.9541	4.6025	3.9287	3.1157	3.5085	4.8026					
R.TVFESLDQAWSLLR.I +3																			3.7254						
R.YNEIVNLTLPDGTVR.Q +2		4.6676	4.97		4.615	4.8524	4.8352	4.9645	4.8502	3.9359	4.6202	4.8409	4.3377	4.6959	5.0766	5.0152	4.9489	4.6776		3.5853		4.717	4.848	4.6025	
gi|6319726|ref|NP_009808.1|		13.2	10.5	2.7	13.2	10.5	10.5	23.5	23.5	7.8	10.5	25.7	13.2	32.2	14.3	18.1	20.5	11.6	18.6	27.6	6.8	8.6	18.4	8.9	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by tyrosine or high concentrations of phenylalanine or tryptophan; Aro4p [Saccharomyces cerevisiae]
K.AQLPAGSNGLM*IDYSHGNSNK.D +2																			4.7762						
K.AQLPAGSNGLMIDYSHGNSNK.D +2																	3.9469	4.8495		2.9395					
K.GDLSIMR.A +2												2.9954													
K.GLINDPDVNNTFNINK.G +2		4.1017	3.834		4.864	5.0121	4.9283	4.6011	4.8016	4.6392	4.8033	4.1307	4.684	4.3011		4.1671					5.2062		5.3774		
K.GNEHCFVILR.G +2													3.2411	2.9962	2.8465		2.9612		2.6468	3.2481					
K.HGVAAITTTK.G +1									2.3139				2.6321	2.8014	2.8073			2.1237	2.1498						
K.HGVAAITTTK.G +2		3.7316	3.6197	3.5918		3.0873	3.5267	3.7327	2.9243		3.4227		3.8246	3.0488	3.2341	3.6071	2.9404			2.7055			3.5855		
K.NGTDGTLNVAVDACQAAAHSHHFM*GVTK.H +3														3.6337											
K.VNQGAEEDVR.I +2		3.2535										2.7684					3.0874					3.3079			
K.YGVSITDACIGWETTEDVLR.K +2					4.0252			4.1141	5.1582			3.274		3.5328	4.5433					3.6732			3.306	3.7917	
R.EAIDIITGK.D +1																		2.7274			2.8768	2.9455	2.5803		
R.EAIDIITGKDDR.V +2																	3.0302	3.6632							
R.ELASGLSFPVGFK.N +2		4.0643	4.5798		4.6066	4.4611	4.6669	4.3143	4.4568	3.0742	3.9249	4.0322	3.9938	3.9754	3.9628	4.6309	4.2424			3.4862		4.0423	4.2307	3.6393	
R.ILGYDPLASPALLQVQIPATPTSLETAK.R +2								3.7205	4.1872			3.5618				3.9413			3.5248	3.4498					
R.VLVIVGPCSIHDLEAAQEYALR.L +3														4.1196											
gi|6320077|ref|NP_010157.1|		4	4	3.4	10.8	12.2	12.3	11	20.8	8.7	10.4	15.4	25	31.6	21.9	23.5	15.8	10.3	13.4	18.1	8.6	3.1	12.9	15.8	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Npl4p and Ufd1p participates in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation by the proteasome; Cdc48p [Saccharomyces cerevisiae]
K.AEQEPEVDPVPYITK.E +2					4.7366	4.6306	4.7615	4.771	4.6867	4.0213	4.315	3.9346	3.8526	4.0038	4.1411	4.177		3.6421	4.3189		4.4248		3.6105	4.1834	
K.ATQGFSGADLLYIVQR.A +2		3.5311	3.4535	4.1376			4.8513		5.3546			4.8813	5.355	4.4652		5.222	2.7214		4.7876	3.5086					
K.AVATEVSANFISVK.G +2												4.2965	4.4348	4.696	4.7752	4.5425	4.1851	4.6876	4.4036				4.3791	4.2686	
K.ETVEYPVLHPDQYTK.F +2													4.0948	3.5368	3.2513	3.4098	2.9204								
K.GPELLSM*WYGESESNIR.D +2													4.9763	4.8304	3.0719										
K.GPELLSMWYGESESNIR.D +2																		3.2149					2.9901		
K.LADDVDLEALAAETHGYVGADIASLCSEAAM*QQIR.E +3														6.2555											
K.NAPAIIFIDEIDSIAPK.R +2		4.9029			5.4432	4.8968		4.9208	4.6604			4.8871	4.9001	4.1139	3.4025	4.4576	4.8464		4.6325	2.7453				3.5058	
K.NAPAIIFIDEIDSIAPK.R +3														3.8775											
K.PYFVEAYRPVR.K +2																	2.9894			2.6211					
K.RSVSDAELR.R +2																	2.85								
K.TPLEPGLELTAIAK.A +2					3.333	3.0209	3.3004	3.2508	3.4308	2.6552	2.7986	2.5512	3.4952	3.4177	3.4356	3.6679		2.9669		3.8389		3.3994	2.7839	3.2263	
K.VEGEDVEM*TDEGAK.A +2																								2.9306	
K.VEGEDVEMTDEGAK.A +2							3.4863	3.7104	4.1492				4.4331			4.2416	3.7066								
R.AAAPTVVFLDELDSIAK.A +2			4.8005		5.2065	4.7474	4.6837	5.1138	4.372	4.1901		5.0553	5.3102	5.3361	5.5012	5.4364			4.9391	3.1873	3.1503				
R.AAAPTVVFLDELDSIAK.A +3													5.51	5.8545	5.6672	5.5205				3.7887			4.9964		
R.AVANETGAFFFLINGPEVM*SK.M +2														4.468		2.7432			3.8835	2.7771					
R.AVANETGAFFFLINGPEVMSK.M +2																				2.7773					
R.EDEENNM*NEVGYDDIGGCR.K +2																								2.7951	
R.EDEENNMNEVGYDDIGGCR.K +2									5.1536		4.8844												4.1309	4.7593	
R.EVDIGIPDATGR.L +2					3.1914	2.9475			2.812		2.6221								3.7091					3.2404	
R.FALGNSNPSALR.E +2				3.7917		3.7542	3.8209		3.9018	3.2634	2.793	3.6094	3.8792	3.9934	3.7663	3.6375	3.5844	3.6384			3.3023	3.8926	3.341	3.8866	
R.GGSLGDAGGASDR.V +2																					2.8398				
R.GVLMYGPPGTGK.T +2																2.6268				2.5298					
R.ISVLPIADTIEGITGNLFDVFLK.P +2																				4.5471					
R.ISVLPIADTIEGITGNLFDVFLK.P +3																				5.3569					
R.LDQLIYVPLPDENAR.L +2					4.0033	4.3238	4.0618	3.6045	3.8221	3.7752	3.7655	3.8615	4.1264	4.2512	4.3373	4.1904	3.6146				3.7962			3.382	
R.LGDLVTIHPCPDIK.Y +2									2.9593				3.9803	3.843	3.578	3.6147		3.997							
R.LSILNAQLR.K +2									3.1176			3.5625	3.6183	3.4896			3.287								
R.SNVVVIAATNRPNSIDPALR.+3													4.5629	4.5108	3.9704					4.1136					
R.VVSQLLTLMDGM*K.A +2														3.0133	2.5052										
gi|6321498|ref|NP_011575.1|		4.8	2.8	5.4	9.6	8.5	10.5	10.4	22.5	6.6	9.5	16.8	27.2	23.1	20.3	20.4	18.4	15.8	13.5	27.3	7.5	6.8	8	12.2	Formylglycinamidine-ribonucleotide (FGAM)-synthetase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway; Ade6p [Saccharomyces cerevisiae]
K.ATNIAHVCGLQDK.V +1																	3.0448								
K.ATNIAHVCGLQDK.V +2									3.7748				3.4483	3.5878						3.7469					
K.DIIPGCENWPSFER.N +2					2.6145				2.8326									2.8941							
K.DINSYTNSTSVINELR.S +2					5.3095	5.0978	4.8894	4.3342	5.1635	4.0823	4.4272	4.7858	5.0565		3.8662					4.6373	5.6373	5.6169	5.6553	4.0355	
K.DNSSEESVFLNGMAGSK.L +2										3.6535	4.5425	3.2262				5.2448		3.9566			2.6038	4.5795	5.2868	4.6614	
K.EDIVLAYHDR.S +2											2.6607				2.6725						3.6257				
K.EVTAPLSLNITAFAPVFNTSK.T +2				4.8173	4.7368	4.8899	4.926	5.2317	5.1432		4.193	3.7767	3.6785	4.8868	2.9749	4.0368	4.3052	2.8728	4.5163	4.7288			3.1471	3.021	
K.EVTAPLSLNITAFAPVFNTSK.T +3																				3.6294					
K.EYISIVGKPSFQSQEIK.I +2													3.4512				3.843		3.5457	3.5546					
K.IFNADWTIDGIK.Q +2							4.2873		4.9043			4.0694	4.1381	3.2872	4.1103	4.0056	3.8039	3.6393	4.2501				4.3201	4.2147	
K.IGLELSSQRPK.V +2				2.669																					
K.IINSTTNDVIYANSR.S +2											4.2596						4.9906	5.4349		3.6443	4.7137	4.8081		4.556	
K.LIVEDPLLK.T +1														2.3262	2.388										
K.LPIAVAHGEGK.A +1									2.6967									2.9773							
K.LPIAVAHGEGK.A +2		3.9337	3.9056	4.034				3.6041	3.6524	3.4428	3.1745	3.0579	3.8877	3.853	3.5805	3.4118	3.7585		3.1753	2.9858					
K.LSANWM*SPASHQGEGSK.L +2																			3.758						
K.LSANWMSPASHQGEGSK.L +2															2.6902		3.8972								
K.LSVAESLLNIFAADVK.S +2				5.3094	5.075	5.0374		4.0948	5.1251			3.7575	5.3846	5.5667	4.812	5.3837			3.7467	4.5606					
K.LYEAVQALGLDLCPALGVAIPVGK.D +2									3.7591			4.0248		4.009	2.6588	3.4124				2.7434					
K.LYEAVQALGLDLCPALGVAIPVGK.D +3													5.5047	4.9644	4.8522					3.5398					
K.PSFQSQEIK.I +2											2.728		2.6639												
K.PVNALISASASAK.L +2			3.7827														3.5604	3.3459							
K.QQFTLFQM*IR.N +2																			2.6324						
K.SFLITIGDR.S +2													3.2478	3.2905	3.3481	3.4393		3.2121	3.3129	3.3315			3.0512		
K.SLGASALLQVYNQVGNK.S +2					3.3328			5.0123	4.6266			4.5274	4.8324	5.2805	4.8508	3.2872	3.4326	3.6478		4.7494	3.9883			2.5537	
K.SPTVYDNAILK.G +2									2.6636				2.8935	2.5332				2.8715		2.5962					
K.SVLYHEGVR.S +2																						2.7113			
K.TAEEEFASITDDR.D +2						4.4431						4.0181	2.6311					2.5629			3.3317	4.6086		4.387	
K.TAEEEFASITDDRDPGLQYALTYNPADDM*K.I +3									4.7527							3.7953				5.7051					
K.TAEEEFASITDDRDPGLQYALTYNPADDMK.I +3		6.5423							4.1153																
K.TTPIDLEM*PILFGKPPK.M +2													2.7694	3.249						3.0043					
K.TVPGFPLLENLNDISLK.C +2					3.1026		2.6794	3.9183	2.9952				2.5866	2.6867	2.641										
K.VETHNHPTAVSPFPGAATGSSGGEIR.D +3													5.4202	5.1552											
K.VLSLEPGMSPMEIWCNESQER.Y +2																	3.9028							2.9397	
K.YEEWGGYGPWIR.L +2					3.7567	3.6607	3.4479		2.6552			2.6521	3.5172	2.8212	3.3316	3.5469	3.2996	2.9578	3.6	3.7751					
R.APFAVVGHATAEQK.L +2		5.1747	4.8172	5.127					4.3527	4.0887		4.74	4.8461	4.7982	5.17	5.1221	2.8757	3.4778	4.2417	4.7962	4.0395				
R.DPGLQYALTYNPADDMK.I +2					2.87		2.7128	2.941	2.7117																
R.ERAPFAVVGHATAEQK.L +3																		3.9293							
R.ETITEALNLPEANLSEIPSLQDAIQR.V +2									3.5411																
R.ETITEALNLPEANLSEIPSLQDAIQR.V +3						5.7927	5.4774	5.7	4.9097			5.3222				5.7955	4.5342								

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.FPFNPNGSTNGIAGIK.S +2													2.8657	2.7779	2.9677					3.0606			2.8801	2.8444	
R.GLALLIK.T +1																2.0634									
R.LEANSWYPEGK.Y +2						3.7323	3.1379		3.3099	3.4042	3.4555		4.0059						3.7385						
R.LKDIIPGCENWPSFER.N +2														3.0659											
R.NTDDSVLVLVDLSAK.Q +2													4.3043	4.5948	4.3594	3.2727				4.358					
R.NVSEQYEAR.V +2												2.7098													
R.QDTFAFGACNGCQFLSR.L +2																								2.6446	
R.QLNDAVANNLPSSALGEDTYLIR.V +2									3.7135									3.2979	3.9678	3.7108		3.5361			
R.QLNDAVANNLPSSALGEDTYLIR.V +3													4.0116												
R.SCYIHYVNGIAQNLSEQDTK.L +2																	4.2401			3.167					
R.SDGGLLITLLEM*AFASR.C +2																3.3446				3.5619					
R.SELEQTWSK.T +1																				1.8347					
R.SELEQTWSK.T +2											2.9937	2.9855													
R.VCMVQISQEK.D +2										3.0521	2.7565														
R.VLAM*M*PHPER.V +2										2.7669															
R.VLAMMPHPER.V +2		3.0331											2.946	3.0506	2.8302		2.7451	3.3013		2.8123					
R.VLNLPSVGSK.S +1																			2.2554						
R.VLNLPSVGSK.S +2							2.627												2.7958						
R.YVDNYGNVTER.F +2												3.1567	3.4595	3.0653	3.0562	3.405	3.317								
R.YVLGVSPQDLSIFEEICK.R +2									4.0816				3.5581	5.1003	4.8736	4.1033				2.8843			2.5215		
gi|6322581|ref|NP_012655.1|		13.3	8.2	5.3	19.4	21.7	19.2	25.8	39.5	11.4	20.5	26.2	48.7	47.6	36	36.8	19	28.8	15.9	37	13.3	5.1	16	34.1	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; Atp2p [Saccharomyces cerevisiae]
K.AHGGFSVFTGVGER.T +2													3.947	4.8145	3.7934										
K.ETGVINLEGESK.V +2		3.1935																2.7432							
K.IGLFGGAGVGK.T +1															1.911	1.8062									
K.IGLFGGAGVGK.T +2									3.1061		3.0791		3.4138	3.276	3.1287	3.3751	2.6869	2.6841		2.833	2.8572		2.6882	2.8611	
K.LVLEVAQHLGENTVR.T +2													5.3987	3.6394					3.1997	2.6845					
K.SLQDIAILGM*DELSEQDK.L +2														2.5226		3.5122			4.8983						
K.TVFIQELINNIAK.A +2					4.4486			2.8725	4.4391			3.6377	4.6897	4.969	4.621	3.199		3.4723	3.8504	4.7494				2.8617	
K.VALVFGQM*NEPPGAR.A +2									4.1711	3.1072		3.2973	4.786	2.8582						3.0565				2.7058	
K.VALVFGQMNEPPGAR.A +2			2.5498		3.4153	2.8587	2.7213	4.0139	2.8921	2.565	4.0178	3.3617		3.6546	3.7835	3.7687		3.3223		4.9118			3.1779	3.8347	
K.VLDTGGPISVPVGR.E +2		4.5716	4.4677	4.0214		4.4268	4.4604	3.8785	4.6125	4.4085	4.2128	3.8957	4.2614	4.1635	4.3444	4.2142	4.1451	2.9957		4.5848				3.4659	
K.VQETLQTYK.S +2									2.8809			2.8181													
K.VVDLLAPYAR.G +2					3.57	2.6924	3.4801				2.7076	3.1303	3.4266	3.4558	3.4082	3.4189	2.9262	3.5983		2.7588	3.3008			3.2423	
K.YDNIPEHAFYM*VGGIEDVVAK.A +2															3.9363										
K.YDNIPEHAFYM*VGGIEDVVAK.A +3													5.5892												
R.DEEGQDVLLFIDNIFR.F +2					4.4742	4.6287	4.8133	4.6876	4.7758			4.6765	4.2248	4.5655	2.7883	4.5938				3.7003				2.8994	
R.FLSQPFAVAEVFTGIPGK.L +2					3.3393			3.4922	3.9549			3.1521		2.6329		3.0724				2.9731				2.5643	
R.FLSQPFAVAEVFTGIPGK.L +3													3.5435												
R.FTQAGSEVSALLGR.I +2					4.1043	4.6454	4.7236	4.582	4.2563		3.634	3.8386	4.4484	4.333	4.4398	4.4914		4.069		3.6754	4.4895	4.7481	4.2633	4.4675	
R.GISELGIYPAVDPLDSK.S +2		3.7866				3.4336	3.2213	4.2631	3.988	3.6143	3.4026			3.6546	3.7835	3.7687		3.9032					4.0338	2.9298	
R.IINVIGEPIDER.G +2		3.9102				4.124	4.184	4.0661	3.9153	3.6809	3.7552	3.8839	3.8834	4.0454	3.8185	4.2663	3.6795	3.2412			3.1186			3.6456	
R.IPSAVGYQPTLATDM*GLLQER.I +2													4.2684						3.4296						
R.IPSAVGYQPTLATDMGLLQER.I +2									3.2054								3.2197			2.7457	3.696			4.1995	
R.KPIHADPPSFAEQSTSAEILETGIK.V +3													4.0028	4.6214											
R.LLDAAVVGQEHYDVASK.V +2									3.0434				5.1274	4.8942	4.9994	4.8426	4.9749	3.7563		3.9113					
R.TIAMDGTEGLVR.G +2									3.9417		3.6956				3.3984	3.704	3.141	3.5047		3.1975		3.7872	3.5351		
R.VALTGLTIAEYFR.D +2		2.9258	3.3254	2.8283	3.5809	3.8655		3.501	4.7365			3.9981	4.6603	3.9968	3.8716				4.0775	2.7375			3.2518	2.6077	
gi|6324533|ref|NP_014602.1|		16.9	38	16.9	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	16.9	21.1	21.1	30.3	7.7	16.9	21.1	16.9	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S19 and rat S15 ribosomal proteins; Rps15p [Saccharomyces cerevisiae]
K.LAAPENEKPAPVR.T +1																						2.4919			
K.LAAPENEKPAPVR.T +2		3.8167	3.5285	3.6152	3.4095	3.8628	3.9921	3.4787	3.3562	3.1467	3.791	3.654	3.5339	3.6909	3.5317	3.3819	3.6181			3.1474		2.6083		3.1174	
K.LLEM*STEDFVK.L +2					3.4863	3.7185				3.5649	3.4434	3.247	3.6099	3.5318	3.187		2.6797		3.628	3.4143	3.3875	3.6782			
K.LLEMSTEDFVK.L +1																2.4829	2.4819	2.8342		2.7535					
K.LLEMSTEDFVK.L +2		3.6446	3.7816	3.9331	4.0082	3.9739	3.9848	4.0732	4.0276	3.6882	3.8889	3.7735	3.5499	3.7755	3.906	3.9993	3.7744	3.8146	2.7397	3.9252	3.6348	3.5066	3.9009	3.8931	
R.GMTSKPAGFMK.K +2			2.9536																						
R.NMNIVPEM*IGSVVGIYNGK.A +2						2.7543			4.1215	3.9849	4.3954	4.3696	5.6829	5.3559	4.011	4.4078							3.8398		
R.NM*IIVPEM*IGSVVGIYNGK.A +3													5.5284	5.1001	4.4349										
R.NM*IIVPEMIGSVVGIYNGK.A +2					3.7655		4.8548	4.9276	5.1654		3.5852	5.2582		4.9434	4.2927	5.5395		3.3195	5.0934	3.4374			5.3519		
R.NMIIVPEM*IGSVVGIYNGK.A +2											3.79	3.8654								4.5193					
R.NMIIVPEMIGSVVGIYNGK.A +2			2.9852		6.1154	3.4437	6.0144	6.3389	6.0738			4.8542				5.113		3.2886		3.6528			4.7133		
gi|82795241|ref|NP_009845.2|		4.3	8.4	4.3	6.3	6.3	6.3	6.3	11.5	6.3	9.7	14	20.1	23.3	18.1	16.4	19.7	11.9	9.1	25	13.8	5.8	11.5	12.1	Vacuolar aminopeptidase Y, processed to mature form by Prb1p; Ape3p [Saccharomyces cerevisiae]
K.DYASVVPPR.H +2											2.5941														
K.EGLHGTLGEPTK.H +2		2.6831	2.7448	2.9356									2.6686	2.7842	2.5398	2.7637	2.6639								
K.FGFTAVVIYDNEPK.S +2												3.4903	4.8267	4.9737	4.2822	4.4909				3.895				2.7713	
K.HGDPDNIVALGAHSDSVEEGPGINDDGSGTISLLNVAK.Q +3														6.728						4.5346					
K.HTVATVGVPYK.V +1															3.3262		3.1572	2.9075		2.6807					
K.HTVATVGVPYK.V +2		2.9366	3.3235	3.1461					2.9932				3.1836	3.122		2.9144	2.8297			2.6287			3.477		
K.LIAHSVATYADSFEGFPK.R +2												4.4419	5.25	5.6304	5.1856		2.7849		2.7607	4.2759					
K.LIAHSVATYADSFEGFPK.R +3																				3.6556					
K.LVEIPNLGCEEK.D +2					3.8148	3.7584	3.9009	3.7571	3.6762	3.4315	3.6083	3.4019	3.2058		3.8699	3.5772	3.5784				3.2829		4.0198	3.7909	
K.NLYVDYYK.A +1									2.5044				2.7354	2.6553	2.6885	2.5427	2.3583	2.8188	2.6795	2.547	2.5707		2.4867	2.4955	
K.SKEGLHGTLGEPTK.H +2													3.1829	2.6046											
K.TQNIIADTK.H +1																					2.3052	2.3165	2.514	2.5556	
K.TQNIIADTK.H +2									2.8437		2.9997	3.1184	3.45			2.6944									
R.SDYVGFINNGIPAGGIATGAEK.N +2			5.2952		5.5203	5.6858	5.9092	5.5862	5.5474	4.5268	4.823	5.7058	5.4877	5.6292	5.1272	5.8457	5.2225	3.9032		4.4164	4.4053	5.9958	5.9876	5.3348	
R.SDYVGFINNGIPAGGIATGAEK.N +3													4.4853												
R.VFM*DYDM*M*ASPNYEYEIYDANNK.E +2																			4.1526		2.912				
R.VFMDYDMMASPNYEYEIYDANNK.E +2																	3.7652	4.1732		3.0995					
8		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|10383761|ref|NP_009900.2|	3.5	8		4.9	13	13	11.3	11.6	23.9	10.1	11.3	13.3	29.4	25.4	23.9	19.4	13.5	8.1	7	23.2	8.8	4.9	8.6	4.6	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase, phosphoribosyl-AMP cyclohydrolase, and histidinol dehydrogenase activities; catalyzes the second, third, ninth and tenth steps in histidine biosynthesis; His4p [Saccharomyces cerevisiae]
K.EALDLSIENVR.K +2					3.2617		3.4445		3.6354		3.2078	3.2917	3.0248	3.5408	3.4508	3.4996				2.8763	3.5146			3.6393	
K.EEEVPLVALSLPSGK.F +2	2.6034			3.126	4.3628	4.5839	4.4254	4.4522	4.3821	4.1369	3.7647	4.2752	4.3166	4.139	4.4922	4.0732	3.1532	3.6534			3.744		3.8597	3.7795	
K.FHAAQLPTETLEVETQPGVLCSR.F +3		5.0965													4.4189										
K.FITAQNITPEGLENIGR.A +2		4.7985			4.7083	4.055	4.971	5.1022	3.6783	4.5898	4.3051	4.4031	4.8926	5.1364				4.9761	5.4021	3.3528		3.1987	4.9553		
K.FITAQNITPEGLENIGR.A +3													4.6571												
K.FIVEQENVGFCHLETM*SCFGEFK.H +3														4.846											
K.FSDDEIIAFLNNGVSSLFIASQDAK.T +2																				3.4548					
K.FSDDEIIAFLNNGVSSLFIASQDAK.T +3														4.3423											
K.GNSALLEYTEK.F +2						3.7418			3.1538	2.6529	2.8324						3.4258								
K.HGLVGLESLLK.Q +2														3.2317						3.1019					
K.IKEEAEELTEAK.G +2																			2.73	3.3783					
K.ILGPGNQFVTAAK.M +2	3.63	4.0695		3.9222	4.3465	3.8147	4.1715	4.2871	4.1475	2.7348		2.8457	3.953	3.9511	3.5331	3.8418	3.7002								
K.IQEIQDAVHNQALQLPR.V +2									5.0711				5.4203	5.2864	4.7252	5.4119									
K.IQEIQDAVHNQALQLPR.V +3									4.0811				4.4916	4.4314	3.9813	4.0352									
K.IVLAGGAQAVAAM*AYGTETIPK.V +2																					4.9043				
K.IVLAGGAQAVAAMAYGTETIPK.V +2																				2.703					
K.LLQSTDCDSDALK.F +2					4.4284	4.2683		4.6296	4.1657	3.4723	3.8923	3.9883	3.4898			3.8849							4.5291		
K.LSNPVLNAPFPEEYFEGLTEEM*K.E +3													3.7645												
K.LSNPVLNAPFPEEYFEGLTEEMK.E +2					3.8387	3.6606	3.4641	3.4813	3.3644							3.5939									
K.LSNPVLNAPFPEEYFEGLTEEMK.E +3					4.2285		3.5173		3.5052																
K.LTGPIHLDVVK.A +2		3.3247		3.3336									3.8649	3.6777	2.9646	3.3004			3.008	3.0556					
K.LVDNAGSVFVGAYTPESCGDYSSGTNHTLPTYGYAR.Q +3									4.8705				4.1206		5.3643		4.8221			4.4395					
K.TAEHLVEQLNVPK.E +2												3.0238	3.9966	3.9589	3.9191	3.665	3.9966	3.7353		3.6696					
K.TSEIM*HLVNPIIENVR.D +2													3.2054	3.2041					2.7429						
K.TSEIM*HLVNPIIENVR.D +3													4.8928												
K.TSEIMHLVNPIIENVR.D +2																				2.7945					
K.VSPEVVYVAEK.V +1																					2.1575				
K.VSPEVVYVAEK.V +2									6.2645					2.6521											
R.CLGLVYSSK.K +2													2.5277	3.1813		2.7115	2.5077	2.5214							
R.LFNDSALLDAK.I +2					4.1789	4.046	4.3763	4.2389	4.457	3.2872	3.6994		4.0563	4.6196	3.4271		3.6479	4.3597		4.5463	4.1182	4.0455		4.2265	
R.LQDAPEESYTR.R +2											3.3044	3.2716	2.8908		2.9652	3.0685						3.2834	3.0647		
R.QYSGANTATFQK.F +2									2.8627			2.6493			2.9356								2.9473		
R.TDRPDGLYTTLVVDQYER.C +2													4.1674		2.9883	4.2982									
R.TDRPDGLYTTLVVDQYER.C +3													3.9285												
gi|6321721|ref|NP_011798.1|	7.3	11.5		12.8	12.1	4.2	19.5	15.7	16	10.9	19.5	19.5	16	19.8	19.8	19.8	13.1	12.5	12.8	12.8	8.9	16.6	12.8	8.9	Endo-beta-1,3-glucanase, major protein of the cell wall, involved in cell wall maintenance; Bgl2p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.AALQTYLPK.I +2					3.2083		2.8007	2.9018	3.0112	2.8902	2.7346	3.0107	3.0921	2.9565	3.1367	2.7903									
K.ESTVAGFLVGSEALYR.N +2				2.8801	4.6979		5.4875	5.0664	4.9383		4.2668	4.8283	5.2364	5.2844	4.8654	5.1032	3.0335	4.0023	4.8482	4.5385	4.8742	3.1602	3.9688	5.0889	
K.HWGVFTSSDNLK.Y +2													3.6046	3.315	3.3379	3.1089			3.2032	2.8208					
K.STSDYETELQALK.S +2		4.3178		4.9094	4.9075	4.8713	4.9142	4.7199	4.6933	4.2827	4.8562	4.6588	4.7911	4.7393	4.697	4.4678	3.5954					4.7321	4.7344		
R.NDLTASQLSDK.I +1																							2.8284		
R.NDLTASQLSDK.I +2	3.7796	3.6435		3.6522			3.6549	3.6394			2.8643	2.7926						2.8782				3.6444			
R.SVVADISDSDGK.S +1																	2.8531	2.6049	3.4303	3.1117	2.7808	3.0766		2.3169	
R.SVVADISDSDGK.S +2	3.9891	4.1383					3.5237		3.5238	3.5112	3.6818	3.82		3.7313	3.8296	3.9833			3.9347						
gi|6323768|ref|NP_013839.1|	3.5	6.6		6.9	17.9	28	28	32.3	37.8	24.3	22.1	39	42.1	50.7	42.7	38	20.1	18.8	31.2	51.2	17.6	14.7	11.7	7.4	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade16p; ade16 ade17 mutants require adenine and histidine; Ade17p [Saccharomyces cerevisiae]
K.ADNWWFR.Q +2													2.7571	2.756						2.5633					
K.AFEHTADYDAAISDFFR.K +2													5.4767	6.857	3.8557					5.5662					
K.DYSEFLSELSSNGEISQDLR.N +2						3.4027			5.7905	4.305	3.6394	3.9973		4.8342	4.8763	5.2155			5.0276	3.1927	5.297	5.6727	3.7278		
K.ELSASLNLPAAASFK.H +2					4.0576	4.1144	4.3825	3.6951		3.1579	3.8875	3.078	3.7276		2.9322	3.2241					3.1679			4.2572	
K.FEEIPKPFTPEER.K +2													3.151		2.7047	2.8184	3.2707			3.005					
K.HVSPAGAAVGIPLSDVEK.Q +2		5.3725												5.2841	3.4044		5.2699			4.9772					
K.HVSPAGAAVGIPLSDVEK.Q +3													3.9466	3.9324											
K.LTNVSLSSDAFFPFPDNVYR.A +2					4.4755		4.7971	4.3986	4.576	2.5695	3.2762	4.7267	5.1526	4.3786	5.2065	4.6398				3.3187					
K.NLTEQAIIDLTVATIAIK.Y +2								4.0814						3.2835		3.1647			3.5065	2.6923					
K.PAQAYVSQQDSLPFK.V +2						4.6344	4.5501		4.2373	4.1553	4.6293	4.3793	4.7616	4.4595	4.5535	4.7066	4.4329	4.558	3.4191		4.3541	4.5325	4.6205		
K.QVYFVADIENLSPLACAYAR.A +2																			3.7213	3.0285					
K.RNDAIINQSTFK.E +2													3.9796	4.4689	3.8868		3.2068	4.174	4.1026	4.3513					
K.SNAIDLFVTGQIPTEEPELSEYQSK.F +2						4.6399	3.608	3.1706	4.122							4.4847		4.4313							
K.SNAIDLFVTGQIPTEEPELSEYQSK.F +3									3.6118			3.5555				3.6665									
K.TAILSVYDK.T +1									2.3244				2.2172					2.1998		1.9945		2.2685	1.9915	2.1064	
K.TAILSVYDK.T +2						2.947			2.6868			2.5245	2.9296	2.9012		2.6226		2.874		2.6339		2.5867			
K.TGLLDLAR.G +1													2.2735												
K.TGLLDLAR.G +2													2.9095	2.9543	2.965	2.9798	2.546				2.8402	2.6431	2.9067	2.8298	
K.TLHPAVHGGILAR.D +2														2.7623						3.0637					
K.VDYVVCNLYPFK.E +2					3.8518	3.6918	3.6455	3.9061	3.4429		3.5194	3.2136	3.2777	3.4406	3.1277	2.8657	3.199	3.5233		2.8974		3.0537		3.685	
K.VGVTIPEAVEEIDIGGVTLLR.A +2					3.9305	3.9609	4.1908	4.6284	4.3164			4.4161	4.5709	3.0286	3.1662	5.0439			3.1563	4.2012					
K.VGVTIPEAVEEIDIGGVTLLR.A +3													4.0629	4.5602		3.5473									
K.VLCGSPGYINLLDALNSWPLVK.E +2								2.8493	3.3885			2.6927	4.7214	2.8025	3.1384					3.7308					
K.VLCGSPGYINLLDALNSWPLVK.E +3													4.0319												
K.VVFSAADSFDLVYVENPIR.L +2																			3.1525						
K.YCILQIDPNYVPEAVER.R +2					5.8672	5.7954	5.9594	5.5564	5.4618	4.7454	4.8627	5.0839	5.5971	5.816	4.2277	5.5695		5.1204	4.3635	6.3305	4.966		5.4866		
K.YIAAPSGSVMDK.V +2												2.9462										2.6063			
K.YTQSNSVCYAR.N +2									2.7825	2.5837		2.5867													
R.DAGFPIEDVSAITHAPEM*LGGR.V +2													4.5106	4.3459	3.3637				3.1045						
R.EVSDGVIAPGYEPEALAILSK.K +2	4.3446	3.8084		3.2322	3.5596	4.4931	4.2102	3.8818	4.1982	3.0042	2.5951	3.667	3.2837	3.2136	3.2418	3.6712	3.3392	3.0825	4.362	3.1317	3.1643				
R.EVSDGVIAPGYEPEALAILSK.K +3																			3.582						
R.M*SSFGDWIALSNIVDVPTAK.I +2							2.7575	3.3258	4.5344					4.8345						2.765					
R.MSSFGDWIALSNIVDVPTAK.I +2				3.813				3.1238	3.1136								2.5418			3.3554					
R.NDAIINQSTFK.E +2						3.6536			3.6671	3.0143	3.5472	3.6554		3.5345		3.5721						3.0628			
R.NGMVVGLGAGQQSR.I +2										3.3916															
R.VTILSDPK.D +2																					2.5713				
R.YGANPHQKPAQAYVSQQDSLPFK.V +3														5.4248						4.6434					
3	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6321236|ref|NP_011313.1|	5.2	5.4	11.2		13.8	13.8	22.8	14	21.4	11.6	22.2	20.2	35.2	36.8	26.4	25	21	15.6	21.8	33.6	11	6.4	15.2	15.8	Aromatic aminotransferase, expression is regulated by general control of amino acid biosynthesis; Aro8p [Saccharomyces cerevisiae]
K.DFSYLFSDETNAR.K +2			4.9231		5.1511	5.3248	5.4091	5.3515	5.0036	3.9893	4.3797	5.0693	5.1322	4.9946	4.7244	4.877	4.2621	4.768		4.204	4.717	4.5302	4.5619		
K.DWDVLATAGNTNAWESTLR.V +2			6.0686		4.5928	4.666	5.4686		6.1341		3.4036	6.107	4.5785	6.4588	5.5085	6.1321	5.5344		5.1712	4.4838	6.0603	5.3625	4.7554	5.595	
K.DYFPWDNLSVDSPKPPFPQGIGAPIDEQNCIK.Y +3														4.3675											
K.EVSNPNIIFFR.G +2			2.9697		3.02	2.6945	2.901	2.8556	2.9326	2.5956	2.9594		2.7474	3.3044				3.248		3.1311			2.8446	2.8618	
K.GYLDWLLGLR.H +2													3.9831						2.6096	4.1379					
K.LLYTIPTGQNPTTGTSIADHR.K +2									3.9155				3.974	3.8911	3.6	4.1187	3.8269		2.7532						
K.RLGDTLYEEFGISK.- +2		3.1887																		3.3329					
K.SANPSNDIPLSR.A +2	2.8954				3.3047	3.2854	3.2898		3.2164	2.7757		3.1422				2.7226								2.9501	
K.SEGETEPPQPAESK.E +2	3.2716						3.6272	3.1632			3.2181	3.2195	3.1018			2.9867								3.0783	
K.SLANTFLSLDTEGR.V +2					4.9803	4.7873	4.6007	4.4797	4.9147		4.6807	4.3317	4.4475	4.7574	4.4218	4.8575	5.0233	4.6222	4.3791	4.7309	4.0589		5.0969		
K.VM*ENWTPGAPKPK.L +2													3.092	3.6895											
K.VMENWTPGAPKPK.L +2		3.6948	3.4369										3.6828	3.4636	3.1921		3.4719	3.2674		3.4429					
K.YDFLIVEDEPYYFLQM*NPYIK.D +2																				2.5497					
K.YNSDPYQLEQSLYHK.V +2													4.7568	4.729	3.3616	4.5042	4.1726		3.7478	3.7534					
R.ALQYGFSAGQPELLNFIR.D +2							4.8065	5.3453	5.4189		3.4764	5.4406	5.3746	5.6626	5.6434	4.8218		2.6917	2.5678	2.9511					
R.DCAIDALYK.Y +1											2.2089							2.6045		2.2369	2.6827		2.1973		
R.DCAIDALYK.Y +2										2.8166			2.8823	2.78											
R.GTYAAVSPEK.L +2																							2.9213	3.1823	
R.GVLVVPGSWFK.S +2												3.0371	3.0371	3.2948	3.0508		2.7675			2.7199					
R.LGDTLYEEFGISK.- +2							4.3237			3.322	3.3218								3.8748					4.9076	
R.LGWITGSSK.I +1													2.176	2.3533	2.2585										
gi|6325326|ref|NP_015394.1|	4.4	14.3	13		24.2	24.2	24.2	24.2	29.4	8.9	15.4	24.2	39.9	42	32.8	28	33.4	22.2	11.3	38.2	11.6	18.8	11.6	15.4	Spermidine synthase, involved in biosynthesis of spermidine and also in biosynthesis of pantothenic acid; spermidine is required for growth of wild-type cells; Spe3p [Saccharomyces cerevisiae]
K.EYFQLLNSALTEK.G +2	4.8566	5.0811	5.0344		4.8242	5.032	5.2145	4.9082	4.8646	4.2019	4.5029	4.8223	4.9095	4.8314	4.6675	4.8478	4.8745	5.0689		4.3577					
K.EYLPEM*AASYSHPK.V +2																		3.2145							
K.EYLPEMAASYSHPK.V +2													3.1996	3.3898	3.2277		3.82	2.5396		3.7662					
K.HDSVEEAWLCDIDEAVIR.L +2																									
K.HDSVEEAWLCDIDEAVIR.L +3													4.1502	4.9581											
K.IHEASFVLPTWAAK.E +2		3.6945	3.5888										3.0318	4.512	3.8836										
K.KIHEASFVLPTWAAK.E +2																				3.0235					
K.KVLVIGGGDGGVLR.E +2																			2.6382	3.1565					
K.STTYGNVLVLDNVIQATER.D +2					4.8548	5.6496	5.6191	4.7547	4.6365		4.7341	4.8305	5.0423	5.5187	5.219	5.2306	4.2398	4.9746	4.5316	3.7506	5.0084	4.5511	5.3504	4.385	
K.STTYGNVLVLDNVIQATER.D +3													4.5592												
K.THIGDGFQFLR.D +2			3.1371										2.9124	2.9897		2.5116	2.639	3.0518		2.5116					
K.VLVIGGGDGGVLR.E +2					4.2066	4.4033	4.1899	4.2883	4.0902	4.0776	4.1846	4.1491	3.799	2.9676	3.7946	4.2448			4.0245			4.1776			
K.YQDVLIFK.S +1															2.4541			2.4393				2.3751			
R.DEFAYQEM*IAHLALNSHPNPK.K +3														5.2232											
R.DYQNTFDVIITDSSDPEGPAETLFQK.E +2					4.551	5.0744	4.402	3.4424	3.7992			3.8591				5.0865	3.6002			3.5127				3.8558	
R.EISDTM*WPGQAM*TLK.V +2													4.3392								3.5068				
R.EISDTMWPGQAM*TLK.V +2															3.3603										
R.EISDTMWPGQAMTLK.V +2		3.7325							3.5446								3.6973					2.5643	3.8411		
2	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6324637|ref|NP_014706.1|	17.8	29.5	27.4	16.3	13.4	4.7	13.4	16.3	24.3		10.9	22.2	37.7	29.5	35.7	33.3	21.7	24.3	24.8	30.2	14	13.2	12.4	13.7	Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3 and rat L3 ribosomal proteins; involved in the replication and maintenance of killer double stranded RNA virus; Rpl3p [Saccharomyces cerevisiae]
K.AGM*TTIVR.D +2													2.8668												
K.AGMTTIVR.D +2				2.7202	2.9696	2.9101	3.0186	3.0411	3.0836			2.8177	3.0072	2.8996	2.968	3.1519				3.0396				2.7163	
K.AHLAEIQLNGGSISEK.V +2	3.7271	3.795	5.6765	5.546					5.1484			2.5306	5.6238	5.676	5.2206	5.6066	4.8926	2.7762	5.7155	5.4986					
K.ALEEVSLK.W +1												1.996	1.9914	2.0468	2.2563							1.9412			
K.GDDEANGATSFDR.T +1																						2.1024			
K.GDDEANGATSFDR.T +2		4.475			4.5082		4.6335	4.5936	4.517		3.2306	4.371	3.3303		3.1485	3.2248	4.1263	3.9409	2.6679		4.5323			3.4043	
K.GHGFEGVTHR.W +1																				2.0362					
K.GHGFEGVTHR.W +2		3.1444	3.0711						2.5069		2.6689		2.5576	2.8445	2.6851	2.859		3.0013		2.9867					
K.HAFMPGTLK.K +2													2.7168												
K.HAFMGTLK.K +1														1.8802	2.1794		2.5268	2.5151		2.3999					
K.HAFMGTLK.K +2		2.6209	2.6889	2.7356												2.7621	2.594								
K.HAFMGTLKK.D +2																				2.7964					
K.KAHLAEIQLNGGSISEK.V +2													4.2839							2.5713					
K.KTITPMGGFVHYGEIK.N +2																				3.0689					
K.PVALTSFLGYK.A +1																2.647		2.4797	2.4131	2.6803	2.2553		2.4706		
K.PVALTSFLGYK.A +2		3.7596	3.8779					4.0228	3.7991			3.4916	3.6022	4.0206	3.9399	3.8593	3.7404	3.7551	3.5767	3.5928	3.3936			3.0267	
K.TITPM*GGFVHYGEIK.N +2									3.8443				3.9565	3.8347	3.4085	3.6451			2.9077	2.9846					
K.TITPMGGFVHYGEIK.N +2	4.5385	4.8195	4.5713										2.6857	4.2014	4.1832	4.4102	4.5037			3.9713					
K.TVAVDSVFEQNEM*IDAIAVTK.G +2					2.7483				5.3314			6.0526	5.7433	5.7141	5.6201	5.6827	4.7858	5.5756	3.8449	5.0036		3.3678	4.2518	4.0802	
K.TVAVDSVFEQNEM*IDAIAVTK.G +3													5.134	4.9636					3.6672						
K.TVAVDSVFEQNEMIDAIAVTK.G +2		5.3436	5.6817		5.922		5.3927	5.1966	5.68			5.1702			5.66	4.9394	5.3244	3.248		4.5811	4.6099			4.6007	
K.TVAVDSVFEQNEMIDAIAVTK.G +3							5.2147		4.4944			4.9574			5.0503		3.6986			4.0153					
K.YAQDGAGIER.E +2	3.1535				3.2631	3.2432	3.1532	3.2294			2.8157		2.6708		2.6548	2.5637									

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.KALEEVSLK.W +1																						2.2126			
R.KALEEVSLK.W +2											2.701	3.2369	2.8132		2.7195						2.8522				
R.KTPLAQKKAHLAEIQLNGGSISEK.V +3												3.7737	3.701												
R.SKPVALTSFLGYK.A +1																				2.7211					
R.SKPVALTSFLGYK.A +2	3.2416	4.4404	4.1657										4.0525	3.6861	2.8202	3.4585			3.9159	3.7435					
R.SLTTVWAEHLSDEVK.R +2	4.5563	4.7211	4.8643	4.7888									4.634	4.8031	4.5608	4.595		2.8966	4.7541	4.4019					
R.VGKGDDEANGATSFDR.T +2		4.5986		3.8419															3.8847	4.1275			4.5081		
R.VLVHTQIR.K +2			2.5468																						
1	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320269|ref|NP_010349.1|	45.7	32.5	39.1	38.4	45.7	38.4	38.4	31.8	38.4	45.7	31.1	38.4	38.4	32.5	38.4	27.2	27.2		26.5	34.4	17.9	12.6	25.8	31.1	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosomal proteins; Rps13p [Saccharomyces cerevisiae]
K.GISSSAIPYSR.N +1																			2.3867						
K.GISSSAIPYSR.N +2	3.7288				3.717					3.4108	3.4173													3.3461	
K.GLTPSQIGVLLR.D +2	3.5164	3.8354	3.7161	3.5342	3.7575	3.5384	3.5222	3.5649	3.4755	2.7511		3.3372	3.269	3.6533	3.0719	3.3392	2.6792			2.7386				3.3608	
K.LSSESVIEQIVK.Y +2	4.3242	4.4337	4.5145	4.7337	4.4482	4.4504	4.3493	4.3845	4.2853	4.5983	4.3781	4.3353	4.4422	4.5339	4.3699	4.5897	3.6462		4.4277	4.261		3.9487	3.4532		
K.SNGLAPEIPEDLYYLIK.K +2	4.2685	4.4967	4.656	3.463	4.6093	4.7757	4.5538	4.6501	4.0772	2.8271	3.7836	3.6582	3.8667	3.709	3.8221	3.7842	2.8273		3.82	3.5524	2.8641		2.6374	3.038	
R.KGLTPSQIGVLLR.D +2		2.9816	3.2123											2.9142						3.2282					
R.NAPAWFK.L +1	2.0631	2.0594	1.9495	2.0842	2.1939	2.2045	2.1431	2.1664	1.9754	1.8934	2.015	1.8369	1.8598	1.9136	1.9726							2.1137		1.8197	
R.TVAVLPPNWK.Y +1									2.2658												1.9737				
R.TVAVLPPNWK.Y +2	2.8841		2.8569	2.6163	2.7494	2.7654	3.1168		3.1228	2.9194		3.0106	2.8496		3.0256					2.7228			2.5377		
gi|6323090|ref|NP_013162.1|	18.2	18.2	41.3	55.4	41.3	18.2	41.3	41.3	41.3	32.2	55.4	55.4	47.1	61.2	41.3	55.4	41.3		41.3	41.3	41.3	55.4	55.4	32.2	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl22Bp and to rat L22 ribosomal protein; Rpl22ap [Saccharomyces cerevisiae]
K.TFTVDVSSPTENGVFDPASYAK.Y +2	6.3556	6.0457	6.0824	5.953	6.1678	6.0893	6.1986	6.0176	5.613	5.4986	5.5867	5.5635	5.7871	5.7409	5.2172	5.5629	4.7235		5.3905	4.9742	5.612	5.4885	4.3766	5.7673	
K.TFTVDVSSPTENGVFDPASYAK.Y +3													4.1572	4.9326											
K.VEGAVGNLGNAVTVTEDGTVVTVVSTAK.F +2					4.2256		5.5103	3.3059	5.3215			4.8893	5.453	4.5444	5.6294	5.3665	2.5284		3.6041	4.1824	3.6306	4.5787	2.7689		
K.VEGAVGNLGNAVTVTEDGTVVTVVSTAK.F +3			4.8831	5.2962	5.6495		5.2641	5.8485	4.9718		3.8287	4.2644	4.7744	5.5764	5.4559	4.7468	4.2396		3.5665	4.7536					
K.YLIDHIK.V +1													1.9053	1.9286											
R.LAFYQVTPEEDEEEEDEE.- +2				4.1013						3.4819	4.5428	3.7998		3.9053		4.3568						4.0726	3.2411	3.9522	
gi|6324445|ref|NP_014514.1|	26.1	32.4	32.4	32.4	42.3	32.4	42.3	35.9	33.1	35.9	42.3	35.9	36.6	33.8	43	36.6	35.9		34.5	35.2	26.8	35.9	33.1	26.1	Primary rRNA-binding ribosomal protein component of the large (60S) ribosomal subunit, has similarity to E. coli L23 and rat L23a ribosomal proteins; binds to 26S rRNA via a conserved C-terminal motif; Rpl25p [Saccharomyces cerevisiae]
K.ELYEVDVLK.V +1		2.683	2.8367	2.8731	2.9963	2.7098	2.941		2.5295		2.4628			3.0079	3.1841				2.8773	3.1265			2.7245		
K.ELYEVDVLK.V +2									2.6818																
K.KVEDGNILVFQVSM*K.A +2													4.4479	4.2855	4.0654	3.6567			2.9922	2.9156					
K.VEDGNILVFQVSM*K.A +2							4.5895	3.0652	4.7179	4.0511	3.539	3.9932	4.492	4.593	4.9022	4.5218					3.2605				
K.VEDGNILVFQVSMK.A +2					4.1557				5.0144			4.2552			4.1658		2.6174			3.2146		3.2606	4.3714		
K.VIEQPITSETAMK.K +2						4.2037				2.8869	2.9927	3.7837	4.3449		3.5482	3.8704			4.0655	3.2141				3.3797	
K.VIEQPITSETAMK.K +1																				2.3819					
K.VIEQPITSETAMK.K +2	4.174	4.2409	4.0966	4.0377	4.1583	4.2201	4.2944	4.2541		3.9594	3.4187	4.1758	3.8901			3.5509	3.9055					4.1559	3.971		
K.VNTLVRPNGTK.K +2	3.551	3.6393	3.5424	3.6515	4.034	3.9746	3.8309	3.8823	3.446	2.9248	3.517	3.7928	2.6484	3.2994	3.4066	3.6524	2.9547		3.2394		3.1524	2.982	3.153	3.828	
K.VNTLVRPNGTKK.A +2																			3.0133						
R.LTADYDALDIANR.I +1									2.4681																
R.LTADYDALDIANR.I +2	4.984	4.9296	5.0246	5.0467	5.1269	5.1495	5.0985	5.1409	5.0205	4.9774	5.0807	4.8648	5.0269	4.8631	5.0675	5.1142	4.9202			4.6022	3.4257	5.0603		4.9389	
3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	
gi|6320128|ref|NP_010208.1|	23.9	14.2	14.2	31.9	14.2	14.2	23.9	23.9	14.2	23.9	14.2	14.2	20.4	20.4	20.4	14.2	23.9	31.9	14.2	14.2		22.1	14.2	23.9	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity to rat L31 ribosomal protein; associates with the karyopherin Sxm1p; Rpl31ap [Saccharomyces cerevisiae]
K.GLQTVVVEEDA.- +1	2.4148			2.1646						2.4582							2.5232	2.5039						2.3016	
K.GLQTVVVEEDA.- +2				3.2843													2.7919								
K.LHMGTDDVR.L +2				3.0111														2.6755				2.798			
K.NPLFSYVEPVLVASAK.G +2	5.5669	5.6404	5.5338	5.5356	5.6901	5.3456	5.6161	5.5465	5.3553	4.2115	4.9931	5.2077	5.1081	5.0144	5.2643	5.3945	4.5083	2.7227	4.4521	4.2915		2.8123	5.4835	5.0198	
K.NPLFSYVEPVLVASAK.G +3													3.9845			3.8279			4.4257	3.6982			3.852		
R.LAPELNQAIWK.R +2							2.5723	2.5101																	
R.NEEEDAKNPLFSYVEPVLVASAK.G +2													5.3055	5.8521	5.2656										
R.NEEEDAKNPLFSYVEPVLVASAK.G +3													5.4756	5.9809	5.3224										
gi|6321315|ref|NP_011392.1|	28.3	31.5	28.3	34.3	11	6.7	13.8	13.8	33.1	11	11	16.1	38.2	39.4	30.3	37.8	32.3	18.1	38.2	38.2		11	13.8	11	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins; Rps2p [Saccharomyces cerevisiae]
K.AAFVAIGNTYGFLTPNLWAEQPLPVSPLDIYSDEASAQK.K +3									3.9789																
K.AVVVVGDSNGHVGLGIK.T +2									4.0703			3.3464	3.6918	5.3655	3.78	2.9445	3.7724	4.135	3.5673	5.1542					
K.EFQIIDTLLPGLQDEVM*NIK.P +2													2.6986			3.7608	2.8956		3.5155	3.2635					
K.EFQIIDTLLPGLQDEVM*NIK.P +3													4.0266	4.3735					4.6533	5.0577					
K.EFQIIDTLLPGLQDEVM*NIKPVQK.Q +3														3.9581											
K.EFQIIDTLLPGLQDEVMNIK.P +2	5.2901	5.1014	5.5778	5.0325													3.6353			4.9575					
K.EFQIIDTLLPGLQDEVMNIK.P +3																				3.6066					
K.ITTIEEIFLHSLPVK.E +2		4.6792		3.0796									3.3391	4.6131	3.5449	3.8046			3.92	3.5133					
K.KLLQLAGVEDVYTQSNGK.T +2													4.1684		4.6994		6.0287		4.8616	4.7309					
K.KLLQLAGVEDVYTQSNGK.T +3																				4.1766					
K.LLQLAGVEDVYTQSNGK.T +2	5.7097	6.4134	6.3155	5.8844	6.378	6.2688	6.6234	6.3738	6.2308	6.1389	6.3446	6.1172	5.8436	6.0776	5.8394	5.9777	5.4382	3.8134	5.6573	5.6448		5.9332	4.0496	6.5099	
K.LLQLAGVEDVYTQSNGK.T +3													4.0867												
R.AGIIIAK.L +1	1.927		1.9756	2.0392			1.986	1.9504				1.8535											1.9948		
R.GSGIVASPAVK.K +1											2.0011		1.9936	2.0963	1.9449	1.9942	2.1	2.1819	1.8971	1.9404		2.0921	2.0403	1.894	
R.GSGIVASPAVK.K +2	3.0863	3.1457	2.7652		2.7338		2.5716	2.5899	2.6437	2.8746								2.7208							
R.GSGIVASPAVKK.L +2	3.0467	2.816	3.0425	3.2612														3.2225							
R.GYWGTNLGQPHSLATK.T +2	5.2643	5.4134	5.3791	5.3896									4.9732	4.7267	4.0071	4.952	4.8717		5.2038	5.0133					
gi|6322120|ref|NP_012195.1|	13.3	32.6	32.6	32.6	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4	34.1	33.3	33.3	33.3	32.6	24.4	20	38.5		13.3	17.8	13.3	Protein component of the small (40S) ribosomal subunit; identical to Rps24Ap and has similarity to rat S24 ribosomal protein; Rps24bp [Saccharomyces cerevisiae]
K.DAVSVFGFR.T +1			2.4052				2.3635						2.6175	2.1361		2.1364									
K.DAVSVFGFR.T +2	3.3895	3.4801	3.5215	3.5478	3.5112	3.487	3.4317	3.4529	3.4579	3.5272	3.4529	3.4194	3.2842	3.4084	3.2489	3.5029	3.3842	3.5679		3.4387		3.4891	3.317	3.4655	
K.KIFGTGK.R +1																				1.9142					
K.QFVVDVLHPNR.A +2		3.0826	2.7886	2.6108									2.8055	2.5587	3.1589	2.5878	3.1645		2.9938	3.2204					
K.SVGFGLVYNSVAEAK.K +2		4.6375	5.0354	4.3873	4.8493	5.0844	4.9088	5.0223	4.8485	3.7733	4.2862	4.1364	4.8294	4.7926	4.8156	4.8509	3.4316	3.6075	4.5088	4.0001			4.0235		
K.VISNPLLAR.K +2	3.4974	3.5346	3.5184	3.5144	3.4036	3.416	3.4817	3.4599	3.1476	3.4134	3.2203	3.2547	3.1807	3.343	3.222	3.4256	3.2144	3.2687		3.3007		2.8824		2.633	
R.KQFVVDVLHPNR.A +2													4.177	4.0642					3.176	4.0069					
R.KQFVVDVLHPNR.A +3													3.9527	4.0972						3.6561					
R.KVISNPLLAR.K +2													2.7137		2.7263	2.8205									
gi|6322794|ref|NP_012867.1|	16.8	29.9	21.6	29.9	23.4	23.4	23.4	23.4	43.1	25.1	28.1	25.1	38.3	43.1	38.3	38.3	29.9	19.2	18	22.8		16.8	22.8	16.8	Protein that associates with ribosomes; homolog of translationally controlled tumor protein; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and relocates to the mitochondrial outer surface upon oxidative stress; Tma19p [Saccharomyces cerevisiae]
K.AKLQETNPEEVPK.F +2																		3.3627							
K.DIFSNDELLSDAYDAK.L +2	5.9302	6.0991	5.9599	5.8957	6.1948	6.1466	6.0181	6.107	5.7253	5.7885	5.8103	5.8075	5.8024	5.9636	5.837	5.827	6.1117		6.0039	5.9316		5.7365	3.4382	5.7871	
K.DWEFFTGESM*DPDAM*VVM*LNYR.E +2															4.3066	4.842									
K.DWEFFTGESM*DPDAM*VVM*LNYR.E +3													6.2078	5.8934	5.7015										
K.DWEFFTGESM*DPDAM*VVMLNYR.E +2									3.5394							2.929									
K.HGIVEEKI.- +1																		2.2095		2.1939					
K.HGIVEEKI.- +2		2.8929	3.0552	2.9314																					
K.LQETNPEEVPK.F +2					3.882	3.6535	3.5896	3.8249	3.6882	3.0792	3.1937	3.9107	3.9372	3.5863	4.0173	3.8364			3.9494						
K.LQETNPEEVPKFEK.G +2		4.6421		4.7831					4.2631	3.4321		3.7383	4.8328	4.5245	3.9026	4.5727	4.7832	4.6634	4.9419	4.7668			3.3422		
R.EDGTTPFVAIWK.H +1																1.9206									
R.EDGTTPFVAIWK.H +2	3.1215	3.08	3.165	3.2903	3.2531	3.3725	3.2425	3.2667	3.1411	2.8698	3.1707	2.8376	3.0128	2.9219	2.9835	2.9161	2.7464					2.7162		2.8083	
R.LQQTAFDK.K +1									2.2039		1.8959			2.1232			2.0378	2.009					2.0088		
gi|6323324|ref|NP_013396.1|	11	14.2	14.2	14.2	15.5	20.5	15.5	15.5	20.5	20.5	20.5	15.5	23.7	17.8	20.5	16	20.5	24.7	17.4	17.8		20.5	20.5	11	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog; Gsp1p [Saccharomyces cerevisiae]
gi|6324759|ref|NP_014828.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; interacts with Kap121p, Kap123p and Pdr6p (karyophilin betas); Gsp1p homolog that is not required for viability; Gsp2p [Saccharomyces cerevisiae]
K.FDVWDTAGQEK.F +1					2.6947	2.5686					2.5288						2.0608			2.7023					
K.FDVWDTAGQEK.F +2	3.9293	3.6555	3.3822	4.0765	4.2619	4.1938	4.1585	4.1814	3.9823	4.047	4.1001	3.9055	4.1935	4.0828	3.4507	3.7739		3.2002				4.0372	3.9775		
K.LVLVGDGGTGK.T +1					2.4855				2.238	1.9023	2.0573		2.4314	2.034	2.1208	2.5988	2.4005		2.4351	2.3151		2.4294	2.2897	2.4969	
K.LVLVGDGGTGK.T +2					2.8508				2.748		2.8344			2.8093		2.6106		3.0747	2.8595						
K.NLQYYDISAK.S +1					3.0234						2.4709		2.6902	2.9256	2.8918		2.7599	2.4837	2.806	2.6962		2.7879	2.8971		
K.NLQYYDISAK.S +2					3.244	3.369	3.3541	3.329	3.1533	3.1465	3.0023	2.9865	2.9585							2.8893					
K.PFLWLAR.K +2		2.6883	2.5872	2.6588									2.5712	2.5139						2.5064					
K.RHLTGEFEK.K +2																		2.5845							
R.VCENIPIVLCGNK.V +2	4.7542	4.5608	4.6251	4.5061	4.6282	4.6456	4.8398	4.7626	4.6006	4.5762	4.7767	4.8177	2.9593		4.5459	4.6458	4.6711	2.8093				4.6443	3.3582	4.4609	
R.VCENIPIVLCGNKVDVK.E +2																			3.1859						

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6325126|ref|NP_015194.1|	8.4	24.6	32.3	24.6	16.5	19.2	16.5	16.5	23.6	19.2	16.5	25.9	23.9	37.4	42.4	37	25.9	21.2	32.3	34.7		17.2	23.2	9.8	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal proteins; binds 5S rRNA and is required for 60S subunit assembly; Rpl5p [Saccharomyces cerevisiae]
K.GASDGGLYVPHSENR.F +2		4.523	4.1564	4.6025	3.7642	4.4942	3.7253	4.2257	3.5832	3.3709	3.8947	4.1394			3.7993	4.0977	4.0352	4.322	4.395			2.836	3.8889		
K.GVEEVEGEYELTEAVEDGPR.P +2												4.8105			2.8474	5.3983	3.7057					5.594	5.5677	5.593	
K.GVEEVEGEYELTEAVEDGPRPFK.V +2			5.9716										5.7095	5.0448	4.9979	5.8031	4.9468		3.008	3.3468					
K.GVEEVEGEYELTEAVEDGPRPFK.V +3			3.6815																						
K.GYLADDIDADSLEDIYTSAHEAIR.A +2		5.32												5.2638	4.2379	4.0588			3.8161	5.0271					
K.GYLADDIDADSLEDIYTSAHEAIR.A +3		5.043	4.6247	4.2157										4.7683					3.7403						
K.IAALAGQQ.- +1	2.2041	2.3503	2.4281	2.552	2.381	2.4201	2.3337	2.4164	2.4132	2.3868	2.4719	2.3775		2.4165	2.4046				2.5906	2.1844		2.3542	2.2643		
K.LGLDETYK.G +1						1.9526			1.9175	1.8497				1.9385	1.9393										
K.LGLDETYK.G +2						2.6637			2.7915			2.7522										2.5634			
K.VFLDIGLQR.T +2		3.6785	3.7173	3.776	3.6609	3.7136	3.7918	3.7248		2.9262	3.4005	3.4379	3.6912	3.586	3.604	3.6989		3.7763	3.2147	3.7936			3.6678	3.8155	
R.FPGWDFETEEIDPELLR.S +2	5.6902	5.7619	5.8051	5.4049	5.5621	5.5604	5.504	5.7168	5.3791	3.8867	5.3386	5.1905	5.245	5.552	5.4063	5.3068	4.4905	4.6697	5.1694	5.1623			3.7626		
R.SYIFGGHVSQYM*EELADDDEER.F +2													5.259		5.2904	5.3449		3.5096							
R.SYIFGGHVSQYM*EELADDDEER.F +3									5.0027				4.7392	5.1186	5.4772	5.2073									
R.SYIFGGHVSQYMEELADDDEER.F +2																	4.0813			5.3643					
6	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	
gi|37362684|ref|NP_013969.2|	13.5	33.7	19.7	33.7	33.1	19.1	23	33.7	33.7	33.1	17.4	33.7	38.2	38.2	37.6	34.3	21.9	32.6	23.6	34.3	21.9		23.6	17.4	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity to rat L18a ribosomal protein; Rpl20ap [Saccharomyces cerevisiae]
gi|6324888|ref|NP_014957.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Ap and has similarity to rat L18a ribosomal protein; Rpl20bp [Saccharomyces cerevisiae]
K.ASGEIVSINQINEAHPTK.V +2		4.6154		4.6426	4.7683			5.0294	4.298	3.8496		3.8914	4.6647	4.6928	4.3996	4.6428	4.4373	4.3989		4.7429	3.8164		4.2136		
K.KASGEIVSINQINEAHPTK.V +2													4.0505			4.1626		4.8267		4.4102					
K.KASGEIVSINQINEAHPTK.V +3														4.5074											
K.NFGVWVR.Y +1									2.4072									2.3671			2.4961				
K.NFGVWVR.Y +2		2.6087		2.5449	2.7458		2.7131	2.6621		2.5932	2.601		2.5083	2.5401	2.537						2.5424				
R.IFASNEVIAK.S +1													2.5217										2.4321		
R.IFASNEVIAK.S +2	3.3765	3.46	3.4707	3.3903	3.3211	3.3784	3.5503	3.3927	3.0841	3.3743	3.2111	2.8591	3.4509	3.0871	2.9989	3.5007			3.2663	3.2308					
R.LPTESVPEPK.L +2					2.7047	3.0531	2.9254	2.53	2.5695	2.7198		2.7963	2.6242		2.7966									3.0149	
R.RLPTESVPEPK.L +2		3.1978	3.205	3.2883				2.9638	2.7332			2.6956	2.9302	2.5587	2.9772	3.2444		2.5194	2.7344	3.0623					
R.VAAVETLYQDM*AAR.H +2									4.7595	4.41	4.622	4.9932	4.7295	4.8348	4.213				3.7242		5.1571			4.553	
R.VAAVETLYQDMAAR.H +2	5.198	5.2198	5.3916	5.2586	5.2584	5.3039	5.2423	5.26	5.1035	5.188	4.9752	5.0895	4.8868	4.8932	5.2928	5.1283	4.5482	5.1613	3.732	5.2708	4.5122		5.1209	5.157	
R.YWYFLQK.L +1												2.3869	2.4114		2.3785	2.3284	2.1606	2.2522	2.2216	2.3772				2.5378	
R.YWYFLQK.L +2												2.5113		2.5751		2.5379									
gi|6320121|ref|NP_010201.1|	16.1	25.1	14.6	24.6	33.7	23.6	33.7	37.7	33.7	29.1	33.7	37.2	37.7	41.7	32.2	37.2	27.6	13.1	28.1	17.6	23.1		21.6	18.6	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Bp; not essential for viability; has similarity to rat L13 ribosomal protein; Rpl13ap [Saccharomyces cerevisiae]
gi|6323791|ref|NP_013862.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Ap; not essential for viability; has similarity to rat L13 ribosomal protein; Rpl13bp [Saccharomyces cerevisiae]
K.AAGLTAAYAR.T +1																1.8058	1.9814								
K.AAGLTAAYAR.T +2	3.6105	3.6775		3.2769	3.653	3.6135	3.7148	3.679	3.535	3.4367	3.5078	3.4793	3.644	3.4793	3.2645	3.5678	3.4596		3.1264						
K.AEAEAEK.K +1												2.111													
K.APEAEQVLSAAATFPIAQPATDVEAR.A +2						5.7467	4.4748	4.8015	5.5768	3.5821	4.1181	3.5515	4.424	5.8112	5.6558	6.1675	5.1848	4.6633	5.1715	4.6987	5.3109		5.7766	4.9145	
K.APEAEQVLSAAATFPIAQPATDVEAR.A +3					3.6276	4.0649	4.5917		4.1601			4.1723	5.295	5.0927	4.8061	4.3976		6.0457							
K.VHFDQAGK.K +1													2.5861	2.5864	2.159		2.6237								
K.VHFDQAGK.K +2		2.5846	2.5226	2.7088				2.5494						2.5771											
K.VHFDQAGKK.V +2		2.9001	2.6069																2.7894						
R.AVQDNGESAFR.T +2	3.436	3.2586		3.6074	3.7299		3.6194	3.1047	3.2319	2.5241	3.4105	3.3826	3.6701	3.0499		3.3399									
R.GFTLAEVK.A +1														1.8098									1.8767		
R.GFTLAEVK.A +2																2.555									
R.NQEIFDANVQR.L +1													2.5432												
R.NQEIFDANVQR.L +2	4.1805	4.1626	4.1782	4.0818	4.2686	4.1667	4.2196	4.2414	4.1337	4.1923	4.2916	4.0806	3.9523	4.2166	4.1865		3.2559		3.686		3.8046			4.081	
R.PLDLLRPVVR.A +2																2.5815									
R.TIGIAVDHR.R +2		3.1324	3.1814	3.0152	2.5515		3.0266	3.123	3.023		2.9734	2.9913	2.5874	3.1622	3.2279	3.0601				2.9375	3.0811		2.5919		
gi|6321408|ref|NP_011485.1|	27.6	56.2	45.7	27.6	45.7	16.2	45.7	45.7	56.2	56.2	34.3	56.2	57.1	57.1	39	57.1	56.2	39	46.7	57.1	45.7		56.2	44.8	Protein component of the large (60S) ribosomal subunit, has similarity to rat L30 ribosomal protein; involved in pre-rRNA processing in the nucleolus; autoregulates splicing of its transcript; Rpl30p [Saccharomyces cerevisiae]
K.LIIIAANTPVLR.K +2	4.9098	4.7644	4.8465	4.8798	4.6162		4.6901	4.5681	4.5257	4.2391		4.4621	4.6492	4.551	4.3782	4.377	4.5816	4.6671	4.267	4.6881	4.3913		4.3467		
K.LIIIAANTPVLRK.S +2																			3.3487	3.6221					
K.SELEYYAM*LSK.T +2										2.9312			4.0281	4.5277				3.5825							
K.SELEYYAMLSK.T +2		3.1457							4.3533	2.8112		3.898		4.3319	4.4268	4.7167	4.6882	4.9041					4.5333	4.3957	
K.VYYFQGGNNELGTAVGK.L +2	5.3983	5.4736	5.3817	5.2856	5.4877	5.4723	5.6671	5.6356	5.2588	5.5607	5.2715	4.9591	5.1827	5.3367	5.1916	5.1534	5.3592	3.6172	4.3111	5.443	5.061		5.4584	4.7986	
R.KSELEYYAM*LSK.T +2													4.2347	4.8149	3.1144	4.0915		4.2282							
R.KSELEYYAMLSK.T +1															2.6294										
R.KSELEYYAMLSK.T +2															4.1053	4.5379				4.7633					
R.VGVVSILEAGDSDILTTLA.- +2		2.581	5.2564		4.2443		4.7131	4.6909	4.1026	4.431	4.4069	4.4285	3.4761	4.4647		2.762	3.8484		3.0086	3.3172	2.6445		3.099	3.0317	
3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6323196|ref|NP_013268.1|	27.6	38.8	38.8	27.6	16.4	21.7	21.7	21.7	38.8	16.4	27.6	10.5	38.8	32.9	32.9	38.8	38.8	21.7	27.6	38.8	10.5	10.5		10.5	Fusion protein that is cleaved to yield a ribosomal protein of the small (40S) subunit and ubiquitin; ubiquitin may facilitate assembly of the ribosomal protein into ribosomes; interacts genetically with translation factor eIF2B; Rps31p [Saccharomyces cerevisiae]
K.ESTLHLVLR.L +1														2.3537	2.2148		1.9811			1.8263					
K.ESTLHLVLR.L +2	3.3516	3.3083	3.2416	3.2456					2.9851		2.8269		3.1258	3.0807	2.8848	2.9317			2.9657	2.7551					
K.LAVLSYYK.V +1	2.1174	2.0231	2.0435	1.9542		2.0637	2.1201	2.1516	2.1091		2.0282		2.1274	1.9941	1.9987	2.013	2.152			1.818					
K.TITLEVESSDTIDNVK.S +2	4.632	5.3672	5.5956	5.4874	5.5034	5.7555	5.4482	5.4958	5.2562	4.7403	4.2168	5.1052	5.4286	5.4919	5.4366	5.4203	5.0955	5.3335	4.8579	5.0609	5.2195	4.6059		5.5392	
R.ECSNPTCGAGVFLANHK.D +2		4.8742	4.6856						4.3827				4.7534	4.8636	4.3871	4.4854	4.6095	4.3191	4.8064	3.6545					
R.TLSDYNIQK.E +1																	2.0144								
R.TLSDYNIQK.E +2	2.8443	2.7501	2.786	2.9168	2.7091	2.6232	2.7089	2.8297	2.6207	2.6881	2.6612		2.793			2.5757	2.5899			2.711					
1	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	
gi|6320228|ref|NP_010308.1|	41.7	47.4	46.8	39.7	28.8	26.3	37.2	32.1	42.3	24.4	30.8	32.7	36.5	45.5	34	41	29.5	17.9	24.4	40.4	14.7	7.1	10.9		Protein component of the small (40S) ribosomal subunit; identical to Rps11Bp and has similarity to E. coli S17 and rat S11 ribosomal proteins; Rps11ap [Saccharomyces cerevisiae]
K.CPFTGLVSIR.G +2	3.6482	3.5539	3.5512	3.6545	3.6909		3.7226	3.6961	3.4961		3.1637	3.4205	3.4825	3.5676	2.9066	3.6636	3.0706		3.1123	3.4218			3.5518		
K.ILTGTVVSTK.M +2	2.9099	2.7771	2.8122	2.6746	2.9034	2.7883	2.6784	2.8794	2.5597	2.9234		2.8252													
K.KCPFTGLVSIR.G +2		2.7185																							
K.NAGLGFK.T +1	1.9261	1.8679	1.9323	2.0118	1.8366	1.8519	2.0793	1.8947	1.8685		1.8531	1.8037		1.8057	1.8791	1.8452		1.8527							
K.NVPVHVSPAFR.V +1													2.3619				1.8845	2.5564		2.5196					
K.NVPVHVSPAFR.V +2	2.5304	2.6491	2.6772						2.6557					2.5932		2.5865	2.6468								
K.TAIEGSYIDK.K +1																			2.3245	2.3595	2.2757	2.2619			
K.TAIEGSYIDK.K +2	2.9072	2.7995	2.9475	3.0811			2.7939	2.7679	3.0183		2.8004	2.7759	3.0977		3.1048			2.6234							
K.TAIEGSYIDKK.C +1					1.9681																				
K.TAIEGSYIDKK.C +2					2.7808	2.9176	2.5834		2.5205		2.7421	2.7561	3.1833	2.9186	2.7278	2.8367			3.3111			2.6353		
K.VSAAAGK.A +1					1.8987		2.0596			1.9262	2.1616			1.826						1.9731			2.0362		
R.AYLHYIPK.Y +2		3.3088	3.4016	3.3083						3.0385			3.1846	3.2879	3.0514	3.1572	3.0275			3.4145					
R.VQVGDIVTVGQCR.P +2						4.2419	4.4638	3.6812	4.5632	4.125	4.5179	4.2221	3.6808		4.0741	4.2374				3.7334	4.0221				
R.VQVGDIVTVGQCRPISK.T +2	4.5418	4.9662	4.9916	5.009					4.5294				4.6918	4.6177	4.4905	4.5137	4.5372		4.2516	4.6906					
gi|6321335|ref|NP_011412.1|	10.1	23.5	23.5	22.8	22.1	22.1	22.1	22.1	22.1	22.1	22.1	16.1	17.4	33.6	24.2	22.1	23.5	16.1	17.4	29.5	16.1	16.1	16.1		Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli L15 and rat L27a ribosomal proteins; may have peptidyl transferase activity; can mutate to cycloheximide resistance; Rpl28p [Saccharomyces cerevisiae]
K.ETAPVIDTLAAGYGK.I +1															2.043					1.9691					
K.ETAPVIDTLAAGYGK.I +2	4.1501	4.1841	4.1464	4.2916	4.3502	4.313	4.3429	4.2746	4.0312	4.3722	4.3038	4.1383	3.6974	4.2923	4.0468	4.0936	3.137	3.7546	3.5324		4.193	3.7228	4.3128		
K.GRIPNVPVIVK.A +2		3.4898	3.4968										3.3861	2.8186	3.2669		2.8981		2.6842	3.0907					
K.LWTLIPEDK.R +1					2.1099				2.0972							2.4067					2.1193				
K.LWTLIPEDK.R +2		2.7052	2.8405	2.7773	2.8236	2.9299	2.8148	2.6523	2.7683	2.9421	2.906			2.9512		2.6884	2.82	2.692			2.7012	2.6809	2.7758		
K.LWTLIPEDKR.D +2				2.7601											2.7891					2.8384					
K.YHPGYFGK.V +1														1.8059						1.9912					
R.GHVSAGK.G +1														1.9366											
R.IPNVPVIVK.A +2		2.759	2.6339	2.7308	2.7282	2.6673	2.7452	2.7195	2.6005	2.5345	2.6225	2.724	2.7865	2.5031	2.513	2.7018									
gi|6323077|ref|NP_013149.1|	19.8	25.4	37.7	25.4	27.4	42.1	27.8	37.3	25.4	9.9	25	37.7	35.3	35.3	30.6	44.4	24.2	18.7	15.1	30.6	24.6	15.1	20.6		Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Ap; required for maturation of 18S rRNA along with Rps0Ap; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal; Rps0bp [Saccharomyces cerevisiae]
K.EASYVNIPVIALTDLDSPSEFVDVAIPCNNR.G +3			4.6995		3.9417	3.9007	4.0779	4.9114				4.7526				4.0469	3.9452								
K.FAAHTGATPIAGR.F +1								3.0262	3.0535				3.0509	3.2203	2.6382	3.1719	3.1014	3.0132	2.3892		1.8393				
K.FAAHTGATPIAGR.F +2	3.8306	3.698	3.8367	3.6269	3.5065			3.8076	3.4751		3.2173	3.4836	3.4091	3.8463	3.0042	3.3895	3.238	2.7916	2.8689	2.5943		3.6635	2.6962		
R.FTPGSFTNYITR.S +2	3.1798	2.9116	2.6113	2.6306		2.5233			2.6081			2.8374	2.8706	3.3248		2.6949		2.9668							
R.IIAAIPNPEDVVAISSR.T +2	4.2864	4.7559	4.5832	4.1886	4.5958	4.2475	4.3382	4.3809	4.0002	4.4164	4.3671	4.163	3.9252	3.9096	3.759	3.9815	3.8239			3.0166		2.7124	3.6437		
R.IIAAIPNPEDVVAISSR.T +3													4.7885	4.7565	4.5727					3.6892	4.8099				
R.LVIVTDPR.L +2	2.8359	2.6171	3.0756	3.0893	3.0369	3.0581	3.2226	3.1962	3.0693	2.6941	2.5775	2.8109	2.556	3.0079	2.8631			2.82		2.6075	2.825	3.2905	2.9517		
R.NPEEVEQVAEEAAAAEEGEEEEVK.E +2						2.5158															3.43				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.NVQVHQEPYVFNAR.P +2													4.4404	4.4794	4.5897	3.8511		2.8566		3.6439			2.7349		
R.NVQVHQEPYVFNARPDGVHVINVGK.T +3														5.19						4.5889					
R.PDGVHVINVGK.T +2								3.8413			2.8806		4.2396	3.5379	3.8276	3.9227			2.8794						
R.TQPWSIMPDLYFYR.N +2						3.8274	3.5025	4.0414	3.9057		3.3039	3.5963	3.5954	3.824	3.8317	3.6398			3.5603	3.6794					
R.TQPWSIMPDLYFYR.N +2		3.9378	4.1948	3.2105								2.6457								3.3269					
gi|6325036|ref|NP_015104.1|	12.4	17.5	12.4	27.2	20.3	26.3	14.7	33.2	29.5	18	17.5	29.5	40.6	36.9	40.6	33.2	11.5	12.9	33.6	20.3	34.1	11.1	23		N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal; Rpl1ap [Saccharomyces cerevisiae]
K.AGKPPTPVSHNDDLYGK.V +2																		4.2528		3.4927					
K.FPTPVSHNDDLYGK.V +1																	3.0089								
K.FPTPVSHNDDLYGK.V +2	4.0776	4.4106	4.381	4.2339				4.3664	4.1774	3.8402		3.126	3.984	4.0555	4.0138	4.1715	3.9865			3.2555			3.6591		
K.KYNAFIASEVLIK.Q +2																			2.7767						
K.LPNCPRPNM*SICIFGDAFDVDR.A +3																			4.5989						
K.NWQNIVGSLVVK.S +2		3.351		3.6234	3.6466	3.6011	3.5426	3.725	3.4632	3.4249	3.3705	3.4988	3.3303	3.3559	3.3761	3.5454	3.0641	2.998	3.0818		3.3848	3.3697			
K.SCGVDAM*SVDDLKK.L +2													4.7094						4.3565						
K.SCGVDAMSVDDLK.K +2	4.712	5.1076	4.9509	4.9047		3.9991			3.0288	4.1599	4.1555	4.2638										4.7309			
K.SCGVDAMSVDDLKK.L +2								4.3084	4.9146	3.9678	3.2042	4.1839	4.6622	4.6231	4.5272	4.7494				3.9271	4.2457				
K.YNAFIASEVLIK.Q +2					3.3403	3.7669		3.6444	3.6201			2.835	3.81	3.7929	2.8949	2.8274					2.7961		2.8832		
R.LLGPQLSK.A +1					1.9177	2.0902		1.9435					1.9992		1.8996	2.0821							1.8577		
R.LLGPQLSK.A +2				2.5378			2.6679														2.5103				
R.NFLETVELQVGLK.N +2				5.6802	5.7616	5.9531	3.886	5.5525	5.7732		3.6139	5.4836	5.7872	5.8078	5.8106	5.3957			5.4	5.8008	3.3438				
R.PNM*SICIFGDAFDVDR.A +2													4.9513	5.0516	5.0624						3.8678		4.0413		
4	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6321203|ref|NP_011280.1|		1.9		5.9	9.1	13.6	7.7	3.2	12.8	10.5	20.6	12.8	15.7	15	11	14.7	21.4	16.5	11.5	15.3	6.2	12.3	5.4	14.8	Bifunctional enzyme of the 'de novo' purine nucleotide biosynthetic pathway, contains aminoimidazole ribotide synthetase and glycinamide ribotide synthetase activities; Ade5,7p [Saccharomyces cerevisiae]
-.M*LNILVLGNGAR.E +2												2.569	4.7536				2.719			3.7549					
-.MLNILVLGNGAR.E +2					3.8294			4.1398	3.1227						4.251					4.0164					
K.GLNTGGM*GAYAPAPVATPSLLK.T +2													5.0634			3.6693		3.7382	4.5379	4.463				3.8292	
K.GLNTGGMGAYAPAPVATPSLLK.T +2											3.4045					3.281	3.4345	4.5293		3.5517				4.5084	
K.GVIIPSSIDESVQAIK.D +2						4.332	4.6568		4.7588	3.6755	3.1458	3.4406		4.0296		4.7119						3.8707		3.2502	
K.IIQHVALPWDAPCPWDESK.T +2														3.6834											
K.ITLDTDKLPPHTQIFQAGTK.Y +3														4.4382											
K.IYVAPGNGGTATMDPSR.V +2										3.5934	3.1198													3.2993	
K.LPPHTQIFQAGTK.Y +2																		2.7661							
K.TIDSQIVKPTIDGM*R.R +2													2.889												
K.TIDSQIVKPTIDGMR.R +2																	2.8173			2.8547					
K.TLGEGILEPTK.I +2									3.0224		3.313	3.0425		3.4735	3.3659				3.1436			3.3768			
K.TNQLVPEVLEYNVR.F +2					4.1067	3.4857	3.5236	3.6255	4.0237	3.3178	3.073	3.0895	3.8357	4.0282	3.7217	4.3756	4.0479	3.0203		2.8411				2.7083	
K.VAITYADSGVSVDNGNNLVQTIK.E +2					3.0288	3.8335			3.7416		2.9161				4.4892	4.5998	5.6455	5.0541	5.1601	3.8897	5.1444	2.7705		3.5581	
K.YDSATDSLLTNGGR.V +2										3.59	3.9301						3.9703					4.344			
R.FGDPETQAVLSLLDDQTDLAQVFLAAAEHR.L +3				6.7163																					
R.LDSVNIGIDDTR.S +2					3.8482	4.1153				3.5769	4.1241	3.7253						3.9672			3.9848	3.6666			
R.LLLGLAHITGGGLVENIPR.A +2																			2.719						
R.LLLGLAHITGGGLVENIPR.A +3																				4.5149					
R.QNEDTLLVGATDGVGTK.L +2				5.0097		4.5116	5.1069						3.8769				4.7875		4.9703				4.4025	3.5454	
R.SAVTVVVAAGGYPESYAK.G +2													4.4773	4.6663	3.5649	2.9667	3.0668			3.0879					
R.TAVDTVYEAVK.C +2										2.7028	3.2391	3.647						3.2249				3.6088	3.6253		
R.TFNM*GVGM*VLIVK.R +2													3.0319												
R.VDMSTWEVPR.V +2											2.9293			2.9638	3.2859	3.4128	2.804	2.7649						2.6451	
R.VINWDITPDVANFAR.L +2		4.605				4.8582	4.5095		4.0204		4.2011	3.5346	4.7696			4.1355	4.1343	3.0598			2.7183		3.3885		
R.VLSVTSTAQDLR.T +2					4.077	3.6428			3.8219			3.4692		4.0153			2.7798	3.7296				4.0431			
gi|6322815|ref|NP_012889.1|		4.4		3.8	4.8	7.8	8	18.2	20	5.6	9.6	19.2	31.9	32.1	26.9	22.8	23.4	15.4	17.6	26.1	8.4	7.8	10.8	12.2	UDP-glucose pyrophosphorylase (UGPase), catalyses the reversible formation of UDP-Glc from glucose 1-phosphate and UTP, involved in a wide variety of metabolic pathways, expression modulated by Pho85p through Pho4p; Ugp1p [Saccharomyces cerevisiae]
K.FENELDSFFTLFR.R +2					4.0842		3.4457	4.7666	4.55		3.9122	4.2534	4.8013	3.9856	4.6771	3.4781	2.8775	3.4414	3.181						
K.FTNFNTNNLWINLK.A +2		2.9584						3.4757	3.9397			4.1841	3.968	3.6652	3.0659	3.8894	3.6133	3.1839							
K.GGTLISYDGQVR.L +2						2.7591				2.9245	3.1993		2.9398					3.6652				3.4784			
K.ILNHM*IETGAEYIM*ELTDK.T +3														3.6108											
K.LNGGLGTSM*GCVGPK.S +2														4.1999	3.3681					3.4613	2.8457				
K.LNGGLGTSMGCVGPK.S +2												3.2639			4.1207		3.9601							3.6242	
K.RLIESSNLEMEIIPNQK.T +2																				3.6045					
K.SPNPDEVVKYEIISQQPENVSNLSK.L +2																	3.3722								
K.SPNPDEVVKYEIISQQPENVSNLSK.L +3																			3.7421	4.8011					
K.TCSDLLLVK.S +2													2.7006	2.645		2.768									
K.THSTYAFESNTNSVAASQM*R.N +2																			4.068						
K.THSTYAFESNTNSVAASQM*R.N +3													4.5363	5.0463											
K.THSTYAFESNTNSVAASQMR.N +2															2.644		6.1221	5.5998							
K.YEIISQQPENVSNLSK.L +2						5.2793	5.581	5.1621	5.2954	5.4809	4.816	5.2937	5.3062		5.2011	5.5966				4.5816		5.6338	5.3566		
R.DGHEINVLQLETACGAAIR.H +2									6.2601				6.3634		6.5584		6.4402			5.8515					
R.DGHEINVLQLETACGAAIR.H +3													3.5926												
R.EGNTFLDLSVR.Q +2				3.0179	3.2134	3.1718	3.1121	3.5184	3.1158		2.7268	2.877	3.3587	3.2663	3.0805	3.2746	2.7038			3.0488		3.2267	3.0515	2.6273	
R.EILFVSNGDNLGATVDLK.I +2									4.2306			3.4945		2.9809	4.2081	3.6188				3.1931	3.4175		2.9978		
R.FGPNPLIK.L +2		2.7554		2.6487									2.5565	2.7198	2.7225	2.7926								2.5267	
R.GTVIIVCSDGHK.I +2								2.6355						3.2011											
R.HFDGAHGVVVPR.S +2													3.6911	3.6407					2.9987	3.4834					
R.HFDGAHGVVVPR.S +3														3.9067						3.5003					
R.LIESSNLEM*EIIPNQK.T +2													4.0027												
R.LIESSNLEMEIIPNQK.T +2								3.0452								3.9502									
R.LLEVAQVPK.E +2								3.2915	3.9567		3.8696	4.0713	3.7157	3.8463		3.8441					3.2715		3.8313	3.3791	
R.QYDSDVPLLLM*NSFNTDK.D +2																		2.8655	3.8658						
R.QYDSDVPLLLMNSFNTDK.D +2																								2.8355	
2		X		X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	
gi|6325229|ref|NP_015297.1|	7			3.8	29.6	32.9	31.2	38.2	47.7	17.3	30.7	35.4	45	48.7	42.2	42.2	42.2	26.6	38.4	44.5	19.6	17.1	27.9	26.9	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase), cytosolic enzyme that transfers an acetyl group from one acetyl-CoA molecule to another, forming acetoacetyl-CoA; involved in the first step in mevalonate biosynthesis; Erg10p [Saccharomyces cerevisiae]
K.AIILGAQSIK.C +1						2.3605	2.2342	2.3824				2.8397	2.4896	2.5491	2.4049	2.4797	2.3923			2.445	2.4116	2.3189	2.2068	2.5718	
K.AIILGAQSIK.C +2					3.5185	3.3578	3.7077	3.5177	3.3258			3.3792					3.184			2.857	3.3831			2.7524	
K.DFDEIIFGNVLSANLGQAPAR.Q +2							2.9413	5.344	5.8381		2.9582	5.4173	5.3038	3.9957	5.302	3.8348	3.3764		4.3557	4.8212			3.3347		
K.DFDEIIFGNVLSANLGQAPAR.Q +3													4.2397		3.6985										
K.EGKFDNEIVPVTIK.G +2																	3.6812		3.4166	2.9601					
K.ENGTVTAANASPINDGAAAVILVSEK.V +2					2.9228	3.9344										4.7274	3.1163	5.2781	3.2681	4.32	4.4503		3.2303	4.3429	
K.ENGTVTAANASPINDGAAAVILVSEK.V +3					4.1331	5.2338	5.1157	4.4164	4.5454		3.9614	4.6921	4.5909	6.3113	5.9102	5.7795		4.6387		5.5915	5.0037				
K.FDNEIVPVTIK.G +1					2.2595																				
K.FDNEIVPVTIK.G +2					4.3125	4.4851	4.4037	4.6512	4.3913	3.5587	4.1537	4.3083		3.7984		4.2758			3.936		3.8077		4.2967	4.0013	
K.FGQTVLVDGVER.D +2					4.2689	4.1976	4.4101	4.2608	4.3279	3.875	4.0155	4.1253	4.158	4.1532	4.4127	4.3523						4.2231	4.1239	4.2679	
K.GWGEAAHQPADFTWAPSLAVPK.A +2														4.2904											
K.IGVAAICNGGGGASSIVIEK.I +2					5.9008	6.4279	6.1619	6.193	6.256	2.7362		5.6775	5.7193	6.5421	6.1201	6.3395	4.5718	3.4933	4.8878	5.1907	6.4323	4.1354	4.0844	4.939	
K.IGVAAICNGGGGASSIVIEK.I +3													4.32	5.3843											
K.IGVAAICNGGGGASSIVIEKI.- +2																		3.0336		3.834					
K.NLKPLAIIK.G +2																2.5153									
K.TAVELGAVALK.G +1					2.4492	2.4019			2.3055		2.3014		2.1168	2.3773			2.2236	2.4558			2.3846		2.2614		
K.TAVELGAVALK.G +2					3.0184	3.2256	3.1924	3.0464	3.1356		2.5588			3.1431									3.2281		
K.VNVYGGAVALGHPLGCSGAR.V +2									4.1518				5.9961	5.4164	5.6109		4.8183	3.367	4.7895	4.6051					
K.VNVYGGAVALGHPLGCSGAR.V +3													3.7471		3.81										
R.DGLNDAYDGLAM*GVHAEK.C +2													3.9406						4.6134						
R.DGLNDAYDGLAMGVHAEK.C +2									3.7822						5.0405	5.0811	5.6157			3.9642					
R.EQQDNFAIESYQK.S +2						4.3359		4.531	4.4413	3.831	3.9503	4.2371	4.8579	4.8276	4.3971	4.1117						3.8802			
R.QVALAAGLSNHIVASTVNK.V +2																			2.8543	4.2699					
R.TPIGSFQGSLSSK.T +2	3.9955				3.681	4.2225	4.1564	4.096	4.1937	3.3875	3.78	3.384	3.7828	4.1503	3.9517	3.9918	3.6842	3.3767		2.8945		3.5348		3.9593	
R.VVVTLLSILQQEGGK.I +2	4.8795			5.1033	4.9533	4.9671		4.8304	4.7815		3.7054	4.7681	5.1422	5.013	4.8073	4.9298	5.0815	4.6811	4.8386	5.068				4.3831	
R.VVVTLLSILQQEGGK.I +3														4.9454					4.7016						
1	X			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6319597|ref|NP_009679.1|		5.5	5.5		9.6	11.5	13.5	13.5	16.9	17.5	22.2	19	26.5	30.1	26.5	26.8	12.3	21.1	11.8	27	13.6	12.4	11.2	14.2	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bearing tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end formation; Grs1p [Saccharomyces cerevisiae]
K.EYEEILAK.I +1											2.6416			2.688				2.3656							
K.GYLRPETAQGQFLNFNK.L +2													4.7731	4.5746	3.817				2.5458	4.288					
K.IDDSGVSIGK.R +1																				2.2248					
K.IDGYSGPELGELM*EK.Y +2								3.3087	2.9636	3.1005	3.022	3.3611	4.2347	3.8504		2.5195		3.1108	4.1342	3.9263	2.7924	3.6247			

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.IDGYSGPELGELMEK.Y +2					4.8475	4.4269	4.4683	4.4013	4.7284	2.9885	3.9459	3.7545			3.1666	4.2921		4.1183		3.139	4.4008	4.6944	3.6532		
K.LDDDVVKEYEEILAK.I +2																				4.1502					
K.LDNPIEVTK.W +1																								2.4326	
K.LDNPIEVTK.W +2											2.7636														
K.TPFASASIGK.S +1									2.5534				2.7234	2.3745	2.7859	2.2388	2.0692			2.3187		2.1704		2.3651	
K.TPFASASIGK.S +2																2.7839									
K.TSYGWIECVGCADR.S +2										3.0995	2.9002	3.6236	3.8153	4.1484	3.5811	4.3263				2.5413	4.0863			3.5635	
K.VDGVDGEVELDDK.L +2									4.7088		4.1079					4.6426		4.4451							
K.VESHLLNMSQDDLASK.A +2																4.0569	4.8277	4.9215		4.2518					
K.VLLVPLSNHK.D +2		2.5362	2.8235										2.6144	2.5027	2.6431					2.7239					
K.WEIDLTK.K +1														2.0496											
K.YDIGNPVTGETLESPR.A +2					5.0853	5.03	5.2251	5.1963	5.3995	4.6296	5.2031	4.903	4.5749	4.8037	4.2636	4.9288					4.1794	4.9793	4.5829	4.5327	
R.ADHLVEEVLEAR.L +2													4.1005	4.1668	3.8429	3.5749	3.4292		3.2894	2.8457					
R.AFNLM*FETAIGPSGQLK.G +2														3.3106					3.5607						
R.AFNLMFETAIGPSGQLK.G +2																				2.6292					
R.DITYNGASWEEGTK.D +2		3.8803	3.0674								4.7593							4.1482				2.7178			
R.DVQEAGSTEPIVK.T +2			3.9986					3.69	3.9664	3.1656	3.8683	3.8138	4.2592	3.4376	4.1317	4.009		3.8032							
R.EFLM*AEIEHFVDPLDK.S +2														3.9147											
R.EYVPSVIEPSFGIGR.I +2					3.7032	3.7715	3.4336	3.7127	3.4914	4.1093	3.6557	3.4228	3.7582	3.8747	3.785	3.5291	3.0942	3.3366			3.1776	3.6595		3.639	
R.GLVEDANAAAK.D +2													2.9134		2.5408	3.3477									
R.GLVEDANAAAKDDAEK.K +2																	4.5526	5.0368							
R.M*VDNETLGYFIAR.I +2										2.819			3.76		2.83										
R.MVDNETLGYFIAR.I +2						2.9763	2.734	3.1572				2.5711			3.6846	3.4258	4.7921	4.5837		4.2968		3.3072	3.0693	4.3207	
R.NDELGTPFGVTIDFESAK.D +2					5.4413	5.6375	5.0661	5.31	4.7301	3.0831	3.4097	4.6642	4.5084	5.1588	4.1867	4.9833		4.9068	2.9219	3.9089	3.4432		5.004	5.3448	
R.SAYDLTVHSK.K +2												2.6454													
R.SVLSFPPLVAPTK.V +2		3.5692					3.5031		2.8938	3.1758	3.2924	3.3389	3.371	2.8933	3.3586	3.4419				3.0975	3.3682		2.7333		
gi|6319695|ref|NP_009777.1|		4	2		5.8	7.5	8.3	5.6	11.4	3.8	8.6	11.1	16.4	16	10.8	12.5	6.7	12.2	10.3	11.6	8.8	6.1	7.4	6	Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to isoform Pyc1p but differentially regulated; mutations in the human homolog are associated with lactic acidosis; Pyc2p [Saccharomyces cerevisiae]
K.ADVHDTHQIGAPM*AGVIIEVK.V +3													5.145						4.1024						
K.AGITWIGPPAEVIDSVGDK.V +2					4.2267	4.8689	3.7623	4.1219	3.6901	2.561	3.1047	3.4917	4.4862	3.6918	4.0422	3.5746			3.5865		3.1579	3.3873	2.7581		
K.CSCSGSTYEIVR.R +2									3.6705																
K.DGESVDASDLLVVLEEETLPPSQK.K +2					4.717	4.8713	4.5669	4.3661	3.6523				3.3917	3.3664	3.891	3.6533		3.019							
K.DNGVDIFR.V +2																				2.5529			2.7267		
K.IREDLQNRFGDIDECDVASYNMYPR.V +3																							3.6965		
K.IVQM*GTHILGIK.D +2													3.814	3.8022	3.8491					3.0534					
K.IVQMGTHILGIK.D +2		3.8009												3.8417	3.6314		2.6318			3.1151					
K.LLHYLADLAVNGSSIK.G +2												3.0615													
K.LQAVGDLNKK.T +2																			2.5715						
K.LTCRPGLELEPFDLEK.I +2													4.3034	3.9475	3.9392					4.1173					
K.LTCRPGLELEPFDLEK.I +3													3.7524												
K.NFLAPAEPDEEIEVTIEQGK.T +2							4.4022		4.5573			2.9784		4.2466	3.6593	4.3054		4.5856		2.8994	3.835			3.4348	
K.SNPSVPHLHDAQGNVINVTK.S +2														3.7118					2.625						
K.SQNIQSVAKPK.A +2		3.2145																2.9361							
K.VDFIHPGYGFLSENSEFADK.V +2													4.9104												
K.VDFIHPGYGFLSENSEFADK.V +3													4.7061	4.798											
K.VVGDLAQFMVSNK.L +2		2.5208	2.9471		3.3718				3.8937		2.7409	2.7824	3.801	4.0227	3.9742	3.9194	3.7362				3.9273			4.2046	
K.YNLDYYLEVVEK.I +2												2.6617	4.1224	3.8497	4.5105	4.8456			2.7684						
R.DAHQSLLATR.V +2																		2.9245							
R.DAILTDAVK.L +1											2.284														
R.DNFSLLGEK.N +1																				2.029					
R.DNFSLLGEK.N +2																					2.7503			2.5525	
R.EANYLLGDIVK.V +2		3.6024	3.4332				3.266	3.6315	3.7088		2.9454	3.2569		3.2667	3.0602	3.2351	3.3593	3.1661	3.1879			2.9921	3.1882		
R.EGDDVADAFQR.A +2									3.2958		3.5797	3.0344	2.909			2.6785		3.1633	2.918			3.2052			
R.ELDAYWAEMR.L +2																				2.9143					
R.ETYGDLSVLPTK.N +2						3.1531	3.055			2.5024	2.6051												2.8364	2.7126	
R.FGDIDECDVASYNM*YPR.V +2												2.5729							4.3788	4.5034	4.768				
R.FGDIDECDVASYNMYPR.V +2																	3.967			3.7305	3.6394	3.5002	3.9511	4.7756	
R.GANGVAYSSLPDNAIDHFVK.Q +2																				2.54					
R.HYFIEINPR.I +2													2.5354												
R.LDGGNAYAGATISPHYDSMLVK.C +2																		3.5833							
R.LLYSCFEADLK.G +2																		3.5214							
R.NAGTAEFLVDNQNR.H +2										4.3419	4.572		5.0521			4.8574	4.2218				4.7133	4.1012			
R.PGLELEPFDLEK.I +2						2.7656			3.5496					2.9766	2.8339	3.4545									
R.QFNGTLLMDTTWR.D +2																				2.7027					
R.TAFGNGTCFVER.F +2																		3.3172							
R.TIAIYSHEDR.L +2						2.6658							2.9285	3.2254											
R.VFDALNDLEQLK.V +2					4.7882	4.7266	4.9047	4.8527	4.756		3.7348	4.2394	4.4843	4.6736		4.8476	4.6167	4.3628		3.3653	4.2152		4.0062		
gi|6321594|ref|NP_011671.1|		6.5	7.3		22.3	25.2	18.9	17.8	30.6	20.9	25.2	27	41.6	46.9	23.7	37.3	29.2	25.6	27	33.1	12.6	9.3	18.3	18.1	Cystathionine beta-synthase, catalyzes the synthesis of cystathionine from serine and homocysteine, the first committed step in cysteine biosynthesis; Cys4p [Saccharomyces cerevisiae]
K.ALGAEIIR.T +2														2.5202		2.6163									
K.ALGIKPQIYAK.L +2		3.3922											3.2583	3.3114	3.3537		2.9445	2.7709		3.1256					
K.DLHLKPVSVK.E +2														2.6821						2.8296					
K.DNGFDQLPVLTEDGK.L +2			4.1901		4.6455	4.6589	4.8264	4.7569	4.2507	3.7751	4.3648	3.2599	4.8745	4.7566	4.1904	4.1228	3.9041	3.4221	4.466		3.8682	4.066	3.0716	3.7762	
K.FVDDEWLK.K +2														2.516									2.5721		
K.IQIVGADPFGSILAQPENLNK.T +2					5.5172	5.96	5.8502	4.86	5.638	2.7919	4.9193	4.1334	5.3015	5.872	6.0071	5.362	4.7606	5.0402	6.2849	5.9179	4.5469		3.2061		
K.IQIVGADPFGSILAQPENLNK.T +3													5.6947	5.1592	5.4769					4.1242			4.5654		
K.KLNNFNDVSSYNENK.S +2													5.9575	5.0807				4.896		3.8983					
K.KNNLWDDDVLAR.F +2													3.8407			2.6792									
K.LELYNPGGSIK.D +2													2.9372	2.7905		2.6767	3.1053								
K.LNNFNDVSSYNENK.S +2						3.8288				4.0303	4.2768		4.4475			4.1613			3.1882						
K.LSGLVTLSELLR.K +2									3.79			3.5129	4.5235	4.4607			3.8527	2.6796	3.551	4.0304			3.2131	2.8019	
K.LSNNSNNDNTIK.G +2						3.3822			3.3102	3.2302	3.1335	3.2979	3.2963	3.2788	2.815	3.6688				3.3914	3.3578				
K.NNLWDDDVLAR.F +2							3.1847		3.6147	2.8992	3.2099	3.0551					3.8198	3.188		2.5532				2.9545	
K.NSSAVITDGLKPIHIVTK.M +2													4.4677	4.7985											
K.NSSAVITDGLKPIHIVTK.M +3													3.5975												
K.TDITDYK.V +1																				1.9283					
K.TDITDYKVEGIGYDFVPQVLDR.K +2																				3.0779					
K.VEGIGYDFVPQVLDR.K +2					4.7568	5.1188	5.0628	5.1399	5.0889	3.9274	4.0365	4.899	4.859	4.4793	5.1882	5.1016	4.0265	3.5745		3.0502	3.8806	4.724	4.5985	4.7588	
K.YADVFGNATVK.D +2					2.9623	2.7451			3.1087			2.9062	3.0674	2.839	3.0279	2.9037			2.8382						
R.AVVAGAGTGGTISGISK.Y +2					5.3738	5.1591		5.4498	5.1699	5.4144	5.1449	4.1168	4.5083	5.3596		4.5776						5.0938		5.5441	
R.FDSSKLEASTTK.Y +2																			3.1009						
R.HNVIDLVGNTPLIALK.K +2																			3.6911						
R.KLSINNSNNDNTIK.G +2																			4.0779						
R.QLEDLNLFDNLR.A +2					3.3685		2.9277							2.9828	2.5913	3.2318	3.0513	2.7122		3.701					
R.STLIEPTSGNTGIGLALIGAIK.G +2		4.4869	4.4527		5.3977	5.8568	5.6936	5.6261	5.5013		3.2613	4.3231	5.3908	3.5851	4.07	4.0091	5.2794		4.5167	3.6908			5.8134	4.8981	
R.STLIEPTSGNTGIGLALIGAIK.G +3													5.0279		3.7679										
R.TPTAAAWDSPESHIGVAK.K +2									3.5501				4.0787	4.8693		3.1791	4.2843	3.9994		4.8385					
R.TPTAAAWDSPESHIGVAK.K +3														3.6877											
gi|6321643|ref|NP_011720.1|		6.6	4.7		11.7	11.2	14.8	14.8	17.1	7.4	10.4	16.1	23	22.2	14.9	18.7	15.1	13	10.6	18.1	9.3	9.7	8.8	6	Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase, involved in single carbon metabolism and required for biosynthesis of purines, thymidylate, methionine, and histidine; Ade3p [Saccharomyces cerevisiae]
K.AALEAGAFEAVTSNHWAEGGK.G +2															6.4825	5.5592				4.0826					
K.CVGDVEFNEAIK.Y +2								3.0367						3.1629				3.5523					3.4094		
K.DVDGFGPTNIGELNK.K +2					4.3576	4.5613	4.7803	4.5948	3.9388	3.5806	4.0605	3.6615	3.9583	3.7617	3.9544	4.3191	3.0015	3.3645				4.3081			
K.DVDGFGPTNIGELNKK.N +2																	2.9077	3.5765							
K.EQGFGNLPICIAK.T +2		3.2603			3.3181	2.9447	3.3763	3.4062	3.495	2.862	2.9227	3.1277		3.1866	2.9712	3.3656									
K.FETDTEGEIAAIR.K +2					4.3874	4.1216	4.0719	3.906	4.4108	3.6041	4.1365	4.313	4.0077	4.2372		3.814		3.7519			4.0544	4.2331	4.1395	4.0526	
K.FETDTEGEIAAIRK.A +2																		4.2181		3.0791					
K.GVPTGFTFPIR.D +2														2.8883									2.5197		
K.LLTPVPSDIDISR.A +2						2.5134	2.8755	2.7995	2.748		2.7592	2.7416	2.9028						2.652	2.7217					
K.M*YGGAAIDILPEAQR.K +2									3.2846			3.2787	4.2689	4.3987	3.8109	3.8888		4.0001	4.1979		3.2063				
K.MYGGAAIDILPEAQR.K +2					3.6661		2.7952	4.3499								3.3529					3.3348	4.2996	4.5621	4.2924	
K.PLQIPPLPLK.L +2																			2.6876	2.9151					
K.QFGVPVVVAINK.F +2							3.0177						2.9519							2.8055					
K.RVVDINDR.M +2																				2.7416					
K.SHGGAPDVKPGQPLPSAYTEENIEFVEK.G +3													5.286	5.0562			4.6307								
K.SLNSTVTITHSK.T +2		3.0775	3.1532		2.8031							2.7644			3.3332					2.7093					
K.STTTM*GLVQALTAHLGK.P +2														3.7699											
K.TEAGYVVTEAGFDFTM*GGER.F +2																						3.9261			
K.TNPDDLTPEEINK.F +2		3.7796							2.9536				3.3735			3.3461	3.7039								
K.TQYSLSHDATLK.G +2									3.3832		3.1971	3.2444		3.7168		3.1271	3.272				3.0289				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.TVVIDVGTNYVADPSK.K +2														5.2595	5.0625	5.4928				3.7615					
K.TVVIDVGTNYVADPSKK.S +2													4.2217	4.0871	3.4842		3.7929	4.074		3.6752					
K.YILVSGITPTPLGEGK.S +2							4.8606	4.5662	5.0279	4.3242		4.9301	4.8631	4.8331	4.5363	4.864	4.7736	4.7951	4.4365	3.9996	3.6301	4.5185		4.9884	
R.LNIDPDTITIK.R +2					2.8413	3.4831	2.7385	3.0498	2.9336				2.7491			2.9504		3.1025	2.6302						
R.QITIGQAPTEK.N +2		2.7455										2.685													
R.QMEESSKPLQIPPLPLK.L +2													3.1622												
R.SDIVGSPVAELLK.S +2		3.7973	3.6512		3.7133	3.5855	3.8355	3.7341	3.6131	3.313	3.2433	3.6384	3.5459	4.1393	3.1113	3.4674	3.529	3.6311		3.7557	2.8115	3.8443	4.0067	3.1827	
R.SPVTVEDVGCTGALTALLR.D +2			4.5864		3.2376	6.7454	6.1215	5.7666	5.4733		5.3352	5.641	5.2614	6.5962	5.4218	7.2246	4.457		5.9193	4.5591	6.5834		5.6046		
R.SPVTVEDVGCTGALTALLR.D +3													4.2696	3.9285	3.9502	4.0939			3.5347						
R.SSGLTPNAVVLVATVR.A +2													2.9502						2.6705	2.5399					
R.VVVAADVNR.S +2						2.9742			2.7259					2.855			2.8713	2.8772							
gi|6322012|ref|NP_012088.1|		12	14.9		14.9	14.9	21.4	14.9	21.6	18.4	20.3	21.4	25	22	21.8	27.5	17.8	24.9	25	23.5	11.9	14.9	18.5	15.5	Inosine monophosphate dehydrogenase, catalyzes the first step of GMP biosynthesis, expression is induced by mycophenolic acid resulting in resistance to the drug, expression is repressed by nutrient limitation; Imd2p [Saccharomyces cerevisiae]
K.ESFPGLEVIAGNVVTR.E +2							4.8463		3.5396			2.8759	3.0913			3.6023		4.1392	3.9044				2.6558		
K.GNLVSMLSR.T +2																				2.938					
K.NPVTGAQGITLSEGNEILK.K +2		6.1584	6.1961		6.6906	6.1313	6.5625	6.0588	6.143	5.8717	5.3127	5.8825	6.8637	6.2463	5.8466	6.0527	5.5624	5.2941	6.0202	5.1802		6.7044	6.233	5.8445	
K.NPVTGAQGITLSEGNEILK.K +3													4.2899	4.7673											
K.NPVTGAQGITLSEGNEILKK.I +2									4.5582				5.0257	4.9282		5.4284			3.7879						
K.NPVTGAQGITLSEGNEILKK.I +3														3.9774											
K.NYENGFINNPIVISPTTTVGEAK.S +2		4.6099	5.8055		4.7503	5.297	4.88	4.8164	4.7772	3.8481	4.1399	4.3831	4.5934	5.5503	5.0538	4.7751	4.6763	4.0917	4.9272	4.7821	4.6626	3.0574	4.8267	4.48	
K.NYENGFINNPIVISPTTTVGEAK.S +3						4.5561		5.2067	3.7108		3.8598		4.6627	5.4392	4.0768		4.8462	4.6876		6.2168				4.7523	
K.YGFAGFPVTTDGK.R +2																3.2011									
R.DIQFVEDNSLLVQDVMPTK.N +2							5.2001		4.5524	3.6006	3.6839	4.015	3.634	3.9161	4.5558	4.8779		3.9191	3.7665	3.6691	5.0558		4.901	2.8836	
R.DIQFVEDNSLLVQDVMPTK.N +3														5.1713											
R.DIQFVEDNSLLVQDVMTK.N +2									4.2852							4.3566	4.5248								
R.EQAANLIAAGADGLR.I +1									2.5733																
R.EQAANLIAAGADGLR.I +2			4.5531		4.672	4.7825	4.7581	4.7828	4.5999	4.7525	4.5345	4.6073	4.9458		4.2697	4.5431	4.3255	5.1225	4.3588			4.6913			
R.EQAANLIAAGADGLR.I +3														4.4129						4.2676					
R.GMGSIDAMQK.T +2											2.6548														
R.TASAQLEGGVHNLHSYEK.R +2													4.9829	4.8521	3.1837	3.3026	4.7076	4.2446	2.6855	3.2225					
R.YFSESDSVLVAQGVSGAVVDK.G +2		5.9993	5.731		6.2921	5.919	6.0219	6.1313	6.2703	4.5902	4.9199	6.417	6.2792	6.0096	6.1684	6.2208		5.8755	3.5251	5.5607	3.9034	5.9741	3.6325	5.8171	
R.YFSESDSVLVAQGVSGAVVDK.G +3													3.8966	5.986				3.5647	3.9027			4.2958	3.8759		
	5	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6321837|ref|NP_011913.1|	3.3		3.4		4.8	10.2	3.3	6	6.2	4.3	2.7	11	17.2	16.4	16	15.7	7.6	12	3	16.5	4.3	5.8	8.6	6.3	Arginine/alanine aminopeptidase, overproduction stimulates glycogen accumulation; Aap1p [Saccharomyces cerevisiae]
K.AVVFNTVAR.L +2											2.5323		2.9423									2.556			
K.DSTGIDNTLVLNEK.S +2											3.7621														
K.DVCSVMNIWTK.R +2														2.6245											
K.EEEDTTIYPILLALK.D +2													3.9798	3.8079	3.5877	3.2971						2.7891	3.6127		
K.FGQFAANLAAR.T +2					3.084			3.681	4.0088	2.897			3.7753	4.0971	2.8534	3.8902					2.9892				
K.FTLDLVLNK.L +2																		3.1555							
K.GFDQTLAQALDTIR.S +2	3.2773												4.0515	4.554	4.3661	4.2052	3.8872	4.4388		4.2209			2.9684	4.0156	
K.IFNIYQNPVSSEEK.I +2						4.7826	4.7315		5.1264	3.0228		3.4368	3.3842		4.5459	4.5398	4.4861	3.047	3.861				3.1774	5.0135	
K.INGDQSGIFITSYSDER.W +2						3.0153												3.0988					3.6343		
K.LSELGWNIGEDDSFAIQR.L +2															4.0917										
K.NEDSFVVWEQIINSLSALK.S +2																				3.2333					
K.STWVFEPEDILNALDK.F +2					3.1349	3.9443								3.4112	3.0309	3.3329				3.7474					
K.TGDLWDALADASGK.D +2			4.9252			4.2475		4.4192	4.9159			4.342	4.3436	5.0535	4.847	5.0802	4.2065	4.853		3.5444	4.739		5.1066	4.517	
K.VTLFSAACTSGNEK.M +2												3.1725					4.0575	4.43		4.8124		3.2166			
K.VWEQYVTDNLQR.A +2						4.2564		3.8412		3.8936		3.5054	4.2169	4.73	4.3036	4.2423		4.4905	4.2256	4.4659	4.1296	4.6395		3.9269	
K.WLGEETFIK.G +1																		2.0754							
K.WLGEETFIK.G +2													3.092	2.9363	3.0993	2.6245	2.6511			2.6625					
R.EVLPNNVTPLHYDITLEPNFR.A +2																				3.6463					
R.FFEDTFNIEYPLPK.M +2	2.8573				4.3724	4.0076	3.6465	3.9543	2.7733			3.2765	3.377	3.8805	4.4253	4.1962				3.097					
R.IEGVNAIEVNK.N +2												3.049	3.8508												
R.VGFPVLSVK.E +2													2.903	2.5968											
R.VGLVADAK.A +1																				1.9126					
R.VIDLLLDIENSSLDR.I +2			2.5734									4.0544	4.5109	3.3005		3.6957									
	1 X		X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6324907|ref|NP_014977.1|		15.9	11.2	16.3	16.3	20.6	20.2	20.2	24.5	29.2	22.7	24.5	26.2	15.5	15.5	20.2		17.2	10.3	29.6	9.9	19.3	12.9	20.2	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma4p [Saccharomyces cerevisiae]
K.ADQEYEIEK.T +2							3.2033	3.1833	3.0971	3.0617		3.0458	3.1499			3.0346			2.7536						
K.AMLSQQITK.S +2														2.6083	2.7665					2.7491		2.9536			
K.DLVSGGVVVSNASDK.I +2											4.4371		3.7131							4.6555					
K.IEINNTLEER.L +2						3.3246			3.0684	2.9345		3.1543	3.1356												
K.LLSEEALPAIR.L +2		3.623			3.8013	4.0575	4.0577	3.9823	3.9126	3.7344	3.755	3.4868				3.5313		3.9301		3.0962				3.9458	
R.APLEEIVISNDYLNK.D +2		5.2423	5.1182	4.6442	4.5584	4.7649	5.2697	5.4019	4.6877	3.3183	5.2822	4.6916	4.8968	5.1985	5.3816	5.0275		4.2092	3.5143	4.5199				3.5006	
R.DVDLIESMK.D +1																						2.2281		2.518	
R.DVDLIESMK.D +2																							2.6461		
R.DVDLIESMKDDIMR.E +2																				4.0413					
R.EQSLDGIFEETK.E +2				3.543	3.4486	3.7157	3.728	3.7427	3.4667	3.3175	3.1005	3.1134	3.1991	3.6036	3.2891	3.2704		2.8659			3.2674	2.9967	3.2562	3.3075	
R.EQSLDGIFEETKEK.L +2																		2.9956		2.7927					
R.NETNNIDGNFK.S +1																					2.5521				
R.NETNNIDGNFK.S +2		3.2448	3.0864	3.6942						2.6365											2.8467				
	1	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X	X	X	X	X	X	
gi|6325006|ref|NP_015074.1|	29	20		33	31	40	31	31	31	31	40	28	23	23	23	33	23	23		24	9	21	21	9	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Ap and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA; Rpl36bp [Saccharomyces cerevisiae]
K.AKVEEM*NNIIAASR.R +2													3.721												
K.AKVEEMNNIIAASR.R +2				4.2995									4.1888	4.244	2.5493	3.0852	4.3456	4.5086		4.0501					
K.KVTQMTPAPK.I +2	3.1246	3.1746																		2.986					
K.TGIAIGLNK.G +1					2.7177	2.4778	2.7729		2.5618	2.2899	2.4728	2.6195	2.208	2.3303	2.6143	2.5062	2.6807	2.6265			2.5555	2.1993	2.6755	2.4583	
K.TGIAIGLNK.G +2	3.2906			3.4164	3.3571	3.1307	3.2124	3.2336	3.2907	3.1821	3.2443	3.2479	3.0511		3.0074	3.0347	3.2586	2.5085			3.1926	3.1811	3.4239	3.3165	
K.VEEM*NNIIAASR.R +2										4.092			4.1953	3.7484											
K.VEEMNNIIAASR.R +2					4.7537	4.7242	4.7177	4.6901	4.4674	4.5173	4.5944		4.5799	4.5565	4.1519	4.2271	3.7764	3.4634				4.5602	4.4548		
K.VTQMTPAPK.I +1						2.1934																			
K.VTQMTPAPK.I +2						2.8853					2.6634	2.5111													
R.EIAGLSPYER.R +2	2.6369	2.6592		2.569	2.7706	2.906	2.9159	2.9484	2.7494	2.7893	2.7001	2.63				2.6781									
	1 X	X		X	X	X	X	X	X	X	X	X	X	X	X		X	X		X	X	X	X	X	
gi|6322910|ref|NP_012983.1|	36.8	55.2	29.9	29.9	63.2	55.2	73.6	65.5	73.6	65.5	65.5	55.2	44.8	52.9	52.9	44.8	44.8			29.9	25.3	26.4	29.9	36.8	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Bp and has similarity to rat S21 ribosomal protein; Rps21ap [Saccharomyces cerevisiae]
K.ADDHASVQINVAK.V +1						3.3389			2.713		2.1481									2.9973					
K.ADDHASVQINVAK.V +2	2.6302	3.2622			3.9253	3.7081	3.8605	3.7982	3.6258	2.8576	3.4742	3.6681	3.4669	3.4153	3.2144	3.845	3.4621				3.1543	3.689		3.0632	
K.GQLVELYVPR.K +2	4.0097	4.1332	4.0513	4.0886	4.0633	3.8532	4.0117	4.0026	3.9262	3.8338	4.0701	3.9228	3.8515	3.5668	3.8824	4.0365	3.9225			4.0858		3.9657	4.1672	4.0227	
K.NVWSYSR.- +1					1.8373		1.8889		1.9821					2.025	1.9937										
R.AIPGEYVTYALSGYVR.S +2		4.652	4.8552	3.6163	5.495	2.8654	4.9933	5.2846	4.5235	2.674	3.473	4.9717	5.3075	5.0002	4.3387	4.163	3.2098			4.6746			4.7775		
R.GESDDSLNR.L +2							2.9554	2.7599	2.825	2.5348	2.8175										2.5134			2.9062	
R.LAQNDGLLK.N +2	2.8365	2.8923			2.8757	3.0539	2.8551	2.8832	2.7809	2.7772	2.7514	2.9782													
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X			X	X	X	X	X	
gi|6321987|ref|NP_012063.1|		15.5	8	15.5	28.7	28.7	19.5	19.5	36.8	28.7	32.8	40.8	32.2	45.4	20.1	40.8	36.8	28.7	16.1	29.9		32.8	25.3	24.7	Alpha subunit of the heteromeric nascent polypeptide-associated complex (NAC) involved in protein sorting and translocation, associated with cytoplasmic ribosomes; Egd2p [Saccharomyces cerevisiae]
K.AHNGDLVNAIM*SLSK.- +2													4.3786	4.5455					3.934						
K.AHNGDLVNAIMSLSK.- +2																				4.8038					
K.DDIELVVQQTNVSK.N +2					4.1899	4.4915	4.1286	3.8769	4.4689	3.7719	2.5896	4.0379	4.5531	4.3237	4.2531	4.0188	3.7028	4.2289				4.6179	4.3887		
K.DNQIYAIEKPEVFR.S +2		4.3553	3.9002	3.7134					4.1509			3.8725	4.3196	4.218	4.0688	4.0821	4.2279			4.0896					
K.DNQIYAIEKPEVFR.S +3														3.781											
K.LAAAQQQAQASGIM*PSNEDVATK.S +2																				3.7107					
K.LAAAQQQAQASGIM*PSNEDVATK.S +3										4.016	4.0412			5.1144						4.5399				3.9439	
K.LAAAQQQAQASGIMPSNEDVATK.S +2					4.4298	5.819			5.9302	4.9099	5.7034	4.9578				5.0724	5.3432	3.9969		6.0924			3.9089	5.4476	
K.LAAAQQQAQASGIMPSNEDVATK.S +3						4.5245			4.7766	4.3848	4.873			4.7147				3.9488				4.1069	4.0477	4.1011	
K.VDNFTQK.L +1							2.3048	1.9501			2.0139	2.0789			1.945	2.0756						1.981	1.9523		
K.VDNFTQK.L +2							2.6224					2.512												2.561	
R.SAGGNYVVFGEAK.V +1						2.3304	2.2122			1.8065														2.1166	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.SAGGNYVVFGEAK.V +2		3.6735		3.629	3.9315	3.9611	3.9615	3.9441	3.778	3.7945	3.6547	3.5268	4.0009	3.6545		3.6237	2.9736	3.6864	3.1196			3.7803			
1		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	
gi|6323371|ref|NP_013444.1|	15.1	16.3	18.6	16.3	18.6	19.6	18.6	18.6	22.4	19.6	19.6	19.6	25.3	28.5	22.4	22.4	19.6		12.8	18.6	19.6		16.7	7.4	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphorylated on serine 302; Rpp0p [Saccharomyces cerevisiae]
K.GNVGFVFTNEPLTEIK.N +2	4.3131	4.9514	5.0101	5.1998	5.21	4.9019	4.7433	4.9444	4.8491	4.3628	4.2265	4.067	5.1686	5.2313	5.2838	4.8014	4.4299			5.0167	5.0457				
K.KAEYFAK.L +1																			2.1646				2.0851		
K.LREYLEEYK.S +2													2.5746	2.5178											
K.SLFVVGVDNVSSQQM*HEVR.K +2									4.3097				5.2967	5.5708	4.0735	5.183				3.4835					
K.SLFVVGVDNVSSQQMHEVR.K +2														4.7577	5.147					4.6858					
K.TSFFQALGVPTK.I +2	3.9097	4.2336	4.2601	4.4335	4.2286	4.3478	3.9454	4.3295	3.9974	3.2882	4.2721	3.7617	4.008	4.2151	4.0501	4.013	2.518		3.5927	4.1126	3.5199		3.799	3.761	
R.AGAVAPEDIWVR.A +1															2.3282						2.5948				
R.AGAVAPEDIWVR.A +2	3.7853	3.6863	3.9533	4.0902	4.0763	4.1825	3.8909	3.9738	4.1951	3.32	3.7433	3.0158	3.1856	3.5003	2.8749	3.369	3.2155						3.665		
R.AVVLMGK.N +1	1.8265		1.8672		2.1949		1.8861	1.9236																	
R.GFLSDLPDFEK.L +1																	2.7197		2.5754	2.5365	2.3134				
R.GFLSDLPDFEK.L +2		3.4726	3.4262	3.5515	3.547	3.2848	3.3238	3.3993	3.4946	3.2796	3.2553	3.2679	3.2551	3.3324	3.5644	3.3577	3.1903		3.4179	3.2186	3.3228		3.0491	3.171	
R.GTIEIVSDVK.V +1																	2.1885				2.2906		1.8811		
R.GTIEIVSDVK.V +2						3.5183				3.5321	2.8274	3.0725		3.3007			3.2916		3.1571				3.7957		
gi|6323577|ref|NP_013648.1|	30.6	38.8	38	27.1	16.1	12.9	25.5	22.7	38.4	14.9	18.8	34.9	44.7	42.7	34.9	40.8	25.1		29	36.1	6.3		6.7	6.3	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to rat S3a ribosomal protein; Rps1bp [Saccharomyces cerevisiae]
K.APSTFENR.N +2	2.6367	2.5869	2.5835		2.5954	2.673	2.6269	2.5743																	
K.DIFPLQNIHVR.K +2	3.2583	3.7511	3.5785	3.3676									3.273	3.5094	3.334	3.2988			3.0101	3.1613					
K.FDVGALM*ALHGEGSGEEK.G +2									3.7194			2.5221	3.9706		3.4001		3.2251								
K.FDVGALMALHGEGSGEEK.G +2	4.4116	4.6376	5.172											4.3868		2.5645	3.875								
K.KVSGFKDEVLETV.- +2																				2.541					
K.LRVDEVQGK.N +2		2.8052	3.0528	2.903			2.743	2.913	2.864	2.6102	2.7261		2.728	2.869	2.7838	2.6597				2.6692			2.8821		
K.NASDALK.G +1							1.8576																		
K.NLLTNFHGM*DFTTDK.L +2									4.3889			3.7493	4.5269	4.486	4.0846	4.144			4.5344	4.3308					
K.NLLTNFHGMDFTTDK.L +2	4.7953	4.9059	4.9058	4.3062										4.7324	2.982		4.0901			4.4302					
K.TSDDYVLR.I +2		3.1088		2.8695			3.2868	3.1204	3.3909	3.0881	3.4065	2.5708		3.0857						3.1024					
K.VISEILTR.E +2										2.5371	2.9113								2.9935		2.7014			2.7095	
K.VSGFKDEVLETV.- +2		2.8558			2.9719	3.0437	3.2307	3.1326	2.5787			2.8286	3.1143	2.9167		2.8687			2.6129						
R.EVQNSTLAQLTSK.L +2					4.1643	4.2912	4.4089	4.3992		4.0307	3.4884		4.3761			3.7447	3.7935								
R.HSYAQSSHIR.A +2		2.7289	2.8269						2.8889		2.6363	2.9456	2.9075	2.7888	3.0027					2.7131					
R.IFAIAFTR.K +2	3.1685	3.1196	3.1906	3.3588	2.9713		2.972	2.9376	3.1746			2.8778	3.1179	3.0888	3.1721	3.0187			3.0496	2.7406	2.6666		3.0489	2.6342	
R.IFAIAFTRK.Q +2																			2.8235						
R.VDEVQGK.N +1											2.0092														
R.VVEVCLADLQGSEDHSFR.K +2	2.5678		4.4592	5.0973					5.6909			4.774	5.6893	6.043	5.8593	5.75	4.8417		4.2441	4.4691					
R.VVEVCLADLQGSEDHSFR.K +3													3.6999												
R.VVEVCLADLQGSEDHSFRK.V +2																			2.9286						
2	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X		X	X	
gi|6319666|ref|NP_009748.1|	10.3	30.3	17.9	25.1	13.8	8.2	12.3	14.9	28.7	20.5	20	22.1	42.6	24.6	29.7	34.9	30.3	9.7	20	17.4			8.7	16.9	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Ap and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9bp [Saccharomyces cerevisiae]
K.AEASGEAAEEAEDEE.- +2										3.4058	4.5215	4.2603				5.1878								3.7089	
K.HIDFAPTSPFGGAR.P +2		3.6826		3.8504					2.7916				3.0065	3.7191	3.3135	3.1483	3.2592		3.1314						
K.KLDYVLALK.V +1															2.5151		2.3434								
K.KLDYVLALK.V +2													3.1389	2.8877		3.0897									
K.LAGEFGLK.N +1							2.1503				1.8331				2.198										
K.LAGEFGLK.N +2							2.6008																2.5472		
K.LDYVLALK.V +2													2.9188	3.3709	3.0926	3.4369			2.6777	2.8742					
K.QIVNIPSFM*VR.L +2									2.5703				2.8974			2.6343									
K.QIVNIPSFMVR.L +2	3.2003	3.3175	3.6403	3.4668	2.9895			3.3397				2.6425			2.7322	3.1314	2.7593	3.0644							
K.RLFEGNALIR.R +2		3.1755																	2.9356	3.1045					
K.RPYESSR.L +2			2.7065											2.5196	2.5205										
K.VEDFLER.R +1				1.8086																					
K.VEDFLER.R +2					2.7617	2.8029	2.6278		2.6336	2.716	2.6804		2.9015						2.9941						
R.KAEASGEAAEEAEDEE.- +2		5.1897											5.2061			4.2754	4.0977			2.8184					
R.LFEGNALIR.R +2	3.3663	3.5296	3.3047	3.3917	3.4398	3.4275	3.3346	3.5089	3.1657	3.3035	3.2543	3.0788	3.1829	3.2907	3.0964	3.4434	3.1396		3.2073	3.3722			3.0812	3.0928	
R.LQTQVYK.L +2									2.7821																
R.RLQTQVYK.L +2		2.8588	2.8128	2.508									2.7144												
R.VGVLSEDK.K +1														1.9374											
R.VGVLSEDK.K +2									2.5717			2.5521						2.8185							
R.VGVLSEDKK.K +2								2.6413		2.5062			2.5192	2.6539		2.6918								2.7619	
gi|6320963|ref|NP_011042.1|	25.5	32.1	32.1	25.5	31.4	31.4	31.4	31.4	31.4	25.5	25.5	25.5	37.2	31.4	25.5	37.2	25.5	32.1	31.4	33.6			25.5	10.9	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Ap and has similarity to E. coli L14 and rat L23 ribosomal proteins; Rpl23bp [Saccharomyces cerevisiae]
K.ECADLWPR.V +2													2.8524												
K.KVMPAIVVR.Q +2		2.5561	2.6468															2.5214							
K.VMPAIVVR.Q +1			1.8953																1.8269						
K.VMPAIVVR.Q +2					2.826	2.6472	2.7987	2.6279	2.6615							2.6106									
R.ISLGLPVGAIM*NCADNSGAR.N +2		3.0448				3.9715	4.5067	4.5556	3.4201	4.8841	4.48	4.7881	4.8691	4.1212	4.1044	4.5625	3.3302	3.7818	4.9204	4.1894			3.8107		
R.ISLGLPVGAIM*NCADNSGAR.N +3													3.915	3.7694											
R.ISLGLPVGAIMNCADNSGAR.N +2	5.2013	5.5101	5.3834	5.2941	5.2883	5.6169	5.4086	5.3658	4.9265	3.182	5.3286	4.3609		4.6622	4.6437	5.1817	4.4	4.3423	2.9304	3.2763			3.7588		
R.LNRLPAASLGDMVM*ATVK.K +3																				3.6214					
R.LPAASLGDM*VM*ATVK.K +2					4.2492	3.8545			4.0076	4.3598		3.7051	4.7999	4.6873	4.3332	4.5213	3.6376		4.5487	4.3545			3.5295		
R.LPAASLGDM*VMATVK.K +2						4.4204	4.0413	4.6309	3.7913	3.231		3.8874		4.6495	4.9085	4.485		4.4406	2.7735	3.797			3.6436	3.0474	
R.LPAASLGDMVM*ATVK.K +2					3.3855		4.7084	4.3065	4.0514	3.9053	4.2668	4.2414	4.1471	4.2544	4.9528			4.1606		3.3629			3.592		
R.LPAASLGDMVMATVK.K +2	4.6842	4.9568	5.3469	5.1708	5.1758	4.7637	4.6102	5.0337	4.3091			4.5614			4.9824	4.8447	4.468		3.0796	5.3044			3.1357	3.5964	
R.NLYIIAVK.G +2													2.6693	2.7863		2.5698				2.6198					
gi|6325176|ref|NP_015244.1|	10.2	21.8	17.8	24.9	13.7	8.1	12.2	14.7	28.4	21.3	12.2	14.2	34	24.4	29.4	26.4	21.8	9.6	19.8	9.1			8.6	9.1	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins; Rps9ap [Saccharomyces cerevisiae]
K.AEASGEAADEADEADEE.- +2										2.7746															
K.HIDFAPTSPFGGAR.P +2		3.6826		3.8504					2.7916				3.0065	3.7191	3.3135	3.1483	3.2592		3.1314						
K.KLDYVLALK.V +1															2.5151		2.3434								
K.KLDYVLALK.V +2													3.1389	2.8877		3.0897									
K.LAGEFGLK.N +1							2.1503				1.8331				2.198										
K.LAGEFGLK.N +2							2.6008																2.5472		
K.LDYVLALK.V +2													2.9188	3.3709	3.0926	3.4369			2.6777	2.8742					
K.QIVNIPSFM*VR.L +2									2.5703				2.8974			2.6343									
K.QIVNIPSFMVR.L +2	3.2003	3.3175	3.6403	3.4668	2.9895			3.3397				2.6425			2.7322	3.1314	2.7593	3.0644							
K.RLFEGNALIR.R +2		3.1755																	2.9356	3.1045					
K.RPYESSR.L +2			2.7065											2.5196	2.5205										
K.VEDFLER.R +1				1.8086																					
K.VEDFLER.R +2					2.7617	2.8029	2.6278		2.6336	2.716	2.6804		2.9015						2.9941						
R.LFEGNALIR.R +2	3.3663	3.5296	3.3047	3.3917	3.4398	3.4275	3.3346	3.5089	3.1657	3.3035	3.2543	3.0788	3.1829	3.2907	3.0964	3.4434	3.1396		3.2073	3.3722			3.0812	3.0928	
R.LQTQVYK.L +2									2.7821																
R.RLQTQVYK.L +2		2.8588	2.8128	2.508									2.7144												
R.VGVLSEDK.K +1														1.9374											
R.VGVLSEDK.K +2									2.5717			2.5521						2.8185							
R.VGVLSEDKK.K +2								2.6413		2.5062			2.5192	2.6539		2.6918								2.7619	
3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X	
gi|6319585|ref|NP_009667.1|		8.8	8.8	22.4	19.7	27.9	27.9	17	27.9	27.2	35.4	27.9	29.9	14.3	22.4	25.2	25.2	14.3	25.2	23.1	27.2	35.4	33.3		Calmodulin; Ca++ binding protein that regulates Ca++ independent processes (mitosis, bud growth, actin organization, endocytosis, etc.) and Ca++ dependent processes (stress-activated pathways), targets include Nuf1p, Myo2p and calcineurin; Cmd1p [Saccharomyces cerevisiae]
K.DNNGSISSSELATVM*R.S +2																			4.3854		3.5692				
K.DNNGSISSSELATVMR.S +2					2.7798	5.0162	3.2226		3.092	2.7654	3.1908	3.615				4.9106	4.3064				4.6728	3.0646	3.2926		
K.EAFALFDK.D +1													2.4161	2.6401	2.4964	2.5259	2.5458	2.2324	2.5386						
K.HVLTSIGEK.L +1																				1.9516					
K.HVLTSIGEK.L +2				2.6339																					
K.LTDAEVDDM*LR.E +2													2.7876												
K.LTDAEVDDMLR.E +2				3.9657						4.0941	4.2304										3.7921	4.1135			
K.NGDGLISAAELK.H +2						2.8439	3.1481	3.2568	3.1688		3.3132	3.1112	2.9728		2.9296					3.895		2.8361			
K.SNDSEQELLEAFK.V +2		4.9207	4.9788	5.0935	4.9119	5.1892	4.9333	4.8309	4.8862	4.8671	4.5304	4.6363	4.6784	4.5582	4.4625	4.7744	4.8465	5.0672	4.809	4.1106	4.7859	4.7999	4.7441		
R.EVSDGSGEINIQQFAALLSK.- +2																							3.277		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6320432|ref|NP_010512.1|		13.5	9	14	18.9	29.3	33.3	18.9	54.1	19.4	38.7	37.8	50.5	50.5	41.9	36	28.8	14	19.8	43.7	9	12.2	16.7		Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence; Adk1p [Saccharomyces cerevisiae]
K.AIELKVDDELLVAR.I +2																				3.6386					
K.DDVTGEALVQR.S +2													2.8189												
K.DELTNNPACK.N +2					3.4206	3.4957	3.4964	3.4848	3.4556		3.2364		3.1056	2.7424	3.1893	3.1428									
K.EDM*KDDVTGEALVQR.S +2													3.6543												
K.EDMKDDVTGEALVQR.S +2									3.8851	3.6589	3.7173	3.7194	3.8385	4.5038	4.4994	4.3297		3.665							
K.GTQAPNLQER.F +2			3.1437			3.1407	2.9495		3.02	2.9418	2.8093	2.6283					2.8085								
K.GTQLGLEAK.K +1									2.0813																
K.IFNPPKEDM*KDDVTGEALVQR.S +3													3.7816						3.6783						
K.IFNPPKEDMKDDVTGEALVQR.S +2																	3.3122	5.0267		4.2113					
K.IFNPPKEDMKDDVTGEALVQR.S +3				4.8303										3.5159	3.9149	4.4395	4.1779	4.2287		4.7275					
K.IM*DQGGLVSDDIM*VNM*IK.D +2														4.5473											
K.IM*DQGGLVSDDIM*VNM*IKDELTNNPACK.N +3													4.2099												
K.IMDQGGLVSDDIM*VNMIK.D +2																						3.111			
K.IMDQGGLVSDDIMVNMIK.D +2									2.8381													4.768	3.7173		
K.NGFILDGFPR.T +2		3.7919	3.1025	3.0669					3.6938		3.3283	3.6563	3.6473	3.7539	3.6383	3.8355	3.5439	3.74	3.0731				3.5393		
K.TGIWAGVDASQPPATVWADILNK.L +2					5.4206	4.9987	5.0496	5.4568	6.2448		4.0236	4.8436	4.9562	5.4131	4.7181	5.6065	3.6965			4.4187					
K.TGIWAGVDASQPPATVWADILNK.L +3					4.9882				5.3767			4.2968	5.9816	5.1966	4.3188	4.038									
K.VDDELLVAR.I +2		3.7846			3.7592	3.6597	3.7446		3.597	3.7626	3.6878											3.7623			
R.FHAAHLATGDM*LR.S +2						2.7399	3.5157						3.7503	3.9155	2.9978				2.99	3.1095					
R.FHAAHLATGDMLR.S +2																				4.1094					
R.LAAYHAQTEPIVDFYK.K +2									4.8276			3.5501	5.5576	5.431	5.1517	5.1715									
R.LAAYHAQTEPIVDFYKK.T +2																				4.7001					
R.LAAYHAQTEPIVDFYKK.T +3													4.258	4.2181											
R.MVLIGPPGAGK.G +1																					2.0088				
R.MVLIGPPGAGK.G +2		3.0527																							
R.SDDNADALK.K +1										1.8944										2.0462	1.876		2.3879		
R.SDDNADALK.K +2							2.7815	3.0193		2.8767	2.8794	3.0611													
R.SDDNADALKK.R +2												2.6522													
	2	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6323294|ref|NP_013366.1|	41.8	31.3	41.8	31.3	41.8		41.8	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3		Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Ap and has similarity to rat S28 ribosomal protein; Rps28bp [Saccharomyces cerevisiae]
gi|6324741|ref|NP_014810.1|	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Bp and has similarity to rat S28 ribosomal protein; Rps28ap [Saccharomyces cerevisiae]
K.TPVTLAK.V +1	1.8834		1.8806		1.8058		1.8186																		
R.ENDILVLMESER.E +2										3.6722		3.0692	4.1838	4.5304		3.5738		3.4932							
R.ENDILVLMESER.E +2	4.635	4.856	4.8621	4.8151	5.0316		4.6637	4.744	4.3343	3.4052	4.5502	4.513	4.3311	4.7419	4.2593	4.5528	4.1415	4.2814	4.3315	4.1327	4.4668	4.5693	3.8228		
R.VEFLEDTSR.T +1			2.1905						2.4492				2.1899	2.2129	2.2135	2.3026		2.3405	2.6189	2.144		1.9712			
R.VEFLEDTSR.T +2	3.3425	3.357	3.3302	3.4516	3.4106		3.3782	3.2087	3.2969	3.2959	3.5355	3.2901	3.363	3.3824		3.2863	3.1748	3.2509	3.0928		2.9065	3.0171	3.6828		
	1 X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6320781|ref|NP_010860.1|	24.2	35.8	35.8	44.8	44.8	33.3	39.4	44.8	44.8	44.8	39.4	44.8	49.1	53.9	44.8	44.8	37.6		20.6	41.2	21.8	26.1	16.4		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Bp; rpl12a rpl12b double mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins; Rpl12ap [Saccharomyces cerevisiae]
K.EILGTAQSVGCR.V +2	3.6519	3.5608	3.6204	3.5636	3.6068	3.5886	3.7164	3.6565	3.8754	3.5012	3.4413	3.554	3.4868	3.8147	3.6701	3.5687					3.3125		3.6489		
K.HSGNIQLDEIIEIAR.Q +2														5.1741					3.1435	2.7381					
K.HSGNIQLDEIIEIAR.Q +3														5.2136											
K.IGPLGLSPK.K +1									2.3187						2.1991	2.1127	2.1363				2.0492	2.0342			
K.IGPLGLSPK.K +2	2.7439	2.7428	2.6721	2.7557	2.6274	2.5188		2.6829	2.6277	2.5638		2.5203	2.5687	2.5431		2.509					2.6053				
K.NPHDIIEGINAGEIEIPEN.- +2		4.1817	4.7333	4.1099	5.0217		5.1542	5.1258	5.015	3.7902	4.2062	5.3525	4.5555	4.8431	4.1517	4.8834	3.8571			4.1766					
R.AVGGEVGASAALAPK.I +1					2.6326											3.009	2.5221			2.539		2.4504			
R.AVGGEVGASAALAPK.I +2				4.1977	4.3174	4.238	4.1091	4.1716	4.2466	3.894	4.1422	3.4485	3.7408	4.2833	3.9313	4.5151	4.2337				4.1456		4.141		
R.QAAASVVPSASSLVITALK.E +2	4.0215	4.5677	4.2514	3.7958	5.3444	5.2415	4.7693	5.362	4.5607	4.2028	3.8204	3.7606	3.9542	4.2248	3.2954	3.9629	3.7279		3.4288	3.7307		4.7352			
R.QAAASVVPSASSLVITALK.E +3													4.9791	5.4857	4.8999	4.6977									
R.TLASVTK.E +1													1.8565												
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X		
gi|6323481|ref|NP_013553.1|	20.5	18.8	13.6	14.2	25	31.2	31.2	25	35.8	16.5	21.6	29.5	43.8	31.2	36.9	31.8	23.3	10.2	25	22.2		21.6	10.2		Protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6bp [Saccharomyces cerevisiae]
K.EANLFPEQQTK.E +2	2.6709				3.2299	2.9436	3.1224		3.0022	3.1114	3.2269	2.6078	3.7511			2.5227			3.609						
K.FNVEYFAK.E +1					2.1533		2.2377	2.2321	1.883		2.1313	2.3414	2.0968	2.1153	2.1516	2.0742	2.1934	2.221				2.0716			
K.FNVEYFAK.E +2											2.9599	2.5496	2.5962									2.9538	3.05		
K.HLEDNTLLVTGPFK.V +2			4.5678										4.0303	4.7089	4.1573	4.1195				4.56					
K.KEANLFPEQQTK.E +2											3.8977											2.9967			
K.QYLSASFSLK.N +2															2.5659										
K.VSVEGVNVEK.F +1													2.4428	2.4266			1.9814	2.3137	2.2445	2.4262		2.5268	1.9507		
K.VSVEGVNVEK.F +2	3.2692	3.2783	3.316	3.4879	3.3433	3.2658	3.304	3.3065	3.2187	2.8895	3.2142	3.0891	3.0481		3.168		3.1073								
K.WYPSEDVAAPK.K +2						2.5454	2.5842	2.8598	2.5326				2.533												
R.ASLVPGTVLILLAGR.F +2	4.3113	4.4825		5.2002	4.5562	4.7701	4.4429	3.8105	4.4516			4.5931	4.9157	4.7364	4.347	4.5158	2.5852		4.4852	4.5688					
R.ASLVPGTVLILLAGR.F +3						4.2606							4.2606	4.4605	3.8821					4.2417					
R.YVIATSTK.V +1		2.3793				2.2629			2.2103	2.1409	2.2906	2.0095	2.3414	2.1249	3.3024	2.3491	2.0628		2.1045			2.3199			
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X		
gi|6320065|ref|NP_010145.1|	19.2	19.2	29.2	19.2	28.3	9.2	28.3	28.3	21.7	28.3	16.7	20.8	30.8	30.8	23.3	29.2	29.2	21.7	29.2	29.2	28.3		28.3		Protein component of the large (60S) ribosomal subunit, identical to Rpl35Ap and has similarity to rat L35 ribosomal protein; Rpl35bp [Saccharomyces cerevisiae]
K.EQLASQLVDLK.K +2					3.2886	3.2145	3.2582	3.2045	3.417	3.2907	3.1477	2.967	2.7761	3.1667	3.1917	3.1067		2.6548			2.7889		3.0053		
K.EQLASQLVDLKK.E +2			3.8382						2.9906				3.7031	3.7577	3.1108	3.638	3.7146	3.8647	3.9973	3.81					
K.FEASQVTEK.Q +1											2.0082		2.38			2.0856	2.0826		2.2515	2.2361	2.2157		2.3292		
K.FEASQVTEK.Q +2	3.0568	3.1681	2.8839	3.1058	2.999		2.8414	2.7857		2.6467	2.7284			2.882			2.9452								
K.SIACVLTVINEQQR.E +2	4.631	4.886	4.9205	4.9901	4.8663		4.7909	4.8338	4.5326	3.3857		4.6034	4.955	4.7722	5.0352	4.6239	4.8051	4.8615	4.0888	4.6675	4.1966		4.5789		
K.SIACVLTVINEQQR.E +3												3.8267	5.075	5.2535				5.0483		4.5928	4.7168		3.8894		
K.SKEQLASQLVDLK.K +2															2.8804										
K.SKEQLASQLVDLKK.E +2														4.2892											
K.SKEQLASQLVDLKK.E +3													3.8937	4.104											
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X		
gi|6321464|ref|NP_011541.1|	9.3	19.4	21.3	19.4	18.5	18.5	18.5	27.8	36.1	18.5	26.9	28.7	30.6	31.5	27.8	28.7	19.4	30.6	28.7	28.7	19.4	18.5			Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein; Rps25ap [Saccharomyces cerevisiae]
gi|6323365|ref|NP_013437.1|	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Ap and has similarity to rat S25 ribosomal protein; Rps25bp [Saccharomyces cerevisiae]
K.AAAALAGGK.K +1	1.942		2.8894		3.0041	2.9179	2.9644	3.054	2.9335	2.7713	2.8121	3.0905	2.8313	2.703	2.7345	2.7633	2.5864		2.352	2.1756	2.2143	2.4894			
K.AAAALAGGKK.S +2	3.3369	3.3305	3.4053	3.3769								2.7871		2.9936		3.0731	3.218	3.2828	2.7916	2.9082	2.9234				
K.DRAQHAVILDQEK.Y +2			3.816															4.1941							
K.EGIIKPISK.H +1									1.9994		2.4694														
R.AQHAVILDQEK.Y +1						2.9792	2.791						3.2255		2.94		3.0924			3.3302		3.1618			
R.AQHAVILDQEK.Y +2		3.4403	3.3822	3.4431	3.3292	3.2093	3.322	3.251	2.9705	3.4357	3.2325	2.9976			3.1861	2.7702			3.0317		2.7108	2.8056			
R.AQHAVILDQEKYDR.I +2													4.5662	4.3638											
R.YVSVSVLVDR.L +2								3.4703	3.6737			3.6669	3.9685	3.4896	3.5853	3.6369		3.3223	3.6501	3.9354					
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			
gi|14318569|ref|NP_116702.1|			5.6		18.3	19.1	18.3	19.3	29.7	16.8	16.6	16	29.5	40.7	21.8	26.8	13.1	21.8	13.1	32.6	17	22.2	19.1	16.6	Probable di- and tri-peptidase; forms a complex with Dug2p and Dug3p to degrade glutathione (GSH) and other peptides containing a gamma-glu-X bond in an alternative pathway to GSH degradation by gamma-glutamyl transpeptidase (Ecm38p); Dug1p [Saccharomyces cerevisiae]
K.AIQIPAVSSDESLR.S +2					3.8841	3.6859	3.6837	3.7354	4.2401	3.4049	3.6766	3.2356	4.168									3.7767	3.6721	4.0733	
K.ASGQEFPVNLVTCFEGM*EESGSLK.L +2										2.6638						2.9023					3.544	3.132			
K.ASGQEFPVNLVTCFEGM*EESGSLK.L +3														3.5482											
K.ASGQEFPVNLVTCFEGMEESGSLK.L +2						4.5347			2.802		3.1232					3.8745							3.3329	4.1131	
K.DIEFSVEELNAATGSK.T +2					4.9999	5.5039	5.2995	5.0814	5.4878	2.5403		5.2918	3.7521	4.9532	5.4442	5.8677	4.9367	5.0352	5.2228	4.8576	4.6868	5.5577	5.5719		
K.EANGYFK.G +1																				1.8349					
K.FISEQLSQSGFHDIK.M +2									3.6994				4.4267	4.6994	4.6974	4.7192		4.6224		4.5708					
K.GVDAVCISDNYWLGTK.K +2								3.4163	3.1235				3.8252	4.1115	3.8749	3.9082		4.603		3.9294					
K.IDSLKPQFFSR.L +2			2.6795										3.3875	3.1276	2.7765	2.932		3.2122		2.8891					
K.ILIDGIDEM*VAPLTEK.E +2										4.2282		4.7026	5.2188	5.116	5.07	5.0392		4.795			2.8233	2.906		4.132	
K.ILIDGIDEMVAPLTEK.E +2			4.1109		5.116	5.282	5.2661	5.2484	4.2131	2.733	2.8085	3.6905		3.6103	4.0643	4.207	4.1646		2.9855	4.2882	5.029		5.0306	3.233	
K.LDISNFVGGM*K.T +2												2.7052	3.4969	3.6662	3.3803				3.6784	3.0869				2.7452	
K.LDISNFVGGMK.T +2					3.3086	3.5257	3.7761		3.6251						3.5778	3.6619	3.7604	3.6036		2.9944	3.7238	3.6005	3.731	3.6698	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.LVYGVDPDFTR.E +2					2.849	2.9916	3.2136	2.9696	2.8697	2.89	2.9335									2.5304		2.9767	2.9469		
K.TMAAYLQYYSESPEN.- +2											2.5169									3.1675	2.6269	2.7263		3.3838	
K.TVLVYGHYDVQPAQLEDGWDTEPFK.L +3														6.1006											
R.GVTDDTGPLLSWINVVDAFK.A +2					5.7581		5.281	5.1786	4.9803			4.7564	5.5775	4.7337	4.3202	5.1018	3.9883	3.245	4.5271	5.2412					
R.TELIHDGAYWVSDPFNAQFTAAK.K +2														4.4232											
R.TELIHDGAYWVSDPFNAQFTAAK.K +3													4.6495	4.7767											
R.YPSLSIHGVEGAFSAQGAK.T +3														4.8479						4.7835					
gi|6321429|ref|NP_011506.1|			3.7		8.7	9.5	14.4	10	13.9	3.6	11.6	9.6	28.6	26.3	20.4	15.3	24.4	21.4	8.5	25.7	13.4	8.1	12.2	14.8	Isopropylmalate isomerase, catalyzes the second step in the leucine biosynthesis pathway; Leu1p [Saccharomyces cerevisiae]
K.ANVDTDAIIPK.Q +2					3.3185	3.4007	3.8885	2.652	3.4966	2.8316			2.9654	3.0578	2.7943	2.8981							3.2628		
K.DDQGKDQETDFVLNVEPWR.E +2													4.4225							2.9014					
K.DQETDFVLNVEPWR.E +2					3.7247	2.887	3.5358	3.2575	4.0339			3.5154	3.3713				3.5076		3.3072	3.0582		3.0821	4.0208	3.298	
K.ELESAAYDHAEPVQPEDAPQDIANDELK.D +3														3.6264	3.9878	4.1965	3.6921								
K.ELESAAYDHAEPVQPEDAPQDIANDELKDIPVK.S +3													5.1164				5.1904	5.0951		3.6229					
K.HCLVNGLDDIGITLQK.E +2													4.4564	5.4503	3.5292										
K.IFQEAGFEWR.E +2							3.1516		3.3544		3.1455	3.2592	3.1526	3.2309	3.0772	3.3376	2.8443			3.3737	2.6331		2.9464	2.7275	
K.ILDSDGNVLVDHFEIEPFR.K +2													4.7481	4.7175	3.2248					2.891					
K.LAM*VVPGSGLVK.K +2													3.4711	2.9992						2.7722	3.2308				
K.LAMVVPGSGLVK.K +2			3.22		3.0085	2.7532	2.9011	3.006	3.0656		3.1635				3.0842	2.7629	2.8964								
K.LCVDLPNQK.I +2																		3.2081						2.8595	
K.PFLTLEGISAPLDK.A +2						3.8536	4.0776						4.7751	5.2132	4.9384	4.5468	4.421	4.9299		5.017					
K.QFGVPYFGM*SDAR.Q +2													2.7289												
K.SDDTPAKPSSSGM*KPFLTLEGISAPLDK.A +3														4.1248											
K.SIIAPSYGDIFYNNSFK.N +2			3.6539		5.2057		5.3012	4.7505	5.0481	3.5806	4.1819	4.0191	4.6567	4.9242	3.4449	5.2137	2.5689	3.3333	5.1081	2.9572	5.0881	2.574		4.5812	
K.VFIGSCTNGR.I +2								2.6071	2.6047								2.5803	2.7004							
K.YSFLEGGSK.L +1																				2.2904			1.8884		
R.AGM*IKPDETTFQYTK.G +2														3.9918				3.4249	4.1189	3.6199					
R.AGMIKPDETTFQYTK.G +2																	4.5118								
R.ALAYM*GLEPNTPLK.S +2						3.0614		2.979	2.5514			3.3003	4.4684	3.8927	3.4741	3.5206		4.1503			3.9946				
R.ALAYMGLEPNTPLK.S +2					4.4483	3.5629	4.0345	3.8803	3.7686		3.8524	3.8979			2.8235	3.7328	4.2351			3.5595		4.5453		3.5087	
R.EAEILVVTGDNFGCGSSR.E +2													4.5417	4.3115	4.2444		5.0301	4.5609		4.5761	5.0023	5.3957	5.5777	5.2172	
R.EAGCSICLGM*NPDILDAYER.C +2																			5.1218	3.3609	4.5802				
R.EAGCSICLGMNPDILDAYER.C +2							4.4625		4.5409		3.8616	3.5201					4.5819	4.422		4.1508			3.6848	4.2256	
R.LDQGIIIDK.L +2						3.5692							3.2206												
R.M*SMCNMAIEAGAR.A +2																					3.0491				
R.MSMCNMAIEAGAR.A +2																3.3549	3.9067						3.7648	3.6052	
R.RVDCTLATVDHNIPTESR.K +3													4.0299												
R.VDCTLATVDHNIPTESR.K +2											3.9867		3.7434	4.0506				3.0898							
gi|6323509|ref|NP_013580.1|			7.7		12.4	12.4	17.9	16.1	20.6	8.8	19.8	17.7	30.5	18.7	17.5	19.1	14.9	14.5	16.3	32.8	13.8	9.2	13.4	8.8	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase, catalyzes the formation of HMG-CoA from acetyl-CoA and acetoacetyl-CoA; involved in the second step in mevalonate biosynthesis; Erg13p [Saccharomyces cerevisiae]
K.ALDQVYK.S +1													2.3123				1.8678								
K.ALDQVYK.S +2																							2.7755		
K.DYEAAIELR.E +2											3.0912										3.2587	3.0395		3.2606	
K.GAARPTGGAGTVAM*WIGPDAPIVFDSVR.A +3																				4.5119					
K.GIQIYIPTQCVNQSELEK.F +2							4.5379	4.5748	5.1332		2.5617	4.5783	4.3268		4.3285	4.4517	4.4132	3.137	4.0064	3.6421	4.9707		4.6929	4.6337	
K.GLVSDPAGSDALNVLK.Y +2			4.5002		4.649	4.6465	4.7133	4.8419	4.7808	4.0145	4.4604	4.445	4.3518	5.1107	4.1441	4.1656		4.5813		4.0008	4.3676				
K.IVGDVQHIIK.E +2													3.5095	3.5736	3.306	3.0055	3.5716	3.4928							
K.PQGSIEHLQSGVYYLTNIDDK.F +2																				2.9313					
K.SYNIDTNK.I +1									2.1628			2.1516													
K.TFVNVAKPFHK.E +2													3.0537	3.4471					3.174	2.5526					
K.TRPQNVGIK.G +2			2.7601			2.6472																			
K.YFDYNVFHVPTCK.L +2			4.1143										4.6093		3.1592		3.9248			2.8356					
K.YTIGLGQTNM*SFVNDR.E +2																					3.5927				
K.YTIGLGQTNMSFVNDR.E +2																3.7022									
R.ANPQLFPEVDAELATR.D +2					3.8077	3.8242	3.8962	3.6855	3.0546	3.2271	3.042	3.3638				3.6442	4.226			2.9		3.1964		2.8778	
R.DAIVVCGDIAIYDK.G +2									2.6356														2.917		
R.DYDESLTDK.N +1																	2.6318	2.773	2.4489	2.7529	2.8716	2.6569	2.6233		
R.DYDESLTDK.N +2						2.6237	2.5618				2.5513		2.7598												
R.EDIYSM*SLTVLSK.L +2													3.4214	2.9947											
R.LEVGTETLIDK.S +2					3.4603	3.3195	3.6457	3.1181	3.3322	2.8376	2.7068	3.4306	3.2322		3.1227					3.6977		2.9007		
R.PTGGAGTVAM*WIGPDAPIVFDSVR.A +2													4.9031	4.6599					4.1911						
R.PTGGAGTVAM*WIGPDAPIVFDSVR.A +3													5.3677	5.5172											
R.VGLFSYGSGLAASLYSCK.I +2					5.119		5.6593	5.3147	5.0132		2.6456	5.1341	5.3348	5.6919	4.7643	5.1342		2.9472	4.4863	3.0858			3.0216		
R.VGLFSYGSGLAASLYSCK.I +3													4.6624										4.3821		
gi|6324321|ref|NP_014391.1|			4.3		20.7	24.1	27.8	25.6	28.1	25.6	24.1	24.7	29.3	28.7	31.8	19	25.3	14.8	11.9	25	18.2	12.8	12.2	20.7	Type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; not functionally redundant with Ydj1p due to due to substrate specificity; shares similarity with bacterial DnaJ proteins; Sis1p [Saccharomyces cerevisiae]
K.EISEAFEILNDPQKR.E +2							4.4522	4.1522	4.3301	2.9014		3.9169		3.8885	4.3734	4.6862	3.7678					3.9773			
K.EISEAFEILNDPQKR.E +2													2.7746	2.7428	2.8321	3.4506				3.6936					
K.LYDLLGVSPSANEQELK.K +2					4.6142	4.6764	4.8176	4.6598	4.4582	3.686	3.8517	4.3828	5.0308	3.3575	3.9823	4.651	4.1352	2.7352		3.9714	3.9948	3.0783	4.1801	2.7384	
K.LYDLLGVSPSANEQELKK.G +2														3.1073											
K.NQGDYNPQTGR.R +2							2.8109																		
K.RDGDDLIYTLPLSFK.E +2			3.1388																						
K.TLQFVIQEK.S +2					2.9984	3.1113	3.2305		3.0536		3.0146	2.9284		3.037	2.7369		2.8873		2.6968	2.9423				2.9158	
K.TQIDIQLKPGWK.A +2													3.9518	3.74	3.6312										
K.VDYPISLNDAQK.R +2						3.7978	3.4388	3.401	3.5522	2.5924	3.2546		3.1262		3.8077		3.128						3.7783	3.4739	
K.YKVDYPISLNDAQK.R +2																	3.754			4.502					
R.DGDDLIYTLPLSFK.E +2			4.1926		4.1362	4.3119	4.3325	3.9867	4.1137	3.218	3.0843	3.8053	2.9574	4.6376	4.091	4.4781	3.0946	3.6622			4.2066	4.2098	3.7468	3.7871	
R.EIYDQYGLEAAR.S +2					3.8322	3.8916		3.0956	3.902	3.8636	3.8432	3.8665	3.9771	4.0678	3.657				3.9408	4.1646	4.2757				
R.VQPVQPSQTSTYPGQGM*PTPK.N +2								2.8588	2.8824					3.0229	3.7882	3.9987			4.6311						
R.VQPVQPSQTSTYPGQGM*PTPK.N +3													4.6517												
R.VQPVQPSQTSTYPGQGMPTPK.N +2					3.7274	4.7061	3.857	4.2533	4.3303	3.9084	4.422	3.6969		3.9225	3.9372	4.3591	4.2468	4.2855		4.201	3.8033			2.5353	
R.VQPVQPSQTSTYPGQGMPTPK.N +3												3.6039													
4		X		X		X	X		X	X	X	X		X	X	X		X	X	X	X	X	X	X	
gi|6319809|ref|NP_009890.1|		4.6			13.6	13.6	13.6	10.8	21.4	3.8	12.4	18.6	24.8	25.8	21	27.4	17	7.6	19.2	26.4	16.2	5.4	16.8	19	Glucokinase, catalyzes the phosphorylation of glucose at C6 in the first irreversible step of glucose metabolism; one of three glucose phosphorylating enzymes; expression regulated by non-fermentable carbon sources; Glk1p [Saccharomyces cerevisiae]
K.DVVQLYQEQLSAQGM*PM*IK.V +2																			4.4484						
K.DVVQLYQEQLSAQGM*PM*IK.V +3													4.9984												
K.DVVQLYQEQLSAQGMPM*IK.V +2																				3.3585	2.5762				
K.DVVQLYQEQLSAQGMPMIK.V +2																	2.92								
K.GLPMIPAFVTGSPNGTER.G +2																2.5673		3.7415						2.5057	
K.IPDDLLDDENVTSDDLFGFLAR.R +2					5.9144	5.8028	5.6563	5.6273	5.3332		4.9549	5.1488	5.3373	5.5223	5.4692	5.7499	5.299		4.335	4.5634			5.0112	3.5715	
K.IPDDLLDDENVTSDDLFGFLAR.R +3													4.2684												
K.LDELTAYFIEQMEK.G +2					4.8927	4.2603	3.059		4.8387			2.5723				2.8463									
K.LGFTFSYPVDQTSLNSGTLIR.W +2					5.1225	4.3451	4.2932	3.5244	5.1804		2.5096	4.2722	4.9924	5.3317	4.7922	5.0033	3.9534		4.176	3.4122	3.467		4.2792		
K.LSTNFGFHLEK.R +2		3.5028											2.5684		3.4123	2.7888	2.7608	2.9672	3.6407	2.6968					
K.THM*IINVEWGSFDNELK.H +2														3.9968											
K.YDVVIDQK.L +1																			2.8749	2.9912		3.0268			
K.YDVVIDQK.L +2										2.6926	2.9955							2.9644							
R.AVIQAVDQICDDFEVTPEK.L +2														2.5145							4.3755	4.7348	4.481	3.2597	
R.ETELSLLQSLR.L +2		2.7337			3.7499	3.5672	4.0525	3.6893	3.534	2.7687	3.0731	3.6223	2.846	3.2131	3.6891	3.2603				3.9559	3.6272		3.0731	3.6164	
R.GVLLAADLGGTNFR.I +2									4.7551			3.883	4.7965	4.0228	5.3782	4.1415				5.1032				4.4226	
R.HALALSPLGAEGER.K +2									3.825				4.3003	4.1912	3.9026	3.4575			3.9844	2.9076					
R.VSGM*FLGEVLR.N +2												2.9688	3.9667	3.5996	3.3722	3.6045									
R.VSGMFLGEVLR.N +2									4.1913			3.9747			3.5497	3.6046	3.2677			2.6663	3.3065		3.9509	3.4293	
gi|6320019|ref|NP_010099.1|		6.1			17.5	17.3	11.2	14.5	16.6	14.7	14.3	10.7	25	20.8	22.2	25.7	15.2	26.9	7.7	18.9	13.3	11.9	8.6	21	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys21p; Lys20p [Saccharomyces cerevisiae]
K.AILANPSTYEILDPHDFGM*K.R +2													3.4211	3.3967											
K.AILANPSTYEILDPHDFGM*K.R +3													3.596												
K.KNDSDVPELATIPAAK.R +2																		3.3602							
K.NDSDVPELATIPAAK.R +2																								2.5056	
K.PGDYLSNVNNFQLIDSTLR.E +2																2.2658									
K.SAVEVIEFVK.S +2													3.4066	3.5252	3.3833			3.4013		3.3465	3.3011			3.3032	
K.VAVETGVDGVDVVIGTSK.F +2													2.985			3.5617	4.6453	5.7494				2.5578		4.5734	
R.ALDDFGVDYIELTSPVASEQSR.K +2					6.0178	5.8339	5.1927	5.6637	5.455	4.4183	4.089	5.0125	5.5799	5.8358	5.794	5.4421	5.3698	5.0743	5.0846	4.8725	2.6592	5.5925		2.7083	
R.EGEQFANAFFDTEK.K +2		3.4339			4.1336	4.315	4.0324	4.3274	2.979	3.6359	3.7288			3.8775	3.8167	2.9005	3.2451	2.5434		4.1908	2.5805		3.087		
R.LIDVSVLGIGER.N +2		2.7137			3.4879		2.7297	3.8571	4.335		2.6951	3.9849	3.8731	4.3483	3.9637	4.2073		3.9775		3.9593			3.9738		
R.SDLVDLLNIYK.T +2						3.8873			3.8892				3.7392	3.9014	3.8881	3.8973	3.942	3.7701	3.705	3.4147	3.6437	3.6784	4.0132	3.8564	
R.SLNIDDVDSIIK.N +2									3.6754			3.6776			2.7076			3.1798		3.3439					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.VDQLNLNLTDDQIK.E +2					4.6772	4.3085		4.6561		3.2264			4.342		4.3627	3.8139								4.1023	
R.VGIADTVGCANPR.Q +2					4.1493	3.8625				3.9231	3.6693														
gi|6320071|ref|NP_010151.1|		5.9			17	16.8	13.2	16.4	13.4	14.3	13.9	7.7	28.2	22.5	22.7	20.7	14.8	23.4	7.5	15.7	15.2	11.6	13	17	Homocitrate synthase isozyme, catalyzes the condensation of acetyl-CoA and alpha-ketoglutarate to form homocitrate, which is the first step in the lysine biosynthesis pathway; highly similar to the other isozyme, Lys20p; Lys21p [Saccharomyces cerevisiae]
K.AILANPSTYEILDPHDFGM*K.R +2													3.4211	3.3967											
K.AILANPSTYEILDPHDFGM*K.R +3													3.596												
K.LGDVRPLNIDDVDSIIK.D +2													3.6824		2.908										
K.NFQLIDSTLR.E +2							3.5603	3.5416						3.3884									2.7976		
K.SAVEVIEFVK.S +2													3.4066	3.5252	3.3833			3.4013		3.3465	3.3011			3.3032	
K.SRVDQLNLNLTDDQIK.E +2																		2.6852							
R.ALDDFGVDYIELTSPVASEQSR.K +2					6.0178	5.8339	5.1927	5.6637	5.455	4.4183	4.089	5.0125	5.5799	5.8358	5.794	5.4421	5.3698	5.0743	5.0846	4.8725	2.6592	5.5925		2.7083	
R.EGEQFANAFFDTEK.K +2		3.4339			4.1336	4.315	4.0324	4.3274	2.979	3.6359	3.7288			3.8775	3.8167	2.9005	3.2451	2.5434		4.1908	2.5805		3.087		
R.LIDVSVLGIGER.N +2		2.7137			3.4879		2.7297	3.8571	4.335		2.6951	3.9849	3.8731	4.3483	3.9637	4.2073		3.9775		3.9593			3.9738		
R.MIVAAPDYVR.S +2																					2.6192		2.5221		
R.SDLVDLLNIYK.T +2						3.8873			3.8892				3.7392	3.9014	3.8881	3.8973	3.942	3.7701	3.705	3.4147	3.6437	3.6784	4.0132	3.8564	
R.VAVETGVDGVDVVIGTSK.F +2													2.985			3.5617	4.6453	5.7494				2.5578		4.5734	
R.VDQLNLNLTDDQIK.E +2					4.6772	4.3085		4.6561		3.2264			4.342		4.3627	3.8139								4.1023	
R.VGIADTVGCANPR.Q +2					4.1493	3.8625				3.9231	3.6693														
gi|6320137|ref|NP_010217.1|		5.6			8.4	8.9	3.5	3.5	19.9	5.6	15.4	13.3	25.5	25	17.5	22	13.8	19.4	12.4	22.9	13.8	16.4	23.1	15.2	Mitochondrial NADP-specific isocitrate dehydrogenase, catalyzes the oxidation of isocitrate to alpha-ketoglutarate; not required for mitochondrial respiration and may function to divert alpha-ketoglutarate to biosynthetic processes; Idp1p [Saccharomyces cerevisiae]
K.DIFQEVYEAQYK.S +2					2.7235	4.1359			4.6126		3.4772	4.2115	4.5232	4.8242	4.7028	4.5239	4.578	4.7015	4.5203	4.3891	4.5541	4.8943	4.4329	4.5893	
K.DLALACGNNER.S +2																	3.0074	3.3292		2.5731					
K.FANILESATLNTVQQDGIM*TK.D +2													4.1064					3.2837		4.7827	4.7544	2.5166			
K.FANILESATLNTVQQDGIM*TK.D +3													4.0352	4.7459											
K.FANILESATLNTVQQDGIMTK.D +2									4.7522							3.0487	4.6044	4.2734		4.4456	4.7977		3.7824	4.7775	
K.FEQLGIHYEHR.L +2													3.1475	2.6859	3.0969										
K.GEETSTNSIASIFAWSR.G +2									4.4291		3.0405	4.1163	2.8651	4.1935	4.2551	3.174				3.3719			4.2764	4.4955	
K.ITQDAAEAIKK.Y +2													2.8597	2.8682											
K.KLNLFLSTK.N +2		3.1728																		2.694					
K.LILPYLDVDLK.Y +2						3.0427			3.0123					2.5902	2.5414	3.3507		2.6407			2.6708				
K.LNLFLSTK.N +2																							2.5424		
K.QPVVELDGDEM*TR.I +2																			2.8517						
K.QPVVELDGDEMTR.I +2																		2.6231					2.5782		
K.SKFEQLGIHYEHR.L +2																				3.2666					
K.TFESEAAHGTVTR.H +2											3.8763	3.0483	4.3379						3.9711			4.1406	3.2939		
K.YYDLSVESR.D +2										2.6508	3.3278					2.9703						3.679			
R.NILGGTVFR.E +2					2.6795				2.5178				2.6801	2.6904	2.7167	2.8394									
R.SAYVTTEEFLDAVEK.R +2		3.487			5.7755	5.8591	5.8095	5.6262	5.3519	2.8528	3.3159	5.6001	5.5968	5.647	5.8087	5.5171	5.0746	5.6863	4.157	5.2679	5.1526	5.0951	5.1235	5.5561	
gi|6323335|ref|NP_013407.1|		3.3			7.3	9.5	9	10.3	19.3	8.2	8.1	10.4	21.5	20.6	15.8	16.5	15	13.4	6.9	24.8	6.7	7.1	9.6	4.9	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mitochondrial genome maintenance; component of the mitochondrial nucleoid; mutation leads to glutamate auxotrophy; Aco1p [Saccharomyces cerevisiae]
K.DGNEFMLKPHGDGLPQR.G +2																	2.9189								
K.DMPILIK.A +1																		1.8262							
K.EFGGIVLANACGPCIGQWDR.R +2									4.4564				3.3058	4.5841	4.5331		3.9203	3.9164		3.8599					
K.EFGGIVLANACGPCIGQWDR.R +3													3.6469												
K.EVAVANNWPLDVR.V +2		4.2685			3.6973	4.4018	4.4761	4.2399	4.5055	3.3561	3.7499	3.7616	4.2968	4.2142	4.4571	4.3966				3.9424			4.0972		
K.EVYDFLASATAK.Y +1																				1.9114					
K.EVYDFLASATAK.Y +2					3.6986	3.8439	3.4912	3.655	3.7994	3.218		3.143	3.6328	4.0049	3.4975	3.7554	3.5341		3.4825		3.7362	3.4043		3.1194	
K.ILYGHLDDPHGQDIQR.G +2													4.7404	4.2715				3.879		3.8412					
K.KQGLLPLNFK.N +2																			2.917						
K.NTIVSSYNR.N +2						2.8452				2.9146	2.6788			2.5624		2.8773									
K.NVYTGEYK.G +1													2.4057							2.2845	2.1677		2.5483		
K.PVTVHCDHLIQAQVGGEK.D +2													5.3769	6.0401						3.1932					
K.QNVETLDIVR.K +2						2.6605		2.7778	3.017																
K.SMIEYLEATGR.G +1									1.9491																
K.SMIEYLEATGR.G +2									3.9721		3.0704	3.7141			3.6406		3.3367			3.0475		3.4503		3.6203	
K.TIFTVTPGSEQIR.A +2		3.3881				3.6088	3.658	3.5858	3.6354	3.6378	3.3119	3.5695	3.4856		3.7505	3.838		3.5322					4.2708		
K.TTTDHISM*AGPWLK.Y +2									2.6398				4.07	4.3296					3.957	3.264					
K.TTTDHISMAGPWLK.Y +2													2.9083	3.3077	3.2252	3.6584	3.9702								
K.VNQNLLEDHSFINYK.Q +2									3.2653					5.2761	4.397	5.1828				3.3855					
K.WVVIGDENFGEGSSR.E +2					4.8458		4.722	4.4915	4.7293			4.1665	4.5014	4.6252	4.4911	4.7165	4.0653	3.9851		3.8721	4.7472	4.5701	4.5002	4.5141	
R.DGQLETFK.E +1																			2.276						
R.DGQLETFK.E +2																				2.9294					
R.FLGGFAIITK.S +2									3.3738				3.5955	3.7528	3.3336	3.5817	3.3421		3.3904	2.9571			3.6972		
R.GYDAGENTYQAPPADR.S +2																		4.4753		4.8804			3.0537		
R.IDILGLAELAPGKPVTM*R.V +2													2.9512	3.8147											
R.IDILGLAELAPGKPVTM*R.V +3														4.0793											
R.LNRPFTYAEK.I +2													3.2056			2.9221									
R.VGLIGSCTNSSYEDM*SR.S +2																					3.7578				
R.VGLIGSCTNSSYEDMSR.S +2					4.8762	4.1801	4.3992	4.788	4.5987	3.7875	4.2121	4.584				4.3423	4.8833	4.323		4.8372		3.9038			
	5	X			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6322476|ref|NP_012550.1|	2.9				14.4	16.9	11.8	7.4	16.6	8.5	16.6	15.9	26.5	26.5	19.8	16.8	14.9	13.7	10.8	23.9	5.3	8.9	12.1	9.4	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids; Ilv3p [Saccharomyces cerevisiae]
K.AMQFNTIGVSDGISMGTK.G +2																				3.8179					
K.ANGHLQILYGSLAPGGAVGK.I +2																			3.5537						
K.DVALLTDGR.F +1											2.0458														
K.DVALLTDGR.F +2										2.7095	2.8975					2.8829				2.8804					
K.GQGASQAM*LYATGFK.K +2													2.6252	3.2221						2.6096					
K.GQGASQAMLYATGFK.K +2					4.7524				4.9138	3.7339	4.4906	3.2105			3.7794	3.9064	4.0514							4.4061	
K.IDLLVSDK.E +1						2.0301										2.4678				2.5076	2.4984				
K.KTMELGILPR.D +2																				2.75					
K.LAECDNIGEYIK.K +2					4.1654	3.939	3.9262	3.9712	4.0234	3.1986	3.6615	3.5598	2.8078	4.0283	3.8418		3.8045	3.4527	3.3821	3.4399		3.8102			
K.LVSNASNGCVLDA.- +2																		2.6308							
K.NIDIVSAFQSYGEYISK.Q +2					5.7934	5.4261	3.5751	5.74	6.3428		2.8646	4.5203	5.1813	5.471	3.3485	5.1162	4.8013		5.1466	5.0488			5.5416		
K.NMPGVMMAMGR.H +2																	2.6479								
K.QSWVAPPPR.Y +2															2.5429		2.5368	2.8758							
K.TM*ELGILPR.D +2													3.4185	3.1293	2.5377										
K.TMELGILPR.D +2					3.2911	3.6189	3.3222		3.3306			3.3309		3.1569	3.1039	3.1423				3.0712				3.1452	
K.YLYENNM*LHGNTM*TVTGDTLAER.A +3													5.5137	3.7239				3.5125							
K.YLYENNM*LHGNTMTVTGDTLAER.A +3																		4.0006							
K.YLYENNMLHGNTMTVTGDTLAER.A +2																	4.7902								
K.YSYIITEPK.G +2						3.1167						2.9415	3.0642	3.1577	2.951	3.3871		3.1256				3.3556	3.4954		
K.YVM*ADLINVGGTQSVIK.Y +2													5.2489	5.7227	4.2802	4.4305				2.8817	2.556				
K.YVMADLINVGGTQSVIK.Y +2	4.4376				5.0075	4.8117	5.5611		5.2215		2.5218	4.0177			4.7251	5.785				5.2644				4.6846	
R.DGDEIIIDADNNK.I +2						3.8915			3.4953		4.6979		4.7546	4.7932	4.4795					4.8292			3.8919		
R.DGDEIIIDADNNKIDLLVSDK.E +2																				4.1158					
R.ISDTTPLIGDFKPSGK.Y +2													3.8391	3.6528						2.7082					
R.KQSWVAPPPR.Y +2													2.8134	3.1032	3.2401								2.8668		
R.VFEEEGAFIEALER.G +2					4.4635	4.3694	5.3508	5.3777	5.2462	3.3834	5.0577	5.5728	5.4091	5.4703	5.0943	5.2141		5.2854	5.0258	4.6441	5.545	5.1372	5.2839	5.3515	
	1	X			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320560|ref|NP_010640.1|		11.9	12.2		33.5	34.5	28.2	32.9	38.6	29.8	41.4	38.6	38.6	49.8	37.6	38.6	29.5	27.3	34.8	42		7.8	24.8	25.7	Cytoplasmic thioredoxin reductase, key regulatory enzyme that determines the redox state of the thioredoxin system, which acts as a disulfide reductase system and protects cells against both oxidative and reductive stress; Trr1p [Saccharomyces cerevisiae]
K.FGTEIITETVSK.V +2					4.3247	4	4.0301	3.1716	3.9027		3.6816	3.5606	3.1216	3.1804		3.9262	3.6134	2.5787	2.9637	3.4775		3.7267	4.0059	3.6971	
K.GISACAVCDGAVPIFR.N +2			3.8408			3.3544	4.1263	4.3158	4.1813		3.5364	3.5742	3.4057	4.0684	4.1082	4.3742		3.5272	3.0305					3.393	
K.IEILYNTVALEAK.G +2					3.5573		4.7873	5.0465	3.7143	4.3021	5.0978	3.941	4.6436	4.6008	4.4027	3.7666				4.3481		3.1544		3.3307	
K.IVAGQVDTDEAGYIK.T +2		4.6005			4.5401	4.6014		4.5525	4.7439	4.399	4.3372	4.0465	4.5336		4.0203	5.2332	4.888	3.5545	4.8834					4.277	
K.KNEETDLPVSGLFYAIGHTPATK.I +3														5.7373						3.6241					
K.LWTEFNEDAEPVTTDAILATGASAK.R +2						4.8403	4.1512	4.1948	4.9464	2.7388	2.5395	4.2952	4.9502	3.977	5.1647	5.3633	3.7146	2.5582	4.1942	3.3946			3.6298	3.0345	
K.LWTEFNEDAEPVTTDAILATGASAK.R +3					5.2394	5.2636	5.1892	5.1666	5.4343		3.8498	5.0507		4.244	4.844	5.7293	3.698			4.4354					
K.TVPGSSLTSVPGFFAAGDVQDSK.Y +2		3.6979	4.0838		4.4041	4.087	4.453	3.8894	4.3983	3.072	3.1575	3.6928	3.856	3.7971	3.6869	3.9957	2.5305		3.8396	3.9829			3.9522		
K.TVPGSSLTSVPGFFAAGDVQDSK.Y +3													3.8622	4.4215											
K.VDLSSKPFK.L +2											2.6233			2.6158	3.0135										
K.VTIIGSGPAAHTAAIYLAR.A +2														4.9741					4.2417	3.5082					
R.QAITSAGSGCM*AALDAEK.Y +2													5.5382												
R.QAITSAGSGCMAALDAEK.Y +2					4.7487	5.3276			5.6415	4.5763	4.3885	5.1455	5.413	4.9361	4.9371	3.1872	4.8827	5.1939		5.5776			4.4289		
	1	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6323470|ref|NP_013542.1|		8	11.1		10.6	11.8	13.9	17.2	30.4	14.2	11.3	26.7	30.9	31.6	32.8	30.7	16.7	18.6	17	33	12		9	6.4	L-ornithine transaminase (OTAse), catalyzes the second step of arginine degradation, expression is dually-regulated by allophanate induction and a
K.AEAKPDIVLLGK.A +2										2.6827			3.6566	2.6578	2.9335		3.3544	3.6192		3.728					specific arginine induction process; not nitrogen catabolite repression sensitive; Car2p [Saccharomyces cerevisiae]
K.AIILGAEGNFHGR.T +2									3.2335				3.9471	3.5916	3.4616				2.9011	3.7859					
K.ALTEQAQTLTLSSR.A +2					4.8731	4.9123		4.7432	4.6692	4.4327	4.4367	4.7038	4.8397	4.7628	4.5443	4.6316		3.7096			4.3183			4.7113	
K.NVAAIILEPIQGEAGIVVPPADYFPK.V +2									3.3597			3.138				3.848									
K.TAWDLCLLM*K.D +2													2.8882	3.1548	2.6354				2.6525						
K.TAWDLCLLMK.D +2																				2.783					
R.AAQLGSSFIAQLK.A +2		3.3831	3.575				4.7457	4.745	4.6694	4.4491	4.8006	4.6989	4.7897	4.7984	4.5779	4.8121	3.8793			2.8249	4.7358		4.4119	4.3489	
R.AFHNDVYAQFAK.F +2													3.9677	4.0326						2.6116					
R.GM*GLLTAIVIDPSK.A +2												3.1633		3.8506	4.4045	3.6554		2.9944		4.0158	2.8089				
R.GMGLLTAIVIDPSK.A +2																				3.638					
R.LAPPLVISEEDLQTGVETIAK.C +2		5.5801	5.575		5.879	6.1272	5.6461	6.0074	5.8711	3.611	3.0136	5.3494	5.1603	5.5515	5.2898	4.5678	4.9601		4.3685	4.7177					
R.LAPPLVISEEDLQTGVETIAK.C +3														4.26	4.2845										
R.TFGAISLSTDYEDSK.L +2						4.7653	4.4966	4.3331	4.4797			4.2968	4.6281	4.5257	4.4445	5.0674	3.9168	4.6456	3.6348	4.0322			3.8357		
R.TGELLCYDHYK.A +2													2.9788					3.7389							
R.VAIAALEVIR.D +2					3.8426		3.8515	3.8839	2.7367			3.5971	4.1069	3.9931	3.997	4.1003	3.2477	4.0833	3.6542	4.1496	4.053		3.6875		
R.VAIAALEVIRDEK.L +2			3.8758															3.6857	2.9827	3.8716					
R.YGHAEDFVPILESPEGK.N +2									3.7002						4.0745	2.752				4.5541					
	1	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6324463|ref|NP_014532.1|	40.7	40.7	31.9	20.4	30.1	21.2	39.8	40.7	40.7	40.7	48.7	39.8	40.7	48.7	40.7	40.7	56.6			31	47.8		31	20.4	Peripheral membrane protein of the plasma membrane that interacts with Mid2p; regulates the cell integrity pathway mediated by Pkc1p and Slt2p; Zeo1p [Saccharomyces cerevisiae]
K.AETAAQDVQQK.L +2	3.9521	4.0571			4.0264	4.1203	4.2119	4.1137	3.988	4.2036	3.9755	4.2058	3.6912	3.1441	4.0287	4.0114					2.8366		2.9721	4.0692	
K.AETAAQDVQQKLEETK.E +2																	3.9836								
K.EEQNIADGVEQK.K +1																2.5254									
K.EEQNIADGVEQK.K +2		4.0015	3.9812	4.0525	3.9871	4.1272	3.5007	3.6644	3.6719	3.3596	3.6841	4.2728	3.6911		3.5323	4.1531				3.0453	2.8281		2.5543	3.5518	
K.EQAEASIDNLK.N +1												2.4694		2.8044			1.8927			2.6766	2.3848		2.5651		
K.EQAEASIDNLK.N +2	2.8948	2.7455	2.6361	2.6249	2.879		2.7523	2.7895			2.6489	2.9003	2.8764		2.6998										
K.EQAEASIDNLKNEATPEAEQVK.K +2									3.9201	3.0293					2.9636	3.7885					2.9102				
K.EQAEASIDNLKNEATPEAEQVK.K +3													4.275			3.6853									
K.EQAEASIDNLKNEATPEAEQVKK.E +2																2.6132									
K.EQAEASIDNLKNEATPEAEQVKK.E +3										3.8748			5.7269	5.6246		4.2796									
K.KEEQNIADGVEQK.K +2						3.2089		3.5278	3.9805	3.034	3.1533		3.2792	3.6885	3.1721	4.0335							3.061		
K.KTEAANKVEETKK.Q +2	2.6529		3.8659														3.7389								
K.KTEAANKVEETKK.Q +3			3.5427																						
K.NEATPEAEQVK.K +2	3.1947	2.8784					3.103	3.163	2.6339		3.1488	2.7462			2.6088	2.8408									
K.NEATPEAEQVKK.E +2													3.006												
K.NEATPEAEQVKKEEQNIADGVEQK.K +3		3.8362															4.6297			3.6378					
K.QASAAVSEK.K +1											1.9437			2.4809							1.9797				
	1 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X		X	X	
gi|6323208|ref|NP_013280.1|	13.4	13.4	13.4		21.9	30.3	30.3	19.9	21.9	21.9	30.3	16.9	25.4	38.8	16.9	16.9	25.4	14.9	20.4	16.9	23.9			16.9	Protein of unknown function, transcription is activated by paralogous proteins Yrm1p and Yrr1p along with proteins involved in multidrug resistance; GFP-tagged protein localizes to the cytoplasm and nucleus; YLR179C is not essential; Ylr179cp [Saccharomyces cerevisiae]
K.LALLM*TDPDAPSR.T +2												2.8548							2.7298						
K.LALLMTDPDAPSR.T +2					3.7325	3.9087	3.9686	3.9835	4.0272	2.5562	4.0008	4.098	3.892	3.8945	4.0424	4.0469	3.4165	3.2364		4.0087				4.2025	
K.LGNPM*PM*EATQAAPTIK.F +2													3.7881	3.9053							2.598				
K.LGNPMPMEATQAAPTIK.F +2	4.499	4.1047	4.4762			2.9598	2.9194	3.1317			4.4329						4.3565	3.4911							
K.VENIISWGYGTPGAGAYDYIK.E +2					5.4878	5.1366	5.4629		5.7243	4.2725	4.1572	5.2238	5.6087	5.7194	5.0696	5.7776	5.2255		4.2426	5.1534	5.4929			5.6017	
K.WSEVCHYIITDIPVEYGPGGDIIAISGK.G +3														5.1977											
R.NNYIGPGPPK.N +2	2.9447	2.8317	2.6307		2.8115	3.0494	3.136	2.9537	2.6429	2.8898	2.8198										2.7112				
R.YVFFLCK.Q +2																			2.53						
	1 X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	
gi|6319668|ref|NP_009750.1|	24.4	30	24.4	16.9	16.9	21.9	16.9	16.9	35	35	16.2	21.9	29.4	23.8	18.8	21.9	28.8	10.6	23.8	17.5				5	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Bp and has similarity to rat L21 ribosomal protein; Rpl21ap [Saccharomyces cerevisiae]
K.AQGVAVQLK.R +1						2.1349			1.9754		2.2196	2.2984					2.0806								
K.AQGVAVQLK.R +2	3.124	2.875	2.7492	2.7787	3.1745	3.1358	3.1191	3.2391	2.7866	2.8877		2.5794			2.576	2.924									
K.HGAVHLSTYLK.V +2																				3.4474					
K.RQPAQPR.E +2																	2.5177								
K.SSVGVIINK.M +2		3.0351		3.0249	3.5938	3.2829	3.4839	3.1982	3.23	3.4063		2.9815	3.573			3.5318									
K.TGVVYNVTK.S +1											1.85	1.8771		1.8984					1.8913						
K.TGVVYNVTK.S +2	3.0397	2.9951	3.0165	3.108	2.9084	2.901	3.1297	2.8965	2.8532	2.7565	3.0484	2.922	2.9739	3.0041		2.7865	2.8152	2.7017	2.5545	3.1384					
K.VGDIVDIK.A +1						2.4095			2.3979	2.1912	2.4156	2.4274	2.4866			2.3884		2.3322	2.2542	2.5784				2.4514	
K.VGDIVDIK.A +2						3.1308			3.1006	3.0216	2.8668	3.0102	2.9044	2.9924		3.1096								2.9657	
R.IVSTEGNVPQTLAPVPYETFI.- +2	3.1185	3.8289	3.4195						3.0678	3.9867			3.898	4.1559	3.9541		2.8446		3.1386						
gi|6325178|ref|NP_015246.1|	24.4	30	24.4	16.9	16.9	21.9	16.9	16.9	35	35	16.2	21.9	36.2	30.6	18.8	21.9	28.8	10.6	23.8	17.5				5	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Ap and has similarity to rat L21 ribosomal protein; Rpl21bp [Saccharomyces cerevisiae]
K.AQGVAVQLK.R +1						2.1349			1.9754		2.2196	2.2984					2.0806								
K.AQGVAVQLK.R +2	3.124	2.875	2.7492	2.7787	3.1745	3.1358	3.1191	3.2391	2.7866	2.8877		2.5794			2.576	2.924									
K.HGAVHM*STYLK.I +2													3.0918	3.2206											
K.HGAVHMSTYLK.I +2																				3.1607					
K.RQPAQPR.E +2																	2.5177								
K.SSVGVIINK.M +2		3.0351		3.0249	3.5938	3.2829	3.4839	3.1982	3.23	3.4063		2.9815	3.573			3.5318									
K.TGVVYNVTK.S +1											1.85	1.8771		1.8984					1.8913						
K.TGVVYNVTK.S +2	3.0397	2.9951	3.0165	3.108	2.9084	2.901	3.1297	2.8965	2.8532	2.7565	3.0484	2.922	2.9739	3.0041		2.7865	2.8152	2.7017	2.5545	3.1384					
K.VGDIVDIK.A +1						2.4095			2.3979	2.1912	2.4156	2.4274	2.4866			2.3884		2.3322	2.2542	2.5784				2.4514	
K.VGDIVDIK.A +2						3.1308			3.1006	3.0216	2.8668	3.0102	2.9044	2.9924		3.1096								2.9657	
R.IVSTEGNVPQTLAPVPYETFI.- +2	3.1185	3.8289	3.4195						3.0678	3.9867			3.898	4.1559	3.9541		2.8446		3.1386						
	2 X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				X	
gi|6321619|ref|NP_011696.1|		8.7		6.7	13.6	24.6	13.3	22.3	30.4	13.6	16.8	22.3	33.6	23.2	23.2	28.4	22.9	20.6	13.9	34.5	15.7	10.1	11		Ribonucleotide-diphosphate reductase (RNR), small subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr4p [Saccharomyces cerevisiae]
K.DTEDFQK.L +1																		2.2694							
K.EAEKDEILLMENSR.R +2													4.4763	4.6112	3.2224	3.2086	3.752	4.0978		4.0165					
K.EGIFQAGNYASM*FWLTDK.K +2													3.0592												
K.EGIFQAGNYASMFWLTDK.K +2									2.8141								3.4345			3.5917					
K.EIANLPEVK.H +1																					2.1082				
K.EIANLPEVK.H +2						2.6049																			
K.EYYSNSLPVEK.F +2		3.1369		2.9856			2.8112	3.0374	2.8673		3.1586	3.1742	2.9487			2.7773									
K.IITEAVEIEK.E +1																			2.3586	2.5765	2.6547				
K.IITEAVEIEK.E +2						2.631																	2.7704		
K.IMPGLAMANR.N +2									2.7557																
K.KIMPGLAMANR.N +2																				2.6384					
K.TYIGNLLALSISSDNLVNK.Y +2						3.3314		4.5349	5.0809			4.7876	5.1925	4.7615	3.8085	5.198		2.7284	3.6887	4.4002					
K.YLIENFSAQLQNPEGK.S +2					5.3454	5.6077	5.46	5.1993	5.2257	4.2682	4.1638	5.0583	5.5636	5.2275	4.7041	5.6584	4.9512			4.7897	2.8159	4.9063	4.7364		
K.YYNAVNPFEFM*EDVATAGK.T +2						3.9435			4.114	3.6683	2.8008		5.1902	5.5289	4.5921	4.438			4.6906						
K.YYNAVNPFEFMEDVATAGK.T +2		6.4438			6.5744	6.621	6.3415	6.3694	5.79		4.3556	5.5119	2.7934	5.5056	4.421	6.1803	5.4824	4.5666	3.5863	5.9397	3.9468				
R.LVAFAAK.E +1													2.1596			2.3246						1.9655			
R.WISNDDSLYAER.L +2				3.5611	3.7025	3.5483		3.4422	3.5091	3.0193	3.6826	3.1291	3.2891	3.5355	3.2333	3.1718	3.5571	2.7364		3.9366		3.8804	3.8404		
	1	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6321376|ref|NP_011453.1|		3.1	2		4.8	4.7	3.6	4.6	9.3	2.8	7.6	6.6	10	8.7	7	8.8	5.3	5.7	6	9.4	4.9	4.7	4.2		Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to isoform Pyc2p but differentially regulated; mutations in the human homolog are associated with lactic acidosis; Pyc1p [Saccharomyces cerevisiae]
K.AGITWIGPPAEVIDSVGDK.V +2					4.2267	4.8689	3.7623	4.1219	3.6901	2.561	3.1047	3.4917	4.4862	3.6918	4.0422	3.5746			3.5865		3.1579	3.3873	2.7581		
K.CSCSGSTYEIVR.R +2									3.6705																
K.DNGVDIFR.V +2																				2.5529			2.7267		
K.IVQM*GTHILGIK.D +2													3.814	3.8022	3.8491					3.0534					
K.IVQMGTHILGIK.D +2		3.8009												3.8417	3.6314		2.6318			3.1151					
K.LQAVGDLNKK.T +2																			2.5715						
K.LTCRPGLELEPFDLEK.I +2													4.3034	3.9475	3.9392					4.1173					
K.LTCRPGLELEPFDLEK.I +3													3.7524												
K.SNPSVPHLHDAQGNVINVTK.S +2														3.7118					2.625						
K.VVGDLAQFMVSNK.L +2		2.5208	2.9471		3.3718				3.8937		2.7409	2.7824	3.801	4.0227	3.9742	3.9194	3.7362				3.9273				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.YNLDYYLEIAEK.I +2					4.1759	3.4039		3.3325				2.6548	3.1778		3.3131	3.1327									
R.DAHQSLLATR.V +2																		2.9245							
R.DAILTDAVK.L +1											2.284														
R.EANYLLGDIVK.V +2		3.6024	3.4332				3.266	3.6315	3.7088		2.9454	3.2569		3.2667	3.0602	3.2351	3.3593	3.1661	3.1879			2.9921	3.1882		
R.EGDDVADAFQR.A +2									3.2958		3.5797	3.0344	2.909			2.6785		3.1633	2.918			3.2052			
R.ELDAYWAEMR.L +2																				2.9143					
R.GANGVAYSSLPDNAIDHFVK.Q +2																				2.54					
R.HYFIEINPR.I +2													2.5354												
R.LLYSCFEADLK.G +2																		3.5214							
R.NAGTAEFLVDNQNR.H +2										4.3419	4.572		5.0521			4.8574	4.2218				4.7133	4.1012			
R.PGLELEPFDLEK.I +2						2.7656			3.5496					2.9766	2.8339	3.4545									
R.QFNGTLLMDTTWR.D +2																				2.7027					
R.SFLSPLETDEEIEVVIEQGK.T +2									2.6792											3.5784					
R.TAFGNGTCFVER.F +2																		3.3172							
R.VFDALNDLEQLK.V +2					4.7882	4.7266	4.9047	4.8527	4.756		3.7348	4.2394	4.4843	4.6736		4.8476	4.6167	4.3628		3.3653	4.2152		4.0062		
1		X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6323567|ref|NP_013638.1|	14.2	18.8		14.2	31.2	31.2	31.2	18.8	35.8	16.5	14.8	23.3	31.2	38.1	43.2	25.6	31.2	17	26.7	29		21.6	10.2		N-terminally acetylated protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosomal protein; binds to 5.8S rRNA; Rpl6ap [Saccharomyces cerevisiae]
K.EANLFPEQQNK.E +2					3.0463	2.976	3.2164		2.8372	2.9821				2.8366	2.8159										
K.FNVEYFAK.E +1					2.1533		2.2377	2.2321	1.883		2.1313	2.3414	2.0968	2.1153	2.1516	2.0742	2.1934	2.221				2.0716			
K.FNVEYFAK.E +2											2.9599	2.5496	2.5962									2.9538	3.05		
K.HLEDNTLLISGPFK.V +2													4.4219	4.5461	4.2839	4.3212	4.4978		4.0436	3.388					
K.KEANLFPEQQNK.E +2														3.606						4.3375		4.3211			
K.QYLSASFSLK.N +2															2.5659										
K.VSVEGVNVEK.F +1													2.4428	2.4266			1.9814	2.3137	2.2445	2.4262		2.5268	1.9507		
K.VSVEGVNVEK.F +2	3.2692	3.2783		3.4879	3.3433	3.2658	3.304	3.3065	3.2187	2.8895	3.2142	3.0891	3.0481		3.168		3.1073								
K.WYPSEDVAALK.K +2					2.6674	2.509	2.5248		2.5708																
K.WYPSEDVAALKK.T +2																		2.5997							
R.ASLVPGTVLILLAGR.F +2	4.3113	4.4825		5.2002	4.5562	4.7701	4.4429	3.8105	4.4516			4.5931	4.9157	4.7364	4.347	4.5158	2.5852		4.4852	4.5688					
R.ASLVPGTVLILLAGR.F +3													4.2606	4.4605	3.8821					4.2417					
R.YVIATSTK.V +1		2.3793				2.2629			2.2103	2.1409	2.2906	2.0095	2.3414	2.1249	2.3024	2.3491	2.0628		2.1045			2.3199			
1	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X		
gi|6322284|ref|NP_012358.1|	21.2	34.2	27.2	31	15.8	15.8	15.8	31	36.4	29.3	21.2	21.2	29.3	32.6	25.5	23.9	27.2	34.2	23.9	31.5			23.9		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Ap and has similarity to E. coli L22 and rat L17 ribosomal proteins; Rpl17bp [Saccharomyces cerevisiae]
K.FVQGLLQNAAANAEAK.G +2	5.98	6.0261	6.1774	5.9087	6.1165	6.0566	6.2933	6.0733	6.0639	5.9101	5.9661	5.9439	6.0486	5.6926	5.7984	6.1171	5.546	5.9671	5.0081	5.2841			5.2415		
K.FVQGLLQNAAANAEAK.G +3													4.4538	4.2017					3.6519						
K.LYVSHIQVNQAPK.Q +1																		2.9403		3.0275					
K.LYVSHIQVNQAPK.Q +2	4.5445	4.5164	4.5916	4.6669				4.1064	4.4762				4.0735	3.7588	4.5017	4.545	4.742	4.087	3.8192	4.4939					
K.YESSPSHIELVVTEK.E +2				5.3603				5.0287	5.0114	4.4496			5.2155	5.3962	5.4134	5.0728	4.9094	4.6002	3.1764	4.8422			4.9548		
K.YESSPSHIELVVTEKEEAVAK.A +2																	4.8662								
K.YESSPSHIELVVTEKEEAVAK.A +3		4.0136															4.1693	3.547		3.7222					
K.YLDQVLDHQR.A +2									2.5366			2.6686	3.3868												
R.ETAQAINGWELTK.A +2		3.7783	3.8162	3.8648	4.1948	4.0585	4.075	4.1275	3.9921	3.918	4.181	3.4928		2.7626				3.9316					2.7394		
R.INKYESSPSHIELVVTEK.E +2														3.1263	2.9402										
R.RFNSSIGR.T +2			3.0164																	2.6712					
R.YGATSTNPAK.S +2	3.1907									2.6865	3.0561														
gi|6322668|ref|NP_012741.1|	21.2	34.2	27.2	36.4	15.8	15.8	15.8	31	36.4	29.3	21.2	21.2	29.3	38	31	29.3	32.6	34.2	23.9	37			23.9		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Bp and has similarity to E. coli L22 and rat L17 ribosomal proteins; copurifies with the Dam1 complex (aka DASH complex); Rpl17ap [Saccharomyces cerevisiae]
K.FVQGLLQNAAANAEAK.G +2	5.98	6.0261	6.1774	5.9087	6.1165	6.0566	6.2933	6.0733	6.0639	5.9101	5.9661	5.9439	6.0486	5.6926	5.7984	6.1171	5.546	5.9671	5.0081	5.2841			5.2415		
K.FVQGLLQNAAANAEAK.G +3													4.4538	4.2017					3.6519						
K.LYVSHIQVNQAPK.Q +1																		2.9403		3.0275					
K.LYVSHIQVNQAPK.Q +2	4.5445	4.5164	4.5916	4.6669				4.1064	4.4762				4.0735	3.7588	4.5017	4.545	4.742	4.087	3.8192	4.4939					
K.YESSPSHIELVVTEK.E +2				5.3603				5.0287	5.0114	4.4496			5.2155	5.3962	5.4134	5.0728	4.9094	4.6002	3.1764	4.8422			4.9548		
K.YESSPSHIELVVTEKEEAVAK.A +2																	4.8662								
K.YESSPSHIELVVTEKEEAVAK.A +3		4.0136															4.1693	3.547		3.7222					
K.YLEQVLDHQR.A +2				3.6218					3.0174			2.9388	3.5751	3.6106	3.6007	3.5942	3.5321			3.371					
R.ETAQAINGWELTK.A +2		3.7783	3.8162	3.8648	4.1948	4.0585	4.075	4.1275	3.9921	3.918	4.181	3.4928		2.7626				3.9316					2.7394		
R.INKYESSPSHIELVVTEK.E +2														3.1263	2.9402										
R.RFNSSIGR.T +2			3.0164																	2.6712					
R.YGATSTNPAK.S +2	3.1907									2.6865	3.0561														
gi|6323057|ref|NP_013129.1|	14.7	29.9	29.9	25.5	10.3	6.9	14.7	6.9	18.6	10.3	10.3	16.7	32.4	29.4	21.1	32.4	19.6	18.6	28.9	17.6			10.3		Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Bp and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA; Rpl15ap [Saccharomyces cerevisiae]
K.GATYGKPTNQGVNELK.Y +2	4.6798	4.6775	4.4425	4.8766			4.4981						3.0174			4.3002	4.1915	4.5586	3.2369						
K.PTNQGVNELK.Y +2												2.7361		2.6015											
K.QGFVIYR.V +1									2.1484				1.9147	2.0416		2.0458			2.0192						
K.RQNTLSLWR.Y +2		3.5659	3.5191																						
K.YFEVILVDPQHK.A +1																				2.5767					
K.YFEVILVDPQHK.A +2		4.5533	4.5075	2.8793									4.3582	4.5399	3.6887	3.6403		3.8209	4.1688	4.563					
K.YFEVILVDPQHK.A +3														3.5785											
K.YLEELQR.K +1									2.0947		1.9626		2.4413	2.2639	2.2772	2.2333							2.2725		
K.YLEELQR.K +2					2.8243				2.773	2.5847	2.5946		3.1128												
R.VLNSYWVNQDSTYK.Y +2	5.1824	5.2026	5.0127	4.9122	5.1365	5.2292	5.0356	5.0726	5.2569	4.9449	5.0278	4.7	4.717	4.7009	4.6121	4.995	4.3812		4.2031	5.0463			4.594		
R.YNWICDPVHK.H +2		3.3395	3.2503	3.4946					3.2158			3.4145	3.3098	3.3792	3.3196	3.2262	3.0998	3.4481	2.9896	3.2733					
3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X		
gi|14318497|ref|NP_116631.1|					14.9	14.5	11.7	9.5	12.7	8.2	14.7	16.9	20.5	21.9	13.5	19.1	23.1	16.1	10.5	13.9	9.9	8	9.1	4.6	Alpha subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs1p to form active enzyme; evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase based on protein sequence, but substrate binding is similar; Frs2p [Saccharomyces cerevisiae]
K.DPLTADLPDDK.T +1																	2.7869	2.3395		2.6734					
K.EGAQILNEGSYEIK.L +2					4.1896	4.0318	2.9649	3.616	3.7385	3.311	3.6124	3.6658	3.9994		3.4414	4.226	3.6029					3.5011			
K.FM*EEFFER.M +2													2.6303	2.6815									2.561		
K.GPEFSTDLTK.L +2											3.0499														
K.LETDLTSDM*VSTNAYK.D +2													5.6501									5.2114			
K.LETDLTSDMVSTNAYK.D +2					5.2652	5.4823			5.0713	3.2567	5.0833	2.9689				5.0296	4.2189	5.1446		4.99	5.2969	4.9158	4.4214		
K.LIQELGQLQIK.D +2					3.1991	3.2536	3.171				3.5003	2.8838		3.4285		4.0041	3.5478	4.0383					3.9321		
K.LQNTDLNELTDETQSILAQIK.N +2					4.5552	5.1873	4.7711	4.905	4.2293			3.4805	6.0657	5.5562	4.7435	2.5775	2.8944		4.1918						
K.NASNELELSAK.L +1																					2.252				
K.NASNELELSAK.L +2						2.8403				2.945			2.9823			2.8278									
K.NNSHLDSIDAK.I +2																	3.0781	2.8286		3.4027			2.587		
K.STLATFPQHGSQDVLSALNSLK.A +2														5.205					2.7472						
K.STLATFPQHGSQDVLSALNSLK.A +3														4.5066						3.9661					
K.VDTVTYDLTK.E +2											2.7358	2.7882				2.6476	2.7341	3.0739	3.1629	3.1686	3.2342	2.8566		2.7847	
K.VSLDFIETNPAAR.L +2					4.2405		4.3201	4.3792	4.4221		3.8837	4.2583	4.2545	4.5691	4.5036	4.2541	2.9059	4.0185			3.0452			4.0845	
R.DLQDTFYIK.D +1																	2.4575	2.1853							
R.DLQDTFYIKDPLTADLPDDK.T +2													4.8239	3.8764	4.5322										
R.DLQDTFYIKDPLTADLPDDK.T +3													3.574	4.7326											
R.VLGWGLSLERPTM*IK.Y +2														3.1543											
gi|37362677|ref|NP_013127.2|					10.8	15.8	12.9	16.7	25.1	6	15.8	18.9	28.7	45.2	28.5	28.5	13.9	18.9	4.5	18.7	8.6	6.2	9.1	5.5	Cytosolic aspartate aminotransferase, involved in nitrogen metabolism; localizes to peroxisomes in oleate-grown cells; Aat2p [Saccharomyces cerevisiae]
K.IIFGTQSDAFQEDR.V +2					4.7774	4.7334	4.7421	4.72	4.5294		4.0648	4.5992	4.6485	4.4621	4.6822	4.5783	4.9532	4.7967			4.0722	4.6937		4.3911	
K.LIHNDSSYNHEYLGITGLPSLTSNAAK.I +3														5.0595											
K.LLETPELTEQWHK.D +2									3.3948				3.8292	3.6743	3.6445	3.56				2.9552					
K.LSTVSPVFVCQSFAK.N +2					3.0286	3.141	3.3347	2.7709	3.5066		3.2992	2.5546	2.8367	3.5851	3.4294	3.4366	3.3694	3.3076							
K.NHIALFDTAYQGFATGDLDK.D +2														7.4141											
K.PAVTSQLAK.I +1																		2.4604	2.1553						
K.PTWANHIM*AIFENQGLK.T +2													2.9274												
K.RLEETHAVYLVASGR.A +2														4.3085											
K.RLEETHAVYLVASGR.A +3														3.9763						4.0469					
K.SLDLNGFLNAIQK.A +2								3.6209	4.5062			4.3706	4.5665	4.8065	4.2327	2.7293	4.2951	3.9536		4.4292	3.8249		4.2447		
K.TATYPYWANETK.S +2						3.1083		3.2174	3.0554		2.9231	3.4426	3.1438	3.2002	2.9702	3.0256		3.294		2.7952		2.696			
K.TIKPAVTSQLAK.I +2														3.5932	3.6003	3.2319									
K.VDLGIGAYR.D +2						3.0894	3.2702		3.4292	2.7669	3.342	3.0485		3.1941						3.092	3.4482		3.4373	2.7313	
R.ASIAGLNQGNVEYVAK.A +2					4.6188	4.5256	4.3505	4.1754	4.4804	3.9589	4.2457	3.3325		4.3188	4.0389	4.2682	4.6581	4.5364		4.5794			4.6667		
R.DDNGKPWVLPSVK.A +2									2.5495				2.7209	3.251											
R.LEETHAVYLVASGR.A +2													3.8715		3.8055	4.5594									

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.VGCFHLALTK.Q +2													3.3953	3.1571	3.1952	3.0775			2.817						
gi|6319326|ref|NP_009409.1|					12.7	12.7	8.8	18.3	25.8	12.7	16	14.4	25.8	27.8	23.2	34.3	17.6	25.8	12.7	22.9	19.3	15	20.3	8.8	N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase, required for 'de novo' purine nucleotide biosynthesis; red pigment accumulates in mutant cells deprived of adenine; Ade1p [Saccharomyces cerevisiae]
K.AEQGEHDENISPAQAAELVGEDLSR.R +2																				2.7932					
K.AEQGEHDENISPAQAAELVGEDLSR.R +3									3.8041				4.149	3.9344	4.0064	4.1348									
K.ESQEFPEPIFTPSTK.A +2					4.121	4.0019	4.1134	4.2234	3.8161	3.7883	3.5223	3.1963	3.8917	4.1065	3.63	3.5683	4.0808	4.0487	3.2073		3.1258	3.4908	3.6079		
K.FEFGIDEK.T +1																							2.6478		
K.LIPLEVIVR.G +2															2.6356	2.5881									
K.TELDGILPLVAR.G +2					4.3891	4.1033	4.5842	4.2409	4.4243	3.2441	3.7922	3.8904	4.1995	4.4192	4.3196	4.4002	4.3358	4.126		3.3995	4.3098	4.2648		4.2028	
K.TGTVHGLK.Q +2																									
K.TIFDYLPAK.L +1																				2.0157					
K.TIFDYLPAK.L +2													2.9367					2.5006				2.806			
K.TNEILVDEVLTPDSSR.F +2								3.5964			2.7322					4.3424	3.6045		4.2204	3.2962	4.7988		3.2489		
K.YIEAYETLTGSK.W +2					3.7199	3.9151		3.3421	3.2482	3.336	3.4159					3.2555		3.4395					4.7171		
R.DWLTANK.L +1																		2.5542	2.5291	2.6204					
R.GYITGSAWK.E +1																		2.2081							
R.ISAYDVIM*ENSIPEK.G +2														3.7473											
R.ISAYDVIMENSIPEK.G +2									4.2606							4.1049		2.6245			3.2979			2.8226	
R.NHLVDIAPGK.T +2											2.6205		3.4885	3.4538	2.7249		2.7078					2.5116	2.9686		
R.RVAELAVK.L +2													2.7831	2.8327											
gi|6319564|ref|NP_009645.1|					18.2	17.8	23.3	12.8	18.2	12.8	23.3	22.1	32.6	39.1	18.6	18.2	27.5	24	20.2	26.7	15.9	21.7	27.9	18.6	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta; may function as a docking site for other proteins required for mitotic and meiotic chromosomal DNA replication and for DNA repair; Pol30p [Saccharomyces cerevisiae]
K.DCVQLVNFQCK.E +2												3.3824	3.4507					3.2813							
K.EDGIIAQAVDDSR.V +2						3.7722	4.107				3.8891	3.4032					3.9126								
K.FEEASLFK.R +1																		2.313	2.1156		2.4845	2.4135			
K.FEEASLFK.R +2																		2.6185							
K.FVADGDIGSGGSVIIKPFVDM*EHPETSIK.L +3														5.9271											
K.IEELQYDSTLSLPSSEFSK.I +2					4.5221	4.5489	4.76	4.6633	4.4586	2.8468	3.5565	4.0891	3.8907	4.4804	4.2761	4.4107	4.3576		4.3522	3.3255	4.5766	3.9265	4.9491	4.4242	
K.LEM*DQPVDLTFGAK.Y +2										3.6497			4.0782	4.5472											
K.LEMDQPVDLTFGAK.Y +2					4.3907	4.2824	4.7985	4.881	4.3771		3.0434					3.9975		4.4855				3.2954	4.7881		
K.LM*DIDADFLK.I +2																				2.7086					
K.LMDIDADFLK.I +2																	2.556						2.7152		
K.SGFLQFFLAPK.F +2													4.0963	3.6292					3.536	3.5511					
R.DLSQLSDSINIM*ITK.E +2													3.188	3.9122				3.4594							
R.DLSQLSDSINIMITK.E +2															4.1807		2.9265	4.042		3.6625		3.0023	3.7151	3.8688	
R.LSSEAPALFQFDLK.S +2					4.5981		4.703		4.8		2.5073	3.7517	4.4416	4.6731	5.0826	4.5255	4.5891	4.6088	4.5135	3.4532	4.6371		4.3908	4.0852	
gi|6320242|ref|NP_010322.1|					5.4	5.4	5.4	5.4	7.4	4.7	5.4	5.4	19.6	16.6	17.1	6.9	8.5	17.6	5.6	17.8	7.4	5.9	7.4	4.2	Lysyl-tRNA synthetase; also identified as a negative regulator of general control of amino acid biosynthesis; Krs1p [Saccharomyces cerevisiae]
K.AAAEGVANLHLDEATGEM*VSK.S +2															2.5353			4.0344							
K.AAAEGVANLHLDEATGEM*VSK.S +3													3.9344	4.2935											
K.AAAEGVANLHLDEATGEMVSK.S +2																	4.8545			3.8336					
K.EICNAYTELNDPFDQR.A +2					4.3487	4.6361	4.4899	4.4486	4.4775		3.9823	4.308			4.2827	4.7112	4.526	4.2384	4.1327	4.1385	3.9086	4.3669	4.5166	4.0482	
K.FHVSISNPEFLAK.Y +2													2.7643	3.8836						3.309					
K.FIEVETPM*M*NVIAGGATAK.P +2													4.7139												
K.FIEVETPMM*NVIAGGATAK.P +2																						2.6469			
K.FPSGDQLHTAETGEFLK.K +2																		3.2462							
K.ILVDNKLECPPPLTNAR.M +2																		3.6437	2.6127						
K.KGGEGEVSVFVSR.V +2													3.702	3.7951	3.4503		3.1913								
K.KTDLFADLDPSQYFETR.S +2														4.1354											
K.RGDIVGVEGYVGR.T +2													3.5712	3.2488						3.2556					
K.TDLFADLDPSQYFETR.S +2					5.4091	5.3436	5.4114	5.8621	5.3114	4.5183	4.0423	4.951	5.191	4.4961	4.7705	5.2989		2.8859		4.002	5.5787		5.1884		
R.EVLLFPTLKPDVLR.E +2															2.5828					3.5659					
R.GDIVGVEGYVGR.T +2									2.7425																
R.IAPELFLK.Q +1																		1.916							
R.INMIEELEK.V +2													2.8898	2.8856	2.8921	3.0224		2.8431						2.8437	
R.LAM*FLTDSNTIR.E +2													3.482	3.6859											
R.LAMFLTDSNTIR.E +2										2.9444					3.5048					3.3374	2.8827		4.0623	
gi|6320764|ref|NP_010843.1|					5.2	8.5	8.7	8.1	27	6.2	9.1	10.9	17.1	17.1	17.1	19.4	10.9	11.7	9.9	25.8	6.5	4.2	7.5	10.5	D-lactate dehydrogenase, part of the retrograde regulon which consists of genes whose expression is stimulated by damage to mitochondria and reduced in cells grown with glutamate as the sole nitrogen source, located in the cytoplasm; Dld3p [Saccharomyces cerevisiae]
K.ALNAVFFGIENFDTVQK.L +2						4.1344			5.4307			4.6084	5.1232	5.9419	4.8575	3.2891	4.5567			5.9772				2.6169	
K.DLYSVSAAVTER.L +2																	3.6173	4.2054		4.4126			2.9188		
K.GSISAEHGIGFHK.K +2													3.523	3.3363											
K.LAVVPQGGNTDLVGASVPVFDEIVLSLR.N +2									3.0508																
K.NHYDPNGILNPYK.Y +2									3.0254				3.2416	3.4475					2.7291						
K.QIEDLLEPFVYEYIASK.K +2							2.9877													2.8797					
K.SELSEILSAFEFM*DR.G +2					3.4268		4.2602	3.5365	3.0521			3.1753	4.4013	4.6429	3.3047	4.6808				2.9649					
K.SELSEILSAFEFMDR.G +2																				2.8605					
K.SVPTACNSYGGMYK.Y +2						2.5183																			
K.VLDSEDLAYFR.S +2					3.4085	3.457	3.5119	3.4139	3.7158	3.1929	3.5216	3.4869	3.3389	3.6548	3.8444	3.5934	3.3729	3.6404		3.8977	3.8562	3.7707		3.4733	
K.YRGQSNLILLPNSTDK.V +2																			3.5182						
R.DFDPVSGTFK.C +1																		1.9722		2.1634	2.1325	2.4778		1.9487	
R.GQSNLILLPNSTDK.V +2								3.7895	3.5237		3.4229						2.8622	3.0889					3.3575	3.7055	
R.GSIECTIEYLK.D +2												2.5583				3.1082		3.5484			3.1073		3.1858		
R.LNAAGLIGDAPKPVVK.S +2									3.6739				4.0825	4.2009	3.773	4.5597									
R.NNCQVGGVVSTNAGGLNFLR.Y +2									3.1513	2.6727	2.8144								3.7742	3.9246					
R.SILSNDEILNSQAPEELASFNQDWM*K.K +3															5.9785	4.1959				3.8716					
gi|6321412|ref|NP_011489.1|					13.9	11	9.8	10.7	22.5	2.3	9.1	19.5	19.9	30	13.7	28.1	13.4	11.5	23.2	30.8	5	3	9.6	11.7	Tryptophan synthase involved in tryptophan biosynthesis, regulated by the general control system of amino acid biosynthesis; Trp5p [Saccharomyces cerevisiae]
K.AGANGFIIVDLPPEEALK.V +2																							2.8507		
K.DEFFAFQK.E +2																2.5792						2.8759	2.8731		
K.DTPLAVGFGVSTR.E +2											3.0036	2.6263	3.394	3.7674	3.7792	3.5276		3.8615	2.9507	3.1188		2.6394		3.2352	
K.DVQSVAEVLPK.L +2						3.0233	2.9452																3.2876		
K.EYVQGILNGAK.H +2									2.8128																
K.GFDEAVADPTFWEDFK.S +2					4.9035			4.377	5.0203	4.5253	3.9787	4.1353	4.8675	3.8312		5.4641	3.9787		4.0458	4.8503				5.0391	
K.INNALAQVLLAK.R +2									4.7204			4.4174	4.4546	4.3147	4.5299	4.6307	4.5238	4.224	4.438	4.2568					
K.IVTLCGDAPEGK.R +2						3.946			3.8882					3.7667						3.5203				3.6514	
K.LLGVEAGGDGVDTK.F +2						3.7359			4.3873							3.9999									
K.NVIAETGAGQHGVATATACAK.F +2						4.5713			6.8265				7.1302	7.0994	5.8646	6.2813	5.0996	3.3258	6.3275	6.4375					
K.NVIAETGAGQHGVATATACAK.F +3													4.4847	4.7442	3.5038		4.1291			4.0305					
K.TM*KPDQHLVINISGR.G +2													3.6193	3.3778											
K.TMKPDQHLVINISGR.G +2																				3.2163					
K.TTYYVVGSAIGPHPYPTLVR.T +2														4.6058					2.5205	2.9213					
K.YVLQDSDGQVHDTHSVSAGLDYPGVGPELAYWK.S +3														5.9972											
R.AQFIAATDAQALLGFK.L +2					4.8969		5.6473	5.6179	5.289			3.2756	5.4258	6.0944	5.0975	3.2751			2.7477	5.1403			4.9515		
R.EHFQSVGSVADGVVIGSK.I +2																5.1318	5.3491			4.8525					
R.FGDFGGQYVPEALHACLR.E +2														5.0941						3.7695					
R.LTEHCQGAQIWLK.R +2													3.3681				3.3978								
R.M*GTTGVQSSVASDLDELISR.V +2									4.7002			3.6216	4.6877	5.4699	3.8825	5.0619		3.3711	4.8287	2.8791	4.8919				
R.MGTTGVQSSVASDLDELISR.V +2					4.2238	4.4499	4.3339	3.3186	3.5756		3.0204					4.4655		2.8191		3.7063				3.3203	
R.NALVTFM*TAGYPTVK.D +2												2.5555	4.3393	4.5022	2.8081										
R.NALVTFMTAGYPTVK.D +2									4.4057		3.3526	4.2244		3.9335		4.2077	3.5683	4.139		3.3291	3.8955		4.051		
R.NEGVTVPIILM*GYYNPILNYGEER.F +2																			2.6105						
R.NEGVTVPIILMGYYNPILNYGEER.F +2					3.1394			3.7377				2.5978				4.3988									
R.NYINDNGLSLIPLVAPSTTDER.L +2					3.3859		2.5839		3.3264			3.1583				3.6534			3.8703	2.9263				2.561	
gi|6322331|ref|NP_012405.1|					6.6	9.3	9	8.5	15.7	4.3	10.3	13.7	10.7	16.1	15	13.6	8.4	12.2	6.4	15.5	9.5	9.9	13.9	12.6	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP; Ura2p [Saccharomyces cerevisiae]
K.AGLLGVESIELTPHIISK.T +2																				3.3796					
K.AIM*GLPLTPYPVEK.L +2						2.6982								3.1182											
K.AIMGLPLTPYPVEK.L +2					2.7942										3.2033	3.2118				2.8795					
K.CIVNPSPASITASAELQSTSAK.R +2																		2.9246			2.9501	2.8036	4.0544	2.7698	
K.DGTVLQGYSFGAEK.S +2						3.9911	4.554		3.3827	3.4664	4.0255	4.3348	3.2517									3.9952	3.8903	3.9239	
K.DSLPLLLAAVEEGK.L +2					4.275	4.6516	4.364	4.4919	4.4822		3.4436		3.6995	4.6604	4.6534	4.5888	4.5773	3.6173		4.1044	4.0521	3.8566	3.8409	4.3126	
K.DYCIIEVNAR.L +2												2.6925					3.0684								
K.EDYDGLFISNGPGDPSVLDDLSQR.L +2						4.4546	2.6797	4.0419	3.9288			3.0166		4.1511	2.9813	3.1662	3.4548	2.5667	3.0671				4.6388	2.5313	
K.EEGIYTILINPNIATIQTSK.G +2																		3.0781		2.8567	3.5612	2.52	2.9662	2.6672	
K.ELTSMDEAESFAEK.V +2						4.2422						2.5204				3.9107	4.4495	3.6433			4.2572				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ELVDLCNVAFSSSPQVLVEK.S +2					3.7645	3.659	4.2852	3.5136	4.0522			3.8129			2.5691	3.4394		5.035		2.5991				3.3573	
K.GHVITTIFFEPSTR.T +2																				3.9748					
K.ILGTSPDMIDSAENR.Y +2					3.0275				3.2353		3.0841			3.3939									3.3669	3.4572	
K.ITAVAELLNQWPTEK.Q +2									4.0696			3.4454	3.74	4.236	3.9571	3.9304				3.771			3.8876		
K.ITGPYNIQFIAK.D +2													3.5098	3.5625	3.2641			2.8635		2.6511				3.14	
K.KGETLQDTIR.T +2														2.6333					2.7917						
K.KNILLSIGSYK.E +2													3.4205												
K.LGLNIPLNEVK.N +2								3.0458	3.084				3.3076	3.3696	3.4027	2.8284	2.9395	2.7642		3.2387		3.0366			
K.LHDLVQFAEK.I +2														2.6482											
K.LLIEAISR.N +2																				2.7479					
K.LTIDDIVLR.L +2					2.9358							2.8597	3.0035	3.1202	3.1818							3.2094			
K.NDLESYLNQAVEVSR.D +2						5.5211	5.8547	5.1906	5.4317		4.4352	4.9026	4.8828	5.281	5.208			5.1476			4.7087	5.2142	2.8397	5.2217	
K.NILLSIGSYK.E +1																				2.1616					
K.NILLSIGSYK.E +2														2.6658				2.7103							
K.SQAANSVDEALAAVK.E +2					4.6543	5.0626			5.1174			3.9808	5.2119					4.3857				4.8935		5.3288	
K.STCACFEPSLDYCVVK.M +2						3.9246		3.4158	3.0515		2.8762				2.5676	2.7186	4.1986	2.5729					4.0276	3.7455	
K.SVGEVMSIGR.T +2																								2.9955	
K.TADLASVLLLTSLQNR.S +2									2.5186			2.5192	3.125	3.7172	3.3429	2.9066				3.3233					
K.TADLASVLLLTSLQNR.S +3																			3.7789						
K.TIM*VNYNPETVSTDYDEADR.L +2																					4.0087	3.5364		3.1021	
K.TIMVNYNPETVSTDYDEADR.L +2									2.866		2.8409									2.5866	4.0492			3.4818	
K.VGYPVLVR.P +2																							2.666		
K.VLGTPIDTIITTEDR.E +2							4.4303	3.7167	4.1808		2.5982	3.5086	4.0454	4.1508	4.0785	4.2948	3.7656	3.6223				4.2818	4.1777	3.6303	
K.VTALFLPLR.E +2												3.3022	3.0938	3.1457	3.0207	3.1207	2.5915						3.1632		
K.VVGVNLIELATK.A +2									4.6093			4.1557	4.5279	4.5967	4.4536	4.4355		4.5092	4.1846	3.6332	4.6469		4.3723		
K.VYFVPVTAEFVR.K +2							2.8917								3.1918					3.1613			2.7675		
K.WLQNEGIPAVYGVDTR.S +2									3.9085		2.8697	3.807					3.6974	3.6508		4.7177	3.7199			2.6645	
K.YTQVLKPIAFPGGLLEDNVK.A +2														4.0344					2.5966	3.173					
R.AAYALGGLGSGFANNEK.E +2					5.5178	4.5359	5.239	6.0235	3.7981	3.6466	4.4179	3.3429		5.5348	5.1741	5.6093	2.9482			6.2676					
R.DELVEELPR.Y +2										3.0304	2.9986				2.9045					3.2765		3.5889	3.1988	3.1325	
R.DYPVVITK.Y +1																				2.1299		2.483			
R.EGVLDLMK.G +1														2.3517											
R.ELFSNAIDEINEK.C +2					3.5694	3.6325	3.408	3.4676	4.1048	3.1092		3.0362	3.7871	3.6734	2.9357	3.4025			3.8138			3.4097	3.6713		
R.ELVAPGAIQNLIR.S +2														3.5843		2.9963									
R.FLDSNEVAIR.R +2									2.726																
R.FNSPEEYAR.L +2														2.9828											
R.GHNIPCTSTISGR.C +2																				3.1211					
R.ILAIDVGMKYNQIR.C +2																									
R.IVNVNPLVSSVK.K +2							3.4238		3.3173		3.2104	3.3872			2.6572	3.3016	3.0317	3.7471	3.259	3.605			3.6439		
R.IVVATAK.I +1											2.0688														
R.LAVDYSVPLVTNVK.C +2									2.8291		3.019	3.2486	3.6564	3.6551	2.8254	2.5817					3.7687		4.1507	3.5111	
R.LFLESGFTYCQLM*PR.S +2																			2.7516						
R.LKDTYIVDNK.I +2																							2.7389		
R.LLMHYQVR.I +2																				2.532					
R.LSNVLEAK.K +2																							2.7663		
R.LYFETINLER.V +2															2.6023	3.0506					3.0411				
R.NITLDVSER.D +2														2.8636										2.535	
R.PSYVLSGAAMNTVYSK.N +2																							3.8498		
R.SAFDVPEWVDPNVQNLVSK.V +2					4.1401	4.2359	4.4645	3.5057	3.7975	3.0561	3.0179	3.8891	4.1175	4.1981	2.9873	4.8086	2.5971		3.6391		4.8396				
R.SISGPVITDVASLK.A +2							3.3508	3.3451	3.9392	2.5067	3.5626	3.3832	3.6746	3.4697	3.7142	3.4149				3.7311	3.8989	3.1118	3.4725		
R.TLACYSDAIVMR.H +2																		2.7308							
R.VFAIANAFAK.K +2					3.7016	3.3246	3.3532	3.4316	3.4029	2.898	3.2457	3.2087	3.3653	3.4053	3.4246	3.265	3.4549	3.4138		3.3636					
R.VVYNGETLVLSGELVSPGAK.G +2																					3.7675	3.9671			
gi|6323056|ref|NP_013128.1|					7.1	15.7	7.1	7.8	16.4	6.8	7.8	13.2	28.8	22	21.7	14.7	15.4	18.3	15.7	32.3	5.9	14	10.5	11.2	Enzyme of 'de novo' purine biosynthesis containing both 5-aminoimidazole-4-carboxamide ribonucleotide transformylase and inosine monophosphate cyclohydrolase activities, isozyme of Ade17p; ade16 ade17 mutants require adenine and histidine; Ade16p [Saccharomyces cerevisiae]
K.AFEHTADYDAAISDFFR.K +2													5.4767	6.857	3.8557					6.5862					
K.ELSASLNLPAAASFK.H +2					4.0576	4.1144	4.3825	3.6951		3.1579	3.8875	3.078	3.7276		2.9322	3.2241					3.1679			4.2572	
K.EVSDGVIAPGYEPEALNILSK.K +2									3.8468					3.9679	3.8252	3.4973	3.901		3.5439	3.3399		3.7676	3.277		
K.FEEVPEPFTK.E +2									2.6496																
K.HVSPAGAAVGLPLSDVER.Q +2																	4.1661								
K.IGVTVQEAVEEIIDIGGVTLLR.A +2																			2.9398						
K.LNNVSLSSDAFPPFPDNVYR.A +2											3.2761		3.7665		3.8751				4.5133	3.9084	3.889		4.4251	3.8634	
K.NGMVVGLGAGQQSR.I +2										3.3916															
K.RNDAIINQSTFK.E +2													3.9796	4.4689	3.8868		3.2068	4.174	4.1026	4.3513					
K.SNAIDLFVTGQR.I +2						2.8957	2.6991	2.6702				3.8138	3.4728	4.0169	4.1191			3.6005				3.6802	3.0203		
K.TAILSVYDK.T +1									2.3244				2.2172					2.1998		1.9945		2.2685	1.9915	2.1064	
K.TAILSVYDK.T +2						2.947			2.6868			2.5245	2.9296	2.9012		2.6226		2.874		2.6339		2.5867			
K.TDNWWLR.Q +2													2.7934												
K.TGLLDLAK.G +2														2.5688											
K.TLHPAVHAGILAR.N +2																				2.6458					
K.VDFVVCNLYPFK.E +2						3.1536			2.9958			3.018	3.4808	3.6987	3.0091	2.8997						2.9164		2.7303	
K.VLCGTPGYINLLDALNSWPLVK.E +2																				2.9089					
K.YCILQIDPNYVPGQM*ESR.E +2																				2.7799		2.7569			
K.YCILQIDPNYVPGQMESR.E +2																	3.8022	2.6016							
R.EAGFPVDDVSSITHAPEMLGGR.V +2																	3.0937								
R.EVFGVTLQQK.R +2																		3.1068						2.6712	
R.ILASGGTANMVR.E +2					3.4145								3.2308					3.0087							
R.M*SSFGDFIALSNIVDVATAK.I +2													4.105	5.2651						3.5032					
R.NDAIINQSTFK.E +2						3.6536			3.6671	3.0143	3.5472	3.6554		3.5345		3.5721						3.0628			
R.PAQAYITQQEELPFK.V +2					3.1677	3.7251	3.8067		2.716				3.9396					4.2583							
R.QVYFVNDMEDLSPLACAYAR.A +2																		2.9605		3.3207					
R.VTILSDPNDYSIFLQDLSK.D +2						4.2895		3.8686	4.1599			3.1519	5.214	4.5284	5.0054	4.6773			4.8909	4.5894					
gi|6323179|ref|NP_013251.1|					12.1	12.8	19	27.1	24.5	27.1	24.2	27.1	29.3	20.9	27.8	29.3	20.9	26	16.1	22.3	17.6	23.8	18.3	20.1	Protein that binds G4 quadruplex and purine motif triplex nucleic acid; acts with Cdc13p to maintain telomere structure; interacts with ribosomes and subtelomeric Y' DNA; multicopy suppressor of tom1 and pop2 mutations; Stm1p [Saccharomyces cerevisiae]
K.ADVPPPSADPSK.A +2								2.5427																	
K.DVTDSATTK.K +1								2.2432		2.1747	2.0305	2.3328			2.215					2.3933			1.8985		
K.EAQADAAAEIAEDAAEAEDAGK.P +2																				3.3532				2.9552	
K.EAQADAAAEIAEDAAEAEDAGKPK.T +2							3.6531	6.1812	6.5892	5.6787	5.1188	5.2213	6.434	6.7523	6.602	6.3799	5.9828	5.7383	6.0881	5.8062					
K.EAYVPATK.V +1							2.4859	2.5007	2.6585	2.2187		2.6578	2.5857		2.5048	2.6021				1.987		2.1327	2.0624		
K.EYLEFDATFVESNTR.K +2						2.6499			4.5278				4.8645		4.8675	5.2447					5.4745	3.8147			
K.KADVPPPSADPSK.A +2					2.6346			3.0432		3.1446	2.5417	3.3668	3.3367	3.5262		3.2424	2.5155	2.6894			3.1674		3.1427	3.4014	
K.KVELDAERIETAEK.E +2																		3.3745							
K.TAQLSLQDYLNQQANNQFNK.V +2					6.3654	6.489	6.5803	6.802	6.9224	6.2844	6.7914	6.4718	6.5231	6.6687	6.9171	6.6658	3.3669	4.8853	6.9046	6.2274	3.679	4.1602	4.6556	6.5455	
K.TAQLSLQDYLNQQANNQFNK.V +3					6.2598	6.2174	6.2066	6.0808	6.1285	4.9078	5.2813	6.4202	6.6324	6.3212	6.2525	6.2739		5.1758				6.4517			
gi|6323873|ref|NP_013944.1|					20	14.9	12	11	19.2	14.7	14.5	19	20.8	24.4	18.5	18.5	12	16.4	13	26.9	12	9.1	10.1	9.3	GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5'-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation; Gua1p [Saccharomyces cerevisiae]
K.ADNIYIEEIKK.A +2													2.5074												
K.AGLYNQISQAFACLLPVK.S +2					4.6406			4.5363	4.3697			3.7804		2.953					2.87	4.1008					
K.GMNDSTVWMSHGDK.L +2																		3.148		3.9401					
K.IIGNTFIHVFER.E +2														4.0256					2.9446	2.976					
K.ISELGWTPK.G +2							3.184		3.3012	3.1979	3.1714	3.2189	2.5444				3.1723								
K.LHGLPTGYK.T +1															2.2952										
K.LMTEAIGDR.F +2											2.5462					2.5758									
K.LVGPTAEVIGAVSGGVDSTVASK.L +2					5.7587	5.4097	5.5826		6.2942	3.6153	3.6663	4.0217	4.8026	5.4124	5.8543	5.4378	3.9946		5.2447	3.4069	4.4395	6.5987	5.507	3.7018	
K.LVGPTAEVIGAVSGGVDSTVASK.L +3													5.4003	5.5792	5.7579			5.5057	5.6549	3.7553			4.4289		
K.NFAVDLCHAK.Q +2													3.4253	3.4028	3.2364	2.521		2.8364		2.8875					
K.QNWTM*ENFIDTEINR.I +2													3.8616						3.1432						
K.QNWTMENFIDTEINR.I +2					4.9042	3.5175	3.0665	4.5925	4.5123			4.1812			3.9097	5.089	4.4021	2.6585		3.9732					
K.THHNVGGLLENM*K.L +2														2.7293											
K.VIDDSNSLFK.G +2					3.3924	3.9029			3.105	2.9654	2.9501	3.4735	3.7174	3.4783	3.192	3.6931		3.2593		2.5086				3.1177	
R.EFNIYAEM*LPCTQK.I +2													3.9408	4.1079	4.0469			3.2995							
R.EFNIYAEMLPCTQK.I +2					3.4733	3.5878									3.2085	3.0526					3.0634		3.8892		
R.FHAILVDNGVLR.L +2																				2.5435					
R.IVNEVDGVAR.V +1																				2.1064	2.3452				
R.IVNEVDGVAR.V +2									3.4144	2.796										3.7729					
R.KADNIYIEEIKK.A +2													3.2278	3.381											
R.KLVGPTAEVIGAVSGGVDSTVASK.L +2																				3.7422					
R.TYDQVIALR.A +2					3.45			3.3353		3.3005	3.343	3.3724										3.6918			
R.VTYDITSKPPATVEWE.- +2					4.7845	4.5833	5.0693	4.6726	4.9452	4.4985	4.7478	4.3487	4.637	4.4439	4.3115	4.666	4.2734			4.27	4.3794	3.5477	4.4242	4.1584	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6325097|ref|NP_015165.1|					5.1	8.9	7.2	4.8	9.9	9.1	10.1	5.1	8.9	12	7.9	15	12.2	12.3	8.6	12.7	11.5	8.8	8.7	12.4	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA; Cdc60p [Saccharomyces cerevisiae]
K.ADM*IAAGEAFVYNEPESQVM*SR.S +2																					2.7508				
K.ADMIAAGEAFVYNEPESQVM*SR.S +2																3.3106						2.8506			
K.ADMIAAGEAFVYNEPESQVMSR.S +2																	3.9163					4.4511			
K.DIFTGEEVEIPPVTK.I +2														2.6203		2.9861	2.7966				2.82			2.8121	
K.EDYYTGTMIYGPYK.G +2					3.3096		3.8195		3.4744		3.0258	2.5901									3.7127		3.7516		
K.GTGVVTCVPSNSPDDYITTK.D +2										3.7477	4.2473						4.392		4.3207	3.913	4.7468	4.3063	4.5388	4.4891	
K.GVLAALDYLR.N +2													3.7028	3.7743	3.8734	3.891		3.5846	4.0294	3.6897			3.6446		
K.IAEFSAISFPYGAK.T +2					3.3312	3.7735			3.2966	2.7985		2.8042	4.5172	4.7407	3.1695	3.9068		4.219		3.5921			2.7622		
K.IEALEFADDAAK.I +2					4.4352	4.3947	4.3866	2.7708	4.0677	3.6433	4.1739	4.1151			4.0273	3.8931	3.834				4.1462			4.4401	
K.IHAPQSVYPELR.I +2													3.3149	3.1242	3.0482		2.7381		2.9652	3.1508					
K.IIDSSSDLDK.S +1																		2.3063							
K.IIDSSSDLDK.S +2																3.2438									
K.LFSEQTLDDNKK.V +2																						3.592			
K.NAFEGVLDWLK.N +2													4.012	4.0187	4.023				3.7013				3.5725		
K.NFDNVPAEEEEIKEETPAEK.D +2																		3.6884							
K.QAIECLEGM*QLFAPEVK.N +2																				3.2952					
K.QAIECLEGMQLFAPEVK.N +2																								2.9739	
K.RGFYKPIVTVPGK.A +2																				2.7222					
K.STGNFMTLEQTVEK.F +2						3.276		4.1917								4.1955								2.6928	
K.TYEQYALTNYK.N +2									3.8103	3.2745	3.8703														
K.VEFSIGFER.M +2														2.7321											
K.YGLFDFQAAR.D +2								3.4075					3.004	3.2352		3.3445	3.0858		2.6782	2.9905			3.5205		
K.YWLTYFPPLCESDCTSLGAR.I +2																			2.5607						
R.EFEYFYPLDVSISGK.D +2									4.0493									3.3528						3.4731	
R.ELQFSEIDTVK.A +2														2.8768				2.8479	2.5889						
R.GFYKPIVTVPGK.A +2													2.7135	2.8003											
R.IAFADAGDTVEDANFDESNANAAILR.L +2						5.4778	3.663		5.1191	2.6116	2.6832					4.5725	5.8176	5.0039		3.5196	5.573	5.4747		4.7067	
R.ILPMETVIATK.G +2							2.5222				2.514			2.7383	2.7201										
R.LANEKPEDVFER.E +2													2.8273					2.5811							
R.QSGEGVTPQEYIGVK.I +2						3.2237										3.7778									
R.SFVTTDANPYYDAFIR.W +2					4.7318	4.8558	4.8428	4.3956	4.889	3.5502	3.893	3.8202	4.643	4.7772	4.7996	5.0564	4.6074	4.1207		4.4089	4.7651	5.29	4.9185	3.9843	
gi|6325151|ref|NP_015219.1|					8.1	12.4	9.8	6.6	19.2	11.1	13.9	13	28.1	22.1	17.6	15.4	10.5	6.1	15.7	15.4	3.9	8.2	9.2	5.3	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm; Sse1p [Saccharomyces cerevisiae]
K.AEEWLYDEGFDSIK.A +2					5.5757	5.3346	5.3543	5.5099	4.9768	4.711	5.0335	5.016	3.3318	4.7785	4.881	4.8151	4.4215	5.0882	4.292	4.3982			4.8301	4.7774	
K.ANITDVCIAVPPWYTEEQR.Y +2									2.9192										2.5833			2.751			
K.DTEGDVDMD:- +1																				1.8013					
K.ENEMLAQDK.L +2								2.8782	2.7259																
K.FEDIHPYSVSYSWDK.Q +2													3.9344	3.5915	3.6255	4.4983									
K.GAAFICAIHSPTLR.V +2													2.5054						2.9914						
K.KDDLTIVAHTFGLDAK.K +2														5.5018						4.0404					
K.KDDLTIVAHTFGLDAK.K +3														4.4766											
K.LEEEYAPFASDAEK.T +2					4.2501	3.855	4.459		4.1313	3.081	3.8999		4.2303	4.3264		4.1179									
K.LSAEEVDFVEIIGGTTR.I +2						4.3563	2.9264		4.9929			4.8519	3.8227	4.9832	4.7551	4.6257									
K.NTLEEYIYTLR.G +2							3.2283	3.364			4.1369	3.8439	4.0584	4.2494	4.1484	3.9107			3.1933	3.8745	3.6654			3.5499	
K.PLSTTLNQDEAIAK.G +2																							3.761		
K.QEASQMAAMAEK.L +2													2.6285												
K.QSISEAFGKPLSTTLNQDEAIAK.G +3													4.0348	4.5957					4.679						
K.QVEDEDHMEVFPAGSSFPSTK.L +2						2.8316			2.6759	3.3037	2.9357						3.3579								
K.YEELASLGNIIR.G +2					4.4352	4.075	4.2101	4.3825	4.0539	4.2624	3.9076	3.7638	4.4607	4.1812	4.2847	4.2691	3.9906	4.3833					3.9831	3.8084	
R.DFDLAITEHFADEFK.T +2														3.9502											
R.EELEELVKPLLER.V +2													3.8547		2.9474					3.1502					
R.GIDIVVNEVSNR.S +2												3.4723					2.7648		2.9936	3.5171					
R.GKLEEEYAPFASDAEK.T +2													4.7335		3.8967			4.4449	3.8524	4.8967					
R.IAGLNPVR.I +2						2.5609					2.6336	2.8054	2.5538		2.6426	2.7257						2.7527	2.5286		
R.IIGLDYHHPDFEQESK.H +2													4.2382												
R.IVNDVTAAGVSYGIFK.T +2					5.0035				4.8421	3.0985	3.6902	4.6855	3.4628	5.6146	4.848	5.0442				4.1177	2.9036	3.0608	3.2169		
R.SKQEASQMAAMAEK.L +2																	3.2539					3.8013			
R.STPSVVGFGPK.N +2									2.6617																
R.YNIADAAR.I +1													2.2673												
gi|9755335|ref|NP_012765.2|					5.6	7.7	8.3	8.3	15.8	4.1	7.9	14.5	16.3	19	16.5	13.8	13.5	12.9	14.3	14.9	11.4	4.5	13.6	9.9	Zinc-dependent metallopeptidase yscII, may have a role in obtaining leucine from dipeptide substrates; sequence coordinates have changed since RT-PCR analysis showed that the adjacent ORF YKL158W comprises the 5' exon of APE2/YKL157W; Ape2p [Saccharomyces cerevisiae]
K.ADEINQIFDAISYSK.G +2					4.7786	4.5332	5.2296		4.9739			4.3064	4.6829	5.2098	4.9268	5.1756	3.8957	2.9962	3.0163				4.5961	4.6479	
K.EAIPALIKPIVFNTVAR.V +2														3.1675											
K.ETQDALDNFTK.Q +2											2.9152														
K.FTGILNDNM*AGFYR.A +2													2.9728	2.8819	3.2995						3.6013				
K.FTGILNDNMAGFYR.A +2							3.9695					3.0017					3.8839	3.5068		3.4228					
K.GFDQSLAQSLDTITSK.A +2								4.0132	4.2621			3.9606	4.1375	4.6951	4.2951	4.3982	3.6603	4.7683	4.1562	3.8669			4.6362	4.2115	
K.HGQFAADLTAK.T +2													3.0379												
K.IGDVTSSEISEEEQQVTTFAFPK.G +2					4.3781		2.8646	4.0295	4.6351		2.5299	4.2662			5.346	5.5511			3.8209		3.3963		4.0693	2.8319	
K.INNPAIDTVTLNTVDTDIHSAK.I +2													5.0692		3.78				2.704						
K.INNPAIDTVTLNTVDTDIHSAK.I +3													3.5699	3.5688											
K.IYLDPISNDEK.L +2						3.5789	3.6538																3.0013		
K.KADEINQIFDAISYSK.G +2													2.922							4.4478					
K.KVTLFNTTPK.M +2														2.6429											
K.LGQQADLLSVEDR.V +2					3.4962	3.8658		3.32	4.1134	2.5773	2.6237	3.0653				3.4601		3.6885							
K.MFTDYCSGNK.E +2																				2.8386					
K.NGVDSSVVLSER.S +2											2.7244														
K.SFVVWDQIINSISSM*K.S +2																			2.8241						
K.SSDSFSTQR.L +2																					2.5947				
K.STWLFEPK.E +2																		2.7351							
K.TEDLWDALADASGK.D +2						5.2028	5.0181	4.9216	4.9297	3.5375	4.4245	4.1894	4.5416	5.0666	4.766	4.9254	4.1813	4.648			3.7873	4.4713	4.8853		
K.TFGIQYPLPK.M +2									2.9158			3.023	2.9897	3.1728	2.8234	3.0491					2.8627			3.1296	
K.TIELEDPTFFK.V +2								3.6119	3.7177	2.5266		3.4869		3.8135		3.4952	2.5931		3.3095	3.2973		3.687	3.55	3.7802	
K.TLSASGYTSTTNFLNLVSK.W +2						2.964			4.0759			3.4217	3.0003	4.0174	3.8335		2.8535		3.8053	3.3434	4.3533		4.6495		
K.VGFPVISVSEDGNGK.I +2									3.2099																
K.VNSEQSGIYITSYTDER.W +2																5.1639	4.4206			4.1471	3.3627	4.1962	5.2729	3.6011	
K.VTM*FGAACAAR.D +2													2.7102	2.7317					2.8908						
K.VTMFGAACAAR.D +2									3.6332				3.7215	3.8014	3.7595		3.078	3.058							
K.WLGEETFIK.G +1																		2.0754							
K.WLGEETFIK.G +2													3.092	2.9363	3.0993	2.6245	2.6511			2.6625					
R.AHQEGVEALWNWVK.K +2																				3.6768					
R.SSHPIEVPVK.K +2													2.5221	2.5491											
R.VGLVADVK.T +1																		1.8429							
R.YLSTADVKPDEDK.T +2																		3.3612		3.6028					
14					X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6322294|ref|NP_012368.1|		7.4		10.8		11.6		6.2	24.7	8.2	13.1	13.1	18.8	24.1	21.6	20.2	18.8	15.3	15.9	23.3	6.2	10.2	10.2	8.8	Farnesyl pyrophosphate synthetase, has both dimethylallyltranstransferase and geranyltranstransferase activities; catalyzes the formation of C15 farnesyl pyrophosphate units for isoprenoid and sterol biosynthesis; Erg20p [Saccharomyces cerevisiae]
K.ADVLTAFLNK.V +1													2.5411		2.4343							1.8832			
K.ADVLTAFLNK.V +2		4.2032		3.9131		4.1436		3.9167	4.0493		3.8376	4.112	4.1804	4.0457	3.9293	4.1752	3.9824	4.1102		3.9128	4.0453	3.8961	4.081	3.9838	
K.ALELASAEQR.K +2						3.8489			3.7422	3.5612	3.5219	3.7623		3.8119	3.5427		3.3998			3.7083					
K.DSVAEAK.C +1										1.9231														1.8393	
K.EACDWYAHSLNYNTPGGK.L +2									3.7666								4.3842			3.8999					
K.IEQLYHEYEESIAK.D +2													4.0513	4.7326	4.1838	3.985	4.2222	4.3872	3.3677	4.5615					
K.LVEELNASLLAYGM*PK.E +2													4.3909	4.6947	4.6991			4.9999	2.8305	4.364					
K.LVEELNASLLAYGMPK.E +2		2.9381		2.7803					2.8762																
K.TVEQLGQEEYEK.V +2				4.1237				3.9419	3.928	2.8508	3.744	4.0693	4.2908		3.8414	3.9934			3.2703		3.7893	4.0866	4.2778		
K.VPEVGEIAINDAFM*LEAAIYK.L +2						3.0989			2.7805					4.8606		3.3992									
K.VPEVGEIAINDAFM*LEAAIYK.L +3														5.4253											
R.GLSVVDTYAILSNK.T +2											4.4052	4.6692	5.1378	5.1843	5.2692	4.8485	3.9276	4.9951	3.4084	4.9672		4.1155	3.6532	2.5111	
1	X		X			X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320548|ref|NP_010628.1|		5.4			7.4	5.1	5.1	6.6	13.5		4.6	10.2	15.7	26.4	20.1	12.9	10.5	8.9	15.3	13.5	5.6	4.6	6.9	4.8	Arginyl-tRNA synthetase, proposed to be cytoplasmic but the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; Ydr341cp [Saccharomyces cerevisiae]
K.DIEEEGDSIPLEQSTNGK.A +2									3.5633		5.4023									5.152		5.122			
K.DLQHVNFGM*VQGM*STR.K +2																			3.3139						

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.DSHPDVNIVDLMR.N +2																3.2562	3.1462								
K.GAVLIDLTK.F +2													2.7034	2.5145											
K.GTVVFLDNILEETK.E +2															4.4436	4.147					3.282		4.1336		
K.ISGVDSSLIFPALEWTNTM*ER.G +2														4.3541	4.4478				3.918	3.2622					
K.ISGVDSSLIFPALEWTNTM*ER.G +3															3.74										
K.ISGVDSSLIFPALEWTNTMER.G +2					3.4965	3.3955	3.7283	3.4107	3.5257								3.5592								
K.KLSIAEPAVAK.D +2		3.1795											3.2671	3.46				3.3441							
K.QFGLLAVGFER.Y +2													3.3915		3.1703	3.0117			2.6346						
K.SDGTTLYLTR.D +2		3.1483									2.8082	2.3936						2.707			3.1245	3.3326	3.2248		
K.VEANGPFIQFFFNPQFLAK.L +2								2.9215	3.971			3.5239	3.1969	2.7443	2.5045										
K.VIIEFSSPNIAK.P +2															2.6472										
K.WINADFSLLK.E +2														3.0514						2.6549				2.5644	
K.YAQIEHPEEVADLVGISAVM*IQDM*QGK.R +3														4.2185											
K.YDVYSGESQVSK.E +2		3.9604											3.9519	4.303	4.0797	4.3991	4.5233		3.8161						
R.GDLLIPIPR.L +2												2.7066		2.5476	2.586	2.7513				2.7924			2.5529	2.5929	
R.LLGQYPDVLR.N +2					2.975	3.0032	3.0949		3.3318			2.9109	3.2282	3.5083	3.1096	3.156		3.5564	3.2046	3.5209	3.0977			3.0285	
R.MLSFEGDTGPYLQYAHSR.L +2																	2.9726								
R.MNYLGDWGK.Q +2													2.7955	2.8695				2.896					2.6219		
R.NYISQELSK.I +2														2.6775											
R.STIIGGFLANLYEK.L +2					3.6639				4.4569			3.4831	4.9373	4.8473	4.8256			3.5859	2.8122	4.37					
R.YGNEEALVK.D +2																3.5785			2.9235						
	1	X			X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6324709|ref|NP_014779.1|			7.3		9.5	10	13	4.9	26	9.5	14.6	17.1	35	35.5	35.5	27.1	16		16.5	22.2	13	17.9	14.6	13	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh2p [Saccharomyces cerevisiae]
K.EYPDLTLETELIDNSVLK.V +2			3.7071		5.1254	5.0105	5.3284	5.3139	4.8253	3.5144	3.6742	3.24	4.3149	5.3484	4.9384	5.0814					4.6668	4.1767	4.2829	4.6738	
K.GPLATPIGK.G +2			2.6197									2.5447	2.5013												
K.ISIFEAVHGSAPDIAGQDK.A +2									3.1521				5.4474	4.7649	3.6103				3.5217	3.3467					
K.ISIIFEAVHGSAPDIAGQDK.A +3													3.7912							3.5163					
K.TFGLFANVRPAK.S +2													3.1081	2.6096	2.7239				2.5709	3.0532					
K.TTYENVDLVLIR.E +2									3.571				3.4916	3.7178	3.9035	2.8791	3.4635					3.097			
K.YTVSFIEGDGIGPEISK.S +2					4.3111				4.3148	3.1568	3.5128	4.1369	4.9377	5.2868	4.6653	5.1075	4.0031			4.1415		3.7602	4.9242		
R.EENGEYSGIEHIVCPGVVQSIK.L +3													4.1488	3.9548	4.0897	4.0825				3.8368					
R.LADGLFVNVAK.E +2							4.041		3.6877					4.0345	3.9129	3.899	3.2		3.8281	3.8937	3.1716			2.7303	
R.TGDLAGTATTSSFTEAVIK.R +2						4.8873	5.4002		4.9165		3.2864	4.5131	3.5241	4.8726	4.1072	5.0712	3.578		4.5793		4.7384	4.8625	5.1916	4.2024	
	1		X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6323967|ref|NP_014038.1|		4.8			8.2	8.8	8.9	6.4	8.9	9.1	13.1	10.7	11.3	11.8	13.4	13.2	7.3	12		11.8	5	4.3	8.9	11.4	Beta-1.3-glucanosyltransferase, required for cell wall assembly; localizes to the cell surface via a glycosylphosphatidylinositol (GPI) anchor; Gas1p [Saccharomyces cerevisiae]
K.ADFYGINM*YEWCGK.S +2							3.6346		3.9423	3.368		3.2526	4.1882	4.2645	4.3103	4.1436				3.2913	3.4871		2.6623		
K.ADFYGINMYEWCGK.S +2		3.7868									2.6714	3.3597				4.072		3.5762		3.4462					
K.ALNDADIYVIADLAAPATSINR.D +2					5.3614	4.9333	4.6144	4.9181	4.6235		2.5013	4.4946	3.7144		4.0265	4.3098				3.4243			4.6966	3.0768	
K.EQLSFVM*NLYYEK.S +2													2.8567	3.2973											
K.IPVGYSSNDDEDTR.V +2																3.5839	3.8969			4.2566					
K.IPVGYSSNDDEDTRVK.M +2																		4.7313		3.7975					
K.KLNTNVIR.V +2																									
K.M*TDYFACGDDDVK.A +2																		2.6959						2.9107	
K.MTDYFACGDDDVK.A +2		3.6237				4.594				4.1446	4.3499						4.8211	4.8157							
K.YGAYSFCTPK.E +2					3.1417					2.9163	2.9115	2.8245		3.3729	3.3247	3.2171		3.8839				3.5456			
R.DDPTWTVDLFNSYK.T +2					5.0185	4.788	4.844	4.7294	4.7223	3.9327	4.1377	4.1356	5.2256	4.2345	4.537	4.6	4.0247	4.9526		4.1065	3.548	4.0361	4.4661	3.9561	
R.KIPVGYSSNDDEDTR.V +2														3.4659	2.5194									3.5493	
	1	X			X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6322848|ref|NP_013920.1|	29			43	31	31	31	31	31	31	31	19	23	33	23	33	33	23			9	21	21	9	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl36Bp and has similarity to rat L36 ribosomal protein; binds to 5.8 S rRNA; Rpl36ap [Saccharomyces cerevisiae]
K.AKVEEM*NNIIAASR.R +2													3.721												
K.AKVEEMNNIIAASR.R +2				4.2995									4.1888	4.244	2.5493	3.0852	4.3456	4.5086							
K.KVTSMTPAPK.I +2	2.9409			3.2303										2.5652			3.2402								
K.TGIAIGLNK.G +1					2.7177	2.4778	2.7729		2.5618	2.2899	2.4728	2.6195	2.208	2.3303	2.6143	2.5062	2.6807	2.6265			2.5555	2.1993	2.6755	2.4583	
K.TGIAIGLNK.G +2	3.2906			3.4164	3.3571	3.1307	3.2124	3.2336	3.2907	3.1821	3.2443	3.2479	3.0511		3.0074	3.0347	3.2586	2.5085			3.1926	3.1811	3.4239	3.3165	
K.VEEM*NNIIAASR.R +2										4.092			4.1953	3.7484											
K.VEEMNNIIAASR.R +2					4.7537	4.7242	4.7177	4.6901	4.4674	4.5173	4.5944		4.5799	4.5565	4.1519	4.2271	3.7764	3.4634				4.5602	4.4548		
R.EIAGLSPYER.R +2	2.6369			2.569	2.7706	2.906	2.9159	2.9484	2.7494	2.7893	2.7001	2.63				2.6781									
	1 X			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X	X	X	
gi|6319625|ref|NP_009707.1|		8.1	11.3		10.8	6.7	10.8	14.5	14.8		11.6	10.8	27	18.3	14.5	25.3	24.4	14.8	15.1	12.2	6.7		11.3	7.6	Large subunit of NADP+ dependent arabinose dehydrogenase, involved in carbohydrate metabolism; small subunit is unidentified; Ara1p [Saccharomyces cerevisiae]
K.DELQELNDFGEK.Y +2					4.1722	4.3925	4.1811	3.89	4.3732		4.2751	4.0272		3.4647		4.0075	4.2903	3.827			4.2096		3.8858	4.2955	
K.DELQELNDFGEKYPVR.F +2													2.6439												
K.TMYAADGDYLETYK.Q +2													3.3973							4.2986					
K.TMYAADGDYLETYK.Q +2											2.9302	2.8911					3.3887							3.9256	
K.TTEIYFSLNNGVR.I +2																							3.377		
K.VWPVLWDEVDR.S +2			2.7875		3.4467	2.9194	2.9301		3.0534			2.5213	3.2428	3.3376		2.7141	3.247	3.4121			2.9008				
R.AIGVSNFSIEYLER.L +2		3.4512	3.191		3.9435		2.8961	4.09	4.4423		3.0882		4.0538	4.4349		3.4587	3.9332	4.2808	4.0232	3.742			3.5186		
R.FIDEPFAAILPEFTGNGPNLDNLK.Y +2								2.8666							3.2752	3.2429			2.9098						
R.FIDEPFAAILPEFTGNGPNLDNLK.Y +3													4.7401		4.0045										
R.HIDTAWAYETEPFVGEAIK.E +2																	3.1311								
R.IPALGLGTANPHEK.L +1																	2.1651								
R.IPALGLGTANPHEK.L +2		4.818	4.7507						4.0898				3.5565	4.6564	3.8936	4.6241		4.8616	3.6499	4.7882					
R.IPALGLGTANPHEK.L +3														3.7199											
R.ISSSIEFASLTK.D +2														2.8385	3.1005	2.7687									
	1	X	X		X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6321522|ref|NP_011599.1|	8	20.1	12.6		20.1	20.1	20.1	20.1	20.1	12.6	24.7	24.7	12.1	24.7	20.1	20.1		21.8	12.1		15.5		20.1	12.1	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Ap; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11bp [Saccharomyces cerevisiae]
gi|6325359|ref|NP_015427.1|	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X		X	X		X		X	X	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Bp; involved in ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and rat L11; Rpl11ap [Saccharomyces cerevisiae]
K.EDTVSWFK.Q +1			2.1754		2.2856	2.2183	2.1165	2.265	1.8423	1.8335	2.2633	2.1451	2.2267	2.2354	2.107	2.2718		2.2395	2.102				2.1799	2.2314	
K.IAVHVTVR.G +2														2.5088											
K.LVLNISVGESGDR.L +2		2.6393			2.8808	2.5681	3.1782	3.7014	3.8399		3.6216	3.8724	3.9372	3.7846	4.4078	3.9374		4.6012	3.8448		2.8666		4.3141	3.0372	
K.TTKEDTVSWFK.Q +2																		2.744							
K.VLEQLSGQTPVQSK.A +1																							2.7724		
K.VLEQLSGQTPVQSK.A +2	4.5794	4.8386	4.6519		4.6174	4.6496	4.8508	4.8422	4.6563	4.5606	4.4853	4.2111		4.5014	3.9922	4.2339		3.9965			4.2081		4.4692		
K.YDADVLDK.- +1											2.1331	2.13													
K.YDADVLDK.- +2		2.5637																							
	1 X	X	X		X	X	X	X	X	X	X	X	X	X	X			X	X		X		X	X	
gi|6322058|ref|NP_012133.1|	11.1	18.1	4.5	13.6	17.1		17.1	17.1	13.6	19.1	22.6	17.1	14.1		9.5	26.1	17.1	12.6	22.6	15.1			12.1	9.5	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; has similarity to Rpl16Bp, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p; Rpl16ap [Saccharomyces cerevisiae]
K.KVASANATAAESDVAK.Q +2																		5.06							
K.LSTSVGWK.Y +1									1.833																
K.RVVVPQALR.V +2		3.5344	3.496													2.8005			3.1436	3.2683					
K.VASANATAAESDVAK.Q +2	5.1256	4.8789		4.9959	5.3165		4.9042	5.0299		4.8708	4.3097	4.1435				3.8709	4.9711		4.2765				3.54		
K.VFEGIPPPYDK.K +2										2.7273	3.0924														
K.VSSAEYYAK.K +1													2.0694					1.9741	2.2445	1.9911			1.9555		
K.VSSAEYYAK.K +2																2.5258									
K.YEDVVAK.L +1	2.1947				2.1544		2.0546	2.1675	1.9968		2.1137	2.1408	2.0459		1.9833	1.9667	2.3721							2.0458	
R.AEELNISGEFFR.N +2		4.4598		3.7531	4.5409		4.7561	4.5585	4.5544	3.5544	3.6663	4.5598	4.74		4.7227	4.4518	2.7942		4.3397	4.2653				4.3349	
	1 X	X	X	X	X		X	X	X	X	X	X	X		X	X	X	X	X	X			X	X	
gi|6322325|ref|NP_012399.1|	36.8	55.2			63.2	55.2	73.6	65.5	73.6	65.5	65.5	55.2	44.8	52.9	52.9	44.8	44.8	29.9		29.9	25.3	26.4		55.2	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Bp and has similarity to rat S21 ribosomal protein; Rps21bp [Saccharomyces cerevisiae]
K.ADDHASVQINVAK.V +1						3.3389			2.713		2.1481											2.9973			
K.ADDHASVQINVAK.V +2	2.6302	3.2622			3.9253	3.7081	3.8605	3.7982	3.6258	2.8576	3.4742	3.6681	3.4669	3.4153	3.2144	3.845	3.4621				3.1543	3.689		3.0632	
K.GQLVELLYVPR.K +2	4.0097	4.1332			4.0633	3.8532	4.0117	4.0026	3.9262	3.8338	4.0701	3.9228	3.8515	3.5668	3.8824	4.0365	3.9225	4.0828		4.0858		3.9657		4.0227	
K.NVWSYSR.- +1					1.8373		1.8889		1.9821					2.025	1.9937										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.AIPGEYITYALSGYVR.S +2		4.3054			5.2763	4.4896	5.3811	5.414	5.4877	3.0513	4.7852	5.2166	5.0814	4.6006	4.7286	4.1445	4.9166	3.0322		4.5846				3.3028	
R.AIPGEYITYALSGYVR.S +3													3.569		3.5135										
R.GESDDSLNR.L +2							2.9554	2.7599	2.825	2.5348	2.8175										2.5134			2.9062	
R.LAQNDGLLK.N +2	2.8365	2.8923			2.8757	3.0539	2.8551	2.8832	2.7809	2.7772	2.7514	2.9782													
	1 X	X			X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X		X	
gi|6320839|ref|NP_010918.1|				5.1	14.7	16.1	16.3	9.6	22.1	9.1	18.2	19.6	24.7	27	20.7	33.6	14.9	16.3	7	14	7.2	4.7	10.5		Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; required for early steps in protein mannosylation; Pmi40p [Saccharomyces cerevisiae]
K.AEPGFVFFIAPHLPVDLEAEDEAFTTYR.A +3																3.5918									
K.FHATNELPFLFK.V +2														4.3096											
K.KLLQAVFSR.V +2																				2.7097					
K.LLQAVFSR.V +1													2.0145												
K.LLQAVFSR.V +2					3.025							2.5784	3.0401	3.3679	2.5118	3.2598		2.995			2.8013	2.681			
K.NLVSM*LTYTYDPVEK.Q +2									2.8669	3.4805			5.0495	4.2051	4.2024	2.9777			4.3204	4.3627	4.7018				
K.NLVSMLTYTYDPVEK.Q +2						4.6744	4.8085		4.7812		3.2228	3.6137			3.6768	4.5599	3.5053	4.8931		4.2371			4.0226		
K.NPSAMLGK.D +1								2.1722	2.1386		2.2028	2.2537	2.1463	2.1827	2.1915	2.1479	2.1349	2.0053			2.1301		2.2535		
K.NSPSDFNKPDLPELIQR.L +2									2.8695				4.2054	4.0814		3.237		3.3483							
K.SVLYNPPIEEFAVLETTFDEK.L +2					4.8792	4.2826	4.7883	4.6722	5.1498		3.4257	4.4155	4.6728	4.3213	4.4444	4.8249	2.8396			3.484					
K.SVLYNPPIEEFAVLETTFDEK.L +3													4.4216	4.8624	3.7618	3.8154									
K.VLSIQAHPDK.A +2				3.3022			3.1052					2.6566		2.8857		2.7945	3.2401								
R.HFEGVDGPSILITTK.G +2													4.2836	3.884	3.9855	4.0158			3.3272	4.2889					
R.HFEGVDGPSILITTK.G +3													3.952												
R.LDAGYQQYDWGK.I +2				4.3443	3.9304	3.8277	3.8398		3.9175	3.8248	4.0433	4.288	4.5999		4.2703	4.3679						2.9091			
R.LNAGEAIFLR.A +2					3.4966				3.6539		3.3561	3.5328	3.5532	3.6264	3.432	3.613	3.1833	3.3398					3.3455		
R.NFIENIQPSAQK.G +2					3.9991	3.8907	3.6281	3.9457	4.1007	3.5887	4.116							3.6602					4.1069		
R.NIVGEETSR.N +2						2.7111																			
	1			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6325114|ref|NP_015182.1|		32.7	39.3	30.8	24.3	24.3	24.3	24.3	31.8	24.3	24.3	24.3	25.2	24.3	24.3	24.3	24.3	31.8			24.3	24.3	24.3		N-terminally acetylated ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Bp and has similarity to rat L35a; rpl33a null mutant exhibits slow growth while rpl33a rpl33b double null mutant is inviable; Rpl33ap [Saccharomyces cerevisiae]
K.IEGVATPQDAQFYLGK.R +2		3.3521	4.6792	5.3711	5.3247	5.2145	5.1838	5.0843	5.1849	5.0094	4.9323	4.8159	5.0411	5.1368	4.9522	5.0554	3.636	4.5911			3.9891	4.3716	4.7731		
K.RIAYVYR.A +2			2.5113	2.5629																2.5771					
K.RVNNPNVSLIK.I +2		2.8587	2.7483										2.5628												
R.IFLYPSNI.- +1		2.1034	2.0721						2.0303									2.1956							
R.VNNPNVSLIK.I +1																2.6835					2.5644				
R.VNNPNVSLIK.I +2			3.01	2.9282	3.0862	3.0242	3.0146	2.954	2.8006	2.6646	2.5558	2.7717	2.9758	2.9913	2.6518	2.7977	2.6191	3.001			2.7614	3.0195	2.9136		
	1	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X	X		
gi|6323729|ref|NP_013800.1|	1.9	1.9	1.9	1.9	7.7	7.7	7.7	1.9	18.9			10.1	19.2	23.7	16.3	11.7	8.3	4.8	14.9	19.2		4.8	8.8		Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production; Adh3p [Saccharomyces cerevisiae]
K.DIPVPEPKPNEILINVK.Y +2									3.3503				3.7077	3.1663	4.1697					2.5771					
K.IQQGTDLAEVAPILCAGVTVYK.A +2					4.8297	5.0596	3.1442		4.1979			3.96		4.2793		4.4758	3.4361		4.9961	3.2323					
K.IQQGTDLAEVAPILCAGVTVYK.A +3													5.9621	5.2179	4.8383	5.9042				4.3008			4.5223		
K.KLGGEVFIDFTK.T +2																			2.7021						
K.LPLVGGHEGAGVVVK.L +2									3.3547				4.4557	3.9738	3.8071	3.7075			3.9412	4.2687					
K.NMVSDIQEATK.G +2													3.0567	2.567				3.5099		3.2541		3.5432	3.5609		
K.SEVFSHVVK.S +2												2.5177					2.7417								
R.PCGTVVLVGLPANAYVK.S +2														2.571											
R.VLGIDAGEEK.E +2									2.9218																
R.YVVDTSK.- +1	2.4713	2.4816	2.4242	2.4586	2.4179	2.4486	2.4358	2.3307	2.3471			2.4336	2.3763	2.2757	2.5312	2.1846		2.063	2.4094	2.4214		2.0289			
	1 X	X	X	X	X	X	X	X	X			X	X	X	X	X	X	X	X	X		X	X		
gi|6322847|ref|NP_012920.1|		13.8	21	41.3	26.1	12.3	12.3	34.1	32.6	14.5		21.7	34.1	33.3	28.3	18.8	20.3	14.5	40.6	29.7	8		8		N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth; Rpl14ap [Saccharomyces cerevisiae]
K.KVLIDGPK.A +1																	1.9641								
K.KVLIDGPK.A +2		2.7307	2.5794	2.6483										2.5053											
K.KWAAAAVCEK.W +2			2.8996	2.7983																2.8126					
K.LAAIVEIIDQK.K +1																					2.6065				
K.LAAIVEIIDQK.K +2		4.8694	4.615	4.6012	4.4845			4.5976	4.5857	4.43		4.5867	4.4918	4.6865	4.5482	4.5432	4.6199	4.3852	4.4126	4.4007	4.3206		4.6316		
K.LAAIVEIIDQKK.V +2			4.2648											2.6495						4.1664					
K.WAAAAVCEK.W +1													2.2222					2.0683		2.3687					
K.WAAAAVCEK.W +2					3.0801	3.2892	3.1138	3.1017		2.8051					3.0752				3.2981						
K.WAASSWAK.K +1					1.9666				1.9985				1.899	1.8203		1.8625			1.8389						
R.AALTDFER.F +2					2.5647	2.5749	2.6105	2.523																	
R.FQVMVLR.K +1									1.9706							2.2523									
R.QAINLGQVVLTPLTFALPR.G +2				3.5195				5.3525	5.4087			4.3013	4.907	4.6417	2.6223				2.709	3.7258					
R.QAINLGQVVLTPLTFALPR.G +3									4.9484				5.6225	4.0845						5.0459					
R.RAALTDFER.F +2				2.9375													2.6458		3.0588						
	1	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X		X		
gi|6321673|ref|NP_011750.1|	11	10.5	13.8		11	11	11	11	11	14	11	14.5	39.1	44.1	43.1	24.6	17.5	17	11.5	20.6		11			Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; Yhb1p [Saccharomyces cerevisiae]
K.ATVPVLEQQGTVITR.T +2	4.6249		4.4192		4.5867	4.8841	4.7716	4.4891	4.6964	4.4068	4.2074	4.4794	4.6949	4.7572	4.826	4.3405		4.0361				4.8416			
K.CNPNRPIYWIQSSYDEK.T +2													3.819		3.7945										
K.EYVASDIVEFTVKPK.F +2		4.6342											4.8105	4.6058	3.1266	4.1948			3.3181	4.7202					
K.FGSGIELESLPITPGQYITVNTHPIR.Q +3														5.1744	3.7419										
K.HVDELLAECANVDK.I +2												2.5956	4.4123	5.4928	5.0057	5.1047	4.7542	5.7119		4.3624					
K.IIVHTDTEPLINAAFLK.E +2													5.0792	5.0133	4.7858				3.2735						
K.IIVHTDTEPLINAAFLK.E +3														4.6036						3.7213					
K.LSAPAGDFAINK.E +2	3.9439				3.5349	3.5701	3.799	3.4984	3.6551	2.6567	3.2271	3.6407	4.1061		3.7306	3.67	3.6692	3.0336		3.5963		3.2223			
K.M*YEEALWPGWKPFDITAK.E +2														4.0063											
K.M*YEEALWPGWKPFDITAK.E +3														4.794											
K.M*YEEALWPGWK.P +2																				2.6833					
K.NIDDLSVLM*DHVK.Q +2													3.8021		2.7845										
K.NIDDLSVLMDHVK.Q +2			3.9446											3.3579	4.2698	3.0895	3.6162			4.2155					
K.NM*LTEHTELLNIFNR.T +2														5.1227											
K.NM*LTEHTELLNIFNR.T +3														4.2695											
K.VGAQPNALATTVLAAAK.N +2	4.3169	4.8435	4.6351		4.5435	4.4841	4.5659	4.7944	4.6471	3.6526	4.191	3.553	4.6184	4.5299	4.8242	4.2138	3.5691	4.2097				4.1804			
R.DDM*HYEPFPGPK.M +2										2.5746			3.2354	3.1823											
R.DDMIHYEPFPGPK.M +2															2.7824	3.5198									
R.ENFPAGLVSEYLHK.D +2													3.4895	2.9811	2.8433		2.5384		2.9901						
R.HYSLCSASTK.N +1																		2.597							
R.HYSLCSASTK.N +2		2.5352	2.6269										2.6613												
	1 X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X			
gi|6320935|ref|NP_011014.1|						6.7	9.3	6.7	13.6	8.9	9.7	15.2	13	10.1	5.9	16.2	9.3	7.7	5.1	7.5	5.1	8.9	5.5	9.3	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp3p; Trp2p [Saccharomyces cerevisiae]
K.ESFLLESAK.T +1																				2.301	1.9747				
K.KGDIIQGVPSQR.V +2													3.7289	3.5636						2.923					
K.LAQLNNPDRK.E +2														2.612											
K.LNQTFESNVGK.E +2									3.4887	3.3504		3.4582	3.2551										3.6181		
K.LTDDSSPIPYPEQPPIK.L +2						4.1102	3.3753	3.4565	3.9315	3.4638	3.165	3.6899				2.8819	3.4114					3.0772			3.3534
K.TGPTEGIETDPLEILEK.E +2						5.0927	4.8769	5.1823	4.8208	3.9584	4.2965	5.0526	3.783	5.0117	4.8099	4.9739	3.6624	4.0858	4.4286	4.1835	5.2781	5.2392	5.2876	4.6266	
K.VAENVPGLPK.L +2												2.5628													
R.AM*ELIAELEGER.R +2														3.3081											
R.GATTEEDDALADQLR.G +2											3.7527		3.5031			3.4841									
R.ICDPLTTSVDK.L +2																						3.0615			
R.SIFPAGTVSGAPK.V +2							2.659		2.9805			3.5453			2.8793	2.742	2.7068	2.922							3.0627
R.VITHPIAGTVK.R +1									2.7182																
R.VITHPIAGTVK.R +2													2.5337			2.5087									
R.YSFIGISPR.K +2												2.973				3.0403		2.6685	2.6271						
	1					X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6323209|ref|NP_013281.1|	3.9	6.8					9.2		14.4	6.3	13.9	12.6	38.2	48.7	42.9	20.4	21.5	28.3	9.7	26.4	8.9	10.5	12.6	8.1	S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam1p [Saccharomyces cerevisiae]
K.DLEDIGAGDQGIM*FGYATDETPEGLPLTILLAHK.L +3														5.7951	3.9898										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ICDQVSDAILDACLAEDPHSK.V +2															3.9864		4.6073			3.9127					
K.ICDQVSDAILDACLAEDPHSK.V +3													4.5911	5.1988	4.5772	4.2994		4.8201		4.4023					
K.IGYDDSAK.G +1																					2.2852				
K.IIVDAYGGASSVGGGAFSGK.D +2							5.6334		5.5444		3.2987		5.6511	6.5879	5.5465	5.9875		2.7975				5.7678	6.3594	5.396	
K.LNMAMADAR.R +2											3.1274	2.5536		3.1662											
K.NFDLRPGVLVK.E +2													3.367	3.52	3.5268	3.4212			3.4581	2.9676					
K.SDEEIIDIISK.N +2		4.2676							4.2505			4.3078	3.3874	4.3852	3.9192	4.1352	4.1587	4.1874	3.2381		4.6477	4.4243	4.1272	4.3645	
K.SLVAAGLCK.R +1																							2.3139		
K.SLVAAGLCK.R +2									3.1647	2.6278	2.8152			3.0108	2.817			2.6118				2.5324			
K.TCNVLVAIEQQSPDIAQGVHEEK.D +3													5.2748	4.7564	4.2546		4.6619								
K.TGM*IM*VFGEITTK.A +2													3.4418												
K.TGM*IMVFGEITTK.A +2														2.7532											
K.TGMIMVFGEITTK.A +2												2.544								3.4129					
R.DGSLAWLRPDTK.T +2													3.1983				2.8792	2.69							
R.DMLDENTK.Y +1																							2.0615		
R.FVIGGPQGDAGLTGR.K +2	4.9725	4.9944					4.5931		4.6626	4.4927	4.4477	3.8785	4.9718	4.8513	4.5475	4.9731	4.8232	4.0961	3.8025	4.1886	3.8902				
R.IDTVVVSAQHADEITTEDLR.A +2														4.8193	4.9114			4.9795		3.8202					
R.IDTVVVSAQHADEITTEDLR.A +3													4.5623	4.8394											
R.KIIVDAYGGASSVGGGAFSGK.D +2																				5.1724					
1	X	X					X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6322639|ref|NP_012712.1|					8.1	8.5	9.9	9.4	16		6.8	8.4	13.7	9.3	9.6	16.1	10.3	9.7	3.5	22.2	8.3	6.2	5.3	6.2	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability; Uba1p [Saccharomyces cerevisiae]
K.EGEDVEVPFITIHL- +2																		3.4953							
K.INEFCHSSGIR.F +2											2.7368	3.2121	2.8808							2.9166					
K.LIDNKTDIEQYK.N +2																		3.2435							
K.LVTDLSVQQPEVLGEGVDVNEDLIK.E +2					3.1718	4.1598	4.3896	4.5785				4.0271				3.4088	3.6638	4.0167		4.733	3.7383	3.4441		3.2585	
K.M*QTSNVLILGLK.G +2													3.3915					2.5237	3.4602						
K.NGFVNLALPFFGFSEPIASPK.G +2					3.6585	3.9832	3.3804	3.1031	3.5394		2.7904	2.9754	3.6635	3.2224	2.5485	3.0386	2.5657			2.9424					
K.NVVLAGVK.S +1						2.2219		2.3704	2.2524				2.1939	2.1364	2.1615	1.9878	2.0324				2.1641	2.2511	2.0917	2.08	
K.NWALLGLGSGSDGYIVVTDNDSIEK.S +2									3.3803																
K.QFM*YFDSLESLPDPK.N +2															2.5945					3.463	2.6549				
K.QQLSNPEFVFSDFAK.F +2					3.1067		3.3652						3.3932	3.7002	3.5087	3.251				3.1216	3.0852				
K.SDDSNSKPNVDEYK.S +2																				3.074					
K.SEVAAEAVCAMNPDLK.G +2																				2.5865		3.3676		3.3061	
K.SMTVFDPEPVQLADLSTQFFLTEK.D +2									3.1354																
K.SVIDHM*IIPEFTPNANLK.I +2																				2.8798					
K.VEVLGPFAFR.I +2									3.2351				3.5651	3.2825	3.2068		2.9492	3.1719	2.8794	3.2869	2.621				
K.VFLVGSGAIGCEM*LK.N +2													5.0717	5.2667	4.5561	4.1898									
K.VFLVGSGAIGCEMLK.N +2							5.3378		4.5826		3.255	4.008		2.9871	3.5138	4.4996	3.8721			3.4006			3.9684		
R.AQNYFIETADR.Q +2						3.8274		3.5061			3.9126					2.7399							4.1355		
R.FSEVEGLDK.L +2								2.5834																	
R.GDIPGVVAFFGGLVAQEVLK.A +2																				2.6007					
R.GLFGNTFVDLGDEFTVLDPTGEEPR.T +2							3.2336		3.6566							3.7045				3.4203					
R.IIPAIATTTSLVTGLVNLELYK.L +2					4.0602	2.6708		3.2264	2.9736				2.6917			4.3907									
R.KPLLESGTLGTK.G +1																				2.0221					
R.KPLLESGTLGTK.G +2													3.6049	3.161				3.1476							
R.LNLPITQLVK.L +2																				3.0878					
R.LTESYSSSR.D +2																2.7734									
R.TGMVSDIEPDGTVTMLDDNR.H +2																							3.7491		
R.TMNDEDANELIK.L +2											3.6327						3.274				3.2705				
R.YDNQIAVFGLDFQK.K +2									4.8988			4.2649	4.8793	4.9484	4.3098	4.7779	3.4927	5.0977	3.5521			4.7712		4.3801	
gi|6324109|ref|NP_014179.1|					6.5	9.5	9.9	10.9	16.9		14.1	14.1	16.9	20.3	20.8	15.7	6.9	13.9	13.2	12.2	9.5	6.5	15.7	9.5	Adenylosuccinate synthase, catalyzes the first committed step in the 'de novo' biosynthesis of adenosine; Ade12p [Saccharomyces cerevisiae]
K.EIPVGISYSIQGK.K +2							3.5534		2.9379				3.3813					2.7657			3.0944				
K.KLDLFPEDLNILGK.V +2														4.8435											
K.LDLFPEDLNILGK.V +2						3.6952			3.3154				3.2013	3.4792	3.8765	3.6512							3.3291	3.2848	
K.LDVLDTFK.E +1															2.0275	2.1132									
K.LDVLDTFK.E +2																2.5376							2.594		
K.LQTIGAEFGVTTGR.K +2											3.0121	3.1877		3.2005	3.5715										
K.LVDLLVGK.Y +1															2.0541										
K.YIEDFVGVPYEWVGTGPAR.E +2							2.9133	3.544	5.3904		3.7451	4.441	4.4376	4.2566	4.591	4.8122	3.345	3.0509	4.2498	3.4998			3.9443		
R.AHLVFDFHQVTDK.L +2														4.238						2.8639					
R.CAGGNNAGHTIVVDGVK.Y +2																		4.361	4.2096						
R.CGWLDLVVLK.Y +2																			3.541	3.1461					
R.VGEGPFPTEQLNENGEK.L +2					4.6566	4.5135		3.6224	4.616		3.8509	4.3858	4.0476	4.1307	3.6563	4.3064					3.4171	3.3608	2.6673	3.2388	
R.YGDFEYDFEAK.L +2					4.3879	4.3363	4.5642	4.1694	4.1724		3.6334	4.094	3.8818	3.9759	4.2434	4.1965	2.6507	4.0336	4.1624	2.997	4.2484	4.2922	3.9784	4.0077	
2					X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6322765|ref|NP_012838.1|					24.6	15	19.8	19.8	29	14.4	24	26.6	35.3	40.4	34.4	39.8		26.6	17.7	19.5	24.9	21.9	14.1	18.9	Mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; Mdh1p [Saccharomyces cerevisiae]
K.DTDM*VLIPAGVPR.K +2														3.3481	2.7177										
K.DTDMVLIPAGVPR.K +2								2.9241	3.1417			3.1674				3.2572				2.8946	3.5861	3.4719	3.5572	2.922	
K.FANAVLSGFK.G +2													3.0339	2.944	3.2111	3.3591		3.3462	2.8126	2.9935	2.8238			2.8575	
K.GFTPEEPDGLNNALK.D +2					2.6713				2.8606					2.9736											
K.GVATDLSHIPTNSVVK.G +2													4.1198	4.0718	4.0527				4.2773	3.1047					
K.LFGVTTLDSIR.A +2							3.5274				2.8131	2.659	3.3968		2.6442	2.9344									
K.NGAGSATLSM*AHAGAK.F +2													3.1408	3.3289											
K.NGAGSATLSMAHAGAK.F +2					2.7411	2.9247	3.1587		2.5625		2.7082		3.1747												
K.SEGIEFFASPVTLGPDGIEK.I +2					5.3392	5.2681	5.2242	5.0023	5.0622	3.7032	3.9121	5.009	4.8349	4.8701	4.4782	5.5708		3.4665			5.3425	4.7431	4.7412		
K.VTVLGAGGGIGQPLSLLLK.L +2					5.3909		5.5795	4.8425	4.6213		3.5341	3.4286	5.1232	5.6283	5.0819	4.358		5.0791	3.6621						
R.DDLFAINASIVR.D +2					3.8541							3.9192	4.0659	4.033	4.2352	4.4058		3.6929		2.7977	2.6518	3.7493		4.3579	
R.DLAAATAESAPNAAILVISNPVNSTVPIVAQVLK.N +3																3.7445									
R.DVIEPSFVDSPLFK.S +2						3.5716		3.7679	3.1579	2.7723		3.3833	3.5028	3.5184	3.3349	3.7144		4.1012	2.8936	3.4542	3.0154	3.2105		2.8252	
R.FISEVENTDPTQER.V +2										3.8905	4.8243							4.1956			4.5411	3.3149	4.2568	3.7312	
1					X	X	X	X	X	X	X	X	X	X	X			X	X	X	X	X	X	X	
gi|6323882|ref|NP_013953.1|					27.3	23.2	23.2	27.3	32.2	9	27	24.7	20.6	36.7	36	33.3	31.8	28.8		23.2	12.4	12.4	26.6	28.5	NADP(+)-dependent dehydrogenase; acts on serine, L-allo-threonine, and other 3-hydroxy acids; green fluorescent protein fusion protein localizes to the cytoplasm and nucleus; may interact with ribosomes, based on co-purification experiments; Tma29p [Saccharomyces cerevisiae]
K.ATALEYLEASNGDMK.L +2																	5.0434	4.3102					5.095	3.9211	
K.DIDILVNNAGK.A +2					4.0847	4.3453		3.3192	4.2243		3.0393			3.3023	2.8435		4.5546	3.3167					4.3553	4.3463	
K.DTTPLM*ADDVADLIVYATSR.K +2						3.0576			3.4734					3.1904	2.8943	2.5224					3.3763	3.1298		2.7444	
K.DTTPLMADDVADLIVYATSR.K +2					5.6634		3.8443	5.5679	6.0694							5.0196	3.8393			3.0472			4.8244	2.9471	
K.FAVGAFTDSLR.K +2					2.5483		2.6129	2.806	2.7948		2.6054	2.6521	3.1378	3.1438	2.54	3.0276	2.6027	3.1167					3.0944		
K.FAVGAFTDSLRK.E +2													2.6389			2.537	2.9088			2.7397					
K.IKPFIENLPQEFK.D +2													3.3848	4.2872											
K.NSGDIVNLGSIAGR.D +2					4.6769	4.5261	4.7973	4.8302	4.3721	3.5036	3.2654	4.0636				4.522	3.93	3.0025					4.8773		
K.PFIENLPQEFK.D +2												2.8559	3.8487	4.125	3.3268										
K.TIDQEFPNAK.V +2										2.5583	3.1698														
K.TVLITGASAGIGK.A +2									4.5071		4.3644	4.4098		4.5644	4.2831	4.8252		3.4072			4.4376	4.6405		4.0904	
K.VHVAQLDITQAEK.I +1																	2.9572								
K.VHVAQLDITQAEK.I +2													4.5404	4.5212	4.1007	3.4954	4.3239	4.3307		4.3649					
R.DAYPTGSIYCASK.F +2											3.6371														
R.VILIAPGLVETEFSLVR.Y +2					5.5751	5.2715	5.2749	5.3088	5.6549			4.4615	4.6495	2.8771	2.7519	5.2189				4.3583				3.9845	
gi|6324225|ref|NP_014295.1|					14.7	8.4	14.7	12	13.7	5.7	13.1	13.6	23.4	20.2	19.1	19.2	17.4	10.5		15.7	9.5	7.3	16.2	15	Alpha-isopropylmalate synthase (2-isopropylmalate synthase); the main isozyme responsible for the first step in the leucine biosynthesis pathway; Leu4p [Saccharomyces cerevisiae]
K.ATIHTYLATSDM*FR.E +2													3.9459	2.7421											
K.ATIHTYLATSDMFR.E +2																				2.8864					
K.DDPSQQATR.W +2										2.7124															
K.EAYNYNDEQYQAISLVNYNVEK.F +2					4.0885		4.3772	3.1166	4.8801		3.0325					4.7915	4.5663	4.6806		4.2452			3.3325	4.1404	
K.EAYNYNDEQYQAISLVNYNVEK.F +3													4.6709	4.7852	3.577	4.0115									
K.EIEVSFPSASQTDFDFTR.Y +2					4.3864	4.5085	4.6418	4.6269	4.582		3.376	2.7687	4.0395	4.7125	4.6048	4.9764		4.0754		4.0232	4.178		4.2214	4.1038	
K.ESIIALAEHAASR.A +2													2.7065												
K.GGAAWVILR.S +2													3.3949	3.2903	3.3246	3.2057	2.7205			3.3495	3.0141				
K.RTVEALTGAK.K +2																		3.0916							
K.WGVGVSEDVGDSSVR.A +2					5.1318	4.9354	5.2066	4.8604	5.2122		4.0752	4.1275	2.53	4.83	4.4487	4.7854	5.009	4.7591		2.9339	2.8111		4.3671		
R.DGNQSLPDPMSVEQK.K +2										2.5105	3.3122	3.3828										3.3496	2.9617		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.DYEAVIR.V +1													2.5589		2.1915		2.1869								
R.GCGVAATELGM*LAGADR.V +2												3.6801	5.1249	5.0204	4.7218									2.571	
R.GCGVAATELGMLAGADR.V +2					5.3511		4.9091									3.6622	4.9631				4.7358				
R.NMQIEFSSAVQDHADSLGR.E +2																	3.3218								
R.SLGLDLPR.N +2																2.6198								2.69	
R.TVEALTGAK.K +1																								2.0104	
R.VEGCLFGNGER.T +2									3.1877	2.9631	3.3543		3.205	3.0177	3.348	3.4819						3.3214	3.3816		
R.YAVENAPDDVSIQCLVQSR.E +2					4.3122	4.8231	4.7645	5.0163	5.2909			4.1845		4.9169	4.312	4.6455									
R.YAVENAPDDVSIQCLVQSR.E +3												5.3033	5.6163	5.4091	3.9738	4.9384	3.6457			4.1692		5.2055	5.6443	4.2129	
	2				X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6323570|ref|NP_013641.1|					10.4	7.9	9.1	6.2	21.6	3.9	9.9	11.3	17.3	19.9	21.4	15.6	15.8	14.9	10.8	26.4		9.9	11.8	4.3	Dihydroxyacetone kinase, required for detoxification of dihydroxyacetone (DHA); involved in stress adaptation; Dak1p [Saccharomyces cerevisiae]
K.ALQSDFEEIK.S +2						3.0384																2.5235			
K.GFALANPSITLVPEEK.I +2							3.2693		3.2213			3.1011	3.6882	3.5755	3.382	3.1085	3.7518	3.1594		3.7897					
K.GM*LSGAVVGEIFASPSTK.Q +2														2.7521											
K.GMLSGAVVGEIFASPSTK.Q +2																				2.6935					
K.GSSTM*IDALEPFVK.E +2																			3.5427						
K.GSSTMIDALEPFVK.E +2																	3.2431	3.1233		3.2644		3.6031			
K.IALISGGGSGHEPTHAGFIGK.G +2														5.8217											
K.IVGAFAEEYSSK.Y +2					3.9722				3.1498						2.8059				2.6869					3.2921	
K.NYTGDVLHFGLSAER.A +2													4.7158												
K.SEPHITELDNQVGDGDCGYTLVAGVK.G +2																	3.3444								
K.SEPHITELDNQVGDGDCGYTLVAGVK.G +3									5.1626						4.2363	4.856	5.3847			4.1923					
K.SFEVTDPVNSSLK.G +2					3.8264	3.5929	3.3941		3.7334	3.0599	3.5839		2.8856	3.9933	3.294	3.745	3.6071	4.0942					3.5573	2.9679	
K.SLGIALDTLYK.Y +2													2.9889	3.2046	3.1871			2.6003		2.624		3.3324	3.1635		
K.SVLDLLNAFTNAPGWPIADFEK.T +2					2.6655			2.6707					2.5568							2.6421					
K.VLDPIPSTEDLISK.Y +2					2.5663		2.6554	2.8518	2.5104			2.732													
R.ALAGTVLVHK.I +2							3.3063		3.488	2.8506	3.1713	3.3955	3.5921		3.4501	3.5555		3.5871		3.3455			2.6534		
R.ASYVGDSSQVEDPGAVGLCEFLK.G +2						3.2722			5.0281		3.2311				4.7532		4.2707	4.1585	4.0829	3.3035		3.4357	3.5539		
R.ASYVGDSSQVEDPGAVGLCEFLK.G +3														5.4524											
R.LVNENASGVLLIVK.N +2												3.349	4.2736	4.2238	4.3219	3.5235			3.1368	3.4671					
R.VAVIGDDVAVGR.E +2									3.7115		3.2782	3.8515				3.842							3.9305		
gi|6324580|ref|NP_014649.1|					19.9	24	24	18.8	25.1	19.1	12.7	19.9	21.1	28.9	19.1	28.9	21.1	16.2	20.2	25.1		12.7	9	11.3	Glutamine-rich cytoplasmic protein of unknown function; contains tetratricopeptide (TPR) repeats, which often mediate protein-protein interactions; has similarity to human SGT, which is a cochaperone that negatively regulates Hsp70; Sgt2p [Saccharomyces cerevisiae]
K.DAESAISIDPSYFR.G +2					3.6788	4.2855	4.033	4.1194	3.939	3.5181	3.7829	3.2668	3.4438	4.2812	3.6486	3.8312	3.2062		3.6484					3.4692	
K.DDAENVEINIPEDDAETK.A +2					4.1666	4.9877	4.5572		4.5255	3.5432	4.2419	3.9549		4.1681	4.1359	4.4688			3.3424			3.5286			
K.DYELAINK.Y +1										2.6155			2.0448												
K.EEIAALIVNYFSSIVEK.K +2														2.771		3.9738									
K.EISEDGADSLNVAM*DCISEAFGFER.E +2									3.5115			2.5219				2.8471								2.5922	
K.EISEDGADSLNVAMDCISEAFGFER.E +2					4.9696	4.0856	3.9586	4.0843	4.0561			2.9865				2.5099				3.5135				3.0869	
K.GQHLADILNSASR.V +2													4.3885	3.7776	3.4911		3.8501		3.3164	4.0533					
K.KDDAENVEINIPEDDAETK.A +2																	4.8585	5.8741		4.3711			2.8471		
K.KKVEQSLNLEK.T +2													4.046	4.1333											
K.KVEQSLNLEK.T +2													2.7257					3.7035	2.6278						
K.VEQSLNLEK.T +2									2.7374					2.7542	2.6055										
K.VLDIEGDNATEAMK.R +2						4.4485	4.5252	4.3781		3.4726						3.9544				4.2886		3.4865			
K.VLDIEGDNATEAMKR.D +2																		3.6342		2.6832					
K.VLPTNAIYYANR.A +2					3.7026	3.848	3.6347	3.9141	3.7881	2.9397	3.6155	3.5378	3.6346	3.8236	3.6951	3.7901	3.1963	3.5378				3.785	3.4826		
K.YAQGKPEEALEAYKK.V +2													4.3313	4.1881			3.165		2.5816	3.8476					
R.EAVSGILGK.S +1									1.962																
	2				X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	
gi|6320789|ref|NP_010868.1|			8			6.2	10.9	14.7	21.7	10.9	14.2	14.7	24	30.5	16.5	17.6	15	9.6	30	24.3	11.4		8.5	12.9	Threonine aldolase, catalyzes the cleavage of L-allo-threonine and L-threonine to glycine; involved in glycine biosynthesis; Gly1p [Saccharomyces cerevisiae]
K.EHPFDCNGPTQIYR.S +2														2.9115			2.9075		2.7116	3.0244					
K.GIPLESPADTNFVFINLK.A +2			5.1079				3.6719	3.6474	3.7619			3.7635	4.6803	5.0366		3.5473	3.9503		5.165	4.1495	3.0739		3.5725		
K.LAISEAFDYAK.E +1																	2.4646	2.4685							
K.LAISEAFDYAK.E +2						3.7475	4.0975	3.9984	3.904		2.8902	3.7016	4.1544	4.0886	3.9757	3.9939	3.8408		3.7191	3.9255	3.8728			3.01	
K.SHYVPDDGDIHGAPTR.L +2									4.0377	3.107	3.033		3.3046	3.8198	3.0343				2.6235	3.5485					
K.SM*GAPIGSVLVGNLK.F +2								2.8397	3.566	3.203	2.9382	3.0052	4.528	4.4365	3.7108	3.4165			3.299	3.504	2.7858				
K.SMGAPIGSVLVGNLK.F +2									3.6419			3.8849			4.1044	3.8477	3.4303	4.3677		3.6371			3.5499	3.3825	
K.SQLLYSHSLAHELAEYCEAK.G +2																				3.9838					
K.SQLLYSHSLAHELAEYCEAK.G +3														4.0839											
R.IWNAAAQSGVPLK.Q +2			4.8493			4.3068	4.2712	4.4026	4.5981		4.0598	4.2687	4.4564	4.7195	4.6435	4.4186			3.0269					3.9683	
R.M*ALVNINNDWK.S +2										2.8965															
R.MALVNINNDWK.S +2									4.082				2.8776	3.8774		4.0123		2.9661						4.3654	
R.SESTEVDVDGNAIR.E +2																			4.3912						
R.THLM*QPPYSILCDYR.A +2																			2.5148						
R.VSFHYQVTR.D +2													2.8302		2.7698										
	1		X			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6322722|ref|NP_012795.1|	4				6.8	12.8	6.8	4.6	10.7	4		11.8	8.6	11.8	10.5	22.5	6.1	6	10.4	7.2	4.4		4.7	8.8	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; Pgm1p [Saccharomyces cerevisiae]
K.EIFDFDLIK.S +2															2.55										
K.IAAVGAANGVR.K +2	3.8004				4.2873	4.0869	3.9701	4.3018	4.0967	4.0653						3.9909								4.0908	
K.IAFGAASDGDGDR.N +2													2.861												
K.LLFDSLNGITGPYGK.A +2					3.9868	3.4614	3.8214	3.8638	3.9073			3.3025				3.8059			2.9893	2.6568					
K.LSICGEESFGTGSNHIR.E +2																3.4411									
K.LVIGQGGLLSTPAASHIIR.T +2														4.064					3.9263						
K.LVIGQGGLLSTPAASHIIR.T +3														4.3004											
K.TIQDEFWNEYGR.T +2	2.693											3.4675	3.5665	3.6382	3.7457	3.7872		3.5087	3.5309				3.5175	3.0476	
K.VVALLSEFVSR.P +2													3.3525	3.1187	3.5841	2.893									
K.YGPLLVDIIDPAK.A +2					3.6143	4.1024	3.798		4.0522			3.9608	4.4006	3.9389	4.2677	4.2483	3.8535		3.9664	3.0922	3.4904				
K.YNLPNGGPAPESVTNAIWEASK.K +2						2.9535			3.1227							3.3843	2.9727	3.6558							
R.DLDGSISENQGLFVK.F +2												3.2725			3.6089	3.4229							3.6874	3.9645	
R.LSGTGSSGATIR.L +2						3.6241				3.4263		3.1406		3.1171		2.9676					3.1321			3.6071	
R.YDYEHIECEQAEK.V +2																				3.4189					
	1 X				X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X		X	X	
gi|6322783|ref|NP_012856.1|		19		15.7	19	19	19	19	26.8	26.8	26.8	26.8	41.2	41.2	19	24.8	24.8	13.7		33.3		13.7		19	Nucleoside diphosphate kinase, catalyzes the transfer of gamma phosphates from nucleoside triphosphates, usually ATP, to nucleoside diphosphates by a mechanism that involves formation of an autophosphorylated enzyme intermediate; Ynk1p [Saccharomyces cerevisiae]
K.EELVDWESNQAK.W +2										3.7348	3.455	2.8224										4.1488			
K.KEELVDWESNQAK.W +2													3.9922	4.0692						3.8325					
K.LLEQHYAEHVGK.P +2													3.6802	3.1479											
K.SGPILATVWEGK.D +2				3.9307	4.2606	4.347	4.1871	4.2198	4.0465	3.7011	3.9224	3.1904	4.0183	3.9021	3.1699	4.0552	3.5319	4.372		3.438				3.6357	
R.GDFGIDLGR.N +2														2.8585		2.8302	2.5462	3.0621				2.642			
R.GLVSQILSR.F +2													3.0674							3.1487					
R.TFIAVKPDGVQR.G +2		3.2119		3.0693					2.9214																
R.TILGATNPLGSAPGTIR.G +2		5.7542			4.7898	4.9063	4.5818	4.8986	5.1258	4.0154	4.7142	4.5282	5.4134	5.1213	5.059	5.1455	4.0701			5.2155				4.8876	
	1	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X		X		X	
gi|6322531|ref|NP_012604.1|					14.5	12.3	15.7	15.7	25.5	14.5	16.6	23.4	45.5	46.8	29.8	28.3	30.2	33.8	11.1	28	15.1	7.4	13.2		Deoxyhypusine hydroxylase, a HEAT-repeat containing metalloenzyme that catalyses hypusine formation; binds to and is required for the modification o Hyp2p (eIF5A); complements S. pombe mmd1 mutants defective in mitochondrial positioning; Lia1p [Saccharomyces cerevisiae]
K.AIEYIAESFVNDK.S +2					3.2167		3.0538	3.2791	3.8366		3.0509	3.4643	4.4159	4.968	4.5264	4.6783	3.509	3.9501		3.121	4.6119	4.8127	4.6766		
K.DATIPELQALLNDPK.Q +2						4.0765	4.0105	4.0084	4.1523	3.3226		3.584	3.3079	3.6366	3.8244	4.0081	3.7513	3.5732	3.9716		3.2033				
K.DKENLQQSLYSSIDPAPPLPLEK.D +3													3.7623	4.5449											
K.ENLQQSLYSSIDPAPPLPLEK.D +2									3.3411	2.6206	3.1908					2.6151	4.9954	4.3416	4.9949	3.0414	5.0119		3.5145		
K.ENLQQSLYSSIDPAPPLPLEK.D +3														3.5662											
K.HEVAYVLGQTK.N +2														3.2622		3.0407									
K.HFQENVDECTLEQLR.D +2														5.0219	3.0029		3.8013								
K.SYLNDEVDVVR.E +2					3.7764	3.8947			3.7379	3.7457	3.7356	3.8028	3.5555	3.6327	3.0718			3.4488				3.9421			
K.TVAEEFATKPEEAK.K +2						3.722						3.3162					2.5642	3.6243		3.3451					
R.DIGTDEAILALATGFSAESSLFK.H +2					5.3442		5.6406	5.0013	5.7998			3.9853	5.5897	5.5126	4.7627	4.6363		2.9816		3.6807					
R.DIGTDEAILALATGFSAESSLFK.H +3													5.6143	4.7351											

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.ETCELAINR.I +2											2.9053		2.6406			2.7224							2.976		
R.HEAAEALGAIASPEVVDVLK.S +2													5.7469	6.67	6.1584		5.3324			2.9307					
R.HEAAEALGAIASPEVVDVLK.S +3													3.8555												
R.HEAAEALGALGDKDSLDDLNK.A +3													4.0338	3.9517											
R.HVMLDQNQEPM*VR.H +2													2.9501					2.7944							
gi|6323332|ref|NP_013404.1|					13.1	13.1	16.8	22.1	25.4	18	21.7	30.3	34	44.7	50.4	44.3	34.4	15.6	27.9	28.3	24.2	29.1	24.2		Protein of unknown function that interacts with Sec72p; Ylr301wp [Saccharomyces cerevisiae]
K.GSTVTSNGLNWEVIEYHA.- +2									4.0345			3.2166			3.3331	3.0574					4.9746	4.2421	3.0195		
K.IPQSYENLKK.G +2														3.014											
K.NNNTIEGLNFIR.L +2					3.971	4.1694	3.9854	3.2911		3.5405	3.9966	2.8831	4.0409	3.1291	3.7948	4.2354	3.8163		3.6904		2.7026	2.9411	3.7788	
K.NWDSGCVEETGAVYPFGADK.E +2					5.4335	5.2596	5.4524	5.3473	5.7434	4.1584	4.5888	4.8491	5.4265	4.4552	4.7093	5.5545	5.2023	4.9623	5.2961	4.5276	5.5913	5.3621	4.1624		
K.NWDSGCVEETGAVYPFGADKESVSFR.E +3													3.8874		4.0895										
K.PSGDELSFPFEWAFAGTNETVK.A +2								3.3166						5	3.4311	3.9927									
K.SEFLLSYGK.E +1													2.0124	1.9097	1.9164		2.1277		2.1098		1.868		2.0479		
K.SEFLLSYGK.E +2													2.9213			2.9993		2.5247	2.9231			2.8023	2.6569		
K.VTDEAYDGLVIVIGR.W +2									4.3518			3.6348	4.5087	4.4776	5.1719	5.0481			3.1523	4.1944					
R.EDLVIVSPNNEK.F +2										3.3889	3.2682											3.5688			
R.ELWQPVDPSREDLVIVSPNNEK.F +2																	4.1951			2.9824					
R.LLFQVGPHPNER.T +2													2.849	3.1548	2.5835	3.6942	3.2037		3.1696	2.8421					
R.WIQGFLSQK.N +2							2.7801		2.9861		2.558	2.8603	3.0149	3.3868	3.2606		2.8602	2.9874							
	2				X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6320710|ref|NP_010790.1|		3.9				9.4	14.6	7.8	16.9	6.2	19.3	15.1	22.1	22.7	14.3	17.4	6.8	16.9	6.8	26.6	6	10.2	9.6		S-adenosylmethionine synthetase, catalyzes transfer of the adenosyl group of ATP to the sulfur atom of methionine; one of two differentially regulated isozymes (Sam1p and Sam2p); Sam2p [Saccharomyces cerevisiae]
K.DMLDENTK.Y +1																							2.0615		
K.ICDQVSDAILDACLEQDPFSK.V +2						3.9171	4.1593	2.9451	3.9731		2.75	3.2286				4.7419		3.6118		4.1014					
K.IGYDDSAK.G +1																					2.2852				
K.IIVDAYGGASSVGGGAFSGK.D +2							5.6334		5.5444		3.2987		5.6511	6.5879	5.5465	5.9875		2.7975				5.7678	6.3594		
K.LNMAMADAR.R +2											3.1274	2.5536		3.1662											
K.NFDLRPGVLVK.E +2													3.367	3.52	3.5268	3.4212			3.4581	2.9676					
K.RIDTVVISAQHADEISTADLR.T +3																				3.8713					
K.SDDEIIEIIK.K +2													2.9029	3.3195								3.5032			
K.SDDEIIEIIKK.N +2																	3.204								
K.SLVAAGLCK.R +1																							2.3139		
K.SLVAAGLCK.R +2								3.2326	3.1647	2.6278	2.8152			3.0108	2.817			2.6118				2.5324			
K.TFLFTSESVGEGHPDK.I +2													4.0419												
K.TGM*IM*VFGEITTK.A +2													3.4418												
K.TGM*IMVFGEITTK.A +2														2.7532											
K.TGMIMVFGEITTK.A +2												2.544								3.4129					
R.FVIGGPQGDAGLTGR.K +2		4.9725				4.5564	4.5931		4.6626	4.4927	4.4477	3.8785	4.9718	4.8513	4.5475	4.9731	4.8232	4.0961	3.8025	4.1886	3.8902				
R.KIIVDAYGGASSVGGGAFSGK.D +2																				5.1724					
	1	X				X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6321859|ref|NP_011935.1|			8.5		17.1	12.9	16.3	8	37.2		11.6	20.2	40.6	37.7	29.2	23.8	34.6	40.1	19.9	25.3	15.8	9.8	20.4		Deoxyhypusine synthase, catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; triggers posttranslational hypusination of translation elongation factor eIF-5A and regulates its intracellular levels; tetrameric; Dys1p [Saccharomyces cerevisiae]
K.CLAPTYLGEFALK.G +2			3.5315						3.5802			2.9988	3.926	4.0534	3.5766	2.5262		4.0567	3.9995				2.601		
K.EINDESSVLYWAHK.N +2									4.4974				4.7027	4.1798	3.7364	4.1902	4.77	4.6213	2.8296	3.8901					
K.FEEWIVPILDK.M +2					3.4248	3.9302	3.7722		3.7811		3.1167	3.2964	3.9944	3.6903	3.6531	3.7959	3.391	2.8635	3.675	3.5575	3.4387	3.4908	3.7676		
K.GCFDEEGYQK.T +2																				2.5655					
K.HGADCLEANQDVDSPIWTPSK.M +2																	5.4979	5.4189		3.763					
K.HGADCLEANQDVDSPIWTPSK.M +3													4.2335	4.3493											
K.HIDELLDDHEK.K +2																				2.7257					
K.INSMSMAAYR.A +2					3.0496		3.2136							2.7306				3.3236							
K.LFADVTTVLPLIVAATFASGK.P +2					2.7839																				
K.LFADVTTVLPLIVAATFASGK.P +3													4.3086		3.5174										
K.LPELLQDAVLK.A +2					3.8193		3.8461		3.7401		3.9182	3.5986	3.8343	3.9805	3.894	3.9883	2.7617	2.7021		3.568			4.003		
K.M*VDAVVTSAGGVEEDLIK.C +2													4.4678	5.7449	4.8276				2.7193		4.4099	4.3536	4.2415		
K.MLEEQDEYVK.K +2											3.3354							3.5591							
K.MVDAVVTSAGGVEEDLIK.C +2						3.7331	4.0839	4.4585	4.6926			3.0868				3.6673	4.8251	3.4971			3.9972				
K.TM*GFQASSVGTACEIIDSMR.S +2																					3.1934				
K.TMGFQASSVGTACEIIDSMR.S +2			2.836						3.5282																
K.TTIFM*GYTSNLISSGVR.E +2																							2.9909		
K.TTIFMGYTSNLISSGVR.E +2									4.4165														3.2938		
K.VQGIDYSKPEATNM*R.A +2													3.3912	3.9187											
K.VQGIDYSKPEATNMR.A +2									3.5455								3.6601	4.3286							
R.AGM*IILGGGLIK.H +2												3.7495	4.3023	4.0305	4.1495	3.7664	3.571		3.8179	4.1449	4.1433				
R.AGMIILGGGLIK.H +2									3.0623			3.2029			3.247	3.3006	3.2487								
R.ATDLIEAMK.T +1																				2.2985		2.271	1.8222		
R.ATDLIEAMK.T +2																			2.7139				3.0704		
R.IGNLLVPNDNYCK.F +2					2.7274	3.1615	2.9994	3.2138	2.9533		2.5629	3.0309	3.112	3.0662	3.0548	2.9824									
R.NGADYAVYINTGQEYDGSDAGARPDEAVSWGK.I +3																	4.0289	3.5373							
R.VDIVGDIR.K +2						2.6151							2.8293	2.8429											
	1		X		X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6325166|ref|NP_015234.1|		2.9		2.9	7.2		2.9	7.2	9.7		8.3	12.6	26.7	35.6	29.6	13.5	9.5	8.7	10.4	23	6.8	7.7	5.4		Cytosolic and mitochondrial glutathione oxidoreductase, converts oxidized glutathione to reduced glutathione; Glr1p [Saccharomyces cerevisiae]
K.ADFDNCVAIHPTSAEELVTM*R.- +3													4.5769	4.947	3.8728										
K.AIFPENIPGFELGTDSDGFFR.L +2					4.293			3.4843	3.5933			3.7446	3.6715	3.4593	3.0324	4.2538			3.0956	3.1513					
K.ALGGTCVNVGCVPK.K +2											2.9244	3.3927					3.5795								
K.HYDYLVIGGGSGGVASAR.R +2														2.545	3.2247	3.4971	4.5436			4.4847					
K.LNSHDQIADEYQNTNVPNIYSLGDVVGK.V +3													4.889	6.0387	3.7955										
K.SHLGM*GSENVGIK.L +2													3.1985	3.3951					3.1923	2.6853					
K.SIDDVDELIWTIGR.K +2		4.6435		3.8667	3.952		3.9024	3.6728	3.4701		2.5235	3.413	3.8515	3.6759	4.0904	4.3002	4.3089	3.6848		3.6919	4.1606	3.074	3.1162		
K.VDVVFGWAR.F +2															3.6555			3.5456		3.0628					
K.VELTPVAIAAGR.K +2									3.5519		3.163	3.291	3.7812	3.3663	3.7505	3.5584						3.5263	3.7239		
K.VMWYASDLATR.V +2																						2.895			
R.DNTTEVYSANHILVATGGK.A +2													4.2086		4.3351			4.0514		3.2273	3.5663				
R.KFDECIQNTITDHYVK.E +2																			2.5319						
R.NDKLDYENVPSVIFSHPEAGSIGISEK.E +3														6.1018											
R.VSHANEYGLYQNLPLDK.E +2														3.6077						2.92					
	1	X		X	X		X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6323104|ref|NP_013176.1|		35.7	31.7	36.2	5	14		5	18.6	10	17.6	17.6	26.2	45.7	32.1	38	10.9	10.9	33	15.4			9		Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family; Rpl10p [Saccharomyces cerevisiae]
K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I +3		5.922	4.7945	6.2951										3.7844	4.0049	4.8435			3.8934						
K.DDGAFVK.F +1									2.3928		2.2809	1.9739		2.3355	1.8826	2.2971									
K.DSNKDVVVEGLR.R +2						3.1164				2.5601	3.1251	2.643	3.0004												
K.DVVVEGLR.R +1		2.3188	2.394	2.3893					1.9684					2.1383	2.3014	2.2786			2.2129						
K.KGSLENNIR.E +2		3.2099	3.1741	2.9611					2.9235		2.7253	2.6189	2.9818	3.2235						2.6098					
K.M*LSCAGADR.L +2																							2.522		
K.MLSCAGADR.L +2		2.5341																							
K.WGFTNLDRPEYLK.K +2													3.9137	4.0532		3.3088				3.5675					
K.WGFTNLDRPEYLKK.R +2																				3.3919					
K.YMTTVSGR.D +1						1.8915																			
R.EAGEVKDDGAFVK.F +2		3.7295	3.4586	3.9497					3.0594				3.8516	3.6164	2.9018	3.3289	3.5284	3.5868	3.7627						
R.EFPEYFAAQA.- +1															2.1495										
R.EFPEYFAAQA.- +2				3.1828						2.6003				2.9496		2.5649									
R.GAWGKPHGLAAR.V +2																			2.7733						
R.VDIGQIIFSVR.T +2		4.0411	4.1021	4.1166	3.8329	3.6865		3.961	3.8493		3.0438	3.7484	3.813	3.8129	3.8265	3.8449	3.7736	3.5863	3.0381	3.7092			3.8492		
R.YKFPGQQK.I +2														2.6376											
	1	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X			X		
gi|6320978|ref|NP_011057.1|	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	37	20.2	12.6			22.7	30.3		20.2			Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Ap and has similarity to rat S26 ribosomal protein; Rps26bp [Saccharomyces cerevisiae]
K.LHYCVSCAIHAR.I +2														3.0362					3.0791	2.8905					
K.VSPAAAAK.K +1														2.0955											
R.DLSEASVYPEYALPK.T +2	4.8104	4.9654	4.7906	4.72	4.7687	5.0088	5.0593	4.8589	4.4826	4.8435	5.0187	4.2906	4.6731	4.6428	4.4532	4.5419			3.2584	4.5918		4.7545			
R.NIVEAAAVR.D +1		2.7571				2.1599		2.0927	2.3278		2.0546		2.4012	2.4378	2.3976					2.1779					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.NIVEAAAVR.D +2	3.2527	3.1846	3.2658	3.3033	3.2419	3.0877	3.32	3.2779	2.9255	3.141	3.1385	2.6379										3.1249			
gi|6321249|ref|NP_011326.1|	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	26.9	30.3	20.2	12.6			22.7	37		20.2			Protein component of the small (40S) ribosomal subunit; nearly identical to Rps26Bp and has similarity to rat S26 ribosomal protein; Rps26ap [Saccharomyces cerevisiae]
K.LHYCVSCAIHAR.I +2														3.0362					3.0791	2.8905					
K.VSPADAAK.K +1													1.9073							2.0131					
R.DLSEASVYPEYALPK.T +2	4.8104	4.9654	4.7906	4.72	4.7687	5.0088	5.0593	4.8589	4.4826	4.8435	5.0187	4.2906	4.6731	4.6428	4.4532	4.5419			3.2584	4.5918		4.7545			
R.NIVEAAAVR.D +1		2.7571				2.1599		2.0927	2.3278		2.0546		2.4012	2.4378	2.3976					2.1779					
R.NIVEAAAVR.D +2	3.2527	3.1846	3.2658	3.3033	3.2419	3.0877	3.32	3.2779	2.9255	3.141	3.1385	2.6379										3.1249			
2	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	X		X			
gi|6325389|ref|NP_015457.1|	7.6	13.8	21.4	21.4	26.2	18.6	23.4	26.2	33.8		26.2	26.2	33.8	33.8	26.2	26.2	26.2	15.2	26.2	26.2					Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; nearly identical to Rps23Ap and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and RPS23B is lethal; Rps23bp [Saccharomyces cerevisiae]
K.AKGDIPGVR.F +2		2.7311	2.563	2.6143																					
K.SSPFGGSSHAK.G +1									2.2696				2.0068	1.8538				1.8215							
K.SSPFGGSSHAK.G +2			2.6325	2.8135														2.507							
K.VSGVSLLALWK.E +2	4.6578	4.5066	4.5812	4.8042	4.1374			4.52	4.5565		3.716	4.3027	4.5766	4.6584	4.4779	3.9922	4.515	4.3855	4.5997	4.5739					
K.VTAFVPNDGCLNFVDENDEVLLAGFGR.K +2					5.4168	5.4695	5.062	5.1414	5.2522		3.7252	4.677	4.7265	5.1122	4.6797	5.0755	3.7314		2.9948	3.0677					
K.VTAFVPNDGCLNFVDENDEVLLAGFGR.K +3					4.3438	4.5215	4.5754	4.8161	6.2118		3.8017	4.4578	3.8417	4.4779		5.7253				3.8847					
R.LLGTAFK.S +1							1.8703																		
1	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X					
gi|116006491|ref|NP_011548.2|	25.2	18.9	25.2	17.3	26	27.6	15	26	18.1	33.1	13.4	13.4	25.2	18.9	24.4	32.3	25.2	18.1		25.2					Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26bp [Saccharomyces cerevisiae]
K.AYFTAPSSER.R +2	2.5746				3.2386	2.9859	3.1243	3.0284		2.877															
K.FAVQVDK.V +1															2.0327										
K.FAVQVDK.V +2						2.6331									2.6054										
K.QSLDVSSDR.R +2																2.5639									
K.VNGASVPINLHPSK.L +2	3.8512	3.9282	4.3261	4.1786	2.8838			3.7429	3.0906	2.6913			3.9532	3.3917	3.4836	3.3669	3.6105	2.7432		3.8375					
R.DDEVLVVR.G +1	2.4918		2.4453	2.5675							2.1918	2.5323	2.2526			2.3803	2.316								
R.DDEVLVVR.G +2																	3.0433			3.0548					
R.RDDEVLVVR.G +2						3.0281				3.4451															
R.RVLLSAPLSK.E +2		3.0792	3.1694										2.8519	2.5656	2.7296	2.5562	3.0541			2.6504					
R.VLLSAPLSK.E +1					2.0481	2.1562	2.2061	2.3308	2.1717		1.8334	1.9635	2.3822		2.1843	2.1227	2.0994	2.0181							
R.VLLSAPLSK.E +2			2.5104		2.6168			2.6499	2.7722	2.5905															
gi|6320801|ref|NP_010880.1|	11.5	11.5	11.5	11.5	26.1	11.5	11.5	26.1	26.1	11.5	11.5	11.5	25.5	25.5	40.1	39.5	22.9	22.9		22.9					Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Anb1p; possible role in translation elongation; undergoes an essential hypusination modification; Hyp2p [Saccharomyces cerevisiae]
K.APEGELGDSLQTAFDEGK.D +2	6.5017	6.3177	6.535	6.4808	6.3649	6.6166	6.3992	6.5107	6.3383	6.2299	6.4353	6.4739	6.2814	6.1284	6.3968	6.1599	6.1185	5.6126		4.0072					
K.DDVKAPEGELGDSLQTAFDEGK.D +2													4.9422		3.3163	4.8854									
K.DDVKAPEGELGDSLQTAFDEGK.D +3														4.0027											
K.KLEDLSPSTHNM*EVPVVK.R +2													3.9918	3.6441											
K.KLEDLSPSTHNM*EVPVVK.R +3													4.2402	3.6062				3.8989							
K.KLEDLSPSTHNMEVPVVK.R +2																	4.36			4.801					
K.KLEDLSPSTHNMEVPVVK.R +3													4.1352	4.6641	3.6032		3.7049			4.2785					
K.LEDLSPSTHNMEVPVVK.R +2													3.2624	3.1591	4.0838	4.0614		3.5908							
K.VHLVAIDIFTGK.K +2																									
R.NEYQLLDIDDGFLSLM*NM*DGDTK.D +2									3.1895																
R.NEYQLLDIDDGFLSLM*NM*DGDTK.D +3															4.0626										
R.NEYQLLDIDDGFLSLMNM*DGDTK.D +2								3.4463								4.0449									
R.NEYQLLDIDDGFLSLMNMDGDTK.D +2					3.1431																				
gi|6323376|ref|NP_013448.1|	25.2	26.8	25.2	17.3	26	27.6	15	26	26	33.1	13.4	21.3	33.1	18.9	32.3	40.2	25.2	18.1		25.2					Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Bp and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA; Rpl26ap [Saccharomyces cerevisiae]
K.AYFTAPSSQR.R +2	3.0679	2.9884			3.3293	3.3749	3.258	3.0056	3.1609	2.7717		3.0768	3.0717		3.0424	2.8353									
K.FAVQVDK.V +1															2.0327										
K.FAVQVDK.V +2						2.6331									2.6054										
K.QSLDVSSDR.R +2																2.5639									
K.VNGASVPINLHPSK.L +2	3.8512	3.9282	4.3261	4.1786	2.8838			3.7429	3.0906	2.6913			3.9532	3.3917	3.4836	3.3669	3.6105	2.7432		3.8375					
R.DDEVLVVR.G +1	2.4918		2.4453	2.5675							2.1918	2.5323	2.2526			2.3803	2.316								
R.DDEVLVVR.G +2																	3.0433			3.0548					
R.RDDEVLVVR.G +2						3.0281				3.4451															
R.RVLLSAPLSK.E +2		3.0792	3.1694										2.8519	2.5656	2.7296	2.5562	3.0541			2.6504					
R.VLLSAPLSK.E +1					2.0481	2.1562	2.2061	2.3308	2.1717		1.8334	1.9635	2.3822		2.1843	2.1227	2.0994	2.0181							
R.VLLSAPLSK.E +2			2.5104		2.6168			2.6499	2.7722	2.5905															
3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		X					
gi|6319931|ref|NP_010012.1|						13.7	10.1		14.5	7.4	10.8	11.7	17.2	17.4	14.2	22	10.3	25.2	11.1	23.5	4.7	10.1	13	6.4	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization; Abp1p [Saccharomyces cerevisiae]
K.AEAPKPEVPEDEPEGEPDVK.D +2											2.6517				3.4191		3.9612	3.8276		4.1424		3.2227			
K.AEAPKPEVPEDEPEGEPDVK.D +3													3.5891	3.7542											
K.EEPEQEEIAPSLPSR.N +2						4.7827	4.8156		5.0218	4.1277	4.2612	4.3487	4.6429			4.7852					4.2392	3.3856	4.7931		
K.ENPWATAEYDYDAAEDNELTFVENDK.I +2						3.9204			2.6479							2.5011		2.5456		3.0905			4.1401		
K.GLFPSNYVSLGN.- +2																						3.6011			
K.GYHVQVTAR.D +2													2.5809		2.6432										
K.IDPSSDIANLK.N +2						2.894																			
K.IIIIGWCPDSAPLK.T +2													4.1623	3.7857	3.1856			3.4412		3.5382			3.751		
K.SPAQLWAER.K +2												3.3041	3.46	3.1139	3.3976	3.3592			2.7197	3.0018			3.2541	3.4529	
R.ASFAANFAAVANNLFK.G +2						3.2983	4.8036		5.0245			3.4972	4.4878	5.4158	4.5854	3.8942		3.7517	3.5229	4.6531					
R.DEDDLDENELLM*K.I +2									5.0231	4.5305	5.2901														
R.DEDDLDENELLMK.I +2						5.3829	5.4888		5.452		4.5761	5.1073				5.5049		3.0497		5.3612	4.136	5.1021	4.7029	3.891	
R.DFDQAPLKPNQSSYKPIGK.I +2													3.3071	3.2163		2.5425									
R.DFDQAPLKPNQSSYKPIGK.I +3													4.0633	4.0212				3.5704							
R.GSDPDTTWLIISPNAK.K +2							3.3236					2.9173			3.2499	3.3553	3.5878	3.6348	4.32						
R.NVASGAPVQKEEPEQEEIAPSLPSR.N +2																				2.7866					
R.NVASGAPVQKEEPEQEEIAPSLPSR.N +3														4.386			4.1355	3.8589	3.9721						
R.VNDNNDDDDWNEPELK.E +2									4.4791	3.5035	4.0042					4.435				3.8845				2.546	
1						X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320788|ref|NP_010867.1|						8.3	10	4.3	13.6		7.4	8.5	26.2	17	16.6	18.3	14.7	12.6	5.7	18.1	9.8	11.9	4.9	9.8	Soluble fumarate reductase, required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; Yel047cp [Saccharomyces cerevisiae]
K.DGSISAVVYEDK.N +2											8.3355														
K.EYAPIELVNLPTTNGQQTTGDGQR.L +2						4.6627					2.709						4.1086	3.84		3.9477	3.9269	3.4342		2.7224	
K.HM*VSANDVVFCSGGFGFSK.E +2																				3.3053					
K.LAETKPELVK.I +2													2.9732			2.6838							3.2176		
K.LANDSPLAIEWLK.N +2							4.4513		4.0936			3.4098	4.3562	4.6641	4.283	4.389		3.5442			4.4604	4.0439	3.9802	4.3148	
K.LDLLAQLGGHSVAR.T +2													4.5388	4.6853	3.7412										
K.LGADLIDM*DQIQVHPTGFIDPNDR.S +3													3.6701												
K.LPPGFEIVSALSNNLK.K +2						3.7921			3.8458				4.124	4.2431	3.7544	3.4441				3.2631					
K.LPPGFEIVSALSNNLK.K +3													4.3476	4.5157	3.7511										
K.NDERLLKGLYAAGEVSGGVHGANR.L +3							3.5491																		
K.YNIPVTILEK.A +2								3.2704					2.6156	2.9268		3.0155	2.9321				2.7937	3.0675		3.0472	
R.ALLVMGEK.M +1									1.8509						2.088										
R.DVVTAAIQK.V +1																	2.5296								
R.GLGGILLNPITGR.R +2									4.0385			3.5859	4.2692	3.8819	4.1539	3.9898	4.0618		3.2545	3.5953					
R.HFHIEDSPR.L +2													2.515					2.9177							
R.LGGSSLLECVVFGR.T +2									3.6791			3.3748	4.128	3.9692	3.8113	3.9181	3.8071	2.8079	3.8887	3.58					
R.TAAESIANDR.K +2							3.1793	3.2192								2.7506						2.9505			
1						X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6325439|ref|NP_015507.1|					4.9		4.7	5.7	9.8		3.9	8.6	13.9	7.4	11.5	6.8	4.6	5.5	8.1	10.7	5.6	4.3	7.2	5.5	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p; Sec23p [Saccharomyces cerevisiae]
K.AETDDGADVIR.W +2																	3.0014								
K.AGYQDDPQYADFK.A +2															2.5496	3.3835			3.0452	3.4571	2.868	4.0646			
K.FYNQIAQR.V +2								2.5271														2.8217			
K.LEAAELLVDR.F +2													3.6073	3.975	4.1675	3.8241					3.4558			3.4539	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.LNPSDNYQDMAR.G +2																	2.5099	2.9679					2.7318		
K.SILNPYCVIDPR.N +2																		3.289							
K.TDANNISESEIGIGATSTWK.M +2					3.5037																3.0894		4.8332	3.6721	
K.VQGLIGHASAVK.K +2												2.5342	2.7189				3.3473					3.1407	2.7505		
R.ATGSALNIASLLLQGCYK.N +2							2.9399	3.8686	3.309			4.9306	4.0747	4.6901	3.2754					3.894					
R.FFLPLEQVEFK.L +2									3.1618				3.1524	2.8979	3.1088	3.0889			2.9661	2.5329			3.0598		
R.FIDTEAGGSQAR.F +2											3.7797		3.932												
R.FTWNVFPSTR.S +2									2.5656				2.8963												
R.ILFASGPGTVAPGLIVNSELK.D +2																			3.1282	3.7629					
R.LAPNFSLYPQFTYYLR.R +2													2.6912						2.7522						
R.NSSWSCPICNSR.N +2																								2.7061	
R.SDANSNVVPVGCLYTPLK.E +2					3.666		3.3512	3.7714	3.2844			2.5512	4.2068	3.5652	3.3585										
R.SQFLSVFNNSPDETAFYR.H +2									5.3516		3.6187	2.8739			2.8334	5.1332		4.1754		3.8106					
	1				X		X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6324378|ref|NP_014448.1|					5.4	14.3		13.2	11		9	8.1	18.8	9.6	7	21.5	11.4	19.1	19.3	10.3	6.1	8.3	8.5	8.3	Saccharopine dehydrogenase (NADP+, L-glutamate-forming); catalyzes the formation of saccharopine from alpha-aminoadipate 6-semialdehyde, which is the seventh step in lysine biosynthesis pathway; Lys9p [Saccharomyces cerevisiae]
K.AISLDVTDDSALDK.V +2						4.3032										3.4825					4.4953		4.2841		
K.DDANEIFSKPIAWNEALK.Q +2													3.0874		3.106										
K.DDANEIFSKPIAWNEALK.Q +3													4.2602												
K.EDLIASIDSK.A +1																								2.1783	
K.EDLIASIDSK.A +2																							2.5982		
K.FGIEWADGTTETR.T +2								3.1255	3.6805				4.3697	4.0266	3.9687	3.8418					3.7227			3.6994	
K.GPGLLAPYSPEINDPIM*K.E +2													3.7041			2.5389		3.6001	4.5189						
K.GPGLLAPYSPEINDPIMK.E +2																		3.3215							
K.IETVSSEDLMATAK.P +2						3.0501					3.5368											3.6288			
K.PYFIYPGYAFVCYPNR.D +2																			3.4195						
K.SFLSYCGGLPAPEDSDNPLGYK.F +2						3.9478		3.3853	3.9003			2.6886				3.8641	3.8089	3.9482	3.9559	3.5078					
K.STSKEDLIASIDSK.A +2																			2.5486						
K.TDVVTSSYISPALR.E +2					4.2205	4.3611		2.7452	4.303		4.1202	2.9907					3.5276					4.593	4.2316	3.5737	
K.VGGYSSM*AATVGYPVAIATK.F +2													3.043					2.528							
K.VGGYSSMAATVGYPVAIATK.F +2																3.4865									
R.GNALDTLCAR.L +2																		2.8049							
R.ILSGFAWLGLFSDAK.I +2														3.4138						3.545					
R.LEELMQYEDNER.D +2											4.6005														
R.TKTDVVTSSYISPALR.E +2																			3.6012						
R.TLANAQALAK.P +2					2.8126			2.5026																	
R.TLANAQALAKPSGSK.A +2													3.926	3.0909			4.296	2.8604							
R.TSTLVDYGK.V +1																				2.017		2.1819			
R.YQGFPEFVK.A +2																2.5057									
	1				X	X		X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320030|ref|NP_010110.1|					3.1	3.1	2.2		4.4		2.9	5.5	4.5	6	1.6	3	3	4.4	8.2	2.9	3.8	5.1	6.9	4.9	NAD(+)-dependent glutamate synthase (GOGAT), synthesizes glutamate from glutamine and alpha-ketoglutarate; with Gln1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source; Glt1p [Saccharomyces cerevisiae]
K.ADHILVSGHDGGTGAAR.W +2													4.6755	3.8976								3.4209	3.0152		
K.DTVELESLCDPVEIAFVK.N +2					5.2165	4.1375			4.8633		2.565	3.053	3.6255		2.7288	4.8981			3.8616					2.6631	
K.EFIGNDEGEVTAIR.T +2									3.7627			2.7436						3.7893							
K.EFISQDSLSLK.V +2																				3.4822			3.0007		
K.GLSGGIIVIKPPK.D +2														2.625											
K.HAIDAGILK.V +2													2.9206												
K.IAQGAKPGEGGELPAHK.V +2																		2.8121				3.2482	3.0561		
K.LASEAIDDGK.K +2																		2.5868							
K.LDLDLDIPEMGK.Y +2																		2.9382				3.7334	2.9737		
K.LIDEAEVTLDR.G +2																	2.7642								
K.LLETNNFPEFTGR.V +2											2.5677	2.6055	4.0997	2.7154			3.7617		3.4286	3.9641					
K.LVSEVGVGIVASGVAK.A +2												3.0459													
K.NIDFAM*QLLESNTK.A +2														4.5577							4.3176				
K.NIDFAMQLLESNTK.A +2									2.6553			3.4681				3.2893									
K.SEGLLGYTDTIDK.I +2					3.8551	4.1487	4.2189		3.898			3.4858							3.6538		3.8194		3.9111		
K.SPILHWNEFQALK.N +2														3.1362											
K.VIVVGGGDTGNDCLGTSVR.H +2																					5.399			3.865	
K.VVDLEDAVPDSK.Q +2											3.4883											4.0607	3.8117		
E.EPTILQPLLVPLYDEK.Q +2					3.8402	3.2936	2.9264		3.0482							2.8222			3.7244				2.8555		
R.FGVTSYYLSDADEIQIK.I +2																							5.0566		
R.GLPVNIDASIINTDR.A +2																			3.6532						
R.GTIATLDDSSYSIDGGK.T +2																						3.9904			
R.IDLLSAEGIDFVTNTEIGK.T +2					4.5019	4.3744	4.0454		4.4105					4.0376										3.5212	
R.ILGNFNHYLK.D +2													2.8378	3.1847											
R.NVNNDNDTLEEGQILENYK.H +2											4.6001						5.0217		5.8894	4.9482	5.137	5.3855	4.6061	4.3849	
R.NVPVDSTILGDVALSR.E +2												2.6929	4.2847	5.0872	4.3535	4.1358			2.5749		4.6047	3.8849		3.778	
R.NVVVQTDGQLR.T +2																								3.0039	
R.QLFAQVTNPPIDPIR.E +2												2.6659	4.63	3.8766									3.8957		
R.SQVALILETGEAR.E +2																			3.2944						
R.TGFTVGVIGSGPAGLACADM*LNR.A +2																	3.2911	3.6126	2.5324						
R.VCPAPCEGACTLGIIEDPVGIK.S +2																		3.7959	4.3252	3.7398					
R.VICASEVGVIPIENSLVVQK.G +2																									
gi|6322569|ref|NP_012643.1|					3.8	4.4	3.8		4.1		4.2	3.4	11.4	9.6	3.9	5.2	7.1	3.7	6.5	4.6	5.4	4.4	7.2	4.7	Large subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; Cpa2p [Saccharomyces cerevisiae]
K.DINIPIAESFACETVDEALEAAER.V +2						2.9426																			
K.DINIPIAESFACETVDEALEAAER.V +3														4.168											
K.ELAAQSLSLAPQILVEK.S +2					2.804		2.7619				2.7267	2.6069	3.7866	3.6292		3.2084	2.6631								
K.FSSILDSIDVDQPEWSELTSVEEAK.L +2					3.0719	3.4316	3.8465		3.7831				3.4008			4.4263	3.5856	2.741							
K.IGLGYTLPELPNPITK.T +2															3.2874					2.7826			3.4113		
K.LTLASDVSPDHPVVM*SK.F +2													3.2823						3.5221						
K.LTLASDVSPDHPVVMSK.F +2																	4.263								
K.LYDNGCNIMGTNPNDIDR.A +2											2.7645									2.2833			3.7431		
K.TIM*INYNPETVSTDFDEVDR.L +2																			3.3231		3.0304				
K.TIMINYNPETVSTDFDEVDR.L +2																						3.3493	3.0444	3.2552	
K.TTVANFEPSLDYIVAK.I +2													3.8102	3.0835	3.7728	3.5756		3.4455	3.3873				3.2392		
K.VLGVNFIEIAVK.A +2													3.2359	3.9814											
R.AESTDDVDYIMR.R +2											3.75				2.9677									3.1827	
R.LYFEELSYER.V +2																							3.0138		
R.NAIDFAIPLFNEPQTALLFAK.C +2									2.9108			2.8632	3.0281	2.5557											
R.NAIDFAIPLFNEPQTALLFAK.C +3													4.423												
R.PSYVLSGAAM*SVVNNEEELK.A +2																					2.9936				
R.SAYALGGLGSGFANNASEM*K.E +2													4.7739						4.4704		5.0045	3.7954			
R.SAYALGGLGSGFANNASEMK.E +2																	4.5591							4.3936	
R.SWDEFIGFK.A +2																						2.6726			
R.VLAIGQALIHENYTVER.V +2														5.4807						3.8582					
	2				X	X	X		X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|37362622|ref|NP_009822.2|					8.6	5.7	10	5.7	11.4		12	11	22.2	31	22.4	14.1	11.4		9	14.1	8.4	7.3	10.2	9.4	Mitochondrial serine hydroxymethyltransferase, involved in one-carbon metabolism; Shm1p [Saccharomyces cerevisiae]
K.AVM*DLLGSELQNK.Y +2													3.7267						3.5842						
K.AVMDLLGSELQNK.Y +2												2.7643	3.3459		4.1047	3.4728	3.7403			3.9147	3.4404	3.868		3.6603	
K.HSITLIPSENFTSK.A +2									2.9801				4.0457	3.7311	3.8382	3.1307				3.1567					
K.KLCNESSEVAALSGEISK.W +2																	3.208								
K.LCNESSEVAALSGEISK.W +2					5.4784	4.9799	5.6534	5.7952	4.644		4.1855	4.2483	5.1315	5.3632	4.941	4.6828			4.2666	3.6369	5.5717		5.0749		
K.LVSGGTDNHLIVIDLSGTQVDGAR.V +3													3.8843	5.195	5.0242										
K.SALFPSGLR.I +2														2.5096											
K.VIVAGTSAYSR.L +2					2.7708	3.7577	3.6892	3.1623	2.5803		3.6341			2.7147										3.5056	
K.YFQSM*PYHVDHTTGLIDYDNLQVLAK.A +3														5.9653											
K.YSEGYPGER.Y +2													2.7629									2.6522	2.5011		
R.ALELYGLDPAK.W +1														3.095	2.8555	2.6205				2.0661	2.7052				
R.ALELYGLDPAK.W +2													2.8816				3.715				2.6821				
R.EEFSQVAK.Y +1																								1.9871	
R.LM*GLDLPDGGHLSHGYQLK.S +2														3.543											
R.VETILSALNIAANK.N +2					4.5884		4.7248		5.0341		5.3152	4.9027	5.0556	5.1569	5.1816	5.0525	4.6008		4.2404	5.1146		4.7624	4.8231	4.4994	
R.VETILSALNIAANKNTIPGDK.S +3							3.5442				3.543		3.7011	3.707	3.6555										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.YYGGNEIIDK.S +2											2.5057	2.6964			2.8413								3.0552		
gi|6323089|ref|NP_013161.1|						5.5	5	3.2	15.8		4.2	13.3	27.1	34.8	25.9	22	10.6		9.1	19.5	3.9	6.4	4.2	5.9	Beta subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs2p to generate active enzyme; sequence is evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase (Msf1p), but substrate binding is similar; Frs1p [Saccharomyces cerevisiae]
K.AEIVLNILTTM*FSR.Y +2														2.9914											
K.FVPLNQTQEFTGDK.L +2						3.4339			2.6311			3.0666				2.5724	2.6714								
K.LSNANFIAKPLPINK.V +2													3.9598	4.165	4.0205				4.1623	3.8705					
K.MSLHAVQSK.E +2																2.5633				3.1926					
K.NSGFEIIQGLLGK.I +2									4.9995			4.0953	4.9425	4.9373	4.828	4.6244	4.6887		3.5539	4.7009	3.0593	2.7059		2.7493	
K.STEQIRPFATAAVLR.N +2									2.622				3.28	3.3676	3.1022	3.4445			2.6802						
K.STEQIRPFATAAVLR.N +3														3.9324											
K.SYASFIALQDK.L +2					3.8439		4.1014		4.0015		3.1099				3.8416									3.6895	
K.TGEEPELK.L +2												2.6881		2.5306											
K.VFETGDVVFK.D +2																					2.8978				
K.YINSCLGLDQSADEIAHCLK.K +2															3.7175					3.7677					
R.GYWIEEDDSVK.T +2													2.8727						3.2533	3.7748		3.0918	3.5942	3.4893	
R.NILIDITATDK.T +2												2.5947	3.0135	3.1508	3.1187	3.2812				2.9061					
R.SLVAM*GTHDLDSIEGPFHYR.A +3														4.264											
R.TEWIADYGAAASGR.G +2											5.0771	4.2648	4.4494	3.2315	4.1249	4.8179	4.2307					5.1094	4.8592		
R.TTLLPGILK.T +1													1.92												
R.VASSQATWVEVLPLTLCSHDENFK.F +3														3.533											
R.VCSLPPLINSEHSK.I +2													3.464	3.4849	2.633	2.9739									
R.YCDEPTTVEPVEIVSEHNGQSR.L +2																	3.6679								
R.YCDEPFTVEPVEIVSEHNGQSR.L +3									4.1632				4.2723	3.908	3.5724	4.4454	3.9978								
R.YDLLCIEGISQSLNEYLER.K +2					4.2324	3.5985	4.6724	5.0784	4.5444			3.2793	5.3132	2.9197	2.5461	4.2163				3.9289					
R.YVHIIEDSPVFPVIM*DSK.D +2													5.9597	3.727						4.6132					
R.YVHIIEDSPVFPVIM*DSK.D +3													3.615	3.5644											
	2				X	X	X	X	X		X	X	X	X	X	X	X		X	X	X	X	X	X	
gi|6319370|ref|NP_009453.1|						4.4	4	4.6	9.4	7.3	9.7	9.5	17.4	16.5	14.5	7.2	4.4	3.9		4.4	5.1	4	7.7	8.4	Alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily conserved enzyme complex required for ATP synthesis; Atp1p [Saccharomyces cerevisiae]
K.AVDALVPIGR.G +2							3.3854						3.1004	3.0674	2.7702	3.3318		2.8573				2.6466			
K.GVSDEANLNETGR.V +2																							4.1591		
K.HALIVYDDLSK.Q +2													3.6503	3.7172	3.3707		3.2277			3.4285					
K.LFLAQYR.E +2													2.5132												
K.LYCVYYAVGQK.R +2												2.8336	2.5791	2.5309										4.0056	
K.SNHNELLTEIR.E +2																		2.5662							
K.TAVALDTILNQK.R +2						4.107	4.1956	4.1037	4.0061	3.2588	4.1287	4.1161		4.0063	3.6636						3.9179				
R.EVAAFAQFGSDLDASTK.Q +2														4.0243											
R.IGEFESSFLSYLK.S +2								3.9769	4.5376		3.4498	4.0633	4.1525	4.1361	4.7696	4.4386	3.5476			3.5634			4.3799	3.052	
R.STVAQLVQTLEQHDAM*K.Y +2													4.7697		3.4933										
R.TGNIVDVPVGPGLLGR.V +2									4.2352	2.7206	4.0094	3.5704	5.0526	4.6883	4.0764	3.6922					4.4038		3.8125		
R.VLAVGDGIAR.V +2									2.8943				2.5041											2.511	
R.VVDALGNPIDGK.G +2						3.67				3.604	3.6894											4.0227		2.658	
	1					X	X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6320662|ref|NP_010742.1|					15.5	15.5	21.9	12.3	37.4		31.6	28.3	39	42.8	38.5	31.6	41.2	22.5		37.4	12.3	25.7	36.4	19.3	Guanylate kinase, converts GMP to GDP; required for growth and mannose outer chain elongation of cell wall N-linked glycoproteins; Guk1p [Saccharomyces cerevisiae]
K.DFIFAEK.- +1														2.2927			2.2855					2.6067	2.2849	2.5139	
K.DYNFVSVDEFK.S +1																2.2744				2.1037	1.9611				
K.DYNFVSVDEFK.S +2					4.2031	4.3512	4.3855	4.4151	4.1791		3.7748	4.2152	4.047	3.9243	4.1887	3.9709	2.6197	3.3637		2.7066	3.3331	3.8874		3.2083	
K.LFAEYPDSFGFSVSSTTR.T +2					5.3832	5.1944	5.6361		5.0397		3.5517	4.6497	5.0562	5.2653	4.2201	5.4491	2.9083			4.054			2.9814	5.1393	
K.NNEFIEWAQFSGNYYGSTVASVK.Q +2									3.7609																
K.RLSAAQAELAYAETGAHDK.V +3																	3.8576			5.6485					
K.TCILDIDM*QGVK.S +2													3.7638	3.9239											
K.TCILDIDMQGVK.S +2							3.7024	3.912				3.8868		3.7165	4.0614	3.5102				3.7147	4.0607				
K.VIVNDDLDK.A +1																	2.138			2.3307					
K.VIVNDDLDK.A +2																									
R.FLFIAPPSVEDLK.K +2													3.4936	3.324	3.3612		3.0716	3.0353		3.9102			3.1385		
R.FLFIAPPSVEDLKK.R +2													2.5449	3.7599											
R.LSAAQAELAYAETGAHDK.V +2									2.8984		4.4933		5.7588	5.5205	4.9844	5.6029		5.1756		4.481		3.7466	5.0533		
R.PIVISGPSGTGK.S +2											2.863	3.242									2.9795				
	1				X	X	X	X	X		X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6323554|ref|NP_013625.1|	2.9				6.3	6.3	6.3	2.9	11			6.9	10.1	6.3	9.8	9.8	7.6	14.5	6.5	16.3		11.6	8.3	8.1	Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; Tub1p [Saccharomyces cerevisiae]
K.GGEEGFSTFFHETGYGK.F +2													3.6102												
K.IGICYEPPTATPNSQLATVDR.A +2									3.7024								4.1773	3.2121		4.0272		4.5061	3.2513	3.0716	
K.TVQLVDWCPTGFK.I +2	3.6476				3.8039	3.9457	3.7382	3.9117	3.646				3.6825	4.0991	3.385	2.7362	3.0357	2.5575							
R.AIYVDLEPNVIDEVR.N +2					3.7235	4.1438	3.6062		3.7694			3.0066	4.4842	4.3629	3.9771	3.4639		3.6993	4.0624	2.5127		3.8202		3.4788	
R.AVCM*LSNTTSIAEAWK.R +2																							4.242		
R.AVCMLSNTTSIAEAWK.R +2												3.4996			3.4211	4.6736		3.9416		3.3076		5.0699	4.5805		
R.FDGSLNVDLNEFQTNLVPYPR.I +2																				2.8901					
R.IHFPLVSYSPVLSK.S +2																			2.699						
	1 X				X	X	X	X	X			X	X	X	X	X	X	X	X	X		X	X	X	
gi|6325292|ref|NP_015360.1|	10	15.4		6.5	7	12.2			11.1	7			22.7	13.2	8.9	9.2	20	7.6	18.9	25.7		14.9	9.2	10	Glutamine synthetase (GS), synthesizes glutamine from glutamate and ammonia; with Glt1p, forms the secondary pathway for glutamate biosynthesis from ammonia; expression regulated by nitrogen source and by amino acid limitation; Gln1p [Saccharomyces cerevisiae]
K.EGYGYFEDR.R +2	2.6995	2.7809																	2.783						
K.GGYPAPQGPYYCGVGAGK.V +2	4.3965	4.1932			3.9389	3.5271			3.8338	4.2056			3.7214	4.2592	4.1756	4.1788	3.8512	3.5299		3.5252				4.1412	
K.LYGSDNDMR.L +2				2.6953																					
K.PVAYYPDPFR.R +2	3.156																3.5171	3.3133		2.5825					
R.GDNIVVLAACYNNDGTPNK.F +2						3.7094														3.9559		2.9152		3.8964	
R.HETASM*TAFSSGVANR.G +2																			5.3295						
R.HETASMTAFSSGVANR.G +2													4.5482	4.6092		2.7236	5.0911								
R.IIAEYVWIDGTGNLR.S +2				3.4935					4.3706					4.8152	4.403				2.5393	3.9828			3.6076		
R.ITSIDQLPEWNFDGSSTNQAPGHDSDIYLK.P +3		5.2711															3.6133		3.9698	4.6761					
R.RGDNIVVLAACYNNDGTPNK.F +2													4.8058							5.356					
R.RPASNIDPYLVTGIM*CETVCGAIDNADM*TK.E +3													6.1392							3.9493					
R.VAEEFGIK.I +1					2.5344	2.5683			2.4126											2.4916					
R.VAEEFGIK.I +2						2.6322				2.5286										2.6939					
	1 X	X		X	X	X			X	X			X	X	X	X	X	X	X	X		X	X	X	
gi|6323391|ref|NP_013463.1|	5.6				7.9	9.8	5.6	5.6	5.6		7.9	7.1	8.9	15.4	9.5	13.5	8.3		4.4	16		7.3	11.2	5.2	Adenylosuccinate lyase, catalyzes two steps in the 'de novo' purine nucleotide biosynthetic pathway; Ade13p [Saccharomyces cerevisiae]
K.ASAQEAIVR.H +2						3.0555					3.0535	2.7031		2.8733		2.5388							3.1892		
K.DLPVLGWTHFQPAQLTTLGK.R +2																				3.1588					
K.DVNNALQPFQK.Y +2					2.9544				3.5246		3.6946								3.2227						
K.ELGLTVVTDEAIEQM*R.K +2													2.771	4.0779	3.411										
K.ELGLTVVTDEAIEQMR.K +2	4.1666				3.3152	4.5029	4.1048	2.536	4.455			4.6385		3.3286	3.7306	4.4328				3.2453		4.9807	4.4546	3.61	
K.GELPFM*ATENIIM*AM*VEK.N +2													2.6345	3.2339											
K.HVEITDDEIAK.A +2														3.4167		2.9447	2.7231						2.807		
K.LVNVINR.L +1											1.8779														
K.LVNVINR.L +2																							2.6314		
K.LWLNLAIAEK.E +2															3.2593				2.8146	3.3514					
K.SQIGSSAMAYK.R +2						2.8168											2.6709								
K.VYPVTGQTYSR.K +2											3.3492														
R.DAYDIIIPK.L +1																2.4158	2.4777								
R.TLDDSAIR.R +1																				1.8088					
R.VLSHQAAAVVK.E +2	2.5373				2.8538	2.7723	2.8231	3.0603						2.9727	2.7823	2.7867				2.9413		2.7625	2.8879		
R.VLSHQAAAVVKEEGGENDLIER.V +3																				4.0323					
R.VTELLGFDK.V +1													2.3277	2.1261	2.4675	2.3377	2.4954			2.1895				2.1295	
R.VTELLGFDK.V +2												3.1616	3.0574		3.274	3.6325									
	1 X				X	X	X	X	X		X	X	X	X	X	X	X		X	X		X	X	X	

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6323530|ref|NP_013601.1|					11.9	21.2	11.9	11.1	31		15.9	41.6	44.7	33.6	26.5	26.5	12.4	15.5	26.1	24.3	21.2		25.7	20.8	One of two orotate phosphoribosyltransferase isozymes (see also URA10) that catalyze the fifth enzymatic step in de novo biosynthesis of pyrimidines, converting orotate into orotidine-5'-phosphate; Ura5p [Saccharomyces cerevisiae]
K.DHGEGGIIVGSALENK.R +2																	4.3926			5.5591	3.6387				
K.EGLSATQTVSK.K +2											2.679														
K.FDVIFGPAYK.G +2												2.7442	2.991	3.0094	3.1673	2.9768			2.5603		2.7219		3.1339	3.4045	
K.FQNIQYAFNR.K +2								3.4243	3.7249		3.5835	3.0948	3.3029	3.4487	3.2689	3.6239		3.4878			3.2611		3.545	3.3674	
K.FQNIQYAFNRK.E +2																			2.6602						
K.GIPLAAIVCVK.L +2														2.6802					2.6179				3.4284		
K.GQVVGSIALDR.Q +2					4.2437		3.9175		3.7894			3.9717		3.9915	4.3116	4.0452	4.3082	4.5713		4.3417	4.3513		4.331	3.656	
K.LLSNLATAYAIAIIQSDLK.F +3													4.5899	5.4631											
K.NFLELAIECQALR.F +2						3.4581			4.9034			3.1938	4.9934		4.8668	4.6521		4.1318	4.6644	4.5468					
K.SKIEQYLQTYGASA.- +2												2.7552	2.5987	3.7522					2.6105	3.1633					
R.ESPYFFNLGLFNTGK.L +2					4.2049	3.7333	3.9043	4.3824	4.0982		3.3313	3.3226	3.8474		3.9994	4.2675							4.0931	2.638	
R.QEVVSTDDKEGLSATQTVSK.K +2						2.7448			3.3061			2.7627	4.0678												
	1				X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6324371|ref|NP_014441.1|					11.4	14.6	16.2	11.4	16.2		8.6	15.2	21.5	24.2	14.1	10.6	11.4	20.2	8.1	19.7	13.4	10.1	10.1		Mevalonate pyrophosphate decarboxylase, essential enzyme involved in the biosynthesis of isoprenoids and sterols, including ergosterol; acts as a homodimer; Mvd1p [Saccharomyces cerevisiae]
K.ACVLVVSDIK.K +2														3.2384	3.2732	3.0597		2.8383							
K.ACVLVVSDIKK.D +2													3.2389	3.7017	2.5673		3.4375	3.234		3.3162					
K.DASLPTLSQWK.L +2					2.7334	3.1565	2.7024	3.2522	3.2051					3.5136	2.791	2.5951				2.9577					
K.DVSSTQGM*QLTVATSELFK.E +2																					3.0864				
K.DVSSTQGMQLTVATSELFK.E +2									3.2125													2.557			
K.FTTEQLEAFNHQFESSNFTAR.E +3													3.5909	3.765											
K.LNLPTNSSISVTLSQDDLR.T +2							3.8744						4.83	4.384				2.7355	2.6087	4.1274			2.9199		
K.LYQLPQSTSEISR.I +2						4.5757			4.671			4.2789					4.2092	4.5138	3.7026		4.6172				
R.DTLWLNGEPHSIDNER.T +2																		4.1052		2.7206					
R.SLFGGYVAWEM*GK.A +2												2.7469	3.6115	3.2956	3.5076										
R.TLTSAATAPEFER.D +2					3.8351	4.3711	3.4912	3.6619			2.5102	3.1893													
R.VILTQVGSGPQETNESLIDAK.T +2					5.6188	5.6954	5.2835	6.0789	5.8755		4.2458	5.7756	5.6224	5.5702	5.4288	5.8908	6.2779	5.2736		5.689	5.5822	5.3553	5.9486		
R.VILTQVGSGPQETNESLIDAK.T +3													4.3761												
	1				X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6321332|ref|NP_011409.1|					34.9	34.9	34.9	34.9	34.9	25.5	34.9	34.9	32.9	49.7	36.2	46.3	30.9	31.5	18.1	34.9	18.8	28.9			Essential light chain for Myo1p, light chain for Myo2p; stabilizes Myo2p by binding to the neck region; interacts with Myo1p, Iqg1p, and Myo2p to coordinate formation and contraction of the actomyosin ring with targeted membrane deposition; Mlc1p [Saccharomyces cerevisiae]
K.DIFTLFDK.K +1													2.4786	2.4547		2.3999		2.1461	2.4421						
K.DSLGDYLR.A +2										2.8073															
K.GVEVDSNGEIDYK.K +2														3.687	3.5073		3.0864					3.7414			
K.GVEVDSNGEIDYKK.F +2														3.1245											
K.LTDAEVDELLK.G +2					4.0702	3.7937	3.7528	3.8294	3.733	3.4721	3.5149	3.584		3.0892		3.3067	3.0696	2.6957		3.3659		3.8055			
R.AIGYNPTNQLVQDIINADSSLR.D +2					5.7256	3.8611	5.8044	5.7553	5.1334		4.487	5.325	5.6815	5.8898	4.9835	5.7313	4.584			5.0577					
R.AIGYNPTNQLVQDIINADSSLR.D +3					4.7618		4.8413	4.6485	3.8316				5.272	5.6613	5.0662	4.4305									
R.DASSLTLDQITGLIEVNEK.E +2					4.9108	5.4558	5.1918	5.2418	5.1522	3.6218	3.7143	4.5759	5.1723	5.262	5.3771	5.3048		4.9095	3.7957	3.713	5.6978	4.8643			
R.YMLTGLGEK.L +1																1.8474		1.9252			2.2211				
	1				X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			
gi|6324088|ref|NP_014158.1|							6.3	6.5	7.3		5.1	5.1	15.6	15.6	16.8	8.9	14.7	18.6	7.5	22.4	9.9	9.5	13.3	6.9	Glucose-6-phosphate dehydrogenase (G6PD), catalyzes the first step of the pentose phosphate pathway; involved in adapting to oxidatve stress; homolog of the human G6PD which is deficient in patients with hemolytic anemia; Zwf1p [Saccharomyces cerevisiae]
K.AVAPIDTDDVLLGQYGK.S +2							4.7567	3.8977	4.4852		3.2003	3.1753			2.9749	3.8227	3.9993	3.7754		4.1934		4.0908	3.8194		
K.M*VSYISGNYDTDEGFDELR.T +2																					2.9154				
K.MVSYISGNYDTDEGFDELR.T +2																	3.8083	3.9027		2.7181			3.3205		
K.NTVISVFGASGDLAK.K +2							3.2668						4.354	5.0795	3.0527		3.0398	3.2201	2.6504					2.7329	
K.SANVDVPHR.L +2											2.6857	2.5517								2.704					
K.TFPALFGLFR.E +2													3.2733	2.9318	3.0644					2.761					
K.TPGLSNATQVTDLNLTYASR.Y +2									4.4413									5.0243		4.6997	5.1522	5.7681	5.681	4.8055	
R.DNIQSVQISFK.E +2																						2.5787			
R.FGNQFLNASWNR.D +2													3.7217	3.8361	3.357	2.8418	2.854	3.582	3.446	3.7796					
R.GGYFDSIGIIR.D +2													3.6663	3.8098			3.0404	3.2087	3.3998	4.2011	3.0588		2.9856		
R.LFYLALPPSVFLTVAK.Q +2								2.6678					2.7813	2.7439	2.7458	3.3418									
R.VIVEKPFGHDLASAR.E +2													3.2915	3.2473											
R.YQDFWIPEAYEVLIR.D +2															2.6305					3.0066					
	1						X	X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|14318501|ref|NP_116635.1|					9.6	14.8			15.2	7	11.8	11.8	14	17.8	16.8	18	16.6	18.8		31.7	15.2	13.6	13.8	7	Dihydrolipoamide dehydrogenase, the lipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase multi-enzyme complexes; Lpd1p [Saccharomyces cerevisiae]
K.AAQLGFNTACVEK.R +2					3.8375	3.5362			4.0365	3.455	3.7162	3.4042	3.9826	4.0949			3.8202	4.1526				3.4978			
K.AEEEGIAAVEMLK.T +2					4.2507	4.1279			3.7453						4.1395	4.2904	4.551			3.4528	3.6653	4.1545	3.8022	4.3248	
K.EAGIDYK.I +1																					1.8394				
K.INVANFQK.A +2														2.805											
K.IVSSTGALSLK.E +1																		2.2373							
K.LGGTCLNVGCIPSK.A +2						4.1378			4.3674		2.7387	3.4895			3.3851	3.8725	3.2744	2.6384		3.7524	2.8782		3.6812		
K.NIIVATGSEVTPFPGIEIDEEK.I +2					5.6661	5.1311			5.697	4.1896	4.0241	4.9479	5.7506	5.9646	5.9395	5.9686	5.1689	6.4892		4.3846	5.91	4.3372	5.8396	4.0997	
K.NIIVATGSEVTPFPGIEIDEEK.I +3													3.8741	5.1976											
K.NVVEIVVEDTK.T +2													4.026		3.97	3.2492				3.157					
K.QENLEAEVLLVAVGR.R +2																				3.9047					
K.SHDVVIIGGGPAGYVAAIK.A +2														5.7968											
K.SHDVVIIGGGPAGYVAAIK.A +3																				3.8187					
K.TNQDTEGFVK.I +2												2.732	2.9259		2.5832	2.8577	3.2077								
K.VTVVEFQPQIGASM*DGEVAK.A +2																					3.4664				
K.VTVVEFQPQIGASMDGEVAK.A +2																3.4502		2.9921		2.761		2.9553	3.2221		
K.VVGDVTFGPM*LAHK.A +2									2.581				3.581	2.7685	2.8605			2.8104							
K.VVGDVTFGPMLAHK.A +2																				2.8651					
R.LVIDDQFNSK.F +2											2.9378									2.848					
R.RPYIAGLGAEK.I +2																	2.6077								
R.VCHAHPTLSEAFK.E +2														3.059											
R.VTPVDGLEGTVK.E +2						2.5221																			
R.VTPVDGLEGTVKEDHILDVK.N +2																				2.9436					
	1				X	X			X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6324258|ref|NP_014328.1|					7.5	5.2	9.3	8.5	12.7	6.6	8.5	12.7	10.6	11	9.3	13.5	6				5.2	7.1	10.8	11.2	Dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to acetyl-CoA; Lat1p [Saccharomyces cerevisiae]
K.ADIESYLEK.S +2						3.1104	3.0807	2.6166	2.9625		3.0173	3.2431	2.6235	3.057		3.2604	2.986					2.9218		2.8049	
K.DIPVNKPAVYVEDK.A +2													3.1752												
K.GLSQISNEIK.E +2																									
K.LSINDLLVK.A +2														2.9773	3.03	2.9834					2.8656	2.9457		2.7472	
K.NVDVSVAVATPTGLLTPIVK.N +2					4.373		4.1203		4.5208			3.0937			4.0038	4.2851	2.5075						4.1887	3.2805	
K.TVIENPLEM*LL.- +2													3.251	3.1295											
K.TVIENPLEMLL.- +2																2.5954									
R.IFASPLAK.T +1														1.9396											
R.LLQSTQGIPSYIVSSK.I +2						4.3734	4.3023	4.1633	4.4626	2.759	3.5991	4.428		3.7474	3.7918	4.4519						4.8262	4.3519	3.7647	
R.VPDANAYWLPNENVIR.K +2					2.6252			3.9029	3.5967	3.215	3.2191	3.1096	4.1612								4.3989		3.3506		
	1				X	X	X	X	X	X	X	X	X	X	X	X	X				X	X	X	X	
gi|6321786|ref|NP_011862.1|		13.8	13.8	34.1	19.6			27.5	32.6			21.7	27.5	33.3	28.3	18.8	20.3		34.1	22.5	8		14.5	12.3	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Ap and has similarity to rat L14 ribosomal protein; Rpl14bp [Saccharomyces cerevisiae]
K.KVLIDGPK.A +1																	1.9641								
K.KVLIDGPK.A +2		2.7307	2.5794	2.6483										2.5053											
K.LAAIVEIIDQK.K +1																					2.6065				
K.LAAIVEIIDQK.K +2		4.8694	4.615	4.6012	4.4845			4.5976	4.5857			4.5867	4.4918	4.6865	4.5482	4.5432	4.6199		4.4126	4.4007	4.3206		4.6316		
K.LAAIVEIIDQKK.V +2			4.2648											2.6495						4.1664					
K.WAAAGVCEK.W +1																							2.14	2.1433	
K.WAAAGVCEK.W +2															2.7548										
K.WAASSWAK.K +1					1.9666				1.9985				1.899	1.8203		1.8625			1.8389					1.9184	
R.AALTDFER.F +2					2.5647			2.523																	
R.FQVMVLR.K +1									1.9706							2.2523									
R.QAINLGQVVLTPLTFALPR.G +2				3.5195				5.3525	5.4087			4.3013	4.907	4.6417	2.6223				2.709	3.7258					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.QAINLGQVVLTPLTFALPR.G +3									4.9484				5.6225	4.0845						5.0459					
R.RAALTDFER.F +2				2.9375													2.6458		3.0588						
	1	X	X	X	X			X	X			X	X	X	X	X	X		X	X	X		X	X	
gi|6324682|ref|NP_014751.1|					5.8	6.1	5.8		4.8	3.3	4.8	5.8	14.2	9.9	8.8	7.6	7.1	7.8		6.8	8.9		7.9	7.3	Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor isozyme, responsible for the residual alpha-IPMS activity detected in a leu4 null mutant; Leu9p [Saccharomyces cerevisiae]
K.DDPSQQATR.W +2										2.7124															
K.EIEVSPPSASQTDFDFTR.Y +2					4.3864	4.5085	4.6418		4.582		3.376	2.7687	4.0395	4.7125	4.6048	4.9764		4.0754		4.0232	4.178		4.2214	4.1038	
K.GGAAWVIMR.S +2																				3.0148					
K.RTVEALTGAK.R +2																		3.0916							
R.ATIHTYLATSDM*FR.E +2													3.9459	2.7421											
R.ATIHTYLATSDMFR.E +2																				2.8864					
R.DYEAVIR.V +1													2.5589		2.1915		2.1869								
R.GCGVAATELGM*LAGADR.V +2												3.6801	5.1249	5.0204	4.7218									2.571	
R.GCGVAATELGMLAGADR.V +2					5.3511		4.9091									3.6622	4.9631				4.7358				
R.TVEALTGAK.R +1																								2.0104	
R.VEGCLFGNGER.T +2									3.1877	2.9631	3.3543		3.205	3.0177	3.348	3.4819							3.3816		
R.YAVENAPDDVGIQCLVQSR.E +2						3.8883											2.5603	3.5034			3.133		3.7792		
R.YAVENAPDDVGIQCLVQSR.E +3													4.0094												
	1				X	X	X		X	X	X	X	X	X	X	X	X	X		X	X		X	X	
gi|6320896|ref|NP_010975.1|					8.1	16.2		9.1	17.2	12.1	16.2	13.1	35	21.9	14.8	36.4	17.2	9.1	12.1	23.9	9.1			9.1	ATP phosphoribosyltransferase, a hexameric enzyme, catalyzes the first step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control; His1p [Saccharomyces cerevisiae]
K.CDLGITGVDQVR.E +2					4.0497	3.7338		3.6677	3.8512	3.1726	3.1124	3.3931				3.3266	3.4475			3.5274				3.6515	
K.FVSGSVEASCALGIGDAIVDLVESGETM*R.A +3																									
K.IDDEGWVAVSSM*IER.K +2													3.5556	3.8258	2.8101						4.2431			3.3272	
K.IDDEGWVAVSSMIER.K +2						5.1366		4.7794	5.2527			4.8295			4.8553	5.1427	4.2078	2.8765	2.7333	3.0902				4.7911	
K.KPEQLIGK.T +2									3.0265		3.2362					3.6066	2.8898			3.6124					
K.LQVQVPVNGEYK.K +2													3.5857	3.3683	3.2986					3.605					
K.SVSILNGADITFHR.S +2																									
K.YFADLEGTTVEK.M +2					4.2247	4.212			4.1175	3.4714	3.6565	3.1783	3.88	2.8925		3.0545	3.7803	2.7708			2.7663				
R.AAGLVDIATVLSTSAYLIESK.N +2																3.2065			3.2672						
R.AAGLVDIATVLSTSAYLIESK.N +3													3.5661												
R.FVSCIYNAPEDK.L +2										3.0089	3.499					3.4512									
R.FVSCIYNAPEDKLPELLK.V +2													3.7862							2.6612					
R.IEGVMTAQR.F +2						3.3953							3.0716	2.907		2.8907									
R.LGASDIM*VFEISNCR.V +2													3.8956	4.331	3.8563	3.2761									
	1				X	X		X	X	X	X	X	X	X	X	X	X	X	X	X	X			X	
gi|6325421|ref|NP_015489.1|					11.5	14.2	11.5	8.9	14.2	6.7	9.2	11.5	17.4	6.7	8.9	18.8	6.4	8.9		11.2		8.9	13.1		Translation initiation factor eIF-4B, has RNA annealing activity; contains an RNA recognition motif and binds to single-stranded RNA; Tif3p [Saccharomyces cerevisiae]
K.EEPALDWGAAR.G +2																							2.9349		
K.TAQLTVEDGDNWEVVGK.K +2					3.7679	5.2118	5.4771	5.334	5.5766	2.6755	3.9881	5.0366	4.4824	4.2001	4.6566	5.6878	4.8757			3.5925		2.6116	5.3089		
K.TAQLTVEDGDNWEVVGKK.- +2																	4.0995	3.9913		2.6878					
R.ADLVAVLK.F +1																							2.0545		
R.ADLVAVLK.F +2																2.9413									
R.EDAPDLDWGAAR.G +2					4.0162	4.0751	3.9979	3.5739	3.6121	3.5334	3.5717	3.6553	3.4547	3.711	3.2729	3.5397									
R.EEVDIDWSAAR.G +2																				3.3353					
R.EEVDIDWTAAR.G +2																				3.5418			3.2745		
R.EEYPVPDAPPYR.A +2						2.6183			2.5318							3.0315									
R.EREEVDIDWTAAR.G +2													2.6222												
R.GGGADVDWSSAR.G +2													2.8007			3.3059									
R.GSNFQGDGREDAPDLDWGAAR.G +2																		3.0374							
R.GSNFQGDGREDAPDLDWGAAR.G +3																				4.4873					
R.SGFGGSFGGR.S +2					3.3378	3.16	3.2691		3.3244		2.8847	3.1091				3.289									
R.TEDDDEDEEAEK.Q +2													2.6277												
R.TVYVSVAAPR.R +2					2.9948	2.5061	2.6927	2.7149	3.2542			3.1744	2.9437		3.6231	3.4443	3.2242			3.2816			3.3649		
	1				X	X	X	X	X	X	X	X	X	X	X	X	X	X		X		X	X		
gi|6321407|ref|NP_011484.1|		9	14.2	9	12.3		13.5	13.5	20.6		13.5	20.6	20.6	20.6	14.2	20.6	14.2		14.2	27.7		11.6			Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Bp and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate; Rpl24ap [Saccharomyces cerevisiae]
-.MKVEIDSFSGAK.I +2																				3.2522					
K.AQRPITGASLDLIK.E +2		4.2371	4.1152	4.1582					3.6502			2.8105	3.7282	4.0325	3.8083	3.6158			3.8832	3.269					
K.AQRPITGASLDLIK.E +3		4.4522											4.6607	5.0085			4.2696		4.5634	4.7467					
K.GITEEVAK.K +1																				1.8814		1.8968			
K.VEIDSFSGAK.I +1																2.0595						1.8937			
K.VEIDSFSGAK.I +2							2.8633	2.9968	2.9618		2.9422	2.7234	2.921	2.8707											
R.IAWTVLFR.K +2			3.129		3.0206				2.913			2.8614	2.8544	3.0788	3.1889	2.9043	2.9841		3.0383	3.003					
R.PITGASLDLIK.E +2					3.489		3.6997	3.4311	3.8233		3.3934	3.0962	3.9136	3.5079	2.9095	3.8126			2.53	3.5013					
R.RIAWTVLFR.K +2																				2.8211					
	1	X	X	X	X		X	X	X		X	X	X	X	X	X	X		X	X		X			
gi|6324808|ref|NP_014877.1|		32.7	39.3	15.9	24.3	24.3	24.3	24.3	31.8		24.3	24.3	10.3	24.3	24.3	24.3	24.3	31.8			9.3				Ribosomal protein L37 of the large (60S) ribosomal subunit, nearly identical to Rpl33Ap and has similarity to rat L35a; rpl33b null mutant exhibits normal growth while rpl33a rpl33b double null mutant is inviable; Rpl33bp [Saccharomyces cerevisiae]
K.IEGVATPQEAQFYLGK.R +2		4.4227	4.4736		4.8236	4.9356	5.0032	5.2834	4.4127		3.2056	3.9749		4.3988	3.5555	4.5868	3.9769	4.1204							
K.RIAYVYR.A +2			2.5113	2.5629																					
K.RVNNPNVSLIK.I +2		2.8587	2.7483										2.5628												
R.IFLYPSNI.- +1		2.1034	2.0721						2.0303									2.1956							
R.VNNPNVSLIK.I +1																2.6835					2.5644				
R.VNNPNVSLIK.I +2			3.01	2.9282	3.0862	3.0242	3.0146	2.954	2.8006		2.5558	2.7717	2.9758	2.9913	2.6518	2.7977	2.6191	3.001			2.7614				
	1	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X			X				
gi|6320122|ref|NP_010202.1|		20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8		20.8	20.8	20.8	20.8	20.8	20.8		20.8	20.8	20.8					Ribosomal stalk protein P1 alpha, involved in the interaction between translational elongation factors and the ribosome; accumulation of P1 in the cytoplasm is regulated by phosphorylation and interaction with the P2 stalk component; Rpp1ap [Saccharomyces cerevisiae]
K.LLTLTNAANVPVENIWADIFAK.A +2		3.7712	4.9401	4.8595	4.8082	4.5445	4.8922	4.6226	4.4421		2.5234	3.9866	4.6548	4.3876	4.2042	4.1729		3.5251	3.1828	3.8019					
K.LLTLTNAANVPVENIWADIFAK.A +3		5.9389	6.2286	6.4914	6.286	6.2769	6.2368	6.2466	5.7913		4.493	5.9546	6.028	5.6278	5.6845	5.5953		5.2765	3.9841	5.3874					
	1	X	X	X	X	X	X	X	X		X	X	X	X	X	X		X	X	X					
gi|6323246|ref|NP_013317.1|							6.7		18.1		8.1	11.6	16.4	14.6	18.9	27.8	17.5	14	6.5	15.4	14.6	13.7	13.7	11.3	Peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; binds to Hsp82p and contributes to chaperone activity; Cpr6p [Saccharomyces cerevisiae]
K.DFM*CQFGDFTNFNGTGGESIYDEK.F +2									3.3687							2.9426					3.9128				
K.DFMCQFGDFTNFNGTGGESIYDEK.F +2									2.9502								3.7331	2.5716				2.8115		4.0014	
K.FEDENFTVK.H +2																						3.1073			
K.HVVFGEVIQGK.R +2													3.7712	3.9747	3.4699	3.248	3.233		2.7413	3.6016					
K.IDDCGVLPDDYQVPENAEATPTDEYGDNYEDVLKQDEK.V +3																4.5806									
K.NFDTVLK.A +1													2.1784												
K.NIGTEQFK.K +1																							2.053		
K.QVLVASSEVLYAEAADEK.A +2									3.606		2.9685	5.364	5.5945	5.6662	5.0962	5.3426	4.5767			3.8665	4.9447	5.7337	3.6061	5.3135	
K.VSIPLNIAICALK.L +2							2.9545		2.7684			2.9448	3.3561	3.0924	2.9565				2.9991				2.7727		
R.IVFELYNDIVPK.T +2							3.2426		3.8475		3.8936	3.5677	4.2482	3.6994	3.9854	3.6634	3.1401	3.3709		3.657	3.3658		3.7028		
R.LIENQQCDQENNKPLR.D +2															3.3753			4.3848		4.1168					
	1						X		X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6320332|ref|NP_010412.1|						2.1			2.8		1.8	5.5	13.7	12.3	8.7	8.9	4.2	7.7	5	13	4.2	1.6	6.2	3.9	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids; Aro1p [Saccharomyces cerevisiae]
K.AQLEDYLLVEGCTR.D +2														3.1236					2.8014						
K.ATDSIPIIFTVR.T +2													2.7202	3.2869						2.5435	3.0225				
K.CYGDSAQFVSDEDLR.F +2						4.9595			4.0089		4.3552						4.238								
K.EVIQNYGDDGYVFSTGGGIVESAESR.K +2																2.8256								2.5582	
K.FGINVETSTTEPYTYYIPK.G +2						4.3541							3.7458	3.9493	2.9784	3.0195				3.2027			4.8211		
K.FVGTAVNFEDNLR.L +2													2.759		4.0458	3.2482	2.6448	3.2248		2.9738					
K.GDNTDWLGIR.N +2														3.1096		2.9603			2.6258					2.6136	
K.HCPSSTYVICNDTNLSK.V +2																		2.6275							
K.HMLTAVHELK.G +2																				2.5822					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.IEYLNNEGSLPIK.V +2																						4.0928	3.0509		
K.ILVAYGLPVSPDEK.W +2												3.9724	4.1452	4.0733				2.8359		4.6791					
K.ITQTATSTTVSGPPVGTLKPLK.H +3													3.6194												
K.LDIM*QYMDELTDAAK.V +2																					2.7585				
K.NFGGAAVTIPLK.L +2												3.2088	2.7884	3.2589											
K.NFIGAFWQPK.F +2												3.4077		3.4709											
K.TACIWNADEFTR.L +2												3.0458				3.1629				2.6418					
K.TPLDILLK.K +2																			2.5052						
K.TTELPDGIQVHGLNSIK.D +2									3.2995				4.3696	3.7465											
K.VIGAVNTVIPLGNK.K +2											2.9813	3.0524	4.6496	4.3799	4.0089	3.8834		4.1749		4.0326	3.2915				
K.VIGAVNTVIPLGNKK.F +2													2.7126												
K.VPYYQQLVLEFK.A +2																				3.4397					
R.AALYALHSLGCK.K +2													3.7827	3.7487	3.7556	3.0496			2.8646	3.7866					
R.ALILAALGEGQCK.I +2									3.6721			3.6888	3.2895	3.5931	3.5969	3.7821	3.8101	3.9176		3.2266	3.6427	3.4569	4.0781	3.5197	
R.FILTDETLVYPFK.D +2													3.3786	3.996	3.7864	3.7765	3.3723	3.2618			2.7835		3.7737	3.5185	
R.FLTSLAALVNSTSSQK.Y +2																			4.5115	2.6883					
R.FNQALTLDVDVVK.F +2												3.1151		3.3991	4.067										
R.ILAMATELAK.F +2																				2.9419			2.6015		
R.LESNASLFLNVVNGAK.N +2																				2.7015					
R.LLTYVVKPGETSK.S +2																	2.9062	2.5652							
R.PIAPLVDSLR.A +2													2.9758	3.0706	2.7453	2.5086									
R.VDHLANYSADFVSK.Q +2													4.4118					4.0457		2.9167					
R.VVQVPTSLLAM*VDSSIGGK.T +2													3.7688		2.8612				4.6163						
R.VVQVPTSLLAMVDSSIGGK.T +2																				2.7402			3.8929		
R.YFGILSPTQVAR.L +2													3.3562	3.3973	3.2344			3.3537					2.8165		
	1					X			X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6319698|ref|NP_009780.1|						12.8	9.8		28.7	9.8	19.7	24.6	19.9	29.5	18	19.9			9.6	13.1	12.8	15.8	17.2	10.9	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex, which is an evolutionarily-conserved multi-protein complex found in mitochondria; Pdb1p [Saccharomyces cerevisiae]
K.ELEDFAFPDTPTIVK.A +2						4.3247	4.0888		3.1841	3.3054	3.3724	4.0888	4.1377	3.5069	3.5695	3.8314				3.7246	3.9444	3.4705			
K.KYGVSAEVINLR.S +2																				2.7347					
K.YGVSAEVINLR.S +2									3.31		3.313	2.9448	3.2923	3.2688	3.1645	3.2673						2.956	3.1739		
R.DDDVFLIGEEVAQYNGAYK.V +2						4.1716			4.8323			3.4763		4.239	4.9097						5.159	2.637	2.5313	2.9663	
R.EALNSAMAEELDR.D +2						3.4621			3.6721		3.5497										3.4298	3.5948			
R.EGTDISIVTYTR.N +2												3.1061				3.2138									
R.GPNGAAVGVGAQHSQDFSPWYGSIPGLK.V +3														3.9314											
R.NVQFSLEAAEILQK.K +2									3.6395				4.4968	3.6759		2.9417			3.0925						
R.VTGADVPTPYAK.E +2									2.6178		3.0156	2.7086	3.3544										3.1612		
R.VVDTPITEYGFTGLAVGAALK.G +2							5.9231		5.834	2.6361	3.2094	5.3616	6.0437	5.4345	6.0764	6.3758			3.9086	5.3799			6.1739	4.4516	
R.VVDTPITEYGFTGLAVGAALK.G +3															4.1849								3.9185		
	1					X	X		X	X	X	X	X	X	X	X			X	X	X	X	X	X	
gi|6323562|ref|NP_013633.1|							12.6	12.6	28.6		19.8	19.8	18.1	28	30.2	31.3	25.3	23.1		34.6	12.6	18.1	24.7	18.1	Mitochondrial peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; involved in protein refolding after import into mitochondria; Cpr3p [Saccharomyces cerevisiae]
K.AIESYGTASGKPR.A +2											3.0137	2.6101	3.1831	3.0487	2.5409	3.0745	3.1328			3.0126			2.638		
K.FADENFVK.K +2									2.76											3.0912					
K.HVVFGEVTK.G +1																		2.8081		2.309					
K.HVVFGEVTK.G +2													2.6205	2.8342	2.5321										
K.HVVFGEVTKGMDIVK.A +2														2.8484											
K.VFFDPAVNGTK.I +2							2.8437	2.5993	2.9494		2.7448	2.7109	3.3918	3.2193		3.4682					2.833		2.8946		
R.IEFELYDNVVPK.T +2							4.1456	4.1934	3.5794		3.2836	3.4436		2.8113	2.5465	3.0884	3.3563	3.6621		3.8638	3.5518	4.1095		4.1852	
R.IIPDFM*QGGDTDLTNGFGGK.S +2															2.9269										
R.IIPDFMQGGDTDLTNGFGGK.S +2									3.2821							4.2374	4.9588	4.2137		3.6269		2.93	3.4675	4.1766	
	1						X	X	X		X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6322707|ref|NP_012780.1|					21.5	16	16	17.4	21.5			16	12.3	17.8	16	40.2	16			22.8	21.5	16	16	21.5	Putative mitochondrial ribosomal protein, has similarity to E. coli ribosomal protein S2; Mrp8p [Saccharomyces cerevisiae]
K.DDDDVIAPLPNADGDIPAISDGVFPK.S +2								2.8744								2.7182									
K.DELDDAFNDVAR.Y +2					4.0026											4.0275					4.0838	3.9187	4.3829	4.8328	
K.ELQGELNFIEER.S +2									2.9087				3.1061	3.7392		2.8652									
K.EQEDFENFLEGK.V +2					3.1474	3.1593	3.1035	3.1403	3.0809			2.9986		3.0847	3.3451	3.2038	2.7584			2.917	2.6445			2.6213	
K.FSKDELDDAFNDVAR.Y +2													2.6354	3.338		3.5445				3.0049					
K.SGSATQFDATDFATNEDLVELVK.E +2					4.2851	4.4563	4.5778		4.3405			3.5328			4.696	6.1946	4.0387			2.727	4.9238	5.5566	5.6843	3.425	
	1				X	X	X	X	X			X	X	X	X	X	X			X	X	X	X	X	
gi|6325290|ref|NP_015358.1|		1.6		1.6	1.6		7.5		11			7.5	9.7	11.9	15.9		9.9	11.2	5.7	12.3		12.1	13.6	7.1	Cytoplasmic and mitochondrial histidine tRNA synthetase; encoded by a single nuclear gene that specifies two messages; efficient mitochondrial localization requires both a presequence and an amino-terminal sequence; Hts1p [Saccharomyces cerevisiae]
K.AGCHIAVILGK.E +2															3.1851										
K.DWADSDMVIR.E +2																	3.5867	3.0534							
K.DWTGYLPER.M +2																		2.5131							
K.HGGVTIDTPVFELR.E +2																				3.7					
K.ILDGIFQIAGVK.D +2														2.5006					3.3327						
K.LIYNLEDQGGELCSLR.Y +2							2.8179		4.9292			3.2974	4.5698	5.1508	2.9138		3.1565					4.0679	5.3803		
K.LSQIHEDGLNEVTR.L +2																		3.8029							
K.SAEDASEFVGVGSIAAGGR.Y +2									5.2145								5.208	4.8475	5.3996	2.9344			5.0691		
R.EAIFSTLSGLFK.K +2													3.3813	3.766	3.5391										
R.LGQEFADDDGELVSAADIVPIVQEK.L +2							3.5487		2.8111											2.5037		4.5611	3.8109	4.356	
R.LGQEFADDDGELVSAADIVPIVQEK.L +3												3.6027	4.246	5.1514	3.5339										
R.YDLTVPFAR.Y +2	3.4396		3.3903	3.2575											2.6116		3.4285	3.1837		2.754					
R.YDNLVNM*FSEASGK.K +2																									
R.YDNLVNMFSEASGK.K +2															3.8082							4.2346	4.464	3.5773	
R.YVAMNNIQSIK.R +2																						2.7615			
	1	X	X	X			X		X			X	X	X	X		X	X	X	X		X	X	X	
gi|6319351|ref|NP_009434.1|						6.9	6.9		6.9	4.5	6.9	6.9	6.9	6.9	6.9	6.9	9.9		6.9	12.2		6.4	9.9	12.2	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2; Pho11p [Saccharomyces cerevisiae]
gi|6322011|ref|NP_012087.1|						X	X		X	X	X	X	X	X	X	X	X	X	X	X		X	X	X	One of three repressible acid phosphatases, a glycoprotein that is transported to the cell surface by the secretory pathway; nearly identical to Pho11p; upregulated by phosphate starvation; Pho12p [Saccharomyces cerevisiae]
K.NLEMETTLANSVNVLNPYTGEM*NAK.R +2																								3.0513	
K.NLEMETTLANSVNVLNPYTGEMNAK.R +2																	2.5559			2.8775			4.1116	4.2129	
R.FSYGQDLETYYQTGPGYDVVR.S +2						5.3743	5.4223		6.0176	4.7383	5.166	5.5312	5.5137	5.7253	5.3535	6.0659	4.4109		5.1933	4.9867		5.6137	6.1267	5.4513	
R.FSYGQDLETYYQTGPGYDVVR.S +3														3.5326											
R.GYSDICNIFTK.D +2						3.7447	3.6079		3.9013		3.1589	3.7122	3.4037	3.6731	3.8207	3.7618			3.5363	3.7138				3.7614	
R.SWYVPQGAR.V +2																						2.5915			
	1					X	X		X	X	X	X	X	X	X	X	X		X	X		X	X	X	
gi|37362609|ref|NP_009355.2|					20.6	20.6	20.6	8.2	20.6		20.6	20.6	20.6	28.8	20.6	20.6		20.6		20.6		12.4	17.1	12.4	H subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv3p [Saccharomyces cerevisiae]
K.LGEGVNVEQVEGLM*SLEQYEK.T +2						4.6277			5.0071		2.7806	4.8565	6.2041	5.7101	5.2542					3.0435		2.7389		3.9975	
K.LGEGVNVEQVEGLM*SLEQYEK.T +3													4.3211												
K.LGEGVNVEQVEGLMSLEQYEK.T +2					5.7329	5.8171	5.9019		5.6015		3.8097	4.8531			4.218	5.9027				4.7356		4.5559	4.3163	4.5795	
K.LGEGVNVEQVEGLMSLEQYEK.T +3																		3.5165							
K.LPFLYSSQGPQAVR.Y +2					3.7947	3.2032	3.1344	3.4349	4.2313		2.5408	4.0235	3.9983	4.0902	3.9646	3.2678				3.5007					
K.TAFVGITK.Y +1																							2.1731		
R.YTSQHEWIAVHQDK.T +2														3.049				4.1288							
	1				X	X	X	X	X		X	X	X	X	X	X		X		X		X	X	X	
gi|6324250|ref|NP_014320.1|			16.6	16.6			9	9	27.6		21.1	16.6	27.1	22.6	20.1	26.6	16.1	24.6		24.1	13.1			17.6	Major isoform of tropomyosin; binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; acetylated by the NatB complex and acetylated form binds actin most efficiently; Tpm1p [Saccharomyces cerevisiae]
K.DLEQENVEK.E +1																		2.405							
K.DLEQENVEK.E +2							3.0123	2.9313			3.1155	2.9856			2.5493	2.593	2.6907	2.5317							
K.ELDEIAASLENL.- +2									4.1066					3.3492	2.5732	3.3415		4.705			2.6565			2.7095	
K.ENQIKSLTVKNQQLEDEIEKLEAGLSDSK.Q +3									3.6066																
K.KELDEIAASLENL.- +2													4.0564	3.3147											
K.KNQQLEEDLEESDTK.L +2																				4.8835					
K.LEAELAESK.Q +1																									
K.LEAESWQEK.Y +2											2.7389					3.2372									

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.LEAESWQEKYEELK.E +2																		3.6774		2.8097					
K.LEAGLSDSK.Q +1													2.416	2.3431	2.1759	2.204	1.8371							2.4148	
K.LEAGLSDSK.Q +2							2.9342	2.9916																	
K.NQQLEDEIEK.L +2											3.0021	3.2728	3.1811		2.7452										
K.NQQLEDEIEKLEAGLSDSK.Q +2			6.3546												4.2328										
K.NQQLEDEIEKLEAGLSDSK.Q +3		4.6188												4.1408						3.6969					
K.NQQLEEDLEESDTK.L +2		5.6406	5.5161						5.3465		5.262	5.4757	5.6862			5.4052	5.5376	5.4322		5.7439	5.2432			5.1988	
R.VAALEEQR.E +2													2.6119												
R.VAALEEQREEWER.K +2														2.8611											
	1	X	X				X	X	X		X	X	X	X	X	X	X	X		X	X			X	
gi|6319602|ref|NP_009684.1|					2.2	4.2	5.3		4.8			12.5	13.7	7.1	15.4	11.9	11.7	18.6	10.1	19.8	14.7	13.5	9.7		Synthase subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; also found in a monomeric form; expression is induced by the stress response and repressed by the Ras-cAMP pathway; Tps1p [Saccharomyces cerevisiae]
K.AQLTSSSGGNIIVVSNR.L +2												3.2475			3.8476			3.8679			4.8524	4.3611			
K.GVLSCDLVGFHTYDYAR.H +2													5.4722		4.5847					3.6199					
K.IIVGVDRLDYIK.G +2																	2.5999								
K.NSSTGQYEYAM*SSGGLVTALEGLK.K +2																3.4631			3.4897		3.1419	4.9076			
K.NSSTGQYEYAMSSGGLVTALEGLK.K +2																		4.0411		3.5414		4.8073	3.1071		
K.VVLVQVAVPSR.G +2					3.0161	3.5911	3.0586					3.4294	3.5997	3.6143	3.8898	3.6918		4.0578	3.3129	3.0114					
K.WFGWPGLEIPDDEK.D +2																	3.6163	2.9425		2.9472					
R.DGM*NLVSYEYIACQEEK.K +2																					4.2541				
R.DGMNLVSYEYIACQEEK.K +2																	3.0689	4.3138		3.3772	3.3346	3.7154			
R.FVNVGAFPIGIDVDK.F +2							4.585		4.4028			4.1563	4.3015	4.6011	4.5741	4.4809	4.4918		3.4268	4.194	3.2265		4.1485		
R.GDVEEYQYLR.S +2						3.2108						2.8606													
R.SVVNELVGR.I +2									2.5889			2.5767	2.6675	2.9411		2.7201		2.8866				2.519	2.6826		
R.VLNVNTLPNGVEYQGR.F +2													4.8012		2.6923										
	1				X	X	X		X			X	X	X	X	X	X	X	X	X	X	X	X		
gi|6323746|ref|NP_013817.1|						9.1	10.8	8.8	29.3	14.1	21.2	26.3	20.9	20.9	22.2	27.9	26.3	6.7		11.4	13.1		13.1		Glucose-6-phosphate 1-epimerase (hexose-6-phosphate mutarotase), likely involved in carbohydrate metabolism; GFP-fusion protein localizes to the nucleus and cytoplasm; mutants show increased resistance to fluconazole; Ymr099cp [Saccharomyces cerevisiae]
K.ENPPTVQFGLKPEIANPELTK.L +2																3.4877	4.1901								
K.EVVLTHPADETTSVHILK.Y +2																	3.2276			2.6596					
K.GVQIHTLK.R +2																		2.8079							
K.SEEQLWLSTAAK.L +2						4.347			4.417		3.6095	2.8922	3.0382	4.4312		4.3101	4.3054	3.9397			4.8052		4.5951		
K.TAIEVENTSSSK.E +2							3.2632		3.1867			3.0633	3.5806	2.7965	2.8682	2.9948									
K.WNAYQLLCK.E +2							2.6987		2.5966		3.01														
R.GGIPLVFPVFGK.N +2									2.8718			3.1684	3.4611	3.3905	3.1009	3.0121	2.9049								
R.IEDIEGTM*VSNLAGM*K.L +2															3.2145						3.1263				
R.IEDIEGTMVSNLAGM*K.L +2										2.5529		3.349			2.5097								4.0549		
R.IEDIEGTMVSNLAGMK.L +2									4.6502		2.5587	2.9159			3.3996					3.3324					
R.NSTWEFLGQIL.E +2							3.333	3.6635	3.5001	2.5543	3.1203	3.0918	3.5521	3.5566		3.4414					3.3911		3.6709		
R.YNLPDTVVWNPWIEK.S +2						4.2848		4.635	4.9127	3.9786	3.479	3.7147	4.5618	4.99	4.7795	5.1725	3.0384								
	1					X	X	X	X	X	X	X	X	X	X	X	X	X		X	X		X		
gi|6322896|ref|NP_012969.1|										14.8	20.3	11.4	20.3	17.7	20.3	17.7	19.9	8.1	14.8	12.2	14.8	19.6	8.9	10.7	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ykr043cp [Saccharomyces cerevisiae]
K.CETIEEIQNVK.S +2											3.319												4.2924	4.0189	
K.SGQYTGLTDLPLTPYGEGQM*LR.T +2										3.0814					4.0291			3.1388	4.3339		3.0435				
K.SGQYTGLTDLPLTPYGEGQM*LR.T +3													3.8361												
K.SGQYTGLTDLPLTPYGEGQMLR.T +2																		4.2142				4.42			
K.SYDDDTVPYVK.L +2											2.8248														
R.DGCENGETTQQIGLR.L +2											4.6899		4.799	4.253		5.0487	4.8632			4.1294					
R.EWEYGDYEGMLTR.E +2												2.5931										3.8945	3.9861		
R.NNQFLNPDNITYIFTSPR.L +2										2.5383	3.4097	2.6182		4.1184	2.9443	5.1623	4.2432		4.3027	4.5275	2.6218	2.9439		2.5235	
R.NNQFLNPDNITYIFTSPR.L +3													3.5348	3.5602											
R.QTVDLVLKPLSDEQR.A +2														3.2982	2.7596	3.5067									
R.VVVDDDLREWEYGDYEGMLTR.E +2																	2.6796								
	1									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|6324911|ref|NP_014980.1|									3.8		4.2	2.9	9.9	11.1	8.2	7.9	7.8	6.9	8.2	7.3	5.7	5.3	6.8	5.5	Cytoplasmic alanyl-tRNA synthetase, required for protein synthesis; point mutation (cdc64-1 allele) causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog; Ala1p [Saccharomyces cerevisiae]
K.DAVDDLESLFK.E +2													3.3354	3.5766	3.4707		2.7377	3.1598	2.505		3.3357	3.0314	2.3298	3.1079	
K.GNVFQGM*GDKPAAIK.D +2																			2.5334						
K.KVSSIKGGK.A +2																				2.7565					
K.LGLEPDTEAR.E +2													2.8403					2.8063							
K.LNVHELSELNDAK.V +2														4.1144				3.3845							
K.NVGVPDDHILPGNAK.D +2													2.9059	2.9714											
K.PIFLGTVDPASDFYTLK.R +2																			3.7478	2.5182					
K.SIYLLAGNDPEGR.Y +2																		3.1632			4.0791				
K.TCFYAEQGGQEYDTGK.I +2																						5.056	4.1512	5.8299	
K.TFFETNENAPYLVK.F +2									4.1902		2.9928	3.7819	4.3617	3.9116	4.1692	4.3785				4.125					
K.YFVILEESGIAK.G +2																						3.6812			
K.YGSANVEGTILK.L +2											3.3318											2.959	3.1445		
R.AVFGETYPDPVR.V +2															2.8393	3.1852							3.0454	2.9295	
R.IQEITSVRPYSGNFGENDK.D +2																		2.7524	3.792	2.9893					
R.IVAVTGTEAFEAQR.L +2															4.1135	3.431	5.2218				4.629		5.1352	4.7692	
R.LAEQFAADLDAADK.L +2														2.8768			4.1789								
R.LYDTYGFPVDLTELM*AEEQGLK.I +2																2.9246									
R.LYDTYGFPVDLTELMAEEQGLK.I +2									2.5009								2.738								
R.LYVTYFEGDEK.L +2														3.3675						3.1333					
R.SNYDTDVFTPLFER.I +2											2.9423	3.376	4.48	4.4454	4.7294	5.1018	2.8365								
R.TLTFALADGGVPNNEGR.G +2													4.3189						2.6614		2.7178				
R.VAHGCYISNAALAK.G +2													4.3758	4.306	3.2767										
	1								X		X	X	X	X	X	X	X	X	X	X	X	X	X	X	
gi|20336767|ref|NP_620387.1|							0.5		2		1.3	1.3	2	3.1	1.1	2	1.1	1.5		1.5	2.1	1.1	2	1.1	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ydr210c-dp [Saccharomyces cerevisiae]
gi|7839178|ref|NP_058165.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ygr161c-dp [Saccharomyces cerevisiae]
gi|7839173|ref|NP_058160.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ygr038c-bp [Saccharomyces cerevisiae]
gi|7839171|ref|NP_058158.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ygr027w-bp [Saccharomyces cerevisiae]
gi|7839164|ref|NP_058152.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ydr365w-bp [Saccharomyces cerevisiae]
gi|7839162|ref|NP_058150.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ydr316w-bp [Saccharomyces cerevisiae]
gi|7839160|ref|NP_058148.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; in YDRCTY1-3 TYB is mutant and probably non-functional; Ydr261c-dp [Saccharomyces cerevisiae]
gi|7839152|ref|NP_058140.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ydr098c-bp [Saccharomyces cerevisiae]
gi|6321008|ref|NP_011087.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Yer160cp [Saccharomyces cerevisiae]
gi|6320985|ref|NP_011064.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Yer138cp [Saccharomyces cerevisiae]
gi|6319486|ref|NP_009567.1|							X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes; Ybr012w-bp [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.DILSVDYTDIM*K.I +2									3.3824				3.4852	3.9588		2.7519				2.8592	3.9005	3.4515	3.7759	3.758	
K.DILSVDYTDIMK.I +2															3.0669	3.2763	3.5861	3.584			2.9941	3.6174	4.0746	4.0565	
K.EVHTNQDPLDVSASK.I +2									3.4929		3.0701	3.035	4.0797	4.1042		3.7934		4.3925		4.1573			2.9099		
K.FLQNSNLGGIIPTVNGKPVR.Q +2														3.0602											
K.VACQLIM*R.G +2							2.5197						2.9027	2.7927	2.8516						2.8702				
K.VACQLIMR.G +2							2.9823		2.9715		2.8153	2.9761	2.9769	3.0626	2.5653	2.871	2.5061				2.6119	2.6608	2.9694	2.5911	
R.LDQFNYDALTFDEDLNR.L +2																					2.9768				
	1						X		X		X	X	X	X	X	X	X	X		X	X	X	X	X	
gi|6321430|ref|NP_011507.1|					6.5	3.6	3.8					6.1	5.6	8.2	4.5	3.3	4.5	3.2	2.4	6.4		9	3.1	5.7	Plasma membrane H+-ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases; Pma1p [Saccharomyces cerevisiae]
K.HYGDQTFSSSTVK.R +2							3.0601							3.2064								4.0935			
K.KADTGIAVEGATDAAR.S +2																		4.5495							
K.KVTAVVESPEGER.I +2																	3.6004			3.8031		2.7858			
K.LSAIESLAGVEILCSDK.T +2					3.3489								3.5584	4.317	4.3593					3.3505		4.1971			
K.TLANTAVVIR.D +2					2.7135							2.6646	2.6243			3.1283	2.5356		2.7541				2.6891		
K.VLEFHPFDPVSK.K +2													2.6873						3.1053						
K.VTAVVESPEGER.I +2													4.1298							3.4347				3.2928	
R.GEGFMVVTATGDNTFVGR.A +2																							4.2153		
R.GYLVAMTGDGVNDAPSLK.K +2																	3.3013			3.2532		2.6987		2.6871	
R.IVTEDCFLQIDQSAITGESLAVDK.H +2												2.6074													
R.IVTEDCFLQIDQSAITGESLAVDK.H +3															4.0436										
R.LGLGGGGDM*PGSELADFVENADGFAEVFPQHK.Y +3														4.5408											
R.PVPEEYLQTDPSYGLTSDEVLK.R +2					3.5137	3.7214	2.8409					2.5559								4.2489				3.3684	
R.QLGLGTNIYNAER.L +2														2.8349				2.7585							
R.SAADIVFLAPGLSAIIDALK.T +2																3.0959									
R.SVEDFMAAMQR.V +2					2.6344	2.9966														3.5223					
	1				X	X	X					X	X	X	X	X	X	X	X	X		X	X	X	
gi|6324702|ref|NP_014771.1|						6.3			8.6	4.4	14.9	13.1	11.6	14	8.9	8.4	8.6		7.5	5.4		8.6	4.4	4.4	Phosphoribosylaminoimidazole carboxylase, catalyzes a step in the 'de novo' purine nucleotide biosynthetic pathway; red pigment accumulates in mutant cells deprived of adenine; Ade2p [Saccharomyces cerevisiae]
K.DFGVPEVTIVSAHR.T +2													3.011												
K.DNICDLCYAPAR.V +2											4.0234									2.947		2.8476			
K.EMIPEALEVLK.D +2																2.5286									
K.GSCLDGVDSLHSIVQM*PR.G +2																			3.9301						
K.GSCLDGVDSLHSIVQMPR.G +2																	3.3699								
K.LETVGYEAYLENK.- +2									3.7999	3.1759	3.5427	3.6624	2.6145	3.1582	3.4075	3.458			2.8822			4.4872	4.639	3.5632	
K.NGIAVTQSVPVEQASETSLLNVGR.D +2						3.4672			3.7031		2.8759	3.1944			3.0267	3.8062						2.9035			
K.NGIAVTQSVPVEQASETSLLNVGR.D +3														3.6008											
K.TVILDAENSPAK.Q +2						3.5259			3.5512	3.4178	3.7791	3.0839	4.2476												
K.VGHINIIASSMAECEQR.L +2																	4.3336			5.2264					
R.ALATPGSSVYLYGK.E +2												2.7754	3.2914	3.006	2.9221		3.0802			3.6465					
R.LLGAYDSSYTTK.M +2											3.5128														
R.SVNGLVFSYPIVETIHK.D +2														3.288											
R.TVGILGGGQLGR.M +2											3.6309	3.5407	3.4101	3.3381					4.0011					3.7294	
	1					X			X	X	X	X	X	X	X	X	X		X	X		X	X	X	
gi|6319424|ref|NP_009506.1|	0.9		0.9	0.9					1.9		1.9	2.8	3	5	1.9		5.9		2.3	2.8		4	5.8	1.9	Key endocytic protein involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; Ede1p [Saccharomyces cerevisiae]
K.EQITNLNSMTASLQSQLNEK.Q +2																						5.1379	3.6381		
K.FVETTVENSNLNVNR.V +2																	4.1215								
K.GFLNLNEFSAALR.M +2	3.1881		4.1337	3.725									3.2137						3.8209	3.0536					
K.KQQFDAIFDSLDK.Q +2														2.7894											
K.LNELTTDLQESQTK.N +2											3.9261	3.876	4.3497	3.6526											
K.LQEMFDDLSQR.K +2												2.8004								2.7912		3.2481	3.2039		
K.LQEMFDDLSQRK.A +2																	2.962								
K.QTEQLEAQVLQVNK.E +2									3.5695			2.8746					3.3574			4.2489					
K.TVEEQHAQLQAK.Y +2																							3.2331		
K.VATPSIPQQPIPLK.N +2													2.5758	3.0445	3.1403										
K.YPAPGTSPSHNEGNSK.K +2														2.515											
R.DDVELPETLEER.D +2											2.823									3.4156		2.6036	2.7831		
R.DNTGNLSHIPGEWEATPATASTDVLSNETTEVIEDGSTTK.R +3																	4.8484								
R.FDGDLNEYGIPR.S +2									2.9366					2.8624	2.6275					2.9907					
R.LEPVVVNQPNR.T +2																							2.6135		
R.LSTGAFSNAASDWSLSFEK.K +2																			3.5542						
R.TPLSSQEQAFYNQK.F +2																							5.4638	4.217	
	1 X		X	X					X		X	X	X	X	X		X		X	X		X	X	X	
gi|6324291|ref|NP_014361.1|					5	14.4	8.6	10	25.3	7.8	7.8	8.6	12.8	14.7	22.8	20.3						8.1	8.1	8.6	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase, which catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle; Idh1p [Saccharomyces cerevisiae]
K.EGVYEAVESLK.R +2						2.8177																2.7487	2.7263		
K.EGVYEAVESLKR.N +2														2.5294											
R.DIGGSSSSTTDFTNEIINK.L +2					5.5048	5.3695	5.5326	5.8326	5.4049	4.7911	4.3528	4.6875		4.9269	4.8106	5.7153				4.8818		4.0907	4.441		
R.DYAVFEPGSR.H +2						2.6998				2.6928	2.7748														
R.ENTEGERSGLEHESVPGVVESLK.V +2									3.8146				4.1558		3.4811	4.2242									
R.FTVTLIPGDGVGK.E +2						3.2406	3.4047		3.6444			2.7147	3.4704	3.8413	3.3734	3.7452								2.9763	
R.IPDIDLIVIR.E +2									3.1894				3.6169	3.8169	3.3425	3.6191									
R.NIITEIGQK.E +2									3.0304							3.0276									
R.TIFEAENIPIDWETINIK.Q +2								3.9984	4.2944						3.4264										
	1				X	X	X	X	X	X	X	X	X	X	X	X						X	X	X	
gi|6320846|ref|NP_010925.1|			19.2		12.8	19.2	12.8	12.8	12.8	19.2	12.8	12.8		19.2	12.8	12.8				12.8			12.8	12.8	Nuclear envelope protein, interacts with GDP-bound Gsp1p and with proteins of the nuclear pore to transport Gsp1p into the nucleus where it is an essential player in nucleocytoplasmic transport; Ntf2p [Saccharomyces cerevisiae]
K.VSLPFQK.V +2														2.6248											
R.NESM*LTFETSQLQGAK.D +2					4.8086	5.1807		4.5354	5.2482	4.8026	4.484	5.2149		5.2721	5.2254	5.4589				5.6515			4.9974	4.8829	
R.NESMLTFETSQLQGAK.D +2			5.53		5.6917	5.7662	5.843	5.6745	5.5517	4.5019	5.8149	5.2635		5.5878	5.6951	5.8167				5.9526			5.2193	4.0272	
R.SQLGNLYR.N +2			2.5138			2.6421				2.529															
	1		X		X	X	X	X	X	X	X	X		X	X	X				X			X	X	
gi|6320576|ref|NP_010656.1|						7.1			21.5		13.1	18.3	16	21.2	21.5	21.5	31.4	15.1	18.3	21.5	9.6	10.3		5.8	2-methylbutyraldehyde reductase, may be involved in isoleucine catabolism; Ypr1p [Saccharomyces cerevisiae]
K.GIVVEAYSPFGSANAPLLK.E +2									4.4401		2.7965	3.4373	3.9747	4.7981	4.5041	4.6413	3.2628		4.6058	3.6921					
K.IFTLPEDDFK.T +2																	3.0326								
K.LNTGASIPVLGFGTWR.S +2									3.7394			3.3689	3.4552		3.3529	3.2271	2.7085		2.7506	2.7653					
K.TWELMQELPK.T +2									3.801					3.4321	3.7074	3.6866		3.5609		3.3396		3.8473		3.4783	
R.DPEAALNK.S +1																					2.0556			2.4211	
R.HIDAAAIYLNEEEVGR.A +2																	4.659								
R.SVDNNGYHSVIAALK.A +2													2.7207	2.9809			3.8953	3.6295							
R.VTDGNVLCIPTLEDGTVDIDTK.E +2						4.8374			5.0107		3.7348	4.7776		4.6948	4.5025	4.5407	4.7372	4.2958	4.6635	3.9185	4.587	4.1408			
	1					X			X		X	X	X	X	X	X	X	X	X	X	X	X		X	
gi|6319378|ref|NP_009460.1|		10	16.9		16.2		6.2	10	16.2		13.8	23.8	17.7		23.8	17.7	17.7	17.7		17.7				13.8	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; overexpression disrupts telomeric silencing; Rpl32p [Saccharomyces cerevisiae]
K.DLETLTM*HTK.T +2											3.0197	3.123													
K.DLETLTMHTK.T +2											3.1656	2.8096	3.3197		3.2433	3.1033	3.1977	2.9904		3.5399				2.7268	
K.TFLVANVK.D +1					1.9147		1.9742				2.0853	1.9892													
K.TFLVANVK.D +2					2.7647		2.7077		2.6396		2.5584				2.6963									2.6147	
K.TYAAEIAHNISAK.N +1																	2.6748								
K.TYAAEIAHNISAK.N +2		4.6474	4.7372		3.7582			4.8916	4.4635			3.7751	3.5565		4.3217	4.5371	4.3992	4.386		4.3865					
R.FRGNISQPK.I +2			2.5052																						
	1	X	X		X		X	X	X		X	X	X		X	X	X	X		X				X	
gi|6324298|ref|NP_014368.1|				18.4		21.4	29.1	28.2	33			21.4		29.1	29.1	28.2	33	23.3	31.1	21.4		21.4	21.4		One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity; Hhf2p [Saccharomyces cerevisiae]
K.SFLESVIR.D +2							2.5738							2.501	2.6527				2.5669						
K.TVTSLDVVYALK.R +2							3.9913		3.5105			3.6912		4.0146	3.9011	4.1549	3.6992	3.899	2.9731	3.6943		3.9408	2.9898		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.DNIQGITKPAIR.R +2				3.095		3.4119		3.2475	3.2352								2.9032	3.3433	2.9977						
R.ISGLIYEEVR.A +2						3.8536	3.891	3.8594	3.9624			3.9426		3.824	4.0572	3.9896	3.2367			3.3595		4.213	4.1045		
R.TLYGFGG.- +1				2.2024				1.9244								1.8436									
	1			X		X	X	X	X			X		X	X	X	X	X	X	X		X	X		
gi|6324982|ref|NP_015050.1|					8.6	12	11.7	12	11.1		8.3	12	7.1	24.6	7.7	15.7		8.9		8.9	10.2		7.7		S-adenosylmethionine-homocysteine methyltransferase, functions along with Mht1p in the conversion of S-adenosylmethionine (AdoMet) to methionine to control the methionine/AdoMet ratio; Sam4p [Saccharomyces cerevisiae]
K.AILSWDESILSR.P +2							2.7006		2.5371		2.6217		3.3344	3.2738	3.1403	2.9923							3.1576		
K.KVLVLDGGQGTELENR.G +2																		4.2564							
K.LDLIGFETIPNIHELK.A +2														4.1897						3.3149					
K.VLVLDGGQGTELENR.G +2					5.0278	3.5675	2.9497	5.3809			3.3479	4.1775				4.2779									
R.DGTTM*EEIAQVIK.D +2								3.1246				3.0168			2.9394			3.8385							
R.DGTTMEEIAQVIK.D +2					4.1814	4.1583		4.2739	3.8753			4.1938		3.9787	4.4993	3.9999		3.8634		4.1207	4.0632		4.2484		
R.EFTGDYGAEPENIDFYQYFK.P +2																					3.0109				
R.EFTGDYGAEPENIDFYQYFKPQLENFNK.N +3														4.5287											
R.TLSEYNNLLNR.I +2						3.1736	3.4171	3.1388	3.2234			2.8938	3.1286	3.1648		2.8531									
	1				X	X	X	X	X		X	X	X	X	X	X		X		X	X		X		
gi|6319552|ref|NP_009634.1|		5.6			5.3	5.3	5.3	5.3	8.5	8.5	8.5	5.3	5.6	5.3	5.6	5.3				5.6			6.4		GPI-anchored protein of unknown function, has a possible role in apical bud growth; GPI-anchoring on the plasma membrane crucial to function; similar to Sps2p and Pst1p; Ecm33p [Saccharomyces cerevisiae]
K.KVNVFNINNNR.Y +2		3.5489											3.4102		2.9821					3.6172					
K.LQSNGAIQGDSFVCK.N +2									4.1144	3.8742	4.4719												2.9059		
K.VGQSLSIVSNDELSK.A +2		3.7561			4.4753	4.3293	4.4346	4.4596	4.2345	3.7394	4.3047	4.0352	4.0221	4.2552	4.2951	4.3022				4.2318			4.496		
K.VNVFNINNNR.Y +2					3.5773	3.8053	3.6685	3.6965	3.7747	3.3882	3.5262	3.493	3.6115	3.6682	3.591	3.5965									
	1	X			X	X	X	X	X	X	X	X	X	X	X	X				X			X		
gi|6323891|ref|NP_013962.1|					6.6	3.4	11.1		7.9		7.9	11.3	11.1	14.3	14.5	11.1		12.3	6.9	13	7.9	14			GTPase activating protein (GAP) for Gsp1p, involved in nuclear transport; Rna1p [Saccharomyces cerevisiae]
K.ALFHLAQNK.K +2													2.7777	2.9794											
K.DSLFELNLNDCLLK.T +2																		3.2011							
K.ELLEVQVDDLAER.L +2					3.1618		3.8502							3.4822	3.2585	3.6291				3.3382					
K.HASLLAK.A +2													2.9147	3.1189				2.807		2.8817					
K.LDLSGNTIGTEASEALAK.C +2							4.4626		3.7852		2.8249	3.0541			3.8063	4.9121				3.5415	4.7552				
K.NLEILDLQDNTFTK.H +2												3.0029	3.69	4.1265	3.7454			3.8721	4.4621			5.067			
R.ESLVEVNFADLYTSR.L +2																						3.8078			
R.LDEDSDALDLLQSK.F +2					5.931	5.6225	5.3345		5.3679		4.635	4.8316	3.5204	4.6102	4.3025	5.0514		2.6625	3.8516	4.7214	2.6889	4.5642			
R.LENGSAVYLALGLK.S +2																						2.7625			
	1				X	X	X		X		X	X	X	X	X			X	X	X	X	X			
gi|6324594|ref|NP_014663.1|					44.3	53.8	44.3	44.3	53.8	29.2	44.3	53.8	29.2	25.5	44.3	53.8			34	44.3		38.7			Mitochondrial matrix co-chaperonin that inhibits the ATPase activity of Hsp60p, a mitochondrial chaperonin; involved in protein folding and sorting in the mitochondria; 10 kD heat shock protein with similarity to E. coli groES; Hsp10p [Saccharomyces cerevisiae]
K.LGNDDEVILFR.D +2					3.7455	3.7674	3.6533	3.68	3.7176	3.333	3.5585	3.5088	3.2163	3.6777	3.5673	3.5419				3.5903		3.8803			
K.LNQAEVVAVGPGFTDANGNK.V +2					4.5128	4.6584	4.7661	4.9799	4.6716	3.8864	5.0787	4.8873	5.2532		3.6601	4.983			2.9733	3.6864		3.1592			
K.TASGLYLPEK.N +1																						1.9759			
K.TASGLYLPEK.N +2						2.8805			3.2044			2.6071				2.8859									
K.VGDQVLIPQFGGSTIK.L +2					3.0687	3.8626	3.8582	3.5004	3.493		3.2219	2.8108		3.0289	3.3813	3.6193			3.6232	3.204					
	1				X	X	X	X	X	X	X	X	X	X	X				X	X		X			
gi|6325300|ref|NP_015368.1|	28.3	52.2	43.5		29.3	29.3			19.6		42.4	29.3	29.3	19.6	29.3	32.6	29.3			34.8	19.6				Protein component of the large (60S) ribosomal subunit, identical to Rpl43Bp and has similarity to rat L37a ribosomal protein; null mutation confers a dominant lethal phenotype; Rpl43ap [Saccharomyces cerevisiae]
K.KLEIQQHAR.Y +2		3.0097	3.2639		3.3055	3.0334					2.801	2.9995	2.7053		2.8986		2.8803								
K.KTVAGGAYTVSTAAAATVR.S +2																				3.9891					
K.RGAAGIWTCSCCK.K +2		3.7433	3.9292																	3.2448					
K.TVAGGAYTVSTAAAATVR.S +2	5.6934	3.5245	4.7497		4.2153	5.699			5.3989		5.2548	5.2041	5.7873	5.7681	5.4491	5.2964	3.1213			3.6318	5.4548				
K.TVAGGAYTVSTAAAATVR.S +3													4.4047	4.621		3.932					3.7644				
R.GAAGIWTCSCCK.K +2											3.0286					3.6884									
R.YDCSFCGK.K +2	2.5288	2.6113																							
	1 X	X	X		X	X			X		X	X	X	X	X	X	X			X	X				
gi|6319568|ref|NP_009650.1|					6.9	7.9			13.7					7.9	7.9	7.9	7.9	7.9	11.3	11.3	9.2	13.3	5.8	6.9	Constitutively expressed acid phosphatase similar to Pho5p; brought to the cell surface by transport vesicles; hydrolyzes thiamin phosphates in the periplasmic space, increasing cellular thiamin uptake; expression is repressed by thiamin; Pho3p [Saccharomyces cerevisiae]
K.DANTLFAWCAYELNAR.G +2					2.782				3.5645										4.1835	3.5845	3.0177	3.9137			
K.SWYVPQGAR.V +2																						2.5915			
K.YDTTYLDDIAK.R +2									3.5393												3.5818		3.1583	3.5397	
R.GYSDVCDIFTEDELVR.Y +2					4.7436	4.4904			5.0984					3.1593	4.5506	4.1468	4.5254	3.0916	4.4901	4.3795	2.6502	4.6102	4.6603		
R.YSYGQDLVSFYQDGPGYDM*IR.S +2						4.4538			4.6632					3.7925	4.561	5.1045		4.5414	3.6161	3.819					
R.YSYGQDLVSFYQDGPGYDMIR.S +2																	4.7015	3.1503		3.8158		3.6959		3.5144	
	1				X	X			X					X	X	X	X	X	X	X	X	X	X	X	
gi|6321574|ref|NP_011651.1|									12		5.8	12	17.8		16.3	16.3	12	12	12	17.4	8.9	10.5	10.9	10.9	20S proteasome beta-type subunit; the only nonessential 20S subunit; Pre9p [Saccharomyces cerevisiae]
K.TTDSSALTYDR.L +2															3.5656	3.7061									
K.TYNEDIPVEILVR.R +2									4.4181			3.6951	3.9442		4.495	4.4343	3.2852	2.7692	4.069	3.3477	4.5145				
K.VDDAIELALK.T +2																					3.4571		3.7928	3.7418	
K.VTSTLLEQDTSTEK.L +2											4.4135									4.5858					
R.KVTSTLLEQDTSTEK.L +2											3.3595		3.7215												
R.TTIFSPEGR.L +2																						2.6534			
R.YGYQLYTSNPSGNYTGWK.A +2									3.9666			3.1234	4.6201		3.6953	4.0766	5.3332	3.4302	5.0663	4.6547		3.1981	3.8005	2.7733	
	1								X		X	X	X		X	X	X	X	X	X	X	X	X	X	
gi|6320175|ref|NP_010255.1|						7.9		7.2			11		11.5	11.5	11.8	11.3		7.7	7.7	6.4	18.7	15.6	7.2	7.7	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp2p [Saccharomyces cerevisiae]
K.AIVLSGGSSM*YPGLPSR.L +2													4.8515	4.5037	3.4358				3.8528		3.5965	2.755			
K.AIVLSGGSSMYPGLPSR.L +2																					3.2201			3.0437	
K.DIM*GDEASEVR.S +2													2.6992								2.9666				
K.DIMIGDEASEVR.S +2								3.4269			3.5024									3.8514					
K.ILLTEPPM*NPLK.N +2														2.9789											
K.LCYVSYDLDLDTK.L +2															2.673	4.1147			2.6418	2.5097	3.6479	3.8093	3.4536	2.841	
R.AGENFPDYTFPSIVGR.P +2						2.6104		2.7333			2.5086		2.8957	3.2974	3.5427	3.392					3.1479	3.5864			
R.ETTALVESYELPDGR.T +2						3.418					3.2298					3.6839		3.5947			3.4813	3.7847	3.771		
R.SYLQISYPM*ENGIIK.N +2																		2.8332							
	1					X		X			X		X	X	X	X		X	X	X	X	X	X	X	
gi|6320527|ref|NP_010607.1|					6.8	13.9			9.2	7.6	13.1		5.5	8.4				4.7	7.9	9.7	15	13.4	26.8	9.2	Cytosolic L-asparaginase, involved in asparagine catabolism; Asp1p [Saccharomyces cerevisiae]
K.DINEDILYK.I +1											2.2434							2.7483		2.6152	2.6577		2.834		
K.EDNLIASGYLSPEK.S +2					5.1489	5.0122			4.757	3.6634	3.9503			2.9568					4.0442		4.8365	3.5269	4.9651	4.065	
K.HVFTGVYGG.- +1									2.0489					2.4137				2.3095						2.0455	
K.ILGTGGTIASK.A +2																							2.8595		
K.LSLPIVYSK.R +2													2.7359	2.6877								2.6102			
K.SQNAAVNGSGIACQQR.S +2																			4.2991	3.857	4.0279		4.0175		
K.TNANSLDSFNVR.Q +2					3.591				4.2464		3.2961		3.9257							3.466				3.8853	
K.VCDIEYEQLCNVDSK.D +2						5.0705				3.1092	5.6435											5.5555	5.4874		
K.YDGIVLATMGAGSLPEEVNETCMK.L +2						2.6331																	4.1122		
R.GVLVSLNDQISSGYYITK.T +2																					2.7376				
R.SMDGMVPIANVPK.K +2																						4.0866	3.3893		
	1				X	X			X	X	X		X	X				X	X	X	X	X	X	X	
gi|6320006|ref|NP_010086.1|						4.3			2.7		2.7	2.7	6.2	9.7	8.7	8		7.7		2.8	8	4	4.3	3	Essential phosphoprotein component (p150) of the COPII coat of secretory pathway vesicles, in complex with Sec13p; required for ER-derived transport vesicle formation; Sec31p [Saccharomyces cerevisiae]
K.AIQNILYPNDIAQR.N +2													3.2396	3.5053				3.0444							
K.EVIHLSYTSPNSGIK.Q +2														2.5526											
K.FAPEAPDLFACASFDNK.I +2													2.6175	2.7125	3.6712	4.4592					4.0723			3.8967	
K.IEVQTLQNLTNTLDEQETETK.Q +2																3.575		3.7838		2.6469	5.4627	4.6442	3.3705	3.547	
K.ISGLESNTTLSEALK.T +2														2.5093	3.448										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.VASIWLSEFPDLEDK.L +2						4.1746								3.4789	3.2205	3.9141		5.3176			2.7034				
K.VIDDVNEEDWNLLEK.L +2											2.7126				2.5627						4.9301	3.9632			
R.DNTVLLWNPESAEQLSQFPAR.G +2						3.1531																			
R.EVDDLVENLDVSQWK.F +2									4.0801			2.5759	4.5605	4.1329	4.3487	4.0389		3.2997			3.894	4.2206	3.7208		
R.NANTPLQTLNQGHQK.G +2													3.4671	3.9058	3.7017	4.3906		3.2121		2.9154					
R.VATATGSDNDPSILIWDLR.N +2						4.3368			4.1174		3.0514	3.1466	4.0465	4.9251	3.7675	4.773		3.5137			4.167		4.9393		
	1					X			X		X	X	X	X	X	X		X		X	X	X	X	X	
gi|6320061|ref|NP_010141.1|								1.5	1.9			1.4	2.6	5.8	4	2.5	2.1	6.2	3.9	2		4.3	1.7	3.7	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime; Rpo21p [Saccharomyces cerevisiae]
K.ALEDIMVHYDNTTR.N +2													2.5445												
K.DLQENLLVLR.G +2														3.1677	3.0945		3.096	3.1709				3.2699		2.9183	
K.EVQFGLFSPEEVR.A +2													3.9699	3.4242	3.6077			3.9077							
K.EVYNVIASDGSYVNYR.H +2																						4.207			
K.MVCETDVPSEDDPTQLVSR.G +2																						4.0495		4.5161	
K.NDLFVIWSEDNDEK.L +2														4.0738				2.6496		2.8621					
K.QSLDTIGGSDAAFEK.R +2												2.9934						3.9418							
K.SLDAETEAEEDHMLK.K +2																		3.6525							
K.TLTYPEVVTPYNIDR.L +2								3.2074	2.7843																
K.TPSLTVYLEPGHAADQEQAK.L +2																		3.5835							
K.TVGSSNGGLIHVVTR.E +2														2.6413											
R.ATGDADEPELR.V +2								2.6394																	
R.DAVTLFCCLLR.S +2																			2.5807						
R.EVFVDGEANWPLPVNIR.R +2															2.9267	3.1841			3.2636					3.9837	
R.FAAIWTLCK.T +2												2.9672				3.1897	2.9778	2.9503	2.9947	3.2407					
R.FDEGTTLLSPK.D +2																						2.8006			
R.GKNEIIQNAQR.D +2																		3.0818							
R.IIQNAQQTFHIDHTKPSDLTIK.D +3														3.7952											
R.TVISGDPNLELDQVGVPK.S +2									4.6969				4.9116		3.8279	4.2267	2.8996		4.5958			2.9473	4.3988	3.8545	
R.VDLLNTDHTLDPSLLESGSEILGDLK.L +3														4.6605											
R.VLSTEEILNIFK.H +2															3.9168				3.7998	3.5258			4.058		
	1							X	X			X	X	X	X	X	X	X	X	X		X	X	X	
gi|6323974|ref|NP_014045.1|							6			12.4	15	12.8	34.6	34.6	21.4	17.5		11.1	11.1	14.5		14.5	17.5	10.7	20S proteasome alpha-type subunit; Pre5p [Saccharomyces cerevisiae]
K.AGVEAISQSLR.D +2											3.6182		4.1843		3.6841									3.3174	
K.CDEHMGLSLAGLAPDAR.V +2													4.0201	3.9498											
K.DTPFTIYDGEAVAK.Y +2							4.3912			3.2322	4.0823	3.6703	4.982			4.0511		3.4531	4.4982			3.7772	3.4759	4.2411	
K.IDGNPDELIK.A +2											3.1583											3.1013			
K.RNADELSSYQK.K +2																				3.1854					
K.SGAHLLEFQPSGNVTELYGTAIGAR.S +3														3.8838											
R.DESLTVDNLSIAIVGK.D +2												3.3432	4.3261	3.8959	4.2716	3.4584									
R.LFQVEYALEAIK.Q +2													4.9324	4.7265	4.6182			2.5269	4.4101	3.8798			4.4473		
R.NADELSSYQK.K +2																						2.9378			
R.NNYDGDTVTFSPTGR.L +2										3.9563													2.9916		
R.SNTHAVLVALK.R +2													3.3323	3.0212	3.2306	3.3799				3.3811					
	1						X			X	X	X	X	X	X	X		X	X	X		X	X	X	
gi|6324783|ref|NP_014852.1|						7.9					6.8	14.7	11	9.3	14.2	13.5	11.9	6.5	7	15.4	7.9		7	10.5	Nicotinate phosphoribosyltransferase, acts in the salvage pathway of NAD+ biosynthesis; required for silencing at rDNA and telomeres and has a role in silencing at mating-type loci; localized to the nucleus; Npt1p [Saccharomyces cerevisiae]
K.AETLFDNGIR.F +2												2.5228													
K.AQDLIMQGIMK.A +2																	2.9087	3.2404						3.0703	
K.DTILYEIPLLSLISEAYFK.F +2												2.763								2.7076					
K.EQFSYLGNLR.F +2														2.67		2.8913									
K.FVDIDWDYENQLEQAEK.K +2						5.2665						3.7041	3.54		4.136	5.3088	5.4875	4.382		4.1207	5.173			3.4671	
K.IICYSDSLNVEK.A +2											2.6308						2.5978								
K.NAGLALTDTFGTDDFLK.S +2						2.5511					3.6562	4.3413	5.0471	4.7413	4.3729	5.5049			3.1796	4.2575	3.0373		3.4095	4.272	
K.SFRPPYSDAYVGVR.Q +2															2.6521	2.881									
K.SLLLGTSNILFAK.K +2													4.3096	4.4827	4.6137				4.2119	4.5333			4.4018		
R.QDSGDPVEYTK.K +2																	2.5713								
	1					X					X	X	X	X	X	X	X	X	X	X	X		X	X	
gi|6323739|ref|NP_013810.1|					7		6.8		16.9				12.2	13.2	16.3	16.6	15.6	8.6	12	20.3	6.7		16.7	11.7	Actin cortical patch component, interacts with the actin depolymerizing factor cofilin; required to restrict cofilin localization to cortical patches; contains WD repeats; Aip1p [Saccharomyces cerevisiae]
K.AQEYSSISWDDTLK.V +2															3.152		3.7627				3.6711		4.0647	3.9895	
K.DGVNNLLWETPSTLVSSGADACIK.R +2					2.9235				4.1456								3.664	4.1596	4.3363	3.3579			3.387		
K.DGVNNLLWETPSTLVSSGADACIK.R +3													3.8544	4.2968	3.7725			4.8251							
K.FATVGADATIR.V +2																3.3361							2.7952		
K.GITALTVNPLISGSYDGR.I +2									3.9095				4.2738	3.4865	3.0392	4.1174	4.193	4.0577	2.6407	4.1248	3.666		4.1049	3.8998	
K.GSQYLCSGDESGK.V +2													2.8089			3.3036			2.8374						
K.ILLYDLQSR.E +2													2.9874	3.005		2.6191					2.5707				
K.INAISWKPAEK.G +2													3.2808					2.9863							
K.LSDLEVSFDLK.T +2														4.2804	3.4445	3.9375									
K.QQLGNQQVGVVATGNGR.I +2																2.71	3.5122						3.3549	2.8685	
K.SEFQVLAGPISDISWDFEGR.R +2									3.333											3.0594					
K.VIVWGWTFDK.E +2															3.1212										
K.VPPVVQFTGHGSSVVTTVK.F +2														5.5393					3.4572	4.4587					
K.YIEDDQEPVQGGIFALSWLDSQK.F +2							3.5342		4.1352						3.9334	3.3392	4.266			3.0712				3.6465	
R.DVEFSPDSGEFVITVGSDR.K +2					3.9336		4.0885		3.9423														4.1203		
R.NFTTHLSYDPTTNAIAYPCGK.S +2																				4.1133					
	1				X		X		X				X	X	X	X	X	X	X	X	X		X	X	
gi|6324950|ref|NP_015019.1|									5		7.5	5.4	7.1	5.4	7.5	4.8	8.5	14.3	6.9	10.4	5.2	9.2	9.8		Mitochondrial aldehyde dehydrogenase, required for growth on ethanol and conversion of acetaldehyde to acetate; activity is K+ dependent; utilizes NADP+ or NAD+ equally as coenzymes; expression is glucose repressed; Ald4p [Saccharomyces cerevisiae]
K.EEIFGPVVTVTK.F +2													2.7785								2.7717	2.9483	2.9057		
K.IAPALVTGNTVVLK.T +2											4.425	3.5952	4.1348	4.1339	4.686			4.1416		4.3251					
K.IVGEAITNHPK.I +2													3.167			3.1659		3.1801	2.824				3.2785		
K.LPNGLEYEQPTGLFINNK.F +2																	3.5733			2.6548					
K.NEGATLITGGER.L +2									2.836		2.5205														
K.TAESTPLSALYVSK.Y +2									3.484			2.8135		3.9867	3.9146	3.7077						2.6869	3.6321		
K.VAFTGSTATGR.H +2																				2.8971					
K.VGDPFDESTFQGAQTSQMQLNK.I +2																						2.9323			
R.AFSNGSWNGIDPIDR.G +2																	3.0774	2.9245			2.5167				
R.EDDVEEAVQAADR.A +2											4.0578														
R.EM*SVDALQNYLQVK.A +2																			3.9483						
R.EMSVDALQNYLQVK.A +2																		2.8299					3.0407		
R.GDVDLVINYLK.S +2															3.0437		3.2404	2.5089	3.3426						
R.HIYQSAAAGLK.K +2																				2.7375					
R.LAELIEQDK.D +2																		2.912							
	1								X		X	X	X	X	X	X	X	X	X	X	X	X	X		
gi|6321427|ref|NP_011504.1|									9.9	8.7	9.5	8.7	24.6	17.9	16.3	15.5	10.3		14.7	31.3	9.1	13.9	11.1		Alpha subunit of the 20S core complex of the 26S proteasome involved in the degradation of ubiquitinated substrates; essential for growth; detected in the mitochondria; Scl1p [Saccharomyces cerevisiae]
K.ATNQTNINSLAVR.G +2									3.1365	3.7054	2.9088					3.1684				3.524			3.8848		
K.DCTVVISQK.K +2										2.6003															
K.FFTLSAENIEER.L +2												3.2682	4.0816	4.3068	4.0551	3.9134			2.9191	2.9431		4.1549			
K.LLDPTTVSYIFCISR.T +2													3.7419		2.8225				4.2376	3.5887			2.9286		
K.NDLEVGVATK.D +2												2.9287	3.2002												
K.SKIDHINEESWEK.V +2																				3.2819					
K.TDPAGYYVGYK.A +2											2.5245		2.8868									2.6152			
K.VVEFAITHM*IDALGTEFSK.N +2														4.7742											
K.YGYDMPCDVLAK.R +2									3.3869								3.6817			3.7884	3.842	3.5727			
R.HITIFSPEGR.L +2																			3.0979						
R.MANLSQYTQR.A +2																					3.4325				
R.TIGM*VVNGPIPDAR.N +2													3.2974	3.2876											
R.TIGMVVNGPIPDAR.N +2															3.7654	3.2407	3.7543			3.3229					
	1								X	X	X	X	X	X	X	X	X		X	X	X	X	X		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6321587|ref|NP_011664.1|		9	14.2	9	12.3				14.2			20.6	20.6	21.9	14.2	14.2	14.2		21.9	20		11.6			Ribosomal protein L30 of the large (60S) ribosomal subunit, nearly identical to Rpl24Ap and has similarity to rat L24 ribosomal protein; not essential for translation but may be required for normal translation rate; Rpl24bp [Saccharomyces cerevisiae]
- M*KVEVDSFSGAK.I +2																			3.4461						
-.MKVEVDSFSGAK.I +2														3.0191											
K.AQRPITGASLDLIK.E +2		4.2371	4.1152	4.1582					3.6502			2.8105	3.7282	4.0325	3.8083	3.6158			3.8832	3.269					
K.AQRPITGASLDLIK.E +3		4.4522											4.6607	5.0085			4.2696		4.5634	4.7467					
K.GITEEVAK.K +1																				1.8814		1.8968			
K.VEVDSFSGAK.I +1													2.2391									2.3006			
K.VEVDSFSGAK.I +2												2.5381													
R.IAWTVLFR.K +2			3.129		3.0206				2.913			2.8614	2.8544	3.0788	3.1889	2.9043	2.9841		3.0383	3.003					
R.PITGASLDLIK.E +2					3.489				3.8233			3.0962	3.9136	3.5079	2.9095	3.8126			2.53	3.5013					
R.RIAWTVLFR.K +2																				2.8211					
	1	X	X	X	X				X			X	X	X	X	X	X		X	X		X			
gi|6324899|ref|NP_014968.1|					8.1		8.1	8.1	11.6		14	17.5	23.9	12.7	22.1	16.4	10.5		23.7	21.1	13.4				Gamma-glutamyl phosphate reductase, catalyzes the second step in proline biosynthesis; Pro2p [Saccharomyces cerevisiae]
K.ANAHAIEEANKIDLAVAK.E +2																			4.1374	4.5552					
K.DVAELEDPVGK.V +1																									
K.DVAELEDPVGK.V +2											4.0973	3.9502					3.8939		4.0088		3.6542				
K.FEVMLQGIK.D +2																				2.8967					
K.FVTSTESAIQHINTHSSR.H +2													5.1582						3.6101						
K.GVDSSGVYWNASTR.F +2																			2.6619						
K.IPVLGHADGICSIYLDEDADLIK.A +3														4.9093											
K.IVNDTIAQFQSETGVPVGSVQLIETR.Q +3															3.8937										
K.TNYPAGCNAM*ETLLINPK.F +2													3.1256		3.2383										
K.TNYPAGCNAMETLLINPK.F +2					4.0037		3.8981	3.1622	4.0786		3.7889	2.6091				3.9278	3.1281			3.425	4.2107				
K.TVDADEEQDFDK.E +2																			3.943						
K.TVDADEEQDFDKEFLSLDLAAK.F +2													4.8258		3.4659										
K.TVDADEEQDFDKEFLSLDLAAK.F +3													4.6273		3.7935	3.8936									
R.GDGQVASDYLGAGGNK.A +2											3.3603	5.0363	4.867		4.0808	4.8327			4.663	5.1723	2.9904				
R.GPVGLDGLVSYQYQIR.G +2									3.4996			3.0669	4.6526	4.5034						4.2998	4.7546				
R.QDVSDLLDQDEYIDLVPR.G +2					3.9564		4.6178	4.5421	4.2506		2.7008	3.7335	3.5178	3.7272	3.4624	4.6763	3.2428		4.5044	3.3182					
	1				X		X	X	X		X	X	X	X	X	X	X		X	X	X				
gi|6323357|ref|NP_013429.1|		19.2	19.2	19.2				19.2	19.2	19.2		19.2	33.3	33.3	33.3	19.2	33.3		35.9	35.9					Protein component of the large (60S) ribosomal subunit, has similarity to rat L38 ribosomal protein; Rpl38p [Saccharomyces cerevisiae]
K.KLIQSLPPTLK.V +2													3.6789	3.6971	3.0101		3.5043		4.0205	3.5846					
K.VRGSSSLYTLVINDAGK.A +2																			3.0337	4.6545					
K.VRGSSSLYTLVINDAGK.A +3																				3.5604					
R.GSSSLYTLVINDAGK.A +2		4.9126	4.776	5.0465				4.6792	5.0325	4.4424		4.8804	4.7431	4.9358	4.6835	4.5139	4.1717		4.4833	4.7738					
	1	X	X	X				X	X	X		X	X	X	X	X	X		X	X					
gi|6324085|ref|NP_014155.1|	12					25.9	25.9	25.9		25.9	25.9	39.8	60.2	25.9	46.3	25.9	39.8	25.9		34.3					Translation initiation factor eIF1; component of a complex involved in recognition of the initiator codon; modulates translation accuracy at the initiation phase; Sui1p [Saccharomyces cerevisiae]
K.DPEM*GEIIQLQGDQR.A +2													4.0187							3.6567					
K.DPEMGEIIQLQGDQR.A +2												2.7167					4.7494			3.4276					
K.SFDPFADTGDDETATSNYIHIR.I +2													4.7426		4.29					3.5853					
K.TLTTVQGVPEEYDLK.R +2						4.4399	4.6433	4.5189		3.6915	3.6406	3.9265	4.4825	4.4893	4.5685	4.4263	4.317	4.1417							
K.VCEFM*ISQLGLQK.K +2										2.9838			4.0421	4.6371	3.0236			3.0402							
K.VCEFMISQLGLQK.K +2	4.1641					3.0534	4.5758	2.776			3.8584	2.9484			3.6931	4.6038	4.2401								
	1 X					X	X	X		X	X	X	X	X	X	X	X	X		X					
gi|6320079|ref|NP_010159.1|					8.3	9	12.8	15.7	19.6		9	12.8	7.7	34.9	12.8	23.4	16.7	21.5		10.6					NADPH-dependent alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; Ydl124wp [Saccharomyces cerevisiae]
K.EVNGLSLEEAWK.D +2																	2.5583								
K.IPAIAIIGTGTR.W +2					3.7981		4.004		4.3646			4.3892	4.1224	4.0429	4.3608	3.9302	3.8082	3.3852		4.2431					
K.ITELGLEHEPLR.L +2													3.229					2.8771							
K.KTAQDDSQPFFEYVK.E +2																		2.6077							
K.M*GTDYVDLYLLHSPFVSK.E +2														3.1887											
K.M*SDSPADGLDLALK.K +2																		3.0511							
K.MSDSPADGLDLALK.K +2														2.7372	3.6301	3.1395									
K.NEETDATFSNSLVEQIVYALK.L +2								3.007	4.0731											3.0696					
K.NIGVSNFAVEDLQR.I +2					4.1215	4.659	4.5008	3.6018	4.4537		4.3298	2.8842		2.8136		2.5868	3.4119	3.6582							
K.RGVLPVTTSSK.P +2														2.778											
K.TAQDDSQPFFEYVK.E +2						4.223	2.6841	4.0286	4.8744		3.5654	3.5953		4.6556	3.6382	4.6791	3.2156	3.878							
K.VAEVKPQVNQIEFSPFLQNQTPGIYK.F +3														5.4991											
R.ISDAQNLFSFDLTAEEVDK.I +2																3.4432									
	1				X	X	X	X	X		X	X	X	X	X	X	X	X		X					
gi|6320073|ref|NP_010153.1|	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	47.2	15.1	15.1	15.1				47.2	15.1								Ribosomal protein P1 beta, component of the ribosomal stalk, which is involved in interaction of translational elongation factors with ribosome; accumulation is regulated by phosphorylation and interaction with the P2 stalk component; Rpp1bp [Saccharomyces cerevisiae]
K.AAGANVDNVWADVYAK.A +2	5.5763	5.7238	5.6529	5.5731	5.4199	5.4632	5.4209	5.5392	5.0684	5.4115	5.4814	5.5902				5.4062	5.5341								
K.EILSGFHNAGPVAGAGAASGAAAAGGDAAAEEEK.E +3									4.1205							4.8054									
	1 X	X	X	X	X	X	X	X	X	X	X	X				X	X								
gi|6320798|ref|NP_010877.1|						7.5		7.8	23.6		7	12.8	8		12.6	11.1	11.8	16.6			7.5		15.1	8.8	Protein with ubiquitin-like N terminus, recognizes and binds damaged DNA (with Rad4p) during nucleotide excision repair; regulates Rad4p levels, subunit of Nuclear Excision Repair Factor 2 (NEF2); homolog of human HR23A and HR23B proteins; Rad23p [Saccharomyces cerevisiae]
K.DGDQVVFMVSQK.K +2																	3.0605						3.7907		
K.EKVPLDLEPSNTILETK.T +2													3.5212												
K.LAQSISCEESQIK.L +2									3.3852		3.3934					2.8092							4.0156		
K.NEEAAANILFSDHAD.- +2									4.1455						3.7673		4.1537	3.1876			4.5742		4.3258	3.821	
K.VPLDLEPSNTILETK.T +2						3.4668		3.2743	3.7642			3.841	4.2074		4.4304	3.8309		3.2216			2.7504				
K.VTEPPIAPESATTPGR.E +2								3.0123	2.8811			2.9242				3.5369		2.6748							
R.QVVSGNPEALAPLLENISAR.Y +2									3.5709			2.8615					2.8668	3.2056					2.7693	2.6697	
R.QVVSGNPEALAPLLENISAR.Y +3															3.8019			3.5438							
R.TESASTPGFVVGTER.N +2						3.8894			3.7566		3.5147		3.9621												
	1					X		X	X		X	X	X		X	X	X	X			X		X	X	
gi|6322097|ref|NP_012172.1|						8.1			10			15.1	22.1	19.4	16.2	16.4	7	12.9	9.7	10			15.1	6.7	Homo-isocitrate dehydrogenase, an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine, in which homo-isocitrate is oxidatively decarboxylated to alpha-ketoadipate; Lys12p [Saccharomyces cerevisiae]
K.ASTQQVVDDVLSR.L +2						3.4585			3.329			2.5238	3.1127	3.7039	3.5673	3.8547	3.0114						3.4394	3.6007	
K.ASTQQVVDDVLSRL.- +2																	3.6724	2.553		2.9197					
K.EQCQGALFGAVQSPTTK.V +2						4.2472						3.7198											3.9956		
K.GIANPIATIR.S +2													3.5464	3.316	3.3452	3.2697		3.2805	3.3506						
K.SLTIGLIPGDGIGK.E +2												2.678	3.9721	4.1578	3.8189	3.5609			3.4174				3.5313		
K.SNVLSQSDGLFR.E +2									4.488			3.6313	4.1694	4.3802	4.2502	4.4638	4.407	4.298		4.1451				3.8393	
K.VEGYSSPIVALR.R +2									3.3236				3.0741	3.8185		3.0893									
K.YNEQIVDSM*YR.L +2																		3.6651	3.3941						
K.YNEQIVDSMVYR.L +2																							4.0089		
R.GQATLTVTHK.S +2													2.6398												
R.IATIALDIALK.R +2													3.1642	3.8773	3.6415					3.5425					
	1					X			X			X	X	X	X	X	X	X	X	X			X	X	
gi|6324328|ref|NP_014398.1|									7.9			4.8	13.4	14.6	13.8	9.4	5.2	4.6	4.8	19	6.9	6.5		9	Citrate synthase, catalyzes the condensation of acetyl coenzyme A and oxaloacetate to form citrate; the rate-limiting enzyme of the TCA cycle; nuclear encoded mitochondrial protein; Cit1p [Saccharomyces cerevisiae]
K.EYWSYTFEDSLDLLGK.L +2																				2.5527					
K.GLVWEGSVLDPEEGIR.F +2									3.6274				3.999	4.4428	3.8169					3.2323		3.8893		2.6658	
K.ITSTDPNADYGK.N +2															2.6159	3.1468								2.986	
K.LPVIASK.I +1																		1.9433							
K.LVSTIYEVAPGVLTK.H +2													3.8715	4.7341	4.0054		3.0314	4.6385		3.1709		3.1573		2.5657	
K.NLAQLLGYENK.D +2												3.4657								3.3817	3.7902				
K.YLWDTLNAGR.V +2									2.694				2.9886							3.4814					
R.AIGVLPQLIIDR.A +2									3.4802			3.0568	3.3431	3.228	3.5893	3.3536			3.2697	2.8979	3.0275				
R.ANQEVLEWLFK.L +2													3.5225	3.2427	3.4351	3.824			3.8908	3.2555					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.AVGAPIERPK.S +2																2.6692	2.5875				2.7232				
R.SEIPEHVIQLLDSLPK.D +2														4.3468											
	1								X			X	X	X	X	X	X	X	X	X	X	X		X	
gi|37362644|ref|NP_011105.2|										6		6.4	5.2	4.8	12.9	17.1	12.6	7.9	13.8	6.9	7.6		6.4	7.6		E1 alpha subunit of the pyruvate dehydrogenase (PDH) complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA, regulated by glucose; Pda1p [Saccharomyces cerevisiae]
K.AVLAELMGR.R +2														2.9025	2.8321										
K.DWCLSGK.G +1																				2.0384					
K.GPLVLEYETYR.Y +2									3.9904			3.6387			3.4828			3.3325							
K.LDSIITSYR.C +2											2.6163		3.0329									3.5555			
K.LSILFEDVYVK.G +2												3.3065	3.6806	3.4655	3.5437	3.3382				3.5013					
K.LWNLPVVFCCENNK.Y +2																2.8457		3.0551	2.6027	3.436			3.5106		
K.M*HLIDLGIATEAEVK.A +2														3.0356					3.4987						
K.M*HLIDLGIATEAEVKAYDKSAR.K +2															2.6834										
K.VNGMDILAVYQASK.F +2									2.979								4.3646	3.9658							
K.YVDEQVELADAAPPPEAK.L +2											3.6454						3.4015					3.7677	2.64		
R.IPEDTWDFK.K +2																2.7632									
R.KYVDEQVELADAAPPPEAK.L +2														3.9591	2.6972	3.0971	3.0088	4.7466							
	1								X		X	X	X	X	X	X	X	X	X	X		X	X		
gi|6321898|ref|NP_011974.1|						7.6	7.6	7.6	14		7.6	7.6	14	19.6	14	7.6	14		13.2	19.6					Mitochondrial thioredoxin reductase involved in protection against oxidative stress, required with Glr1p to maintain the redox state of Trx3p, contains active-site motif (CAVC) present in prokaryotic thioredoxin reductases, binds NADPH and FAD; Trr2p [Saccharomyces cerevisiae]
K.VTIIGSGPAAHTAAIYLAR.A +2														4.9741					4.2417	3.5082					
R.LWTEFNEDAEPVTTDAIILATGASAK.R +2						4.8403	4.1512	4.1948	9.4964		2.5395	4.2952	4.9502	3.977	5.1647	5.3633	3.7146		4.1942	3.3946					
R.LWTEFNEDAEPVTTDAIILATGASAK.R +3						5.2636	5.1892	5.1666	5.4343		3.8498	5.0507		4.244	4.844	5.7293	3.698		4.4354	3.7345					
R.NKPLAVIGGGDSACEEAEFLTK.Y +2																	2.7951			3.0316					
R.NKPLAVIGGGDSACEEAEFLTK.Y +3									4.441				5.1787	6.7272	6.5525					3.824					
	1					X	X	X	X		X	X	X	X	X	X	X		X	X					
gi|6321814|ref|NP_011890.1|					8.1	10.9	8.1	6.7	21.6	5.3		6.7	9.8	14	6.7	17.1			14.8	21.3					Homoserine kinase, conserved protein required for threonine biosynthesis; expression is regulated by the GCN4-mediated general amino acid control pathway; Thr1p [Saccharomyces cerevisiae]
K.AYPTQDLVFNLQR.L +2					4.0516	4.2438	4.3568	4.0347	3.7804			3.6142	4.0117	3.5996	3.0762	4.1994				3.9631					
K.CIAIIPQFELSTADSR.G +2					2.8071		3.7635		3.4255							3.1739			4.7192	3.2783					
K.ESEGYSTVPLR.S +2								2.8684	2.8601	3.1644		2.7875	3.3697			3.2088									
K.VHVSNPIPLGR.G +2									2.8018				2.731	3.2176	3.2358	3.2571			2.5622	3.4588					
R.GLGSSGAAVVAGVILGNEVAQLGFSK.Q +2						2.8024			2.9359					3.6594					2.9521	4.7237					
R.GLGSSGAAVVAGVILGNEVAQLGFSK.Q +3														4.9606					3.5609	4.5415					
R.MLDYCLMIER.H +2																2.9455				3.2523					
R.SDANLITR.T +2										2.6773															
	1				X	X	X	X	X	X		X	X	X	X	X			X	X					
gi|6319509|ref|NP_009591.1|					14.5		14.5	19.7	19.7	14.5	14.5	19.7	18.4	19.7	25	14.5		11.8		19.7					Pyridoxine (pyridoxamine) phosphate oxidase, has homologs in E. coli and Myxococcus xanthus; transcription is under the general control of nitrogen metabolism; Pdx3p [Saccharomyces cerevisiae]
K.DAEDIPCPDYWGGLR.I +2					4.2476		3.7897	4.1096	3.9131	2.603	3.046	3.7505		3.5205	4.0557	3.0251		3.7444		4.4363					
K.QLTDDPIDLFTK.W +2								3.3196	3.1753			2.8918	3.1015	3.323	3.3461			2.8534							
R.ETLPEAITFSSAELPSGR.V +2					4.4509		4.4568	4.401	4.6465	3.3598	3.6048	4.1212	4.582	4.6962	4.4793	4.6175				4.4386					
R.GFTIYSNWGTSR.K +2																				2.7697					
R.IVPLEIEFWQGR.P +2													3.3227		3.6141										
	1				X		X	X	X	X	X	X	X	X	X	X		X		X					
gi|6319793|ref|NP_009874.1|						7.6			4.6				3.2	9.1	9.4	7.6	7.6	9.8	8.1	4.4			6	5.6	Zinc metalloendopeptidase, found in the cytoplasm and intermembrane space of mitochondria; with Cym1p, involved in degradation of mitochondrial proteins and of presequence peptides cleaved from imported proteins; Prd1p [Saccharomyces cerevisiae]
K.DLQNLSICDTWNQLR.Q +2									2.6257							3.2633							3.9232		
K.DYIHSGLELDEGNR.L +2																2.8383		3.2276							
K.EQLEGVPDSILTQFETIK.S +2						3.1491			2.8868					2.7797	3.2562				3.6688	2.6226					
K.IPESLINSLIK.T +2													3.1124	3.2723	3.0281			3.6869	3.0673				3.0802		
K.LDELNIDLSLR.H +2																								2.7497	
K.M*AEDSTTVM*NFLNDLK.D +2																			2.8999						
K.MAEDSTTVMNFLNDLK.D +2						3.6014											3.9632								
K.NELINLSSHYK.T +2														2.6836											
K.TNEIINNSNNFYDSMSK.V +2																		3.3073					4.3444	4.2073	
K.VESPSVSNFVEPFMK.F +2																		2.8604							
K.VPENEAILLDTLKL.K +2														3.1008	3.567	3.2854	3.5403	4.012	3.1156	2.9976					
K.YLLENFNVDLEK.I +2													3.643	3.8314	3.8064	3.2509	3.8022							2.8357	
R.DELASLLGYDTYANYNLYDK.M +2						3.8874																			
R.SYPVTALVCNFSK.S +2															2.6128		2.5292								
	1					X			X				X	X	X	X	X	X	X	X			X	X	
gi|6321401|ref|NP_011478.1|									21.8		7.9		17.1	17.1	17.1	25.5	17.1	9.3		25.5	7.9	7.9		13.4	Nicotinamidase that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; Pnc1p [Saccharomyces cerevisiae]
K.ATAISAAELGYK.T +2									4.4493															3.7943	
K.GEELINPISDLMQDADR.D +2											2.5785		5.6961	5.0835	3.652	3.9611					2.6874	3.1062			
K.GEELINPISDLMQDADR.D +2									3.7789		3.1922						2.6317			2.9101	2.9288	4.1966		5.3246	
K.NTWGSQLVDQIMDQVVTK.H +2									3.1159							2.9112				2.9618					
K.TTVLLDYTRPISDDPEVINK.V +2													3.9971		3.3845	4.3103	4.2741	3.7353		3.1332					
K.TTVLLDYTRPISDDPEVINK.V +3													4.3994	4.8255	3.8411			4.1385							
	1								X		X		X	X	X	X	X	X		X	X	X		X	
gi|6320941|ref|NP_011020.1|									16.6	13.7	19	16.6	21.5	23.4	16.6	22	21.5	13.7	15.6					14.1	Beta subunit of the 20S proteasome involved in ubiquitin-dependent catabolism; human homolog is subunit C10; Pup3p [Saccharomyces cerevisiae]
K.DCVAIACDLR.L +2										3.0814	3.0588		2.7587				3.5707	2.8874							
R.AIEPETFTQLVSSSLYER.R +2									5.4995	3.191	3.9047	4.9147	5.7615	5.4158	5.6009	5.5251	2.8793	3.4472	3.8085					4.9198	
R.DALSGWGAVVYIIK.K +2														3.0263											
R.FGPYFVGPVVAGINSK.S +2									3.9458			4.3808	4.4431	4.4856	4.1386	4.0924	3.2877								
R.FGPYFVGPVVAGINSK.S +3													4.1581												
R.LGSQSLGVSNK.F +2											3.0306					3.4886								3.0529	
R.LGSQSLGVSNKFEK.I +2																			3.2649						
	1								X	X	X	X	X	X	X	X	X	X	X					X	
gi|6324756|ref|NP_014825.1|		17.5	17.5			15.9	15.9		15.9		28.6		17.5	17.5	17.5	28.6		15.9						15.9	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps30Ap and has similarity to rat S30 ribosomal protein; Rps30bp [Saccharomyces cerevisiae]
K.VHGSLAR.A +1																1.8261									
R.FVNVTLVNGK.R +1						2.9478	2.8932		2.8616		2.2191				2.9722	2.8567		3.1467						2.8753	
R.FVNVTLVNGK.R +2		3.5099	3.2934			3.8312	3.7524		3.6802		3.3017		3.2565	3.7275				3.6809						3.1112	
R.MNPGPSVQ.- +2											2.6627														
R.RFVNVTLVNGK.R +2		3.5559	3.6684										3.1275	3.2547	3.0213	3.3258									
	1	X	X			X	X		X		X		X	X	X	X		X						X	
gi|6319413|ref|NP_009495.1|					6.9				16.3			6.9		6.9	13	9.7	11.6	11.6		10.6	14.7	13.5	8.5		UBX (ubiquitin regulatory X) domain-containing protein that regulates Glc7p phosphatase activity and interacts with Cdc48p; interacts with ubiquitylated proteins in vivo and is required for degradation of a ubiquitylated model substrate; Shp1p [Saccharomyces cerevisiae]
K.DADLLNSVVVQR.W +2					2.9952				3.2402			2.8797			2.9703	3.5198	3.1632	3.3272				3.7801	4.183		
K.EGFQVADGPLYR.Y +2														3.1697		3.2473				3.3841					
K.FLYEHVTSNANTDPSR.N +2									3.3193						3.1538		3.7856	4.7142		3.9942					
K.LGGFSGQGQRL.L +2															2.74										
R.LGSTIDAADEVVEDNTSQSQR.R +2																	4.836	4.2059			4.2445	5.0252			
R.NTFAGGETSGLEVTDPSDPNSLLK.D +2									2.6602												4.2302	4.4838	2.692		
R.YDDPANSFYLSELNQGR.A +2					5.1945				5.3796			5.0907		4.7163	5.3613	5.7435				4.5488	4.3304				
	1				X				X			X		X	X	X	X	X		X	X	X	X		
gi|6323182|ref|NP_013254.1|									6.9		7	3.4	7.8	12.6	4.8	7.2	6.3	11.6	7.9	8.8			2.9		Acetyl-coA synthetase isoform which, along with Acs1p, is the nuclear source of acetyl-coA for histone acetlyation; mutants affect global transcription; required for growth on glucose; expressed under anaerobic conditions; Acs2p [Saccharomyces cerevisiae]
K.APQHFYNSQPGK.G +2											3.307			3.2877	2.5973		2.9575								

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.ATHFYVAPTALR.L +2													3.3973	3.2164	2.9238				2.7563	2.5581					
K.DGYLQNNATEGDAEHITPDNLR.R +2											2.5447					4.0082	3.9421	3.5548							
K.DGYLQNNATEGDAEHITPDNLR.R +3													3.7722												
K.EYLHWDAPYTK.V +2														2.663				3.1695		2.8164					
K.IITFGELLR.K +2												2.7166	3.0034	3.142	2.8651		2.5324	2.9879		2.7304			2.6408		
K.IITFGELLRK.V +2																				2.5912					
K.IVDEGLNGVDLVSR.I +2											3.175	2.6255													
K.KIVDEGLNGVDLVSR.I +2																			3.2424						
K.LNASYNCVDR.H +2									2.6614									3.1418							
K.PALIYEADDESDNK.I +2																		4.7695		5.2117					
R.GEIGPFASPK.T +2									2.6218				2.8153												
R.GRVDDVVNVSGHR.L +2																		2.63		3.1415					
R.HAFANPDKPALIYEADDESDNK.I +3														5.3671											
R.TYLPRVSCDAEDRLFLLYTSGSTGSPK.G +2									2.5984							3.4032			2.7333						
R.VDDVVNVSGHR.L +2																							4.1856		
R.VLGSVGEPISPDLWEWYHEK.V +2														3.5964											
	1								X		X	X	X	X	X	X	X	X	X	X			X		
gi|6324993|ref|NP_015061.1|						5.5		5.7	5.5		5.7	8.2	19.1	16.4	13.3	7.6		8.4		5.3			8.4		Fumarase, converts fumaric acid to L-malic acid in the TCA cycle; cytosolic and mitochondrial localization determined by the N-terminal mitochondrial targeting sequence and protein conformation; Fum1p [Saccharomyces cerevisiae]
K.AIQQAADEVASGK.L +2								3.9583			3.8928		4.3142												
K.EFDEWVVPEHM*LGPK.- +2													3.4749												
K.ESALELGVLTEK.E +2						3.0257			3.1705							2.9178									
K.LDDHFPLVVFQTGSGTQSNM*NANEVISNR.A +3													5.7451	6.1541	4.9974										
K.SAAIVNESLGGLDPK.I +2						4.5539		4.4915	9.4442		4.5271	4.0712		4.5435		4.3852		4.324					4.3871		
K.SLM*LVTALNPK.I +2													3.4444	3.3973	2.9433			2.9477		3.3338			3.1964		
K.SLMLVTALNPK.I +2															3.4257					3.1515					
R.LITDAAYSFR.V +2												2.8992	3.8519	3.4999	3.401	3.1361									
R.TETDAFGEIHVPADK.Y +2												2.6616	3.8463	4.0829	3.2931			2.8862		3.4674			2.7283		
	1					X		X	X		X	X	X	X	X	X		X		X			X		
gi|6319814|ref|NP_009895.1|		13.6							28.2			26.4	60	60	49.1	26.4	26.4	51.8	40	26.4		25.5			Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cell from oxidative damage; Grx1p [Saccharomyces cerevisiae]
K.DLIAENEIFVASK.T +2												3.8186	3.8536	4.6913	4.7523	4.4212	4.305	4.6372	3.8286	4.307		4.7816			
K.EGADIQAALYEINGQR.T +2									4.5064			2.9543	4.002	4.5228	4.2782	4.086	3.9263	4.5902	4.5853	4.8899					
K.HIGGNDDLQELR.E +2													3.2606	3.6463				2.5479							
K.TYCPYCHAALNTLFEK.L +2																		2.6891							
K.VLVLQLNDM*K.E +2													3.6089	4.0183	3.5478										
R.ETGELEELLEPILAN.- +2		3.6095							2.8115				3.1731	3.0896	3.4459				3.1623			2.9204			
	1	X							X			X	X	X	X	X	X	X	X	X		X			
gi|6321290|ref|NP_011367.1|							8.2	6.6	13.8	6.6	6.6		18.1	20.5	6.1		9.8	14.4	10.1	21.5					Bifunctional chorismate synthase and flavin reductase, catalyzes the conversion of 5-enolpyruvylshikimate 3-phosphate (EPSP) to form chorismate, which is a precursor to aromatic amino acids; Aro2p [Saccharomyces cerevisiae]
K.DRVEIQSGTEFGK.T +2																	3.6085								
K.DSIGGVVTCVVR.N +2									3.3678				3.0215				2.7152								
K.FLAQNSNVEIVAFVTQIGEIK.M +2																			3.5572						
K.FPRPSHADFTYSEK.Y +2														3.1274						3.1756					
K.GFEIGSGFQGVSVPGSK.H +2							3.8713		3.8738				3.258					3.9904	2.8417	2.9753					
K.SVATISQEQK.T +2																				3.4433					
K.TATYDGEEGILAAK.G +2							4.0481	3.6783		4.3348	3.8046														
K.TLGTPIAM*M*K.N +2														2.5892											
K.TNNSGGVQGGISNGENIYFSVPFK.S +2																		2.9226		2.8306					
R.CPDASVAGLMVK.E +2									3.3595				3.2733	3.7499	2.9046		3.282								
R.DSFDPEFQHLLNTITR.E +2													3.8222	3.485						3.7521					
R.NLPTGLGEPCFDK.L +2														3.0282				2.5246							
R.VEIQSGTEFGK.T +2								3.2815	3.9055	2.6185	3.378		3.5577	3.461	2.8668										
	1						X	X	X	X	X		X	X	X		X	X	X	X					
gi|6321398|ref|NP_011475.1|						8.5		7	12.6	8.5	8.5		13.7	6.4	9.1		8.5	12.9	16.1	15.2					Delta-aminolevulinate dehydratase, a homo-octameric enzyme, catalyzes the conversion of delta-aminolevulinic acid to porphobilinogen, the second step in the heme biosynthetic pathway; localizes to both the cytoplasm and nucleus; Hem2p [Saccharomyces cerevisiae]
K.AGAHCVAPSDMIDGR.I +2																		3.7688		3.7159					
K.DPVGTAADDPAGPVIQGIK.F +2						4.4891			4.9726	4.8816	5.5355				5.6496		5.8746	2.5681	5.2069	5.8918					
K.FSGNLYGPFR.D +2													3.2751	3.3842				2.8457	2.9972						
K.TIAFESHQGFLR.A +2													2.5525	2.936	2.5376				2.9379						
R.LAAVAVNYAK.A +2						3.5308		3.5932	3.6407	2.7498	3.4029						3.5954								
R.LIITYLAPEFLDWLDEEN.- +2																				3.132					
R.LKDYLKPLVAK.G +2													2.962												
R.SVILFGVPLIPGTK.D +2								2.7056	2.7439				2.8384						2.8309						
	1					X		X	X	X	X		X	X	X		X	X	X	X					
gi|6324194|ref|NP_014264.1|		13.2	13.2	13.2				13.2	28.9			28.9	28.9	28.9	28.9	28.9	28.9			38.6					Peptidyl-prolyl cis-trans isomerase (PPIase), binds to the drugs FK506 and rapamycin; also binds to the nonhistone chromatin binding protein Hmo1p and may regulate its assembly or function; Fpr1p [Saccharomyces cerevisiae]
K.TGDLVTIHYTGTLENGQK.F +2									5.0234			3.7112	3.8572	5.2763	5.1707	3.6092	5.5504			4.5491					
K.TGDLVTIHYTGTLENGQK.F +3													3.5821	4.2541											
R.GSPFQCNIGVGQVIK.G +2		4.8369	4.3171	4.0536				4.7733	4.677			3.8615	4.9412	4.7494	4.6095	4.7914	4.2735			4.4874					
R.ISPGDGATFPK.T +1																				1.9879					
	1	X	X	X				X	X			X	X	X	X	X	X			X					
gi|6320078|ref|NP_010158.1|					17.7	17.7	17.7		17.7	10.1	10.1	10.1	28.5	34.2		20.9	20.9			20.9					Adenosine 5'-monophosphoramidase; interacts physically and genetically with Kin28p, a CDK and TFIIK subunit, and genetically with CAK1; member of the histidine triad (HIT) superfamily of nucleotide-binding proteins and similar to Hint; Hnt1p [Saccharomyces cerevisiae]
K.LDTYNVLQNNGK.I +2					4.6038	4.6139	4.5855		4.6273				3.2771												
K.LHDIPDEFLTDAM*PIAK.R +2													4.6268	4.3285		3.807				2.8437					
K.LHDIPDEFLTDAM*PIAK.R +3													4.0413	4.2063											
K.LHDIPDEFLTDAMPIAK.R +2																	4.2112			4.704					
K.LHDIPDEFLTDAMPIAK.R +3																				3.861					
K.SGLIVGWPAQETDFDK.L +2					4.4089	4.7178	4.528		4.5407	3.8015	3.8943	4.2838	4.5464	4.9365		4.5406	4.1543			4.0331					
K.YSYAFLDIQPTAEGHALIIPK.Y +2														2.9261											
	1				X	X	X		X	X	X	X	X	X		X	X			X					
gi|6322426|ref|NP_012500.1|									4.5			4.8	10.1	5.4	6.3	7.5				5.6	4.5	4.1	10.6	6.2	ATPase involved in protein import into the ER, also acts as a chaperone to mediate protein folding in the ER and may play a role in ER export of soluble proteins; regulates the unfolded protein response via interaction with Ire1p; Kar2p [Saccharomyces cerevisiae]
K.DNNLLGK.F +1																				1.8274					
K.DVDDIVLVGGSTR.I +2																						3.7477	3.0194		
K.FEELNLDLFK.K +2													2.9284	2.8676	3.1309										
K.NQVAANPQNTIFDIK.R +2												4.5964			4.4646							4.5183	4.9179		
K.SQIFSTAVDNQPTVMIK.V +2																					3.6126			3.8841	
K.TEILANEQGNR.I +2													3.242	2.8013											
K.VFTPEEISGM*ILGK.M +2													3.1673								2.8519				
K.VFTPEEISGMILGK.M +2																							3.8343		
K.VQQLLESYFDGK.K +2																							2.9262	2.8752	
K.VTHAVTVPAYFNDAQR.Q +2																3.149									
R.IEIDSFVDGIDLSETLTR.A +2									4.3608			3.3547	3.5586		4.4745	5.4189				3.0065			3.7949		
R.ITPSYVAFTDDER.L +2									2.9729											3.7659				2.8681	
R.IVNEPTAAAIAYGLDK.S +2													4.8068	4.2667		4.0579									
	1								X			X	X	X	X	X				X	X	X	X	X	
gi|27808714|ref|NP_014160.2|						6.2			6.8		9.3		5.3	4.6	12.3		11			13.7	7.3		11	7.9	Aminopeptidase of cysteine protease family, has a DNA binding activity and acts as bleomycin hydrolase in vitro; transcription is regulated by galactose via Gal4p; Lap3p [Saccharomyces cerevisiae]
K.ANYFLDQIVSSADQDIDSR.L +2															3.5354		4.3404			2.8673	2.9732		3.6257	3.9003	
K.DLYGDLPYSTTASR.K +2						4.2671															3.5471				
K.EFQSDLTHQLATTVLK.N +2															3.6584					3.7189					
K.LDPSTPVSLINDPR.H +2						3.3529			2.9175		2.7563		3.6279				2.7093						3.0688		
K.NYNADDALLNK.T +2											3.6608														
R.CWLFAATNQLR.L +2														3.4778	3.4325										

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
R.LNVLSELNLK.E +2													3.0708	2.9206	3.2592					2.7659					
R.VFNTVVSTDSTPVTNQK.S +2									4.414		3.7047						4.1217			4.3742			4.1684	2.9737	
	1					X			X		X		X	X	X		X			X	X		X	X	
gi|6320066|ref|NP_010146.1|					8.9	8.9	8.9	8.9				15.3	13.9	15.3		14.4	18.8			23.8				18.8	Rho GDP dissociation inhibitor involved in the localization and regulation of Cdc42p; Rdi1p [Saccharomyces cerevisiae]
K.ESLGLSSDVLPLEFPGDK.R +2					4.372	4.4944	4.563	4.7354				3.2558	4.1569			4.1621	3.6287			3.582				3.4437	
K.IDDHLGSYAPNTK.T +2												3.2898													
K.IQLLVNTEPNPITFDLTNIEK.T +2																	2.6016			3.3794				2.6453	
K.NLDAEDESLAK.W +2																2.7147									
K.TKPFYEVELPESEAPSGFLAR.G +3														4.1058											
K.VQHEIITGLR.Y +2													2.8793	3.0278						2.6468					
	1				X	X	X	X				X	X	X		X	X			X				X	
gi|6319965|ref|NP_010045.1|	4.5					8.3			9.6		7.7	11.5	13.1	7.7	13.1	17				13.1				4.5	Alkaline phosphatase specific for p-nitrophenyl phosphate, involved in dephosphorylation of histone II-A and casein; Pho13p [Saccharomyces cerevisiae]
K.DSVHFVGTNVDSTFPQK.G +2													3.8348		3.1618	3.113				3.6851					
K.DVSCVIAGLDTK.V +2						4.0378						3.339				4.1006									
K.EEQIFTSGYASAVYIR.D +2									3.3761																
K.VWVFGESGIGEELK.L +2	4.0895					4.4487			4.7046		2.7255	3.9707	4.1085	4.5239	4.7364	4.4732				4.3287				5.1277	
R.LAVTLQYLQK.D +2											2.818	3.267	3.8446	3.8474	3.9947	3.9418				3.7649					
	1 X					X			X		X	X	X	X	X	X				X				X	
gi|6322732|ref|NP_012805.1|				9.7		9.3			9.3	9.3	9.3	9.3	16.7	13.9	13.9				8.8					16.7	Co-chaperone that binds to and regulates Hsp90 family chaperones; important for pp60v-src activity in yeast; homologous to the mammalian p23 proteins; Sba1p [Saccharomyces cerevisiae]
K.DLESEYWPR.L +2						3.398			3.3433	3.1787	3.2867	2.954	2.6951	3.0291	3.2724				2.9554					3.2747	
K.ENDEEDEEEIEPEVK.A +2													4.865											3.9103	
K.VANGQHYFLK.L +2				3.9029										2.7266	2.8844				3.1795						
K.VINPQVAWAQR.S +2				3.53		3.4689			3.3059	3.3881	3.3196	2.5248	2.7489	3.1767	3.3444									3.4258	
	1			X		X			X	X	X	X	X	X	X				X					X	
gi|6320930|ref|NP_011009.1|											7.8		8.7	11.3	9	5.4	9.2	6.4	7.3	6.4	6.4		5.2		Threonine deaminase, catalyzes the first step in isoleucine biosynthesis; expression is under general amino acid control; ILV1 locus exhibits highly positioned nucleosomes whose organization is independent of known ILV1 regulation; Ilv1p [Saccharomyces cerevisiae]
K.IGAVFVPVGGGGLIAGIGAYLK.R +2																				2.5224					
K.IPATIVM*PVCTPSIK.Y +2															3.1958										
K.IPATIVMPVCTPSIK.Y +2											2.6826			2.9228						2.6127					
K.LDELQTDNTPDYVR.L +2											3.8625												4.8973		
K.NTYVPILSGANMNFDR.L +2																	3.4104								
K.YISTVHPEIDHTK.N +2													3.7185	3.056											
R.NQGVIACSAGNHAQGVAFAAK.H +2													5.6559	5.514	4.3882		4.5669	5.2596	4.2208						
R.SIVEPSGALSVAGMK.K +2																2.7488									
R.SSVYDVINESPISQGVGLSSR.L +2																			4.203		3.79				
R.TPLPVVGTFADGTSVR.M +2											2.7282		3.7399	3.5285	3.338	2.6187	3.3686	3.5433			3.6509		2.6726		
	1										X		X	X	X	X	X	X	X	X	X		X		
gi|6320983|ref|NP_011062.1|									7.3			7.3	9.8	11.5	6.9	17.3	7.5	5.5		17.5	6.7		6.2		GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins; Gdi1p [Saccharomyces cerevisiae]
K.APLVIADPTYFPEK.C +2									4.498			4.1428	3.9322	4.6058	3.9475	4.2832	3.863			4.1234					
K.EDDLSTHQGLDLDK.N +2																2.7863									
K.FLEWISSYK.E +2																					2.6663				
K.FM*GIAELFEPR.E +2													2.5944							2.9248					
K.FMGIAELFEPR.E +2																	2.8599								
K.SDIYVAIVSDAHNVCSK.G +2															2.5507										
K.SPYLYPM*YGLGELPQGFAR.L +2																				2.7503					
K.VPANEIEAISSPLM*GIFEK.R +2												3.3276	3.8911	4.5821		4.0882				3.043			3.1312		
K.VPANEIEAISSPLMGIFEK.R +2									3.1172																
R.ILLYCQSVAR.Y +2														2.8711		2.6996									
R.LSAIYGGTYM*LDTPIDEVLYK.K +2																2.7809					2.8558				
R.SYDASSHFESMTDDVK.D +2																		3.3084		2.6334					
R.VTGHPLVLK.Q +2														2.8348			2.5559	2.7273					2.5716		
	1								X			X	X	X	X	X	X	X		X	X		X		
gi|6319725|ref|NP_009807.1|									4.3				13.6	8	9.4	11.4	4.9	6.3	4.2	9.8	5.8	4			Imidazole glycerol phosphate synthase (glutamine amidotransferase:cyclase), catalyzes the fifth and sixth steps of histidine biosynthesis and also produces 5-aminoimidazole-4-carboxamide ribotide (AICAR), a purine precursor; His7p [Saccharomyces cerevisiae]
K.AGLNVIENFLK.Q +2									3.0126				3.2048			2.826			3.3866						
K.DGSNSGYDLELIEHVK.D +2													3.3484												
K.ELLM*NDYSNYGLTR.R +2																					3.0417				
K.ELLMNDYSNYGLTR.R +2																		3.3732							
K.IPALESVASLYFR.S +2													3.7251	3.7787	3.8585				3.0344	3.3192					
K.IPVIASSGAGVPEHFEEAFLK.T +2																				2.8638					
K.NNIFATQFHPEK.S +2													2.6004												
K.STGLNYIDFK.L +2														3.1518		3.1954						2.7804			
K.TVFVPLTVGGGIK.D +2									3.1119				3.6139	3.2965	3.3345	3.0527									
K.YGSEEFIAAVNK.N +2																		3.5352		4.2687		3.5167			
K.YYQQGADEVTFLNITSFR.D +2															3.9079	4.4107	2.5022				3.161				
R.DLGVWELTR.A +2														3.6122	3.1357		2.649	2.8703		2.8931					
R.NLGKPVQLAQK.Y +2													3.1628			3.3679									
	1								X				X	X	X	X	X	X	X	X	X	X			
gi|6323681|ref|NP_013752.1|					12				16.1			16.1	10	17.3	17.3		10	16.1		23.3	10	10			Copper chaperone for superoxide dismutase Sod1p, involved in oxidative stress protection; Met-X-Cys-X2-Cys motif within the N-terminal portion is involved in insertion of copper into Sod1p under conditions of copper deprivation; Ccs1p [Saccharomyces cerevisiae]
K.DYSFLGVIAR.S +2									3.4982			2.8264	3.7943	4.0397	3.8088		3.8032	3.811		3.5384	3.5966	4.1404			
K.FDEPIECFNESDLGK.N +2					4.3797				4.3574			3.5048					4.1969	4.531		3.1285	4.2586	4.0663			
K.TFLSAPLPTWQLIGR.S +2					3.814				3.5148			3.4514	4.1639	2.9926	3.2184			3.477		3.0815					
R.GAGKPNSSAVAILETFQK.Y +2														3.3546	2.9902					3.3436					
	1				X				X			X	X	X	X		X	X		X	X	X			
gi|6319430|ref|NP_009512.1|								14.1	14.1			14.1	17.8	17.8	17.8	9.5	15.8		12.4	22		9.5			20S proteasome beta-type subunit; Pre7p [Saccharomyces cerevisiae]
K.GAVYSFDPVGSYER.E +2								4.4032	3.4422			4.1479	2.7615	4.3049	3.974	4.1492	4.014					4.1838			
K.VFDCGDNIVMSANGFAADGDALVK.R +2																	5.4086			2.9866					
R.AGGAAASLIM*PFLDNQVNFK.N +2									3.8091			3.4028	4.5381	4.3648					3.2385	3.3394					
R.AGGAAASLIM*PFLDNQVNFK.N +3														6.2645	3.7765										
R.AGGAAASLIMPFLDNQVNFK.N +2								4.2219	4.4842						2.8096					3.7827					
R.DSFTSATER.H +2																						2.9396			
R.NIQHLLYGK.R +2													2.9612	3.0009	2.6001	2.7199				2.5664					
R.NITDYSINSR.Y +2																			2.5211						
	1							X	X			X	X	X	X	X	X		X	X		X			
gi|6321718|ref|NP_011795.1|						11.4		13.5	16.3		8.5	8.5	13.5	13.5	13.5	8.5			17.1			5.7			Cell wall protein with similarity to glucanases; scw4 scw10 double mutants exhibit defects in mating; Scw4p [Saccharomyces cerevisiae]
K.GETYGVAVPSK.E +2						3.3551			3.3928																
K.NVVITESGWPSKGETYGVAVPSK.E +2																									
K.SASEVASDLAQLTDFPVIR.L +2						4.32		5.0001	4.5291		3.6923	3.9113	3.929	4.6438	4.2296	4.8342			3.3559						
K.VFLGIYYVDQIQDGVNTIK.S +2								3.6768	4.5691				4.364	4.2056	3.1458				3.2621						
K.YWGILSNE.- +1																						2.4353			
R.GITYTPYESSGACK.S +2						2.7682							3.0954						2.9601						
R.LYGTDCNQVENVFK.A +2								5.0766	4.5373		3.5262	4.5967		4.6905	4.6032	4.8519			3.9392			4.2775			
	1					X		X	X		X	X	X	X	X	X			X			X			
gi|6323980|ref|NP_014051.1|		3.3							18.6		9.7		24.4	21.4	11.1	13.6	19.4	10	8.9	27.8					NADPH-dependent cinnamyl alcohol dehydrogenase family member with broad substrate specificity; may be involved in fusel alcohol synthesis or in aldehyde tolerance; Adh6p [Saccharomyces cerevisiae]
K.AM*GAETYVISR.S +2													3.1042												
K.AMGAETYVISR.S +2											3.5185		3.9091												
K.AVSISYSALGSIK.E +2													2.6946						3.7883						
K.FEGIAIQSHEDWK.N +2									2.5679					3.3963	3.6201	2.7834	3.3988			3.0968					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.FVTTYSQPYEDGYVSQGGYANYVR.V +2									4.0976		2.6339					3.7814	3.9526	3.8696		3.9274					
K.IWVETLPVGEAGVHEAFER.M +2													4.074	5.6224											
K.KVGIVGLGGIGSM*GTLISK.A +2																			4.089						
K.M*GADHYIATLEEGDWGEK.Y +2													4.4401	3.5685											
K.M*PLVVGHEIVGK.V +2									3.4664				4.113		3.7217	3.7397		3.2411							
K.MGADHYIATLEEGDWGEK.Y +2																	4.7838			3.2838					
K.MPLVVGHEIVGK.V +2		4.3775							3.7906				4.2394	4.1605	4.1261	3.7957				3.9211					
K.VGIVGLGGIGSM*GTLISK.A +2																			4.8746	2.5166					
K.VGIVGLGGIGSMGTLISK.A +2									4.1281											4.5756					
R.VGVGAQVFSCLECDR.C +2													3.8245	4.5468	3.8776		4.1069			2.9097					
	1	X							X		X		X	X	X	X	X	X	X	X					
gi|6319471|ref|NP_009553.1|				11.5	11.5			11.5	11.5			11.5	19.1	19.1	11.5			18.3	18.3	11.5					One of two nearly identical (see HTB1) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation; Htb2p [Saccharomyces cerevisiae]
gi|6320430|ref|NP_010510.1|				X	X			X	X			X	X	X	X			X	X	X					One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation; Htb1p [Saccharomyces cerevisiae]
K.ETYSSYIYK.V +1																		2.3981	2.3305						
K.SM*SILNSFVNDIFER.I +2				4.6191	4.9252			4.7098	4.9419			5.0035	4.9281	5.1233	4.9819			3.4878	4.5594	4.2649					
K.SMSILNSFVNDIFER.I +2				4.6073	3.2011													3.1106		4.3751					
R.KETYSSYIYK.V +2													3.172	3.0674											
	1			X	X			X	X			X	X	X	X			X	X	X					
gi|6320279|ref|NP_010359.1|													7.5	4.6	2.9	4.1		2.7		2.6	4.7	5.9	6.8	3.9	Phosphatase subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; Tps2p [Saccharomyces cerevisiae]
K.DAIVVNPWDSVAVAK.S +2													2.6875	3.6873		3.3695					3.4713	3.3889	2.8407		
K.DVSCQDWVNLTEK.V +2													3.2476					3.2835			2.8093	2.8181	3.9806	3.139	
K.IQLGESNDDWK.I +2																							2.7845	2.6846	
K.VDMSWQVR.V +2																				3.345					
R.AFETFLAM*YPEWR.D +2													3.1921												
R.DGMNTTALEYVTVK.S +2																					2.7442	3.1965			
R.IINCVTQLPYK.I +2													2.6772		2.7514	3.3467							2.7908	3.0968	
R.LFLFDYDGTLTPIVK.D +2													4.6252	4.2821	4.4807					3.3869					
R.VADLCLITSVR.D +2																		3.047							
R.VNEVMEEFTTR.T +2														2.9243		3.4462						2.8672	3.4542		
	1												X	X	X	X		X		X	X	X	X	X	
gi|6320372|ref|NP_010452.1|						5.9			6.3				6.3	6.3		12.8	5.9			6.3		6.5	6.5	5.9	Essential Hsp90p co-chaperone; necessary for passage through the START phase of the cell cycle; Cdc37p [Saccharomyces cerevisiae]
K.ILQQEEMDESNAEGVETIQLK.S +2																3.1783						2.6643	3.344		
K.LLEVFNDIDIIGIK.A +2									2.5387				3.9325	3.3813		3.4101				3.3328					
K.SLDDSTELEVNLPDFNSK.D +2						3.5291			2.5473							3.4148	2.6015			2.7923				2.8928	
K.VFEDIPIEEAEK.L +2						3.379										3.3665	3.6005					3.366	3.5039	3.3436	
R.ILSNLPESSLTDLPAVTK.F +2													3.5703	4.2317											
	1					X			X				X	X		X	X			X		X	X	X	
gi|6324772|ref|NP_014841.1|						6.8			6.8	6.8	6.8		6.8		6.6	6					6.6		6.6	6.8	Component of mRNP complexes associated with polyribosomes; implicated in secretion and nuclear segregation; multicopy suppressor of BFA (Brefeldin A) sensitivity; Bfr1p [Saccharomyces cerevisiae]
K.DLVNIEPIR.K +2																2.6429									
K.DVSNQFEENQQK.L +2																					4.0817				
K.NTENEQPASIFNK.V +2						4.6621			4.7994	2.6805	4.2796		4.5731											4.9124	
K.VVADDLVLVTPK.K +2															2.8794								3.4551		
R.INEIEESIASGDLSLVQEK.L +2						6.186			6.6935	3.4002	4.4095		5.8885		6.1521	6.4188					6.5646		5.5674	4.9244	
	1					X			X	X	X		X		X	X					X		X	X	
gi|6323669|ref|NP_013740.1|						7.2			11.3				9.8	5.7	5.1	9.6		7		13.2			7	10	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; YMR027W is not an essential gene; Ymr027wp [Saccharomyces cerevisiae]
K.ADVQVALPEGLDAK.L +2						3.9849			3.7561				2.9554	3.8587	3.861	3.2685								4.0507	
K.DFIDILVHDLR.D +2															2.9407					3.3479					
K.DIPYMVSDVMLK.D +2																									
K.IANVPLSFNEYLK.K +2													2.9674	3.4873				2.7677		2.5865			2.8895	2.9809	
K.WETAIGPLATNGITSLSLR.T +2									2.6723				2.7207							4.7764					
R.ALDLFAGEMEK.F +2																2.833									
R.EDSFWTTELDYWNLDANETK.Y +2						3.4556			4.0221							3.9931		3.8552		3.4092			4.8169	3.8884	
	1					X			X				X	X	X	X		X		X			X	X	
gi|6321896|ref|NP_011972.1|									8.9				16.2	13.5	13.5	10.1	8.6		10.1	11.9		15.3	7.3		Aldose reductase involved in methylglyoxal, d-xylose and arabinose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and heavy metals); regulated by the HOG pathway; Gre3p [Saccharomyces cerevisiae]
K.DISALNANIR.F +2																						2.7985			
K.GHITEAHVPIIDTYR.A +2													2.6931												
K.M*PLVGLGCWK.I +2													2.9885							2.5028					
K.MPLVGLGCWK.I +2																				2.8482					
K.SIGVSNFQGSLIQDLLR.G +2									3.5084				4.4833	5.0051	3.9124	3.2566			4.5505	3.6876					
K.TTPTLFENDVIK.K +2									3.2876														2.9645		
K.VSQNHPGSTTSQVLLR.W +2														3.9436	3.3072	3.6689	3.2581		4.0701			2.8491			
R.ALEECVDEGLIK.S +2																	3.3735			3.9595		2.9667	3.9671		
R.FNDPWTWLDGK.F +2													3.1574	3.871	2.991										
R.LFDGACDYGNEK.E +2																						3.7266			
	1								X				X	X	X	X	X		X	X		X	X		
gi|6324716|ref|NP_014785.1|									17.9				19.1	31.6	25.5	14.6		12.2	8.8	9.4	7.6		10.6		Alpha subunit of succinyl-CoA ligase, which is a mitochondrial enzyme of the TCA cycle that catalyzes the nucleotide-dependent conversion of succinyl-CoA to succinate; Lsc1p [Saccharomyces cerevisiae]
K.AEIEAAQFLK.E +2													2.7241	3.4123	3.2247	3.3119		3.3953		3.4961	3.441				
K.AGQTHLGQPVFASVK.D +2													4.1489	4.4815	4.1199			3.6061							
K.ETGATASAIFVPPPIAAAAIK.E +2									2.9773					2.8266	2.77					2.7701			2.6163		
K.LFLEDETTEGIIM*LGEIGGK.A +2														3.0091											
R.DVGVAVVESPGYLGQALLDQFAK.F +2									3.3183				3.9752	4.9951	4.492	4.5904									
R.DVGVAVVESPGYLGQALLDQFAK.F +3													4.8126		4.4585										
R.LVGPNCPGIINPATK.V +2									3.4139				3.8592	3.6314	3.3666	3.4458		3.0947	3.6143		3.8781				
R.SGTLTYEAVQQTTK.T +2																			3.8213				3.9801		
	1								X				X	X	X	X		X	X	X	X		X		
gi|6323547|ref|NP_013618.1|							18		23.2				10	10	10.4	13.6		12.8		22.4	12.8		12.8		20S proteasome beta-type subunit; Pre8p [Saccharomyces cerevisiae]
K.ATNGVVIATEK.K +2																				2.9292					
K.LGQIDYALTAVK.Q +2							2.8786		3.7209				3.3789	4.1733		3.4776		3.6001		4.145	3.3523		3.8122		
K.LTSQEINDR.L +2																2.5261									
K.SSSPLAMSETLSK.V +2									3.3325						3.0609	3.1633									
K.VSLLTPDIGAVYSGM*GPDYR.V +2																		2.8489		3.3285	3.4324		2.6235		
K.VSLLTPDIGAVYSGMGPDYR.V +2							3.6273		3.7109									3.3355		3.1669					
R.YSFSLTTFSPSGK.L +2							3.062		3.3904				3.4559	3.5932	3.032					2.639					
	1						X		X				X	X	X	X		X		X	X		X		
gi|6320899|ref|NP_010978.1|							23.3			23.3	30.2	14	30.2	23.3		23.3			23.3	37.2			14		Member of the p14.5 protein family with similarity to Mmf1p, functionally complements Mmf1p function when targeted to mitochondria; heat shock inducible; high-dosage growth inhibitor; forms a homotrimer in vitro; Hmf1p [Saccharomyces cerevisiae]
K.AEQVIQNIK.N +1																							2.4448		
K.AEQVIQNIK.N +2											3.0306									2.8825					
K.LVEGSIADK.A +1													2.1327							2.0481			2.1519		
K.NVLEASNSSLDR.V +2							3.6267			2.9781	3.9564		4.2162	3.5359		3.8564			4.1171	4.3268					
K.VNNLIFLSGQIPVTPDNK.L +2							5.0934			3.5016	4.6301	4.1678	3.9469	4.6417		4.409			4.6889	4.0967					
K.VNNLIFLSGQIPVTPDNK.L +3														3.6286											
	1						X			X	X	X	X	X		X			X	X			X		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6323619|ref|NP_013690.1|		7			12.3		12.3				12.8	12.3	18.2	18.2	18.2	12.3							12.3		Adenine phosphoribosyltransferase, catalyzes the formation of AMP from adenine and 5-phosphoribosylpyrophosphate; involved in the salvage pathway of purine nucleotide biosynthesis; Apt1p [Saccharomyces cerevisiae]
K.EYGSDLFEIQK.N +2											2.9341														
K.IDYIVGLESR.G +2					3.8321		3.3061					3.2179	3.5175	3.8953	4.0227	3.5198							3.9611		
K.LHLEEAFPEVK.I +2													3.4372	3.6438	3.3239										
K.LNAPVFTLLNAQK.E +2		4.2015			3.6889		3.4374				2.7981	4.3266	4.0504	4.1883	4.3786	3.9846							4.2821		
	1	X			X		X				X	X	X	X	X	X							X		
gi|6319646|ref|NP_009728.1|					3.9	2.9			3.9	1.7	2.9	2.9	6.1		2.9	5.1							2.9		Member of the heat shock protein 70 (HSP70) family; may be involved in protein folding; localized to the cytoplasm; highly homologous to the heat shock protein Sse1p; Sse2p [Saccharomyces cerevisiae]
K.GAAFICAIHSPTLR.V +2													2.5054												
K.YEELASLGNIIR.G +2					4.4352	4.075			4.0539	4.2624	3.9076	3.7638	4.4607		4.2847	4.2691							3.9831		
R.DFDRAITEHFADQFK.D +2					2.8604				2.5424							3.1299									
R.IAGLNPVR.I +2						2.5609					2.6336	2.8054	2.5538		2.6426	2.7257							2.5286		
R.YNIADAAR.I +1													2.2673												
	1				X	X			X	X	X	X	X		X	X							X		
gi|6320235|ref|NP_010315.1|									19.7		16.7		22.7	22.7	19.7	19.7	24.2	19.7		24.7	16.7				Protein with similarity to members of a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; Pst2p [Saccharomyces cerevisiae]
K.GIEAAGGSADIYQVEETLSPEVVK.A +2									4.5575		3.4861				4.965	4.3781	4.5621	4.1697			5.4134				
K.KGIEAAGGSADIYQVEETLSPEVVK.A +2																				2.8399					
K.NVFAELTNM*DEVHGGSPWGAGTIAGSDGSR.S +3													4.646	5.1515											
R.FGNFPAQWK.A +2											2.8141						2.9919			2.5817	2.55				
R.SPSALELQVHEIQGK.T +2									3.885				4.757	4.5719	4.3847	3.6643	4.0879	3.7538		3.3865					
	1								X		X		X	X	X	X	X	X		X	X				
gi|6323958|ref|NP_014029.1|						10			12.2			7.1	9.4	10.6	7.6	7.6	7.1	7.8			4.5				Phosphoribosylpyrophosphate amidotransferase (PRPPAT; amidophosphoribosyltransferase), catalyzes first step of the 'de novo' purine nucleotide biosynthetic pathway; Ade4p [Saccharomyces cerevisiae]
K.DYM*LASESVVFK.A +2																					3.653				
K.FEDGVFTGNYVTGVEDGYIQELEEK.R +2						3.8907			3.6597			3.0631				3.9489	3.3497	3.6679							
K.VLIVDDSIVR.G +2													2.8838												
K.VYFASAAPAIR.Y +2									2.6751			3.0469	3.0401	3.5377	3.4589		3.5325				3.4089				
R.GQDAAGIATCGSR.G +2													4.1074												
R.TCALECANVLGK.P +2						3.7102			4.1409																
R.TCALECANVLGKPYR.E +2																		4.0493							
R.VIYQSLEDLIDCCK.T +2						3.7189			3.3895					2.6783	2.673	3.3206									
R.VNNEDVFHALEGVYR.L +2														3.8383											
R.VSGLAGSM*GIAHLR.Y +2													2.8185	2.5633	3.1347										
R.VSGLAGSMGIAHLR.Y +2													3.5639	3.2158	3.1855										
	1					X			X			X	X	X	X	X	X	X			X				
gi|6323331|ref|NP_013403.1|					6.9		6.9		9.2				7.4		5.8	7.4	5.8	10.7	6.2	17.4					Major exo-1,3-beta-glucanase of the cell wall, involved in cell wall beta-glucan assembly; exists as three differentially glycosylated isoenzymes; Exg1p [Saccharomyces cerevisiae]
K.FLEDSNLAVTTNVLNYILK.K +2					3.1727		2.7262		4.5652				4.0614			3.4502				3.4436					
K.NDYLAPAYEYLR.N +2					2.5504		3.0557								3.0848			2.9618		2.8413					
K.VWVDLHGAAGSQNGFDNSGLR.D +3																				4.2118					
R.KYPNQCGTISN.- +2																									
R.LM*FNGLFPQPLTDR.K +2													2.751						3.4192						
R.TNDDNDEGIPVDEYHFCQYLGK.D +2																		2.7963							
R.TNDDNDEGIPVDEYHFCQYLGK.D +3									4.1971																
R.YVEAQLDAFEMR.G +2																	3.9583			3.3082					
R.YYDYDHGSLGEPIR.G +2															3.1454	2.7228	3.5817	3.8203	2.6105	3.4009					
	1				X		X		X				X		X	X	X	X	X	X					
gi|6322770|ref|NP_012843.1|					7.9	7.9	7.9					8.7	14.5	19.6	11	12			8.7	8.4					Subunit C of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma5p [Saccharomyces cerevisiae]
K.DLITLISNESSQLDADVR.A +2					4.1195	4.5768	3.2301					2.8161		4.2259		2.7761			3.0667						
K.IGSLDTLIVESEELSK.V +2												4.0975	4.3159	4.8343		4.2137			3.0313	3.2695					
K.IIEILQGLNETSTNAYR.T +2														4.4477	3.1334					2.8287					
K.SELIDAFGFLGGNAFM*K.D +2													2.8166												
K.TDSWFNETLIGGR.A +2					2.8775	2.6036	3.4891						3.283	3.9135	3.8504	3.0405									
K.VDNQIGASIGK.I +2													3.4127												
R.EFNYSEELIDQLK.K +2														3.1246	3.5303										
	1				X	X	X					X	X	X	X	X			X	X					
gi|6322127|ref|NP_012202.1|													13.6	25.3	21.4		32.5	26			22.1	32.5	14.3	14.3	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; Arc15p [Saccharomyces cerevisiae]
K.QGGVLLAWLER.I +2													3.2295		3.3045										
K.SVLEALTQVR.Q +2													3.7355	3.9945	3.8781		3.834			4.0796		3.7182	3.705		
R.IDIDAFDPESGR.L +2														3.9701	3.6677		3.6731	3.0526		3.4246	3.66	3.6182	3.6244		
R.ITQVSGVTPIVHYISDR.R +2														3.1442											
R.LTAADLVPPYETTVTLQELQPR.M +2																					2.9904				
R.SLATSGDSLGAVQLLTTDPPYSADAPTK.E +2																	2.9576	2.9348		2.7606					
	1												X	X	X		X	X			X	X	X	X	
gi|6324725|ref|NP_014794.1|									3.6				2.1	2.7		3.9			3.6	3.4		3.6	4.7	4.7	RNA polymerase II second largest subunit B150, part of central core; similar to bacterial beta subunit; Rpb2p [Saccharomyces cerevisiae]
K.AAPSPISHVAEIR.S +2													2.8276	2.8182											
K.AFFLGYMINR.L +2																				3.7412					
K.NCYLSEATESDLYK.L +2																3.9993						4.7557	4.505	2.7509	
K.VAALSGNEGDASPFTDITVEGISK.L +2									4.4752							4.776			4.4174				3.8877	2.8972	
R.LDLAGPLLAQLFK.T +2													3.8478												
R.SAGNIVQVFK.K +2																2.9251									
R.STENGIVDQVLVTTNQDGLK.F +2									3.4996					2.8594					3.3886	3.0644		3.0399	2.666	2.7179	
R.TYEAIDVPGR.E +2																				2.2996					
R.VFVNGVWHGVHR.N +2																				3.1242					
	1								X				X	X		X			X	X		X	X	X	
gi|6321004|ref|NP_011083.1|									10.7		6.5		9.8	6.2	10.4					9.5		7.4	13	9.2	hypothetical protein; Yer156cp [Saccharomyces cerevisiae]
K.ALVAQAIDER.M +2									2.6049		3.1785		2.9178	2.9792	2.7032							3.4939	2.63		
K.DWEASDILVDVGAQYDGVK.F +2																							4.686	3.1536	
K.IIVLPQFCPWK.E +2													3.5488	3.3713	3.2367					3.0207					
K.QFVEALDANDNGISK.Y +2																						4.2127	2.934		
K.VSSSDLDLLYDK.V +2									2.9414		2.5278		2.9361							3.1624				3.3974	
R.ASEFIGGVFVTLVR.G +2															2.7524										
R.GFFETFNEK.Y +1																				2.2549					
R.VSTVPINSTSFQFR.R +2									2.7476																
	1								X		X		X	X	X					X			X	X	
gi|6319685|ref|NP_009767.1|													3.1	2.1	2.2	1.9		1.5	2.3		1.5		1.4	1.3	Urea amidolyase, contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO2 and NH3; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation; Dur1,2p [Saccharomyces cerevisiae]
K.DSITAFQEGQLGER.A +2																							3.6216		
K.ESLDPTVISIIEGAK.K +2														3.6652	3.0351			2.5463			2.9894				
K.ETLPLYGVPIAVK.D +2																					2.7296				
K.LAVVGAHLK.G +2													2.6591	2.8229		2.7317									
K.LGDVLFLPSNEENK.S +2																			2.8082						
K.NPVLFSNAVENLSR.T +2													3.7259	3.45					2.9888						
K.RGSTLSIGK.L +2																								2.7252	
K.STAGGGGIGLQK.V +2																							2.8018		
K.TNLDQFATGLVGTR.S +2															3.9083	3.7325								3.9672	
K.VAAELEYPVMVK.S +2															2.9411	3.2272									
K.VDSEEDIEHIFETVK.H +2													3.0668												

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.VYGCITNIDYLK.S +2																		3.0341							
R.GLPTTAACPSFAYEPSK.D +2																									
R.TGANVIEIDFEPLLELAR.C +2													2.8911												
R.VPAALNNLIGLKPTK.G +2																			3.0111						
	1												X	X	X	X		X	X		X		X	X	
gi|6324535|ref|NP_014604.1|											13.4				13.4	12.2		17.7	13.4	13.4	13.4	17.7		13.4	20S proteasome alpha-type subunit; green fluorescent protein (GFP)-fusion protein relocates from the cytosol to the mitochondrial outer surface upon oxidative stress; Pre6p [Saccharomyces cerevisiae]
K.LYQTEPSGIYSSWSAQTIGR.N +2											3.4157				3.5246	3.4946		4.6888	4.6198	2.924	4.8753	4.5037		2.5655	
R.LTLEDPVTVEYLTR.Y +2											4.0329				4.0344			4.0017	4.0247	3.7369	3.5417	4.4312		4.125	
R.SLLEVVQTGAK.N +2																3.4495		3.4939				3.0654			
	1										X				X	X		X	X	X	X	X		X	
gi|6323752|ref|NP_013823.1|											4	4		6.5	6			5.8		10.5	10	6		4.2	Phosphoglucomutase, catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; Pgm2p [Saccharomyces cerevisiae]
K.DFPELDLGTIGK.N +2														3.6327	3.3483					2.8687	3.6551	3.1454		2.7032	
K.EIFDFDLIK.K +2															2.55										
K.IAAIGAANGIK.K +2											2.7258	2.6377						3.0106		3.0473	3.07				
K.LLFDSMNGVTGPYGK.A +2																				2.8985					
K.SGVVNSAFPADESLK.V +2																									
K.YGPLLVDIIDITK.D +2														4.2745	3.3678										
K.YNLSNGGPAPESVTNAIWEISK.K +2																		3.1085		3.308	2.9034	2.9386			
R.LSGTGSSGATIR.L +2											3.586	3.1406		3.1171							3.1321			3.6071	
	1										X	X		X	X			X		X	X	X		X	
gi|6321816|ref|NP_011892.1|													3	6	2.8	4.3	4.5		3.3	2.8		2.6		2.7	Non-ATPase base subunit of the 19S regulatory particle of the 26S proteasome; may participate in the recognition of several ligands of the proteasome; contains a leucine-rich repeat (LRR) domain, a site for protein?protein interactions; Rpn1p [Saccharomyces cerevisiae]
K.EDDSSLYEASLNALK.E +2													2.7397	4.8129	4.2635	4.1389						3.265		3.0517	
K.FILALNDEGEPIK.V +2														3.4752	3.8345	3.2025	3.3651								
K.ISSAAILGLGIAFAGSK.N +2														2.9308											
K.LIVDNDNWVYK.T +2																						2.5086			
K.LKTDLELLVER.L +2																				2.7917					
K.LPQFVDENTFQR.V +2																								2.5014	
K.SDGSAATSGFEFSK.E +2																			3.2891						
K.SSLADVLSILAM*TYSENGK.H +2																			2.6977						
R.LKEDDSSLYEASLNALK.E +2																	3.8969								
R.LLSDVSDFEGWGHEYIR.H +2																				2.8675					
R.VGQAVETVGQAGRPK.K +2													4.3829	4.1305		3.8385	3.2414								
	1												X	X	X	X	X		X	X		X		X	
gi|6320724|ref|NP_010804.1|													15	17	4.8	7.6		4.8	4.8	10	6.8			4.8	Non-essential protein of unknown function required for transcriptional induction of the early meiotic-specific transcription factor IME1; required for sporulation; expression is regulated by glucose-repression transcription factors Mig1/2p; Emi2p [Saccharomyces cerevisiae]
K.DVTSEELFSYLGR.R +2													3.8765	3.9703	3.6984	4.0769		4.0994	3.8677	3.1212	2.861			2.7769	
K.FSPNPGYHLFEK.R +2													3.1084	2.6595											
K.GLNNTSVGEEK.T +2																				2.7238					
K.LDELTAYFIECMEK.G +2																3.4708									
K.M*GFTFSYPVDQTSLSSGTLIR.W +2																					3.3601				
K.MGFTFSYPVDQTSLSSGTLIR.W +2																									
K.TPFQLCSEVLSR.I +2														3.1636						2.9597					
K.VNAEALEDAVVEICSSLQVDAAK.L +2																									
R.ETELSFLQSLR.L +2													3.3844	3.7191	3.4511	3.2268		3.2268	3.6061					3.3475	
R.GVLLAADLGGTHFR.V +2													4.3027	4.0828						3.4506					
R.HALALSPIGTEGER.K +2													3.1993	3.7872											
R.ISGM*YLGELLR.N +2													2.7333												
R.NILVDLHAR.G +2														2.5267											
	1												X	X	X	X		X	X	X	X			X	
gi|6320249|ref|NP_010329.1|						10.1	10.1		10.1					7.6	19.8		13.4	13.4			16.5			11.6	Coproporphyrinogen III oxidase, an oxygen requiring enzyme that catalyzes the sixth step in the heme biosynthetic pathway; localizes to the mitochondrial inner membrane; transcription is repressed by oxygen and heme (via Rox1p and Hap1p); Hem13p [Saccharomyces cerevisiae]
K.GGVNVSVVYGQLSPAAVSAM*K.A +2																					5.4532				
K.LLEVTTKPR.E +2															2.5465		2.6795	2.5161							
K.M*VEDCFDAFLPSYLTIVK.R +2						2.7442	3.2772		2.564						2.9583									3.7392	
K.MVEDCFDAFLPSYLTIVK.R +2									2.8951																
K.QAEITQGLESIDTVK.F +2						4.0979	3.4593		4.2278					4.2637	4.4068		3.1959	3.1032							
R.GIGGIFFDDYDER.D +2															2.9867						3.0055				
R.GNDGGGGTSMVIQDGTTFEK.G +2																	4.8321	2.7326			3.9492			3.6094	
R.YVEFNLIYDR.G +2														3.0785	2.6507										
	1					X	X		X					X	X		X	X			X			X	
gi|6322116|ref|NP_012191.1|									6.6			4.9	13.9	6.6	5.3	5.8		12.6		10.7				7	3-phosphoglycerate dehydrogenase, catalyzes the first step in serine and glycine biosynthesis; isozyme of Ser3p; Ser33p [Saccharomyces cerevisiae]
K.DQGYQVEFHK.S +2												2.9378								3.2461					
K.GIAVFNSPFSNSR.S +2												3.3016													
K.IAGAALDVYPHEPAK.N +2									3.3784				3.8727					3.9321		4.1071					
K.SDFVTLHVPATPETEK.M +2									3.902				3.6086	3.4477		2.9121									
K.SLDYDQENTVR.V +2																3.3728		3.3846							
K.YINEGNSVGSVNFPEVSLK.S +2													3.1683					3.0552						3.5895	
R.GTVVDIPSLIQAVK.A +2															3.5059			3.7606		2.6138				3.2253	
R.QVSTLDELLNK.S +2															2.941					2.647					
R.SVAELVIGEIISLAR.Q +2													3.1067	4.0204											
	1								X		X		X	X	X	X		X		X				X	
gi|6321606|ref|NP_011683.1|						9.9					23.2	16.3		11.2				13.7		13.7	9.9	9.9	9.9		Clathrin light chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; thought to regulate clathrin function, two Clathrin heavy chains (CHC1) form the clathrin triskelion structural component; Clc1p [Saccharomyces cerevisiae]
K.FPPLEDQNIDFTPNDK.K +2																		2.5738		3.9688					
K.TEQDDILETEASPAK.D +2											4.1817	3.1265													
R.ALQLINQDDADIIGGR.D +2											2.5127			4.4876				4.9648		2.6103					
R.DEFFGQDNTTWDR.A +2						4.5041					3.5538	4.003									4.525	3.7756	4.1128		
R.EAEILGDEFK.T +2						3.1331					2.7937	2.6403		2.685							2.592	2.5609	2.8159		
	1					X					X	X		X				X		X	X	X	X		
gi|6324318|ref|NP_014388.1|									22				21.6	26.6		16.2	29	37.3		16.6		12.9	14.1		Putative protein of unknown function with similarity to phosphoserine phosphatases; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; homozygous diploid mutant shows an increase in glycogen accumulation; Ynl010wp [Saccharomyces cerevisiae]
K.AGEQRPVYFYCGDGVSDLSAAK.E +2																4.3262	4.0802	4.455		2.8552					
K.AGEQRPVYFYCGDGVSDLSAAK.E +3									5.4355				5.8518	5.436		3.9962	5.4376			3.9903					
K.DILASMK.Q +1																							2.0376		
K.DLVTYCK.K +1																		1.8402							
K.DTFEWAQENDVPVIVVSSGM*K.P +2														2.8148											
K.DTFEWAQENDVPVIVVSSGM*KPIK.V +3														3.867											
K.DTFEWAQENDVPVIVVSSGMK.P +2									2.6425								3.0564	4.2073				3.645			
K.ECDLLFAK.R +1																				2.2452					
K.IDIVSNEVEIDAHDQWK.I +2													4.2539	4.6004		5.3181	3.5535	4.0793							
K.IIYKDESPFGHDK.S +2													3.9604					2.6964							
K.VFEGVLDDTK.S +1																				2.7856			2.3417		
K.VFEGVLDDTK.S +2									3.4718								3.3993	3.5055				3.7383	3.7249		
R.LVGQESIHK.I +2																									
R.PVYFYCGDGVSDLSAAK.E +2														3.3332									3.4751		
	1								X				X	X		X	X	X		X		X	X		
gi|6322049|ref|NP_012124.1|									8.3				14	4.9	9.1		8.9		12.7	3.6	6.5		8.3		Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct2p [Saccharomyces cerevisiae]
K.AGEACTIVLR.G +2									2.8087											2.9065			2.9644		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.AVDTEAQNIDGK.K +2													3.8024				2.5239								
K.DHFAELATNAILR.L +2																	2.5443								
K.FGINTFINR.Q +2													3.2162						2.91	2.6182					
K.GSTNLEHIQIIK.I +2																			3.3039						
K.ILIANTTLDTDK.V +2													3.1322												
K.LSDSFLDEGFILAK.K +2													4.302	4.3466	3.6562				4.1869		3.7293				
K.VQDDEVGDGTTSVTVLSAELLR.E +2									2.5059						3.6591		3.2716						2.9118		
R.AVVSSASEAAEVLLR.V +2													3.2091												
R.GATDQTLDEAER.S +2																			2.5554						
R.LASAAALDALTK.A +2									3.6598				3.6085	3.3447	3.4385								4.1771		
R.QLPTILADNAGFDSSELVSK.L +2																			2.6104		3.1177				
	1								X				X	X	X		X		X	X	X		X		
gi|6324761|ref|NP_014830.1|							7.6		6.9				12.1		8.9	5.3	11	11		9.8			6.2		Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchange factor activities, while these activities are found in separate proteins in S. pombe and humans; Tuf1p [Saccharomyces cerevisiae]
K.ELDSAMAGDNAGVLLR.G +2							4.2826		4.3057						3.1986		4.8732	3.4273		4.545					
K.GGANFLDYAAIDK.A +2															3.2656	3.1808				3.2348					
K.ILASLYILSK.E +2													3.677		3.1992										
K.KGEELEIVGHNSTPLK.T +2													2.8533												
K.LLDAVDEYIPTPER.D +2									3.5876								3.1797	3.9065		3.0758					
K.TTVTGIEMFR.K +2													2.758			3.1146									
K.VDTIDDPEMLEILVEMEMR.E +2																	3.9083	3.3594					3.2067		
R.SKPHVNIGTIGHVDHGK.T +2							3.2151						3.0741												
R.TVGTGLITR.I +2																							2.9233		
	1						X		X				X		X	X	X	X		X			X		
gi|6324669|ref|NP_014738.1|						12.8			16.7		11.6		10.9	24.4	12	13.6	10.1						17.1		Ribose-5-phosphate ketol-isomerase, catalyzes the interconversion of ribose 5-phosphate and ribulose 5-phosphate in the pentose phosphate pathway; participates in pyridoxine biosynthesis; Rki1p [Saccharomyces cerevisiae]
K.AYFGNSDGSVEVTEK.- +2											2.6046														
K.FICIPTGFQSR.N +2														2.6153											
K.GGGACLFQEK.L +2																							3.0259		
K.IDALESLGNPLEDAK.R +2									4.0342		3.7388			4.2309	3.1949	4.3736	4.4217						4.7811		
K.IDALESLGNPLEDAKR.A +2																2.9738									
K.IIGIGSGSTVVYVAER.I +2															2.66										
K.LLVGVVETGLFIDNASK.A +2														3.1927											
K.LQLGSIEQYPR.I +2														3.3511			3.465								
K.TFIVVADSR.K +2									2.7809				2.6117	2.9546											
R.IDIAFDGADEVDENLQLIK.G +2						5.3866			3.2559				4.7579			5.1733							5.4119		
R.QGVPIEIVPSSYVR.V +2						2.5406																			
	1					X			X		X		X	X	X	X	X						X		
gi|6324758|ref|NP_014827.1|													12.2	27.8	10.1	15.2	7.6	6.3	12.2	9.6		7.6			3-phosphoserine aminotransferase, catalyzes the formation of phosphoserine from 3-phosphohydroxypyruvate, required for serine and glycine biosynthesis; regulated by the general control of amino acid biosynthesis mediated by Gcn4p; Ser1p [Saccharomyces cerevisiae]
K.AVQNLVDFIK.E +2													3.407	3.6778	3.6888	3.0401	3.6646			2.9918		3.4283			
K.IAPAGYLVTGSWSQK.S +2													3.8749		4.0296	3.8645		3.3921	3.007	2.6339					
K.IDVSQYGVIMAGAQK.N +2														3.171	3.1181	3.8941									
K.ILYEALDANSDFYNVPVDPK.C +2														2.8798		4.5468	3.3046		3.2316			2.8955			
K.NIGLAGLTLYIIK.K +2														4.7315					4.1789	3.1475					
K.NISGASDETLHELGVPITPIAFDYPTVVK.N +3														4.5693											
R.ASIYNALSVK.A +2																		2.8316							
R.EEPQHFGAGPAQM*PTPVLQQAAK.D +3													5.1496	5.1017											
	1												X	X	X	X	X	X	X	X		X			
gi|6321829|ref|NP_011905.1|						20.2			12.3			21.9	13.2	13.2		13.2	21.9	21.9				21.1			Vacuolar H+ ATPase subunit G of the catalytic (V1) sector, involved in vacuolar acidification; Vma10p [Saccharomyces cerevisiae]
K.AEAGVQGELAEIK.K +2						4.3714			4.3113			3.1179										4.4743			
K.AEAGVQGELAEIKK.I +2												2.7353				3.5754									
K.KAEAGVQGELAEIK.K +2									2.7094				3.2398	4.237		3.7767	4.3659	4.9786				2.6187			
K.KAEAGVQGELAEIKK.I +2													4.7834	4.6241											
K.KAEAGVQGELAEIKK.I +3													3.7907	3.8457											
K.NAGGVGELEK.K +2						2.8999																2.6464			
K.NGIATLLQAEK.E +2												2.7993					3.865	3.3207							
	1					X			X			X	X	X		X	X	X				X			
gi|6322667|ref|NP_012740.1|											5.9	5.9	8.7		15.9	8	6.6	7		6.1	9.8				5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes; Prs1p [Saccharomyces cerevisiae]
K.IFVGNSHPELGNMVCQR.L +2																	3.9116								
K.ITAVIPQFPYSK.Q +2															3.1562						2.8936				
K.LVTIDVSPIFAECIR.R +2													3.7563		4.2556	4.1568				3.1435					
K.SDAIDTIVVTNTYPISGER.I +2															3.6702	4.4141		3.1198			4.3939				
R.ENVEDYEDAVVVSK.N +2											4.2184	3.9908													
R.EQLITLVGNVR.G +2												2.5815	3.4279		3.3063		3.0255	3.2032		2.8791	2.7738				
R.LGIEPAPCTLK.K +2											2.7998		2.898		2.736										
	1										X	X	X		X	X	X	X		X	X				
gi|6320607|ref|NP_010687.1|						10.4							10.4	10.4	10.4	10.9	19	37.1	13.6	10.4					Dimeric hypoxanthine-guanine phosphoribosyltransferase, catalyzes the formation of both inosine monophosphate and guanosine monophosphate; mutations in the human homolog HPRT1 can cause Lesch-Nyhan syndrome and Kelley-Seegmiller syndrome; Hpt1p [Saccharomyces cerevisiae]
K.ADLPAEMLNDK.N +2						2.6689																			
K.KADLPAEMLNDK.N +2																		2.6407							
K.NVLIVDEVDDTR.T +2						2.7853								3.6724	3.764	3.8228	3.1523	3.8998	3.5242						
K.QYISYNNVHQLCQVSAER.I +2																		3.2368	2.7589						
K.TNFGIFVLHDK.Q +2													3.6838	3.6644	2.7661					3.1596					
R.MAIEQGNDIFIPEQEHKQ.- +2																	3.1922	2.7856							
R.TQWIDYEQCK.L +2																		2.7453							
R.TTLHYALSELEK.D +2													3.1928			3.0236	2.8587	3.1376		3.0415					
	1					X							X	X	X	X	X	X	X	X					
gi|6322633|ref|NP_012706.1|									17.5			14.6	16.2	38.9	16.2	17.5		6.7	16.2	27.4					Dihydroorotate dehydrogenase, catalyzes the fourth enzymatic step in the de novo biosynthesis of pyrimidines, converting dihydroorotic acid into orotic acid; Ura1p [Saccharomyces cerevisiae]
K.DAFEHLLCGASM*LQIGTELQK.E +2														5.1894											
K.ESVVVKPK.N +2														2.5724											
K.FLNNTYENPFM*NASGVHCM*TTQELDELANSK.A +3													6.2403	6.196	4.7332				4.0527	3.7998					
K.GYTSIDQFR.G +2									2.675					2.6482		2.7387		2.7186							
K.ILNEFPLAYVNSINSIGNGLFIDVEK.E +2									5.07			3.4398				2.951				3.2546					
K.IQDSEFNGITELNLSCPNVPGK.P +2																									
K.IQDSEFNGITELNLSCPNVPGKPQVAYDFDLTK.E +3														5.2767											
K.NGFGGIGGEYVK.P +2																		2.7579							
K.NGFGGIGGEYVKPTALANVR.A +2									2.6237			2.6078	4.0761	3.4927	3.8301	4.2011			3.6199						
K.NGFGGIGGEYVKPTALANVR.A +3									3.6899				3.5664	3.6367											
R.YISVPLGSINSM*GLPNEGIDYYLSYVLNR.Q +3																				4.1627					
	1								X			X	X	X	X	X		X	X	X					
gi|6321474|ref|NP_011551.1|		13.8		25.3	23		13.8	23					23	56.3					39.1	39.1					Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming processes; Acb1p [Saccharomyces cerevisiae]
K.AVNELPTKPSTDELLELYALYK.Q +2				2.7033										3.2507						2.9484					
K.AVNELPTKPSTDELLELYALYK.Q +3				4.6647										4.5493					4.2102						
K.EYIALVDQLIAK.Y +2		4.0035			4.2893		4.2873	4.4174					3.9636	4.2523					3.676	3.9937					
K.SQEDAEKEYIALVDQLIAK.Y +2														5.3487											
K.SQEDAEKEYIALVDQLIAK.Y +3														4.5433											
K.WEAWENLK.G +1													2.2021	2.0892											
K.WEAWENLK.G +2					2.7288			2.6865						2.5729											
	1	X		X	X		X	X					X	X					X	X					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6320861|ref|NP_010940.1|			13.3							8.7	8.7		14.3	15.7	19.9		8.4	9.8		14					Delta 1-pyrroline-5-carboxylate reductase, catalyzes the last step in proline biosynthesis; Pro3p [Saccharomyces cerevisiae]
K.AADETAAAFYPSK.I +1																									
K.AADETAAAFYPSK.I +2										3.1795	4.2914									3.8703					
K.EQKPLVNELISQVGK.Y +2																				2.964					
K.IITCNHDEPSAQQVTDLVETFDESPNGIK.V +3			5.8338										3.8494	4.3686	4.3516										
K.LGIPLQESK.E +2																									
K.PFLAEEVLNGVK.S +2																		4.7607		4.3707					
K.PLVNELISQVGK.Y +2																	3.7182								
K.SGAHPSVLK.H +2			2.5789																						
K.SGIINGVEEAAR.V +2										2.7733	3.0609		3.3875		3.5848		3.3215								
K.YGYGCAVVSYSADVSK.E +2														3.2625	3.3973			2.945							
	1		X							X	X		X	X	X		X	X		X					
gi|6322174|ref|NP_012249.1|													7.3	5.5	5.5	8.5		8.3		5.5			5.5	5.1	Aspartyl protease secreted into the periplasmic space of mating type a cells, helps cells find mating partners, cleaves and inactivates alpha factor allowing cells to recover from alpha-factor-induced cell cycle arrest; Bar1p [Saccharomyces cerevisiae]
K.GYEGAPNEYYPNFPQILK.S +2																2.6427		3.2878							
K.KLVNIQTDGSISGAK.I +2																		2.8713							
K.LVNIQTDGSISGAK.I +2																								2.8691	
K.YATTPVSGVLGIGFPR.R +2													4.1708	2.8942	3.3125	4.0629				3.3883			3.1632		
K.YPVLLDSGTSLLNAPK.V +2													5.1832	5.528	4.969	4.8738		4.1829		2.6628			4.3239	3.3047	
R.SSTYQYLENGR.F +2													2.9588												
	1												X	X	X	X		X		X			X	X	
gi|6324273|ref|NP_014343.1|									10.2		10.2	8.5	18	14.1	14.1	14.1								11.3	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maintenance of mitochondrial osmotic stability and mitochondrial membrane permeability; Por1p [Saccharomyces cerevisiae]
K.DGPLSTNVEAK.L +2													2.9717												
K.LEFANLTPGLK.N +2												2.7072	3.1503	3.2086	3.3479	3.1602									
K.LPNSNVNIEFATR.Y +2											2.733														
K.NELITSLTPGVAK.S +2									4.0053			3.3322	3.3355	4.3624	4.2887	4.1538								3.4877	
K.QTGLGLTQGWSNTNNLQTK.L +2																								2.5519	
K.SAVLNTTFTQPFFTAR.G +2									4.0662		3.5899		3.4527	4.7089	3.7846	4.4956									
	1								X		X	X	X	X	X	X								X	
gi|6324474|ref|NP_014543.1|													2.6	6.6	2.6	2.3		3.9		2		2.4	2.5		Putative metalloprotease; Yol098cp [Saccharomyces cerevisiae]
K.CLNIAHPVEK.L +2																				2.8916					
K.DLSDFDALLQWSQK.D +2													3.2586	3.9397	3.2325								3.1087		
K.IDDVYEPWNPLIK.C +2														4.0076	3.0902	3.578		3.85				3.0654			
K.LCEINSWGFNIYR.G +2														2.7413											
K.LQEIFAEIENGNFEK.E +2														4.26											
K.STDPLFVEAK.L +2																									
K.SVAFVSCHPAK.L +2																2.8248				2.9314					
R.GAGLAYGASMLK.L +2																		2.957							
R.IFVDNKPIIVTAK.P +2													3.1483	3.3518											
R.LATIECGYFETALSK.Y +2																		3.5058							
R.NGNVMLSSLTNR.N +2																						2.7164	2.7747		
	1												X	X	X	X		X		X		X	X		
gi|6321776|ref|NP_011852.1|												9.4	6.9	7.8	12.8			10.3		16.9	8.8		11.6		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs3p [Saccharomyces cerevisiae]
K.AAEILLENR.A +2																		3.028			3.1471				
K.ENVNYMDSIIISPDAGGAK.R +2																					3.0766		2.9631		
K.LAVIDISSVLAESIR.R +2														3.2943	3.5041										
K.SVIAIVTHGVLSGR.A +2															3.0403					3.7207					
R.DQDIFIITQIGSGVVNDR.V +2												3.5404								4.3052			3.1872		
R.ITAIINFPYAR.Q +2												2.5598	3.541		2.6153			2.572		2.9852					
R.LDLNFALIHK.E +2													3.3549	3.5637						3.219					
R.VVCTNTVPFEEK.I +2																		3.3361							
	1											X	X	X	X			X		X	X		X		
gi|6321796|ref|NP_011872.1|								12					15.9	15.9	15.9	9.9			12	15.9			12		Mitochondrial superoxide dismutase; protects cells against oxygen toxicity; Sod2p [Saccharomyces cerevisiae]
K.AIDEQFGSLDELIK.L +2								3.7606					4.7595	4.9521	4.5713	3.5468			4.2413	3.7107			3.945		
K.AIWNVVNWK.E +2													3.021	3.0804	3.2279	2.9433				3.0127					
K.LAGVQGSGWAFIVK.N +2								2.6749					3.5618	3.3425	3.2776				4.0908	3.2479			3.6651		
	1							X					X	X	X	X			X	X			X		
gi|14318481|ref|NP_116616.1|									8.1			5.5	8.1	8.1	5.5	5.5				4.8			4.2		Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymerizes to form microtubules; Tub2p [Saccharomyces cerevisiae]
K.LAVNLVPFPR.L +2									3.5215			3.2397	3.7648	3.6513	3.8088	3.7023				3.0826			3.5625		
K.NMMAAADPR.N +2																							2.9289		
R.LNVYFNEASSGK.W +2									3.2838																
R.M*M*ATFSVLPSPK.T +2													3.3262	3.0217											
R.MMATFSVLPSPK.T +2																				2.9581					
R.SINVDLEPGTIDAVR.N +2									4.3401			3.8966	4.6392	4.5688	4.7546	4.3786									
	1								X			X	X	X	X	X				X			X		
gi|6322845|ref|NP_012918.1|					7.5	13.1	7.5	7.5	12.3								13.1	9.3					11.2		Alpha subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches; Cap1p [Saccharomyces cerevisiae]
K.DINQSNVDDVVCTIR.D +2						4.3761											3.8491	4.2321							
K.GLDIEPYEFTHAK.I +2									2.9045																
K.INWGSAIGSYR.L +2																									
R.DIETNFENDLDLSFFDLNEK.Q +2					4.6525	5.2895	4.751	4.4271	4.2254								3.3366						4.2134		
R.SSYIYDLETR.E +2																		2.5143					3.0566		
	1				X	X	X	X	X								X	X					X		
gi|6324283|ref|NP_014353.1|									6.3				9.2	5.2	5.1		4.6		4.5	5.8		5.5			Leucyl aminopeptidase (leukotriene A4 hydrolase) with epoxide hydrolase activity, metalloenzyme containing one zinc atom; role in vivo is not defined; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ynl045wp [Saccharomyces cerevisiae]
K.CTALQWLNSK.Q +2													2.7935												
K.DCQWEFENDVEK.F +2																	2.8363								
K.SLDTFQFLDTLYEFYPEK.K +2													2.5445												
K.STFTASIESRLPVVFSGIR.I +2									3.2341								2.7989		4.6835	3.376					
K.VPIPAYLIGIASGDLSSAPIGPR.S +2									3.3308				4.6409	4.5996	2.516										
R.ALLDIYQDNIVK.S +2														3.2704						3.0592		3.4555			
R.FSTLVQNLNDNTDPDDAFSTVPYEK.G +2																						3.0526			
R.IIGAIHGEPTR.H +2													2.8551		2.543				2.5564						
R.LALATFDK.F +1																				2.0474					
R.SPEYDQSTLSNYK.D +2																									
	1								X				X	X	X		X		X	X		X			
gi|6321217|ref|NP_011294.1|									14.9				18.1	18.1	13.2	14.9		16.3		11.5		23.6			Protein of unknown function, similar to Listeria monocytogenes major sigma factor (rpoD gene product); the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; Nif3p [Saccharomyces cerevisiae]
K.GLLQDEGHEVVVSK.M +2																		3.8722							
K.SWDNTGLLIDCSTAQVTTADANAK.T +2									3.559							3.2759						4.9341			
K.SYALETVSGETDDLIGYGR.F +2									5.0626				4.0988	3.9266	4.0553	4.0127		2.5198		3.2611		3.4401			
K.TVIVCNHSNTER.G +2																						2.5873			
K.VAVCAGSGSGVFK.Q +2																						3.2903			
R.LSPHTNPQHETAIK.L +2													3.6134	3.2998				3.4301		3.025					
R.VPYVQVASLAAPSAWNQLK.I +2													2.9012	3.5033	2.8294										
	1								X				X	X	X	X		X		X		X			
gi|6322082|ref|NP_012157.1|		1.6	1.6	1.6									2.7	2.7		2.9			3.8	8.4					Component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat; involved in ER to Golgi transport, cargo selection and autophagy; required for the binding of the Sec13 complex to ER membranes; homologous to Lst1p and Lss1p; Sec24p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.IIVSGTLPNLGIGK.L +2		3.5988	3.9715	3.1166									4.0377						3.4917	3.4461					
K.IPQIFQSNLITNFALGPALK.S +2																			2.8227	2.6283					
K.QEIPVVENSEFNQR.V +2																2.8622									
K.SAYHLIGGVGGK.I +2														3.3857						3.4459					
K.SVQDILATYK.K +1													2.0496												
R.ASALNNLESLPLK.Y +2														3.0196		2.9623									
R.LWASSTLVEDK.I +2																									
R.M*LVPSELSNASPDYIR.S +2																				3.1782					
R.NHDDVITYQSLYIVR.G +2																				4.6669					
	1	X	X	X									X	X		X			X	X					
gi|6323886|ref|NP_013957.1|	24.8	38.1	30.5										30.5	30.5	30.5				50.5	50.5					Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Ap and has similarity to rat ribosomal protein S10; Rps10bp [Saccharomyces cerevisiae]
gi|6324867|ref|NP_014936.1|	X	X	X										X	X	X				X	X					Protein component of the small (40S) ribosomal subunit; nearly identical to Rps10Bp and has similarity to rat ribosomal protein S10; Rps10ap [Saccharomyces cerevisiae]
K.ALQSLTSK.G +1	1.9156	1.8677																							
K.IHQYLFQEGVVVAK.K +2		4.8911	5.0941										4.1449	4.9085	4.1241				4.5561	4.7259					
K.IHQYLFQEGVVVAK.K +3													4.1793	4.5257						4.4428					
K.TQFSWQYYYYTLTEEGVEYLR.E +2																			2.5949	3.5315					
R.EYLNLPEHIVPGTYIQER.N +2	4.339	4.3134	4.4896										4.13	3.2641	4.1047				3.0218	2.7911					
	1 X	X	X										X	X	X				X	X					
gi|6324696|ref|NP_014765.1|									19	19			19	23	34.1		19	26.2		26.2					Profilin, actin- and phosphatidylinositol 4,5-bisphosphate-binding protein, plays a role in cytoskeleton organization, required for normal timing of actin polymerization in response to thermal stress; localizes to plasma membrane and cytosol; Pfy1p [Saccharomyces cerevisiae]
K.IVEQLADYLIGVQY.- +2									3.899	3.434			3.6294		2.9835		3.2208	3.6825		3.1095					
K.QTVIIAHYPPTVQAGEATK.I +2														2.7744	3.5915			2.8532		2.6462					
R.HDAEGVVCVR.T +2									2.752	3.1378			2.8691	3.3555	3.122		3.0665								
	1								X	X			X	X	X		X	X		X					
gi|6320917|ref|NP_010996.1|									6.2		6.2	8.5		5	10.6	6.2	8.3			4.8					Mitochondrial aldehyde dehydrogenase, involved in regulation or biosynthesis of electron transport chain components and acetate formation; activated by K+; utilizes NADP+ as the preferred coenzyme; constitutively expressed; Ald5p [Saccharomyces cerevisiae]
K.ALFNLADLVEK.H +2															3.7357		3.6741			2.5696					
K.AMEDDVDEAVAAAK.K +2											2.7508														
K.EEVFGPIVTVSK.F +2												2.6762		3.0524	3.0847										
K.VGDPFDEEVFQGAQTSDK.Q +2									4.0749		3.4636	4.3632			4.1096	4.7382	3.9328								
R.IYIQDTVYEEVLQK.L +2									2.7001			2.868		3.896	3.9123	4.7588	3.7405			3.0044					
	1								X		X	X		X	X	X	X			X					
gi|6321807|ref|NP_011883.1|						5.4	7				4.9		4.9	4.5		4.9	4.9			6.1					Cytosolic asparaginyl-tRNA synthetase, required for protein synthesis, catalyzes the specific attachment of asparagine to its cognate tRNA; Ded81p [Saccharomyces cerevisiae]
K.EATGVDELTTAGSQDHPFK.T +2																				3.6589					
K.M*TDTIGVPIFLTR.F +2														3.4396											
K.TEDNEYQEISASALK.K +2						4.7873					4.3674		4.9453				4.362			4.0351					
K.TPAYALFASQQK.S +2							4.5081				4.055		4.5604	4.542		4.6271	4.6479								
R.EGIDTDAYYWFIDQR.K +2						3.2831	3.4768									2.6279									
R.IDDMDELMAGFK.R +2							3.5105																		
	1					X	X				X		X	X		X	X			X					
gi|82795254|ref|NP_012033.2|									16.1		10.4	16.1	21.3	20.9	15.3	21.3				16.1					6-phosphogluconolactonase, catalyzes the second step of the pentose phosphate pathway; weak multicopy suppressor of los1-1 mutation; homologous to Sol2p and Sol1p; Sol3p [Saccharomyces cerevisiae]
K.NDQLPTALVNK.L +2											2.8558														
K.VSVSGGSLIDALYESLVADESLSSR.V +2									3.937			2.6093	2.8451	3.0323	2.7299	3.3751				2.5703					
R.ASLTHQLGEFIVK.K +2													4.1938	4.2322	3.8465	3.3881									
R.IVPLTDADSNYGAFK.R +2									3.5861		3.2232	3.2229	3.759			4.2695				3.1349					
R.VAWCHDSPKPPSDR.I +3														3.5064											
	1								X		X	X	X	X	X	X				X					
gi|6325337|ref|NP_015405.1|						2.4	4.1		9.4	4.1			9	12.4	9					14.2					Translational elongation factor EF-1 alpha; also encoded by TEF2; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes; Tef1p [Saccharomyces cerevisiae]
K.IGGIGTVPVGR.V +2						3.6212	3.7093		3.5018	3.2451			3.1526		3.4409										
K.PLRLPLQDVYK.I +2																				2.7173					
K.TLLEAIDAIEQPSRPTDK.P +2													4.2294		2.768					3.1227					
K.TLLEAIDAIEQPSRPTDKPLR.L +3														4.2884											
K.YQVTVIDAPGHR.D +2													3.4928	3.5735	3.5754					2.6026					
R.LPLQDVYK.I +2							2.9665		3.0389	2.7278															
R.VETGVIKPGM*VVTFAPAGVTTEVK.S +3									4.6235																
R.VETGVIKPGMVVTFAPAGVTTEVK.S +3														3.928						3.5756					
	1					X	X		X	X			X	X	X					X					
gi|42742310|ref|NP_014942.2|					17.9		17.9		17.9	17.9	17.9	17.9		17.9				17.9							Transcriptional coactivator that bridges the DNA-binding region of Gcn4p and TATA-binding protein Spt15p; suppressor of frameshift mutations; Mbf1p [Saccharomyces cerevisiae]
K.INEKPTVVNDYEAAR.A +2					4.8463		4.5553		2.9658	2.5006	3.7323	3.7052		4.7151				4.2087							
K.INEKPTVVNDYEAAR.A +3																									
R.GNNIGSPLGAPK.K +2					3.3654		3.6962		3.4952	3.1061	3.6011	3.2462		3.237				2.691							
	1				X		X		X	X	X	X		X				X							
gi|6319321|ref|NP_009404.1|												4.7			3.9					4.7	4.8	4.8	5.8	4.7	Subunit of heterotrimeric Replication Factor A (RF-A), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination; Rfa1p [Saccharomyces cerevisiae]
K.LFNVNFLDTSGEIR.A +2												2.8323			3.4989					3.4904			4.0152	4.288	
K.QLLGVDANTLM*SLK.E +2																									
R.AEADYLADELSK.A +2																							4.3752		
R.ATAFNDFATK.F +2																							2.6988		
R.DTVIEECFDESNVPK.T +2																					4.5326	4.1854		3.4514	
R.VIIAEPAIVR.E +2															2.6285										
R.YDNPTGGVYQVYNTR.K +2												2.7516								2.9312	3.8907	3.3026			
R.YTVANLHSLNYR.A +2																									
	1											X			X					X	X	X	X	X	
gi|6322746|ref|NP_012819.1|									8.8				5.3			8.4		7		6.2			5.6	8.4	Vacuolar aminopeptidase, often used as a marker protein in studies of autophagy and cytosol to vacuole targeting (CVT) pathway; Lap4p [Saccharomyces cerevisiae]
K.DVNTEESDLFSTVTLYDNEEIGSLTR.Q +2																2.8236								3.6708	
K.GGLLESVVER.S +2													3.0995					2.9218							
K.GVGVIGSHVDALTVK.L +2									2.8117											3.7673					
K.HFLFAPR.L +2																									
K.SALVDSTPLPVCR.I +2									2.7589									2.8219							
K.SNWQDSIGEDGGK.F +2																		3.677							
R.IAVAPYGGTLNELWLDR.D +2									4.4457				2.5365			4.2622				2.5442			2.9801	3.9789	
R.NGTNLSAFILGK.N +2																							2.5726		
R.SGGTIGPSLASQTGAR.T +2																									
	1								X				X			X		X		X			X	X	
gi|6324475|ref|NP_014544.1|												5.6		8.3		11.1	10.6		8.3			7.2		8.1	Cytoplasmic tryptophanyl-tRNA synthetase, aminoacylates tryptophanyl-tRNA; Wrs1p [Saccharomyces cerevisiae]
K.AVFGFNDSDCIGK.F +2												3.153										3.6193			
K.EQVVTPWDVEGGVDEQGR.A +2																4.3467	4.2695					3.0061		4.6237	
K.LCIETLQEFVK.A +2														2.9785			2.7925								
K.M*SASDDTTAIFM*TDTPK.Q +2																			2.8257						
K.MSASDDTTAIFMTDTPK.Q +2																	3.3027							4.0129	
K.WLQEVFDVPLVIELTDDEK.F +2																2.848									
K.YAFSGGQVSADLHR.E +2														3.4542											
R.ELGGNPDVDVAYQYLSFFK.D +2																			2.561						
R.FFPALQGSTTK.M +2												2.606		3.0857		2.5108									

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
	1											X		X		X	X		X			X		X	
gi|6320440|ref|NP_010520.1|									5.2				5.1					5.8		5.2	7.9	5.8	5.2		Homoaconitase, catalyzes the conversion of homocitrate to homoisocitrate, which is a step in the lysine biosynthesis pathway; Lys4p [Saccharomyces cerevisiae]
K.DALAYLASPAVVAASAVLGK.I +2																									
K.ISSPAEVLSTSEIPFSGVK.T +2									2.5777				2.5528												
K.NPSQIVTTLDHDIQNK.S +2													3.3237												
K.TEIIENPVVEEEVNAQTEAPK.Q +2																		4.0092			5.2392	4.5251			
K.VVVTEGSLDGPVILEQK.V +2																					2.634				
R.LSDLQSAADVVCPTGDLNK.V +2																		3.1006		3.4537		3.2708	4.1206		
R.NSINNALLTLEIPALIK.K +2									2.9568											3.1791	2.5646		2.7074		
	1								X				X					X		X	X	X	X		
gi|14318528|ref|NP_116661.1|									6.2			6.2	2.8		5.8	5	9.2						9.2		Putative X-Pro aminopeptidase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YFR006W is not an essential gene; Yfr006wp [Saccharomyces cerevisiae]
K.DGYENLTGITSDPDEIEK.I +2									4.2139			4.0504				3.9986	4.5413						5.2235		
K.DWYEIESIR.K +2																2.582									
K.ISTAFFIAGEELEGNK.Y +2															3.5734		3.3158								
R.EVYETVLDMQNQAMER.I +2																							3.6721		
R.VFDIDEALYISDLGK.K +2									4.6114			4.2051	5.0352		4.3806		2.9657						3.7974		
	1								X			X	X		X	X	X						X		
gi|6323864|ref|NP_013935.1|													5.6	7.2	5.6		6.3		7	8.8		9.9			Mevalonate kinase, acts in the biosynthesis of isoprenoids and sterols, including ergosterol, from mevalonate; Erg12p [Saccharomyces cerevisiae]
K.FLDDFPAIPM*ILTYTR.I +2																			2.8142						
K.GTDDEAVETNNELYEQLLELIR.I +2														3.2782											
K.LTGAGGGGCSLTLLR.R +2													3.4681		2.9744				3.1119			3.6116			
K.PAVAASVSALR.T +2																				3.7271					
K.SLVFQLFENK.T +2													3.2414	3.5671	3.2274		3.0132			2.6816					
K.WSINDFNAITEDQVNSQK.L +2																	3.0875			2.7747		4.469			
R.DITQEQIDSFK.K +2																						3.8311			
	1												X	X	X		X		X	X		X			
gi|14318577|ref|NP_116710.1|												10.2	8.8	13.1		13.1		11.3		10.9		10.6			Subunit of the 19S regulatory particle of the 26S proteasome lid; synthetically lethal with RPT1, which is an ATPase component of the 19S regulatory particle; physically interacts with Nob1p and Rpn3p; Rpn12p [Saccharomyces cerevisiae]
K.ALLFNNEK.E +2													2.6707												
K.AWDLLQSGSQNISEFDSFTDILK.S +2														2.9162		3.2186									
K.LISLYLLNLLSQNNTTK.F +2																				2.77					
K.NLEDDSLLSYPIK.L +2												2.771		3.983		3.912				3.1552		3.9387			
K.NTELSYDFLPLSNIK.A +2												2.7886	4.0089					4.6286							
K.SLSIAFENGDYAACEK.L +2																		3.5679				2.9788			
	1											X	X	X		X		X		X		X			
gi|6323955|ref|NP_014026.1|													7.1	5.5	5.5		5.5	7.1		5.5	3.6				Vacuolar carboxypeptidase Y (proteinase C), involved in protein degradation in the vacuole and required for full protein degradation during sporulation; Prc1p [Saccharomyces cerevisiae]
K.AWTDVLPWK.Y +2																		2.5745			2.7091				
K.DFICNWLGNK.A +2													2.9671	3.3128	3.2055		3.459	3.1935		3.5597	3.1605				
K.EAVGAEVDHYESCNFDINR.N +2															3.5519		3.9449	3.6674		2.7454					
K.EAVGAEVDHYESCNFDINR.N +3													3.8482	3.7716											
K.YDEEFASQK.V +1																									
K.YDEEFASQK.V +2													2.9572												
gi|6324508|ref|NP_014577.1|													10.4	19.3	13.4		16.5	14		10.4	16.2				Bisphosphate-3'-nucleotidase, involved in salt tolerance and methionine biogenesis; dephosphorylates 3'-phosphoadenosine-5'-phosphate and 3'-phosphoadenosine-5'-phosphosulfate, intermediates of the sulfate assimilation pathway; Met22p [Saccharomyces cerevisiae]
K.DDFLFTNDQFPLK.S +2														3.4907	3.6795						3.4126				
K.KDDFLFTNDQFPLK.S +2													3.613		2.8335		3.7015			2.8487					
K.NDNSPVTTGDYAAQTIIINAIK.S +2																	2.9615	4.1694			4.1254				
K.NDNSPVTTGDYAAQTIIINAIK.S +3														3.6849											
K.VVGEESSSGLSDAFVSGILNEIK.A +2													5.3201	5.9429	5.2995		2.6486			4.4953	4.4747				
R.FWCLDPIDGTK.G +2														3.1733	2.5966			2.6421							
R.GLGAFYSPSSDAESWTK.I +2																		3.5462							
	2												X	X	X		X	X		X	X				
gi|6323932|ref|NP_014003.1|													7.8	9.4	8.6		11.8	7.2	11.8	8.6					Nuclear-enriched ubiquitin-like polyubiquitin-binding protein, required for spindle pole body (SPB) duplication and for transit through the G2/M phase of the cell cycle, involved in proteolysis, interacts with the proteasome; Dsk2p [Saccharomyces cerevisiae]
K.ANGIPVANQR.L +2																									
K.ILKDDQTVESYHIQDGHSVHLVK.S +3														4.7889											
K.SGQDKWEVNVAPESTVLQFK.E +2															3.1435										
K.WEVNVAPESTVLQFK.E +2																	3.542	4.2834	4.1013	3.1009					
R.QLNDM*GFFDFDR.N +2													2.8412	2.8412	2.6725				3.0706						
R.QLNDMGFFDFDR.N +2													2.7124	3.336			2.6552	2.7407							
R.SGGSVQGALDSLLNGDV.- +2													4.8314				4.3951		4.7482	3.868					
	1												X	X	X		X	X	X	X					
gi|6325103|ref|NP_015171.1|													7.9	6.2	6.2	7.9		7.9	8.4	8.1					Vacuolar aspartyl protease (proteinase A), required for the posttranslational precursor maturation of vacuolar proteinases; important for protein turnover after oxidative damage; synthesized as a zymogen, self-activates; Pep4p [Saccharomyces cerevisiae]
K.DTENGGEATFGGIDESK.F +2																				4.462					
K.FDGILGLGYDTISVDK.V +2													4.2689	4.7268	3.2042	4.2568		5.0177	4.4455	3.6291					
K.GDITWLPVR.R +2														2.9538	2.8236										
K.QDFAEATSEPGLTFAFGK.F +2																			3.7648						
K.YYSIYDLGNNAVGLAK.A +2													3.9067			3.6557		3.2964							
	1												X	X	X	X		X	X	X					
gi|6321854|ref|NP_011930.1|													21.6	15	6.9	5.8	7.1	6.9		23.2					2-dehydropantoate 2-reductase, part of the pantothenic acid pathway, structurally homologous to E. coli panE; Pan5p [Saccharomyces cerevisiae]
K.ASCGPVFTSIIDECLQILR.V +2													2.8193	4.4321						2.734					
K.EALAPYLPYINK.N +2													3.174	2.7933			2.5913								
K.KPIDNLVVTTK.T +2													3.7382					3.5188		3.636					
K.LPWTEEEMIQK.K +2																2.624									
K.LYLEGSPIFSYPVEK.C +2													4.5183	3.9921	3.8818		4.0481	3.8018		4.5124					
K.NTNLILIQNGLGVLELLR.E +2																				3.1207					
K.SVVEDDAANNSLVK.L +2													4.467							5.0237					
R.FTNALVVPLFR.S +2													3.3712	3.0693	3.6302	3.5836				3.6707					
	1												X	X	X	X	X	X		X					
gi|14318575|ref|NP_116708.1|									13.2			13.2	13.2	13.2	13.2	13.2				13.2					20S proteasome beta-type subunit; Pre4p [Saccharomyces cerevisiae]
K.TTVQVAEEAIVNAM*R.V +2													3.8003												
K.TTVQVAEEAIVNAMR.V +2									4.5792			4.1174		4.4233	4.6377	5.1452				3.6561					
K.YDNGVIIAADNLGSYGSLLR.F +2									5.0909			3.7913	4.7669	3.4677	2.9543	3.3451				4.417					
	1								X			X	X	X	X	X				X					
gi|6324776|ref|NP_014845.1|				7.3					4.1				4.1	4.1	4.1	4.1				4.1					Imidazoleglycerol-phosphate dehydratase, catalyzes the sixth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control via Gcn4p; His3p [Saccharomyces cerevisiae]
K.ALAVAIR.E +1				1.8663																					
R.ITLHVDCLR.G +1									2.2404				2.4354	2.5751	2.3103	2.0927				2.3727					
R.ITLHVDCLR.G +2				2.9173					2.7027				2.643	2.6861	2.6818	2.6536				2.5398					
	1			X					X				X	X	X	X				X					
gi|6324524|ref|NP_014593.1|																	11.6	6.9			8.1	10.4	7.5	10	Glutathione synthetase, catalyzes the ATP-dependent synthesis of glutathione (GSH) from gamma-glutamylcysteine and glycine; induced by oxidative stress and heat shock; Gsh2p [Saccharomyces cerevisiae]
K.APDLLTQLSGSK.K +2																					3.2242	3.1331		2.9333	
K.FEENPSNASVSPVTIYPTPIPR.K +2																	3.7524	4.4441					4.2941	4.7258	
K.GPIYNDQNMVISDSGYLLSK.A +2																	3.3027								

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.IQQLLTDEGVLGK.Y +2																					3.8901				
K.TTEALALSDSEFTGK.L +2																	4.2779				4.168	4.1478	3.7816	3.839	
R.DTEQEIAVVYYR.T +2																		2.5566				3.6157			
R.TGYTTTDYTSEK.D +2																						2.7893			
	1																X	X			X	X	X	X	
gi|6319591|ref|NP_009673.1|																2.2			3.2	1.6	2.4		2.6	2.8	Alpha aminoadipate reductase, catalyzes the reduction of alpha-aminoadipate to alpha-aminoadipate 6-semialdehyde, which is the fifth step in biosynthesis of lysine; activation requires posttranslational phosphopantetheinylation by Lys5p; Lys2p [Saccharomyces cerevisiae]
K.FVNNWFVEK.D +2																				2.8764					
K.KLVETLPSSYPSR.E +2																			3.1166						
K.LNSIEANFSFDELAEK.I +2																4.39								4.2698	
K.LPLPSIELTQAQISLVASGAGAR.G +2																			2.5124						
K.LQVDLPLGTIFK.Y +2																							2.549		
K.SSGGSSQGEVVENVTANYAEDAK.K +2																					5.4805			3.6148	
R.FDKPDDLSK.F +2																			2.8						
R.IELGEIDTHISQHPLVR.E +2																									
R.TCVVETPTLNSIDK.S +2																				3.4461					
R.TGVVVGPDSNPTLSFTSGSGEGIPK.G +2																							3.1378		
R.TQICGIGEIGEIYVR.A +2																3.1275									
R.VTGDDDIVLYIANNK.I +2																									
R.VVVATSLNPPK.E +2																					2.9822				
	1															X			X	X	X		X	X	
gi|6323843|ref|NP_013914.1|													4.1	2.8	4.4						4.6		3	4.3	P subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv2p [Saccharomyces cerevisiae]
K.DLCSITGFDGISLQPNSGAQGEYTGLR.V +2																					2.6723				
K.HDVVDMITGIGGSK.S +2															2.6226										
K.TAATDITSTQYSR.I +2													4.3015		4.1632								3.4448		
K.TFSIPHGGGGPAGAPICVK.S +2																									
K.VFDIENSSQFLSEDYSNSFPR.E +2																					3.431			3.9927	
K.VVPVWCLQDGSLDLVDLK.N +2													3.0404	3.2239	3.1063								4.5125		
R.EEAAYPLPFLR.Y +2													2.791	2.7725											
R.NLLESPEWYTSYTPYQPEISQGR.L +2																								2.5784	
	1												X	X	X						X		X	X	
gi|6325375|ref|NP_015443.1|													9.2	9.2				7.1		9	10.5			14.1	Methylthioribose-1-phosphate isomerase, catalyzes the isomerization of 5-methylthioribose-1-phosphate to 5-methylthioribulose-1-phosphate in the methionine salvage pathway; Ypr118wp [Saccharomyces cerevisiae]
K.IGTLQLAVICK.Q +2													3.0497	3.6385						3.0755	3.8735				
K.IPSTLITDSSIAYR.I +2																		3.4809			3.002			3.4691	
K.TTIDNVTETGDDIIVEER.N +2																					4.837			4.647	
K.VLDQLLLPYTTK.Y +2													4.0051	3.8407											
K.VVTGTVINPENGSLILNESGEPITGK.V +2																				3.5375				2.824	
K.YVPIHTIDDGYSVIK.S +2													3.7045	3.4971				3.2405							
	1												X	X				X		X	X			X	
gi|6324515|ref|NP_014584.1|						3.1							3.5	3.5						8.4	6.6			5.1	Putative metalloprotease; Yol057wp [Saccharomyces cerevisiae]
K.DISPVIETNIGFIETYR.E +2																					3.4561				
K.EYDETPQGM*LQSFLDR.E +2																					2.8344				
K.EYDETPQGMLQSFLDR.E +2																					2.7663				
K.FGQLAGPFEECR.A +2						2.9277																			
K.LEMNSTNDDFAIK.L +2																				2.966					
K.NQITETYPSGQITLSNAVTK.V +2																								3.3143	
K.NVSLGNILSAAAK.S +2													3.3198	3.8895						3.4018					
K.TEYFPQLTDK.E +2						3.1234														3.1318					
K.VEFIFGDHSR.E +2																				2.5806					
K.VGENSFQIWVASENVK.N +2																								3.3299	
R.AGLLALEYWNPK.T +2													3.9023	4.1796											
R.QFIQSNSYIDDNNK.V +2																				2.585	2.5924				
	1					X							X	X						X	X			X	
gi|6320893|ref|NP_010972.1|													8.5	6.1		4	4.6		5.7					4.6	Aspartate kinase (L-aspartate 4-P-transferase); cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis; Hom3p [Saccharomyces cerevisiae]
K.EVDGIFTADPR.K +2																									
K.FPVQIVDDIVK.H +2																2.5432	3.2153		4.1354					3.7258	
K.LSCLFM*TALCNDR.G +2													2.8491												
K.LSCLFMTALCNDR.G +2																	3.1652							2.6905	
K.NVQNPLGNGTIYPDNVAK.K +2																			3.8568						
R.FILNPALQAK.L +2													3.0087	2.7784		2.9805									
R.IVPVFTGFFGLVPTGLLNGVGR.G +3													3.6731	4.1581											
R.TVDLVMSCGEK.L +2																									
	1												X	X		X	X		X					X	
gi|6323237|ref|NP_013309.1|													8.4	8.4	13.5	12.1		8.1						8.8	Component of both the Nup84 nuclear pore sub-complex and of the COPII complex (Sar1p, Sec13p, Sec16p, Sec23p, Sec24p, Sec31p, Sfb2p, and Sfb3p) which is important for the formation of ER to Golgi transport vesicles; Sec13p [Saccharomyces cerevisiae]
K.FGTILASCSYDGK.V +2																		2.5069							
K.LIDTLTGHEGPVWR.V +2													3.7766	3.9648	3.0277										
R.DVAWSPTVLLR.S +2													3.1084	3.4167	3.1486	2.6957		3.1268						2.8764	
R.SYLASVSQDR.T +2																2.8496									
R.TCIIWTQDNEQGPWK.K +2															4.1022	4.0899								3.6611	
	1												X	X	X	X		X						X	
gi|6324727|ref|NP_014796.1|															1.5				3.2	2.6	3.3	2.6	3.2		Short-lived membrane ABC (ATP-binding cassette) transporter, actively exports various drugs, expression regulated by Pdr1p; also involved in steroid transport, cation resistance, and cellular detoxification during exponential growth; Pdr5p [Saccharomyces cerevisiae]
K.LDPNSENFSSAAWVK.N +2																			2.6237	3.8769			3.6982		
K.NLSASGASADVAYQSTVVNIPYK.I +2																					3.4859	4.6375	4.4846		
K.TTLLDCLAER.V +2															3.2635						3.4507		3.2215		
K.VCVLDDGYQIYYGPADK.A +2																			3.7662		5.0307	2.7907			
K.YADAVVGVAGEGLNVEQR.K +2																									
K.YFEDMGYVCPSR.Q +2																				2.7588					
R.GLDSATALEFIR.A +2															3.4046					3.5651					
R.QTTADFLTSVTSPSER.T +2																			3.2483						
	1														X				X	X	X	X	X		
gi|6322634|ref|NP_012707.1|													3	3					3.7	3.8		3	2.5		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Ykl215cp [Saccharomyces cerevisiae]
K.GFGYYETICGGSGAGADSWR.G +2																						2.9971			
K.GGPLTITDANLFLGR.L +2													2.7575	3.5619					2.931	3.0786					
K.IFGPNEDESLDLETTTLK.F +2																			2.5353			3.4023	2.8093		
K.IPAGSLLSPR.S +2													3.2941	2.9785											
K.SILSGPAGGVIGYSSTCYDK.N +2																				2.9079					
K.VVPLYDTVVEIDER.V +2														2.7939											
R.VTLEDFSEDPYFTK.S +2													3.1603						3.9082	2.9151			4.3823		
	1												X	X					X	X		X	X		
gi|6319527|ref|NP_009609.1|									15.6							9.8	15.4			10.1		9.8	10.1		Putative protein of unknown function; induced by cell wall perturbation; Ybr053cp [Saccharomyces cerevisiae]
K.DLFVTTANAEINDAVR.T +2									3.6988							2.9626						3.8425			
K.ESVGCIFPILDGASQNEIK.Q +2									2.5833							3.3767						3.1218			
K.IPNVLDGNVPLESTK.R +2																	3.0849			2.9872			3.3053		
K.NSNNQSFESPEPDGSAIWFSK.D +2									2.6779								3.6834			3.5634			3.9644		
K.SEWEYVILYSECPELSTDR.A +2																	3.1453								
	1								X							X	X			X		X	X		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6322828|ref|NP_012901.1|													21.6	20.6	27.9					13.7	13.7		13.7		Uridylate kinase, catalyzes the seventh enzymatic step in the de novo biosynthesis of pyrimidines, converting uridine monophosphate (UMP) into uridine 5'-diphosphate (UDP); Ura6p [Saccharomyces cerevisiae]
K.DYSFVHLSAGDLLR.A +2													3.8959	3.8737	2.8409										
K.EGQIVPQEITLALLR.N +2													3.5687	3.0606	3.5121						3.5392		2.9214		
K.ETSM*PVIEYFETK.S +2														2.7221	3.2307										
K.ETSMPVIEYFETK.S +2																				2.8016	2.6111		2.5798		
K.FILFFDCPEDIM*LER.L +2													3.1178		4.1875					2.7533					
K.MDQAISFER.D +2																									
1													X	X	X					X	X		X		
gi|6320510|ref|NP_010590.1|													24.4	17.8				21.3	13.3	28			16.9		Peptidyl-prolyl cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; Cpr5p [Saccharomyces cerevisiae]
K.EVIIVESGELETVPLDNK.D +2																		2.5316		3.4923			3.5394		
K.M*GYLNSIFHR.V +2													3.1376	3.0185					3.258	2.5349					
K.NTNGSQFFITTVPCPWLDGK.H +2													2.7173	3.3958				2.5173	3.5531	2.7594			3.8092		
K.SIFGNTFKDENFDVK.H +2													3.6401							3.3597					
K.VYFDINHGDK.Q +2													2.9335	3.0042				2.6402							
R.VIPNFMIQGGDFTHR.S +2																									
1													X	X				X	X	X			X		
gi|6319558|ref|NP_009640.1|													5.6	2.7	2.7			3		3.7			2.9		Mitochondrial C1-tetrahydrofolate synthase, involved in interconversion between different oxidation states of tetrahydrofolate (THF); provides activities of formyl-THF synthetase, methenyl-THF cyclohydrolase, and methylene-THF dehydrogenase; Mis1p [Saccharomyces cerevisiae]
K.EYTEENIDFVAK.G +2																									
K.GAVELAHAVVDATK.E +2													3.3051	2.9709	2.8356										
K.LPAEITEVELLK.K +2																				3.1199					
K.NFNFLYDVNSSIEDK.L +2																									
K.TFGIPVVVAINR.F +2													2.9599	2.8711	3.0178								2.7944		
K.YVLVAGITPTPLGEGK.S +2													3.1679					3.807		3.5996			4.2719		
R.RVVDINDR.M +2																				2.7416					
R.SSIVGNPIASLLK.N +2													2.8801					2.9368							
1													X	X	X			X		X			X		
gi|6320809|ref|NP_010888.1|												20.6	39.7	39.7	39.7					27			20.6		RNA binding protein, part of U3 snoRNP involved in rRNA processing, part of U4/U6-U5 tri-snRNP involved in mRNA splicing, similar to human 15.5K protein; Snu13p [Saccharomyces cerevisiae]
K.AFPLADAALTQQILDVVQQAANLR.Q +2																									
K.AFPLADAALTQQILDVVQQAANLR.Q +3													6.3266	6.2092	4.76					4.4111					
K.NVPYVFVPSR.V +2												2.7405	3.1373	3.0034	3.1799					2.9226			2.8549		
R.PVIAASITTNDASAIK.T +2												3.2667	3.4983	4.9391	5.1546								4.0396		
1												X	X	X	X					X			X		
gi|6322244|ref|NP_012318.1|						7.1					13.6		14.1			15.7			14.1				15.7		Cytoplasmic protein of unknown function; expression induced by calcium shortage and via the copper sensing transciption factor Mac1p during conditons of copper deficiency; mRNA is cell cycle regulated, peaking in G1 phase; Yjl217wp [Saccharomyces cerevisiae]
K.NTELSQGTWLNKPK.S +2													3.3793						4.0456						
K.SDWSTAVYGGNAR.D +2											3.1284														
K.VTFSEWSLTAPLGK.A +2						3.59					3.1433		3.8869			3.6999			2.7654				4.004		
R.VQGSYESLYDQAGIM*VR.I +2																2.7698									
R.VQGSYESLYDQAGIMVR.I +2																4.3934									
1						X					X		X			X			X				X		
gi|6322525|ref|NP_012599.1|											7.3		8.9	8.7		8.2				12		7.6			Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity; Arp3p [Saccharomyces cerevisiae]
K.DYEEYGPEIVR.N +2											3.1904														
K.FAQFVVENQEK.T +2											3.4707			4.1197								3.9591			
K.GLYNNIVLSGGSTM*FK.D +2																									
K.KDYEEYGPEIVR.N +2													3.4493												
K.LGFAGNDSPSWVFPTAIATAAPSNTK.K +2																4.0803				4.6137					
K.STGVDVSVISHR.K +2																						3.2643			
R.DITLFIQSLLR.E +2													3.9731							3.4047					
R.IAQSELLSGTK.S +2											3.025			3.662		3.4804						2.8768			
R.NAVWFGGSLLAQTAEFK.G +2													3.1488	2.9155						2.6019					
1											X		X	X		X				X		X			
gi|6323278|ref|NP_013350.1|													1.7	2.2	5			2.1	2.4			2.4			Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP; Yef3p [Saccharomyces cerevisiae]
K.ALLPHLTNAIVETNK.W +2															2.7784										
K.AYEELSNTDLEFR.K +2																						2.8454			
K.IAILAAISAM*VDAAK.D +2														4.5279	4.4078										
K.IAILAAISAMVDAAK.D +2																									
K.LVEDPQVIAPFLGK.L +2															3.6717			2.77							
K.LVLAAGTWQR.P +2													3.1535												
K.SNFATIADPEAR.E +2																						3.711			
K.VLEELFQK.L +2													2.8142	2.8049	2.7549			2.7123	3.0189						
R.M*TPSGHNWVSGQGAGPR.I +2																			3.2074						
1													X	X	X			X	X			X			
gi|6323460|ref|NP_013533.1|													9.5	8.9	2.9		5.2			3.7	5.5				Coronin, cortical actin cytoskeletal component that associates with the Arp2p/Arp3p complex to regulate its activity; Crn1p [Saccharomyces cerevisiae]
K.APDQVPLFR.G +2													3.0317	3.1267	3.0136		2.5502								
K.GDLGGFYTVDQSSGILM*PFYDEGNK.I +2																					2.8382				
K.IGIWDIPENYK.F +2																					2.9825				
K.RPQQPTTQETALEEK.K +2													3.2642	3.9327											
K.SASSSSTINHVLK.E +2																				2.7809					
K.SSDIDQVNNAEDPSR.D +2																	4.4834								
K.SVEGPILVSMR.S +2																				2.6838					
K.VGHVLYHIPVAENVLASSSGDYTVK.L +3														4.6609											
R.DTSGWEEADDEPAPIK.I +2																									
R.IEPVSFFVPR.R +2													3.0056	2.5493	2.679		2.7027								
R.SEEFQEDIYPDAPSNKPALTAEEWFSGK.S +3													4.0362												
R.SIYDGSAPSFHEAK.R +2																									
1													X	X	X		X			X	X				
gi|6323383|ref|NP_013455.1|									10.7				8.2	9.3	9.3					10	21.3				Nit protein, one of two proteins in S. cerevisiae with similarity to the Nit domain of NitFhit from fly and worm and to the mouse and human Nit protein which interacts with the Fhit tumor suppressor; nitrilase superfamily member; Nit3p [Saccharomyces cerevisiae]
K.EPSTSVQFLSNLANK.F +2																				3.0283	3.1409				
K.IILVGGTIPELDPK.T +2													4.6823	4.8366	4.5969					4.4027	3.6758				
K.IYNTSIIFNEDGK.L +2														2.6022	2.8888										
K.LVVLPECFNSPYSTDQFR.K +2									3.4818												2.5972				
K.VALVQLSGSSPDK.M +2									3.7515																
R.AVDNQVYVM*LCSPAR.N +2																					2.6742				
R.FPELAM*LSAR.K +2													2.8498												
1									X				X	X	X					X	X				
gi|6324195|ref|NP_014265.1|												8.5	10.1	8.5	10.1	14.4					13.8				Putative protein of unknown function with similarity to dehydrogenases from other model organisms; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YNL134C is not an essential gene; Ynl134cp [Saccharomyces cerevisiae]
K.EYGADELFDYHDADVIEQIK.K +2													4.5667		4.8633										
K.IGPQGALLGCDAAGQIVK.L +2												3.8539	4.9727	4.6048	4.3662	4.6012									
K.NGLDDIPQLLDDIK.H +2												2.6062		3.6852		3.2563					3.3724				
K.QDIPIPELEEGFVLIK.T +2																					3.1028				
K.TVAVAGNPTDWK.H +2																									
K.YNNIPYLVDCVSNTETIQQVYK.C +2																2.8764					3.5936				
1												X	X	X	X	X					X				

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6579194|ref|NP_013844.2|													6.6	5.3	3.6		3.6		3.6	3.4					Large subunit of the nuclear mRNA cap-binding protein complex, interacts with Npl3p to carry nuclear poly(A)+ mRNA to cytoplasm; also involved in nuclear mRNA degradation and telomere maintenance; orthologous to mammalian CBP80; Sto1p [Saccharomyces cerevisiae]
K.NNGLIEATAIEAVFR.N +2														3.7283						2.7057					
K.QAAIALLTM*VVNSK.N +2													3.8813												
K.QAAIALLTMVVNSK.N +2																				2.7426					
K.SIINYFFEELQK.W +2													3.437												
R.EVTELESILGELK.N +2													3.5687	4.3087	3.8016		2.8066		2.5783						
R.LTSNFSEVEDSLPQEFTK.Y +2													3.0637	3.3781	2.7929		2.6798		3.9605						
	1												X	X	X		X		X	X					
gi|6324363|ref|NP_014433.1|													6.7	11.1	6.7	7			9.6	15.2					Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; required for cortical localization of calmodulin; Arc35p [Saccharomyces cerevisiae]
-.M*LHLQPQNLLIQK.T +2														3.0959					2.9483						
K.TIILSFPFELAISK.F +2													4.0131		3.6965	2.6618				2.6641					
K.TLNEAIEALR.K +2														3.8621		3.3073				3.547					
K.TLNEAIEALRK.G +2																			2.7073						
K.VDEDDENDELSAEGR.Q +2																									
R.FITFVLFPR.H +2													3.3107		2.7079				3.1634	2.8086					
R.IVSDFDYTTYHISNTAEDK.S +2																				3.5397					
R.VTIIFETIFQDETDK.I +2														2.5082											
	1												X	X	X	X			X	X					
gi|10383757|ref|NP_009880.2|									18.1				14.6	14.3	10				10	18.1					Diadenosine 5',5''-P1,P4-tetraphosphate phosphorylase I (AP4A phosphorylase), involved in catabolism of bis(5'-nucleosidyl) tetraphosphates; has similarity to Apa2p; Apa1p [Saccharomyces cerevisiae]
K.EHFLPTFNTEPLQDAK.V +2													4.5609	3.9889	3.9928				3.3972	3.8473					
K.IGFNSTGYCGM*LTK.N +2													3.2194												
K.ITEKPELINDILLECGFPNTSGQKPNEYNY.- +3														5.864						4.5823					
K.LLCALDNEESDK.R +2																				4.178					
K.LLCALDNEESDKR.H +2									3.1546																
R.ALTFFQDWLNENPELK.K +2									4.2404				4.3672		4.2465				3.6524						
R.GQTPEGEDPLGKPEEELTVIPEFGGADNK.A +3									3.9022																
	1								X				X	X	X				X	X					
gi|6325220|ref|NP_015288.1|											12.1	12.1	16.6	35.7					35.7	24.8					Subunit beta1 of the nascent polypeptide-associated complex (NAC) involved in protein targeting, associated with cytoplasmic ribosomes; enhances DNA binding of the Gal4p activator; homolog of human BTF3b; Egd1p [Saccharomyces cerevisiae]
K.APADAEK.K +1													1.8146												
K.DEAIPELVEGQTFDADVE.- +2											3.1377														
K.KDEAIPELVEGQTFDADVE.- +2											4.5835	4.045	4.1272	5.0647					3.6549	3.5419					
K.LHAVTIDNVAEANFFK.D +2														5.2842					3.0356	4.4232					
K.LHAVTIDNVAEANFFKDDGK.V +2																				3.9499					
K.VGVQVAAQHNTSVFYGLPQEK.N +2														4.0187					3.3469						
K.VGVQVAAQHNTSVFYGLPQEK.N +3														4.3273											
	1										X	X	X	X					X	X					
gi|6321806|ref|NP_011882.1|													5.4	5.4	6	6.3	5.6			7.8					Argininosuccinate lyase, catalyzes the final step in the arginine biosynthesis pathway; Arg4p [Saccharomyces cerevisiae]
K.LGLLTETELAK.I +2															2.9359					3.0277					
K.NADSLELLR.G +2																	3.0736								
R.DIVNDTLFPALK.G +2													2.9323	3.6131		3.3714				2.605					
R.FGQDLFETFNFEQSVER.R +2															3.3794	3.7846	3.9924								
R.NDQVVTDLR.I +2																									
R.VFGDLTGFLM*SLK.G +2													2.5737	4.3987						2.5051					
	1												X	X	X	X	X			X					
gi|10383791|ref|NP_009958.2|						17							22.2		17	23.7	28.1			22.2					Single-stranded DNA-binding protein essential for mitochondrial genome maintenance; involved in mitochondrial DNA replication; Rim1p [Saccharomyces cerevisiae]
K.GALVYVEADAANYVFER.D +2																2.7861									
K.KLEDAEGQENAASSE.- +2													2.9913				4.6321			3.078					
K.YSIASQPR.R +2						2.6262									2.5798		2.7549								
R.IGSEFTEHTSANNNR.Y +2						4.6227							5.1898		5.3209	4.7256	4.6977			4.3204					
	1					X							X		X	X	X			X					
gi|6320009|ref|NP_010089.1|												13.3	13.3	18.2	21	13.3				11.6					ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p; Arf1p [Saccharomyces cerevisiae]
K.LFSNLFGNK.E +2														2.7688											
K.NISFTVWDVGGQDR.I +2												4.2754	4.0332	4.4223	4.5927	4.5004									
K.QDLPEAMSAAEITEK.L +2																									
R.ILMVGLDGAGK.T +2																				2.6367					
R.NAAWLVFANK.Q +2												3.6768	3.6976	3.7428	3.7957	4.0742				3.4903					
R.NTEGVIFVVDSNDR.S +2															3.4765										
	1											X	X	X	X	X				X					
gi|6320849|ref|NP_010928.1|										7.6	13.1		27.3	21.7		13.1				12.6					20S proteasome beta-type subunit; localizes to the nucleus throughout the cell cycle; Pre1p [Saccharomyces cerevisiae]
K.NKPELYQIDYLGTK.V +2													4.185	4.0832						2.9739					
R.EDYELSPQAVSSFVR.Q +2										3.7821	3.6566		4.1713	4.3781		4.5568									
R.RPYQVNVLIGGYDK.K +2													3.3893	4.012											
R.VQDSVILASSK.A +2											3.0397		3.7122			2.816				3.4769					
	1									X	X		X	X		X				X					
gi|6322459|ref|NP_012533.1|						9.8			12.1				14	24.7	12.1					28.4					20S proteasome beta-type subunit, responsible for cleavage after acidic residues in peptides; Pre3p [Saccharomyces cerevisiae]
K.DNLTAGIIVAGYDDK.N +2									2.9135					2.9327	3.341					2.5774					
K.HSLSQAIK.W +2														2.5152											
K.LPYAIAGSGSTFIYGYCDK.N +2													3.0819	3.3319						3.6785					
K.NKGEVYTIPLGGSVHK.L +2																				2.8101					
R.M*VVLTAAGVER.L +2													3.0673												
R.MVVLTAAGVER.L +2						4.2145			4.2507					3.953	3.5462					3.9543					
R.TTTGAYIANR.V +2						3.1198																			
	1					X			X				X	X	X					X					
gi|6322155|ref|NP_012230.1|													8	8	12.9		9.4	8.7	13.2						Beta subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches; Cap2p [Saccharomyces cerevisiae]
K.DLQDSPFPSAPLR.K +2														4.0135			3.8111								
K.NAAIASSAEEANK.D +2													3.9875		3.3095				2.764						
K.NAAIASSAEEANKDAQAEVIR.G +2																									
K.NAAIASSAEEANKDAQAEVIR.G +3																									
K.TDQNSHM*M*LSGNLTR.Q +2																			2.7379						
K.TDQNSHMMLSGNLTR.Q +2																		2.6377							
R.NLLETVYFEK.T +2													3.0556	3.3166	2.6189			3.1347	2.8424						
R.SPWSNTYYPELSPK.D +2															3.116		3.4816								
	1												X	X	X		X	X	X						
gi|6322261|ref|NP_012335.1|												3.3		3.2	8	8.2	5.4		3.9						Putative mitochondrial aconitase isozyme; similarity to Aco1p, an aconitase required for the TCA cycle; expression induced during growth on glucose, by amino acid starvation via Gcn4p, and repressed on ethanol; Aco2p [Saccharomyces cerevisiae]
K.AGSAINYIGNIIR.R +2														3.2217											
K.DLPSSIATNQEVFDFLESCAK.R +2															3.7735	4.4551	3.8272		4.9179						
K.ILYSHLCDPEESITSSDLSTIR.G +2																	3.5503								
K.ISSGDVLETLNLVDMIAK.D +2																3.0485									
K.QGVLPLTFANESDYDK.I +2															3.1206										
R.DGIIDIFQENGAK.V +2												3.2091			3.2584	3.7051									
R.FLGGEILLVK.S +2																			3.2616						
R.IPFFVTPGSEQIR.A +2												2.6887		3.1473	3.0701	3.0109									
	1											X		X	X	X	X		X						

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6322843|ref|NP_012916.1|						14.4	14.4	14.4	14.4					14.4		14.4									Protein involved in mRNA turnover and ribosome assembly, localizes to the nucleolus; Mrt4p [Saccharomyces cerevisiae]
K.APLTFTIPEGIVYSR.G +2																									
K.ITIDSPYLVCTEGEK.L +2						3.891	3.3158	3.3536	3.3834					3.8022		3.6087									
K.LCSGVTGLLFTDEDVNTVK.E +2						4.2198	4.0299	3.5941	2.8239					3.6814		4.1572									
	1					X	X	X	X					X		X									
gi|6325319|ref|NP_015387.1|									19		17.7	17.7								26.6				16.5	Cytosine deaminase, zinc metalloenzyme that catalyzes the hydrolytic deamination of cytosine to uracil; of biomedical interest because it also catalyzes the deamination of 5-fluorocytosine (5FC) to form anticancer drug 5-fluorouracil (5FU); Fcy1p [Saccharomyces cerevisiae]
K.EGGVPIGGCLINNK.D +2									3.345		2.9505	3.6628													
K.GMDIAYEEAALGYK.E +2											2.9358	2.9135								3.2881					
K.GSATLHGEISTLENCGR.L +2																				3.3033					
K.QFIDERPQDWFEDIGE.- +2									2.9197															2.7336	
R.CVVGENVNFK.S +2																								2.5206	
R.GHEVVVVDDER.C +2																				3.7609					
	1								X		X	X								X				X	
gi|6324511|ref|NP_014580.1|									8.1		8.1							4.4				6	11.1		5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase, involved in nucleotide, histidine, and tryptophan biosynthesis; one of a five related enzymes, which are active as heteromultimeric complexes; Prs5p [Saccharomyces cerevisiae]
K.FVQTTM*LVGDVR.N +2																									
K.FVQTTMLVGDVR.N +2																		2.7318				3.7796			
K.ICENLDIHPSK.V +2																									
K.LQNTSNSTDAGELFNAQNAGYK.L +2									4.0186		4.6324												4.5135		
K.PIAQNYIQHR.I +2																		2.5418							
R.IPDYQDAVIVSPDAGGAK.R +2									3.5717		4.0552											4.3224	3.0106		
R.VDVIDVSCIIGEAIR.R +2																							2.7906		
	1								X		X							X				X	X		
gi|6320056|ref|NP_010136.1|					2.2								1.2	1.2							3		4.6		Alpha subunit of COPI vesicle coatomer complex, which surrounds transport vesicles in the early secretory pathway; Cop1p [Saccharomyces cerevisiae]
K.ADSM*ASDAIPIDFDPYAK.F +2																					3.3538				
K.ADSMASDAIPIDFDPYAK.F +2																							2.6222		
K.NFLQASYFAGEFLK.I +2					3.5723								3.9092	4.1384											
R.AYDDTVSEDQILPYVPGLDVVNEK.M +2																							2.955		
R.ITLLMVDDAEDEK.L +2					3.2253																		2.7771		
R.SSIFAEGGSLPLAYAVAK.A +2																					2.6462				
	1				X								X	X							X		X		
gi|6323871|ref|NP_013942.1|						9.9							8.2			9.4				8.6			7.4		Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall; Gas3p [Saccharomyces cerevisiae]
K.DDFVNLESQLK.N +2																3.8245							3.4446		
K.LDDSGSLTYKDDFVNLESQLK.N +2																									
K.NVFSGGLVYEYTEEANNYGLVK.L +2																				2.7961					
K.NYPNVLGFFSGNEVINDQSDYAK.I +2						2.5984							3.1051			3.2478				2.5921					
K.VNDDLDISK.S +2																									
R.ADPSGTYDSLYLSR.V +2						4.4166																	4.1473		
R.DAYAFQQLGVNTVR.I +2																									
R.FIKPSSATNSESDNEVFFVK.G +3													3.9395												
R.IYSLNPDLNHDK.C +2																									
R.SIPVGYSAADNTDLR.L +2						3.4764										3.1215									
R.TFDEVSEGLYGGLK.N +2																							3.8572		
	1					X							X			X				X			X		
gi|6319721|ref|NP_009803.1|													23.5	23.5	14.8					14.8			18.5		Phospholipid hydroperoxide glutathione peroxidase induced by glucose starvation that protects cells from phospholipid hydroperoxides and nonphospholipid peroxides during oxidative stress; Gpx2p [Saccharomyces cerevisiae]
K.CGFTPQYK.E +2																									
K.GFVILGFPCNQFGK.Q +2													3.6101	2.9309	3.5194					3.3756			3.6955		
K.IDVNGSNADSVYNYLK.S +2																							3.0234		
K.PSSLDQEIQSGLLSK.- +2													3.9285	3.6899											
K.VVLIVNVASK.C +2													2.7048	3.106	2.7915					2.6575					
	1												X	X	X					X			X		
gi|6319926|ref|NP_010007.1|													3.8					3.4		3.8	3.9	7.4			General repressor of transcription, forms complex with Cyc8p, involved in the establishment of repressive chromatin structure through interactions with histones H3 and H4, appears to enhance expression of some genes; Tup1p [Saccharomyces cerevisiae]
K.DSVYSVVFTR.D +2																					2.503				
K.DVENLNTSSSPSSDLYIR.S +2																					4.1922	3.0992			
K.INDTGSATTATTTTATETEIKPK.E +2																									
K.INDTGSATTATTTTATETEIKPK.E +3																						4.061			
K.SLDHTSVVCCVK.F +2																		2.9376							
K.TPNSGTCEVTYIGHK.D +2													3.2365							3.1889					
R.VWDSETGFLVER.L +2													3.4296					3.2915		3.8167		4.0117			
	1												X					X		X	X	X			
gi|6321940|ref|NP_012016.1|															5.4	8.4		6.9			6.9	9			Protein that binds to cruciform DNA structures; Crp1p [Saccharomyces cerevisiae]
K.DEEVFTLDPIVNK.A +2															3.6897	4.3155					2.726				
K.DVILTGTFDDWR.G +2															2.7321	2.5674		3.6646							
K.EEVPEPVAGPIVESSVTEK.S +2																					2.8295				
K.KEEVPEPVAGPIVESSVTEK.S +2																		3.2984							
K.SNESLDDNEEEDGVTGTTTEDVTGTSR.E +2																						2.6586			
K.SPALPQADDPIVETK.E +2																						3.1617			
R.IPEAGGLLCGKPPR.S +2																2.5584									
	1														X	X		X			X	X			
gi|6324938|ref|NP_015007.1|													9.4	12.5	16.3					8.3	8.3				20S proteasome alpha-type subunit; Pre10p [Saccharomyces cerevisiae]
K.CNDGVVFAVEK.L +2																				3.7198	3.0441				
K.GDLLQEAIDFAQK.E +2													3.8034	4.1811	4.2933					4.1602					
K.LVDHHPEGLSAR.E +2														2.7091											
K.TPIPIPAFADR.L +2														2.5072	2.5476										
R.HIGCVYSGLIPDGR.H +2													3.8198		3.0111										
R.NFQVEYAVK.A +2															2.5005										
R.PFGVSTIFGGVDK.N +2																					2.789				
	1												X	X	X					X	X				
gi|6324074|ref|NP_014144.1|													16.3	16.3			24.2	24.2		23.5					Protein with seven cysteine-rich CCHC zinc-finger motifs, similar to human CNBP, proposed to be involved in the RAS/cAMP signaling pathway; Gis2p [Saccharomyces cerevisiae]
K.CYTCGQAGHMSR.D +2																	3.4706			3.0928					
K.DCMKEDGISGLK.C +2																		3.3428		3.7729					
K.IGHLAEDCDSER.L +2																									
R.CFNCNQTGHISR.E +2													3.8578	4.0295			4.3448	4.2182		4.1353					
R.LCYNCNETGHISK.D +2													4.162	3.8628			4.0699	4.2919							
	1												X	X			X	X		X					
gi|6322638|ref|NP_012711.1|													5.6	6		5.2		8.9		5.2					Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp2p; Trp3p [Saccharomyces cerevisiae]
K.DLNMEPLVEVNSK.E +2														3.0474		3.0354				3.6113					
K.TSPISHDNCGIFK.N +2													2.8076					2.5721							
R.LAGADTVLLIVK.M +2																4.4165				3.5169					
R.NILNVSGGTWEENK.S +2													3.3841					4.1732							
R.YHSLAGTESSLPSCLK.V +2														4.2565				4.0946							
	1												X	X		X		X		X					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6319711|ref|NP_009793.1|													7	10.7	10.7	6				7.6					Essential subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; Arc40p [Saccharomyces cerevisiae]
K.APIYSHCFSQDK.S +2														3.3901	3.035										
K.FPFGCLIR.E +2																2.5062									
K.SILAVTCETDCLVYR.V +2													3.4108	4.1758	3.1513	2.6755				2.8275					
K.TITAVDISIHGR.I +2													3.0954												
R.VSNNTPPVLFATLK.D +2														4.2258	3.3925					2.587					
gi|6320276|ref|NP_010356.1|													14.1	22	14.1	14.1				22					Polyamine acetyltransferase; acetylates polyamines (e.g. putrescine, spermidine, spermine) and also aralkylamines (e.g. tryptamine, phenylethylamine); may be involved in transcription and/or DNA replication; Paa1p [Saccharomyces cerevisiae]
K.IVLIAHEPLIPFYER.V +2														4.0954						2.5632					
K.NLATLLLTDYIQK.L +2													5.1196	4.8501	5.0085	4.9293				4.184					
R.LINCPELCSGLFIR.E +2													2.8357	4.208	3.2587	3.5807				3.0358					
	2												X	X	X	X				X					
gi|6322754|ref|NP_012827.1|					5.9	13.4					11.7					13.4		25.1							Cell wall mannoprotein, linked to a beta-1,3- and beta-1,6-glucan heteropolymer through a phosphodiester bond; involved in cell wall organization; Cwp1p [Saccharomyces cerevisiae]
K.DGSSYIFSSK.Q +2											3.3367														
K.EGSESDAATGFSIK.D +2					3.7529	3.0496										2.7318									
K.LGSGSGSFEATITDDGK.L +2																		2.8116							
K.YAVVNEDGSFKEGSESDAATGFSIK.D +2																		2.9813							
R.SGSDLQYLSVYSDNGTLK.L +2						4.3493					3.0192					4.9164		3.9166							
	1				X	X					X					X		X							
gi|6320718|ref|NP_010798.1|					10.9	10.9	10.9									32.7		21.8							Ubiquitin-like protein of the SUMO family, conjugated to lysine residues of target proteins; regulates chromatid cohesion, chromosome segregation, APC-mediated proteolysis, DNA replication and septin ring dynamics; Smt3p [Saccharomyces cerevisiae]
K.VSDGSSEIFFK.I +2					3.8926	3.7459	3.7279									3.737									
R.IQADQTPEDLDM*EDNDIIEAHR.E +3																									
R.IQADQTPEDLDMEDNDIIEAHR.E +2																4.1257		4.3607							
R.IQADQTPEDLDMEDNDIIEAHR.E +3																		3.5182							
	1				X	X	X									X		X							
gi|6324886|ref|NP_014955.1|					2.2		2.2	2.2	2.2	2.2															Protein involved in pre-rRNA processing, 18S rRNA synthesis, and snoRNA synthesis; component of the small subunit processome complex, which is required for processing of pre-18S rRNA; Nop58p [Saccharomyces cerevisiae]
K.M*SLGLAHSIGR.H +2					2.696		2.6645	2.7003	2.6435	2.7467															
	1				X		X	X	X	X															
gi|6322119|ref|NP_012194.1|														10.9								10.9	10.9	10.5	Acidic protein of the mitochondrial matrix involved in oxidative phosphorylation; related to the human complement receptor gC1q-R; Mam33p [Saccharomyces cerevisiae]
K.ENNEYISWLEKM +2														2.6905								3.3577	3.7873		
K.ETLPESTSLDSFNDFLNK.Y +2														3.34								3.4196	3.3886	3.2641	
R.VGDILQSELK.I +2																								3.1605	
	1													X								X	X	X	
gi|6323286|ref|NP_013358.1|											12.8						12.8				12.8			12.8	hypothetical protein; Ylr257wp [Saccharomyces cerevisiae]
K.YSSSGTPENITGEADDEDEDIIR.N +2											3.7281						3.5198				4.4677			4.0522	
R.EGALLTDEVDLENVDASK.V +2											4.0529						3.1558				5.193			5.2999	
	1										X						X				X			X	
gi|6322393|ref|NP_012467.1|														15.1		17.4		7.4						13	Non-essential intracellular esterase that can function as an S-formylglutathione hydrolase; may be involved in the detoxification of formaldehyde, which can be metabolized to S-formylglutathione; similar to human esterase D; Yjl068cp [Saccharomyces cerevisiae]
K.AFWQFQADK.Y +2																		2.7217							
K.AQWEAYDPCLLIK.N +2														3.6728		4.0648		3.895							
K.SCSAFAPIVNPSNVPWGQK.A +2														3.6756		3.8785								4.4186	
K.YGFAIVFPDTSPR.G +2														3.0277											
R.IPTVFYLSGLTCTPDNASEK.A +2																3.4447								2.9937	
	1													X		X		X						X	
gi|6320980|ref|NP_011059.1|													10.3	10.3			9							9	Catalytic subunit of type 1 serine/threonine protein phosphatase, involved in many processes including glycogen metabolism, sporulation, and mitosis; interacts with multiple regulatory subunits; predominantly isolated with Sds22p; Glc7p [Saccharomyces cerevisiae]
K.DIVGWSENDR.G +2																	3.0654							2.8744	
K.TFTDCFNCLPIAAIIDEK.I +2													3.823	4.5555			3.0923							2.522	
R.AHQVVEDGYEFFSK.R +2													3.3343	3.429											
	1												X	X			X							X	
gi|6320334|ref|NP_010414.1|																		5.5			5	3.9	3.9		Fimbrin, actin-bundling protein; cooperates with Scp1p (calponin/transgelin) in the organization and maintenance of the actin cytoskeleton; Sac6p [Saccharomyces cerevisiae]
K.DVSDGENYTILLNQLDPALCSK.A +2																		3.5077							
K.IIVAGSQTGTTHTINEEER.R +2																					3.6091				
R.LLEDDETLEQFLR.L +2																		2.7514			3.6152	3.3641	3.4522		
R.VELDDYVGLVAK.L +2																						3.3018	4.1398		
	1																	X			X	X	X		
gi|6325418|ref|NP_015486.1|																			3.2	4.2		4.1	4.3		Non-essential glycogen phosphorylase required for the mobilization of glycogen, activity is regulated by cyclic AMP-mediated phosphorylation, expression is regulated by stress-response elements and by the HOG MAP kinase pathway; Gph1p [Saccharomyces cerevisiae]
K.LEDVLDQEPDAGLGNGGLGR.L +2																							4.3125		
K.LISETLNDPTEEYLLDMAK.L +2																						3.745	3.5965		
K.SVLSVANVGFFSSDR.C +2																			2.5609						
K.TTLSASQWIGGER.V +2																				3.4416					
R.AESITAVLYPNDNFAQGK.E +2																						3.0239			
R.EIGEDNVFLFGNLSENVEELR.Y +2																									
R.MAFLAIVGSHK.V +2																				2.6891					
R.VLAVAYDFPVPGFK.T +2																			3.7432	2.5177					
	1																		X	X		X	X		
gi|6322919|ref|NP_012992.1|														6.4						8.9		8.9	8.3		Mitochondrial cytochrome-c peroxidase; degrades reactive oxygen species in mitochondria, involved in the response to oxidative stress; Ccp1p [Saccharomyces cerevisiae]
K.EFNDPSNAGLQNGFK.F +2																						3.013			
K.LLENGITFPK.D +2														3.2132											
K.LREDDEYDNYIGYGPVLVR.L +2																				3.1287					
R.EDDEYDNYIGYGPVLVR.L +2																						3.9442	3.5819		
R.EVVALMGAHALGK.T +2														2.8194						3.4971					
R.VDTPEDTTPDNGR.L +2																							3.2463		
	1													X						X		X	X		
gi|6324343|ref|NP_014413.1|													1.7					1				1.3	1.1		Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids; Acc1p [Saccharomyces cerevisiae]
K.GYDNQVIM*NASLQQLIEVLR.N +2																									
K.ILIANNGIAAVK.E +2																		3.2993							
K.IVEWMSYVPAK.R +2																							2.9002		
K.SLAPEVHQQISK.Q +2													2.898												
K.TGLVSVDDDDYQK.G +2																						3.1824	3.8458		
K.VALTVLSHSK.V +2																		2.7196							
K.VIFIGPPGNAM*R.S +2													3.1065												
K.VIFIGPPGNAMR.S +2																									
K.VPCIPWSGTGVDTVHVDEK.T +2																									
K.YYTFNGPNYNENETIR.H +2																						2.676			
R.AIQVEGQPIILTGAPAINK.M +2																									
R.LGGIPLGVIGVETR.T +2													2.9089												
	1												X					X				X	X		

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6320240|ref|NP_010320.1|									7.6										7.8	8.4			7.8		3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by phenylalanine or high concentration of tyrosine or tryptophan; Aro3p [Saccharomyces cerevisiae]
K.GLINDPDMNNSFQINK.G +2																			4.3665	3.0039					
K.GLINDPDMNNSFQINK.G +2																							4.7485		
K.NGTDGGLQVAIDAMR.A +2									2.7526											3.2818					
K.PGVTAIVGTEGNK.D +2																									
R.ELASGLSFPIGFK.N +2									3.1993										3.1708				3.1147		
	1								X										X	X			X		
gi|6320777|ref|NP_010856.1|									6.6									7.4		6.8			6.6		Essential N-acetylglucosamine-phosphate mutase, a hexosephosphate mutase involved in the biosynthesis of chitin; Pcm1p [Saccharomyces cerevisiae]
K.GLSPSSFDSLYCSFDGDADR.V +2																							4.5534		
K.LFIDTANGIGGPQLK.K +2																									
K.LGQFCDEVVEHVK.A +2																		2.7543							
K.LLASEDWDVPAEQVEVINDR.S +2									3.4404																
K.MSPMDWDEEYTDLPNK.L +2																									
K.NTLHCPVSCTK.T +2																		2.82		3.2029					
R.SDVPELLNFECGADYVK.T +2									3.7657									2.9866		2.903			3.3131		
R.SIFQTTDQER.K +2																				2.507					
	1								X									X		X			X		
gi|9755326|ref|NP_061491.1|																29.4	29.4	29.4					29.4		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and to the nucleus; Ybr085c-ap [Saccharomyces cerevisiae]
K.DGEVIANIIGEAK.D +2																4.6329	4.1203	3.8533					4.0313		
K.NYEIQTVLSEDK.S +2																2.9823	4.0774	4.212					4.3482		
	1															X	X	X					X		
gi|6323826|ref|NP_013897.1|																	22.3	11.2		16.3		11.6			DNA damage-responsive protein, expression is increased in response to heat-shock stress or treatments that produce DNA lesions; contains multiple repeats of the amino acid sequence NNNDSYGS; Ddr48p [Saccharomyces cerevisiae]
K.NSYGSSNYGSSNNDDSYGSSNR.G +2																	4.9578			4.0662					
K.SSYGSNNDDSYGSNNDDSYGSSNK.+2																	4.9731	4.4847		3.5247		5.2272			
K.SSYGSSNNDSYGSNNDDSYGSSNK.+2																	4.7454	4.8252		2.6759					
K.SSYGSSSNDDSYGSSNNDDSYGSSNK.+2																	4.5702					5.0317			
	1																X	X		X		X			
gi|6321411|ref|NP_011488.1|					4.3		3.8									4					4.1				Processing alpha glucosidase I, ER type II integral membrane N-glycoprotein involved in assembly of cell wall beta 1,6 glucan and asparagine-linked protein glycosylation; also involved in ER protein quality control and sensing of ER stress; Cwh41p [Saccharomyces cerevisiae]
K.EEGPFELFTSVFPSR.G +2							3.1618																		
K.FMTNNLEANPGLLTEYAK.K +2					2.7652		3.1688																		
K.NPEYETMEVAPGSDCSK.T +2																						2.9205			
K.QFSFGEGPDSIESVEVK.R +2																						2.847			
K.SQTGLIDEYEEILEDEGIWDK.I +2																5.2667									
R.DVFQSLVSDSIR.D +2																2.8945									
R.ETEFDESQFTEIK.L +2																									
R.YYYPEVILDVAGEASNAK.K +2					3.0185																				
	1				X		X									X						X			
gi|6321865|ref|NP_011941.1|														3.9					4.6	4.2	4.3				Glutamine-dependent NAD(+) synthetase, essential for the formation of NAD(+) from nicotinic acid adenine dinucleotide; Qns1p [Saccharomyces cerevisiae]
K.DLSNAIGSYHVDLK.M +2																									
K.IFGGSQIENLALQNIQAR.L +2																			3.126						
K.IFHSCFMGTENSSK.E +2																				2.8294					
K.M*DSLVSSVVSLFEVATGK.K +2																									
K.PGVVEDFILPPEIQK.V +2														3.0146											
K.YDCSSADINPIGGISK.T +2																				5.0478	4.9359				
R.IDIPVELALM*TSR.F +2														3.9176											
R.LVTDAAQNGNEQVIK.D +2																			4.3772		4.3418				
R.SGDDWIPDSPQDLASK.I +2																									
	1													X					X	X	X				
gi|6320393|ref|NP_010474.1|									8.8										7.1	3.8	6				Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, essential protein that is required for the assembly of actin and tubulins in vivo; contains an ATP-binding motif; Cct6p [Saccharomyces cerevisiae]
K.FTYVTENTDPK.S +2																				3.5487					
K.NSGFDPLDVLAM*VEDELDDAQDSDETR.Y +2									2.7334																
K.TEVNSGFFYSSADQR.D +2																					2.9679				
K.VLLTEM*QIQSPTAVLIAR.A +2																			3.8971		5.1388				
R.IITDGFEIAR.K +2																				2.5487					
R.NAITGATGIASNLLLCDELLR.A +2									2.7997										4.3472						
	1								X										X	X	X				
gi|14318532|ref|NP_116665.1|													2.4	2.4				5.8			7				Ubiquitin-specific protease situated in the base subcomplex of the 26S proteasome, releases free ubiquitin from branched polyubiquitin chains; deletion causes hypersensitivity to cycloheximide and other toxic compounds; Ubp6p [Saccharomyces cerevisiae]
K.IESLAGGGESDSALILMYK.G +2																					3.1816				
K.SKAEELTQVPSAR.Q +2																		3.582							
K.SVLPIVLLNTLR.K +2													4.2455	3.7391											
K.VYPITLSTDATSADLK.S +2																		2.9076			3.3768				
gi|6320881|ref|NP_010960.1|													25	18.5				16.8			15.2				Peptide methionine sulfoxide reductase, reverses the oxidation of methionine residues; involved in oxidative damage repair, providing resistance to oxidative stress and regulation of lifespan; Mxr1p [Saccharomyces cerevisiae]
K.IATVIEPIK.N +1																					2.0148				
K.NFYDAEEYHQLYLDK.N +2													3.0059	3.4126											
R.SGLFAHSDADLK.E +2													2.9376					2.9876							
R.VCGGDTDFAEVLQVSYNPK.V +2													2.7669	3.2712				2.5392			5.1179				
	2												X	X				X			X				
gi|6321457|ref|NP_011534.1|						22							22	28.8							22				Subunit F of the eight-subunit V1 peripheral membrane domain of vacuolar H+-ATPase (V-ATPase), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane; Vma7p [Saccharomyces cerevisiae]
K.NFFVYQEGK.T +1						2.2425																			
K.NFFVYQEGK.T +2													2.855								2.6026				
R.DDIAILLINQHIAENIR.A +2														4.0225											
R.VDSFTNAFPAILEIPSK.D +2						4.4138							4.0226	3.787							3.8413				
	1					X							X	X							X				
gi|6321632|ref|NP_011709.1|														9		9			9	9					Dihydrolipoamide dehydrogenase (E3)-binding protein (E3BP) of the mitochondrial pyruvate dehydrogenase (PDH) complex, plays a structural role in the complex by binding and positioning E3 to the dihydrolipoamide acetyltransferase (E2) core; Pdx1p [Saccharomyces cerevisiae]
K.DVDVGEPIAYIADVDDDLATIK.L +2														3.548		4.3059			2.5094	3.4145					
K.YFDPIFEDLVTLSPR.E +2														3.5341		4.0045			2.657	2.6827					
	1													X		X			X	X					
gi|6321692|ref|NP_011769.1|												10	9.6					9.2		13.5					Alpha subunit of the 20S proteasome involved in ubiquitin-dependent catabolism; human homolog is subunit zeta; Pup2p [Saccharomyces cerevisiae]
K.EAELLVLK.I +1																									
K.EGVVLGVEK.R +1																				2.452					
K.LDENNAQLSCITK.Q +2												4.5589	4.9607					4.5246							
K.LGSTAIGIATK.E +2																		3.1326							
K.RATSPLLESDSIEK.I +2																									
R.ATSPLLESDSIEK.I +2												3.18													
R.HIGCAMSGLTADAR.S +2																				4.1842					
R.LFQVEYSLEAIK.L +2													3.5414							3.0634					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
	1											X	X					X		X					
gi|6323717|ref|NP_013788.1|													12	12						13.1					Mitochondrial DNA-binding protein involved in mitochondrial DNA replication and recombination, member of HMG1 DNA-binding protein family; activity may be regulated by protein kinase A phosphorylation; Abf2p [Saccharomyces cerevisiae]
K.ENPTLRPAEISK.I +2													3.8437	3.7542			3.0089								
K.RPTSAYFLYLQDHR.S +3																				3.7411					
R.SQVFAQHPDK.S +2													3.1193	2.8246			2.9884			2.9207					
	1												X	X			X			X					
gi|6323511|ref|NP_013582.1|									8.1				7.2			8.1				8.1					Alpha-tubulin; associates with beta-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p; Tub3p [Saccharomyces cerevisiae]
K.GGEEGFSTFFHETGYGK.F +2													3.6102												
K.IGICYEPPSVIPSSELANVDR.A +2									2.5708							2.8018									
R.AIYVDLEPNVIDEVR.T +2									3.7694				4.4842			3.4639				2.5127					
R.FDGSLNVDLNEFQTNLVPYPR.I +2																				2.8901					
	1								X				X			X				X					
gi|6323975|ref|NP_014046.1|													10.3	15.8	16					12					Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YMR315W is not an essential gene; Ymr315wp [Saccharomyces cerevisiae]
K.AGKPVILEKPIAANLDQAK.E +3														3.708											
K.EVIGSFTYGSAFGATEK.S +2																									
K.IAESTPLPVGVAENWLYLPCIK.I +2													3.5306	3.5632	3.0483					3.2389					
K.IGPVVAFTHNSTGPFVTQNK.Y +2																				4.1847					
K.IGPVVAFTHNSTGPFVTQNK.Y +3															4.0954										
K.LGGSAEDNGDEQIFK.V +2																									
R.SGADDIVFATVQLK.N +2													3.5393	4.6432	3.9205										
	1												X	X	X					X					
gi|6319577|ref|NP_009659.1|													15.9	14.8	19.3				11.4						Hsp70 (Ssa1p) nucleotide exchange factor, cytosolic homolog of Sil1p, which is the nucleotide exchange factor for BiP (Kar2p) in the endoplasmic reticulum; Fes1p [Saccharomyces cerevisiae]
K.AFYALSNLIR.N +2													3.9437	4.0087	4.0882				3.7885						
K.IDENIISVLR.K +2														3.6405	3.6698				2.9444						
K.LWEPLLDVLVQTK.D +2													2.82		3.0621										
R.AAALSIIGTAVQNNLDSQNNFM*K.Y +3													5.2378	5.3361	3.7334										
R.AIALLTAYLSSVK.I +2																			3.4914						
R.LNEDDYLAVK.Y +2																									
	1												X	X	X				X						
gi|6325386|ref|NP_015454.1|														8.6	8.6	8.6		8.6							Protein containing an Lsm domain, may bind RNA and have a role in RNA processing; overproduction suppresses a null mutation in CHC1, which encodes the heavy chain of clathrin; Scd6p [Saccharomyces cerevisiae]
K.NWGPEEIYPNPTVYNSVK.F +2														3.875	3.4683	3.5523		2.789							
K.TISLISVTDNR.Y +2																									
R.YVGLLEDIDSEK.G +2														3.58	2.7653	3.5654		3.0742							
	1													X	X	X		X							
gi|6322452|ref|NP_012526.1|													4.6	4.6	6.5			5.1							Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct8p [Saccharomyces cerevisiae]
K.ELDEMVGEITIDK.N +2																		2.9515							
K.IIITNDAATMLR.E +2																									
K.VAVFTCPLDIANTETK.G +2													4.5484		2.9133										
R.EENIYDMLATK.K +2															2.7625										
R.LGAPTPEELGLVETVK.T +2														3.2489				2.6142							
R.TPGLLQLAIK.Q +2													3.4135	3.5051	3.1153										
	1												X	X	X			X							
gi|6321195|ref|NP_011272.1|									25.4				25.4	17.7		25.4									Putative protein of unknown function; deletion mutant is viable; Ygl242cp [Saccharomyces cerevisiae]
K.EPLGNTALHLCCK.Y +2														2.7729											
K.ILDQDGEIEIDPQNDVDGDTPLHVTVR.Y +3									5.0635				5.1265			4.5422									
K.YGSWEVLDK.I +2																									
R.NNLDLLETVFDSLDNDPEK.I +2									5.4885				3.7212	5.5988		6.1174									
R.YSQEEPEHGTFIAR.N +2																									
	1								X				X	X		X									
gi|6323229|ref|NP_013301.1|									28.1				22.8	36.8	28.1										Subunit of the heterohexameric Gim/prefoldin protein complex involved in the folding of alpha-tubulin, beta-tubulin, and actin; Yke2p [Saccharomyces cerevisiae]
K.IVNEEFDQLEEDTPVYK.L +2									6.2138					5.8974	5.4514										
K.RLEFIETEITR.C +2													3.6217												
K.YQQLQNELEEFIVAR.Q +2									2.8773				3.5282	4.3271	4.3395										
R.LEFIETEITR.C +2														3.0035											
	1								X				X	X	X										
gi|6323537|ref|NP_013608.1|							2.9						2.6	2.9	2.9										Large subunit of trehalose 6-phosphate synthase (Tps1p)/phosphatase (Tps2p) complex, which converts uridine-5'-diphosphoglucose and glucose 6-phosphate to trehalose, homologous to Tps3p and may share function; Tsl1p [Saccharomyces cerevisiae]
K.ILEGLTGADFVGFQTR.E +2							3.4752							3.5968	2.9058										
R.FTPVGIDAFDLQSQLK.D +2							4.4368						2.7923	3.8639	3.4236										
R.M*FVFNIAEPPSSR.M +2													2.7633												
	1						X						X	X	X										
gi|6325273|ref|NP_015341.1|									12.2		11.4		13.5		12.2										Constituent of 66S pre-ribosomal particles, has similarity to human translation initiation factor 6 (eIF6); may be involved in the biogenesis and or stability of 60S ribosomal subunits; Tif6p [Saccharomyces cerevisiae]
R.ETEELISDVLGVEVFR.Q +2									2.6134				3.1373		3.6066										
R.GLLVPTQTTDQELQHLR.N +2													3.2958												
R.LQDAQPESISGNLR.D +2											4.129														
R.TQFENSNEIGVFSK.L +2									3.6207		3.0698				3.2966										
	1								X		X		X		X										
gi|6320142|ref|NP_010222.1|			17.9					17.9					32.1	32.1											Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Ap and has similarity to rat S29 and E. coli S14 ribosomal proteins; Rps29bp [Saccharomyces cerevisiae]
R.KYDLNICR.Q +2													2.706	2.836											
R.VCSSHTGLVR.K +2			3.1237					2.8696					3.068	2.7957											
	1		X					X					X	X											
SHUFFLED_gi|6321019|ref|NP_011098.1|	1.7	1.7	1.7	1.7																					FALSE POSITIVE
K.YNPAIM*DQILQSK.S +2	3.205	3.2791	3.3219	3.2891																					
gi|6325407|ref|NP_015475.1|	5.8	5.8	5.8	5.8																					Protein of unknown function; contains transmembrane domains; involved in secretion of proteins that lack classical secretory signal sequences; component of the detergent-insoluble glycolipid-enriched complexes (DIGs); Nce102p [Saccharomyces cerevisiae]
-.MLALADNILR.I +2	3.215	3.3367	3.2574	3.3021																					
	2 X	X	X	X																					
gi|6325253|ref|NP_015321.1|																			10.3				7.9	10.3	Primary component of eisosomes, which are large immobile patch structures at the cell cortex associated with endocytosis, along with Pil1p and Sur7p ; null mutants show activation of Pkc1p/Ypk1p stress resistance pathways; Lsp1p [Saccharomyces cerevisiae]
K.IPVLEQELVR.A +2																								2.7325	
R.AEAESLVAEAQLSNITR.E +2																			2.702					4.1879	3.3142
R.APTAAELQAPPPPPSSTK.S +2																			4.1067						2.5846
	1																		X				X		X
gi|6321301|ref|NP_011378.1|														2.8			4.5								3.3	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45% sequence identity to mammalian beta'-COP; Sec27p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.NAAASDIFTAVIR.G +2														4.8131			3.6332							3.2812	
R.DLLTDESAEMK.W +2																	2.501								
R.FLEGQEYYEEALNISPDQDQK.F +2																									
R.GNEEVEQDEPLSLQTK.E +2																	3.7106							4.2486	
R.GVNYVDYYPLPDK.P +2																									
R.KNWIIVGSDDFR.I +2														2.5215											
R.SIAVHPTKPYVLSGSDDLTVK.L +2																									
	1													X			X							X	
gi|6325017|ref|NP_015085.1|									14.5												14.5		14.5		Cytoplasmic ankyrin-repeat containing protein of unknown function, proposed to link the processes of 40S ribosomal subunit biogenesis and adaptation to osmotic and oxidative stress; expression repressed by heat shock; Yar1p [Saccharomyces cerevisiae]
K.DIFTTLVSPELLSTCK.E +2									3.3628												4.4317		3.5611		
K.LLCDEYEADPFIR.N +2									3.6329												3.609		4.1962		
	1								X												X		X		
gi|6324206|ref|NP_014276.1|													2.9	4.4									2.7		Protein of unknown function which may contribute to lipid homeostasis and/or apoptosis; sequence similarity to the mammalian Omi/HtrA2 family of serine proteases; Nma111p [Saccharomyces cerevisiae]
K.ETPDLDTFIEIMK.T +2																							3.0014		
K.FPENIGLLVAETVLR.E +2													3.3072	3.186											
K.TNYHYFPTAELK.R +2														2.839											
K.TSGLIIDAEK.G +2																									
R.ALICIQTNIKPITR.G +2																									
R.CNSGILTDNDGTVR.G +2																							3.789		
R.LM*TFDNVPFAISLK.T +2													2.6309												
R.NDTTGIWDYK.N +2																									
R.VSIVDAGFGSISVLQAR.I +2														2.5988											
	1												X	X									X		
gi|6321826|ref|NP_011902.1|																		3.8		8.5		5.2			Delta-1-pyrroline-5-carboxylate dehydrogenase, nuclear-encoded mitochondrial protein involved in utilization of proline as sole nitrogen source; deficiency of the human homolog causes HPII, an autosomal recessive inborn error of metabolism; Put2p [Saccharomyces cerevisiae]
K.AGGPNILSR.F +2																				2.6019					
K.ENFYELTDFK.Y +2																		2.7778		2.8285		3.0143			
K.NVYQAEIDCITELSDFFR.Y +2																				2.8173					
K.SQGWFVGPTVIK.A +2																		2.7497		3.3935					
K.YASDLYAQQPVESADGTWNK.A +2																						4.356			
	1																	X		X		X			
gi|6324552|ref|NP_014621.1|																	3.5			3.5	3.5				Catalytic component of the exosome, involved in RNA processing and degradation; binds Gsp1p/Ran and enhances the GEF activity of Srm1p; implicated in mitotic control; homologous to the E. coli RNase R of the RNase II family; Dis3p [Saccharomyces cerevisiae]
K.FILSDSPLELSAPIGK.H +2																				3.3268					
R.DTFSDFTFPEYYSTAR.V +2																	2.8196				3.4445				
R.LDNLTEDPNSAAFDEVEYK.L +2																	3.6202			4.664	5.4547				
	1																X			X	X				
gi|6320914|ref|NP_010993.1|									5.2									3.5			3.4				Ribonucleotide-diphosphate reductase (RNR), large subunit; the RNR complex catalyzes the rate-limiting step in dNTP synthesis and is regulated by DNA replication and DNA damage checkpoint pathways via localization of the small subunits; Rnr1p [Saccharomyces cerevisiae]
K.AAPIVDDEETEFDIYNSK.V +2									4.0836									2.8949			4.1353				
K.EDSIEGIYDTLK.E +2									3.2046												2.9713				
K.GM*AELNVQESK.V +2																									
K.IADQATENVADISNLK.R +2									2.9765																
R.DLVDLGIWDEGM*K.Q +2																		3.5842							
R.DLGVDLGIWDEGMK.Q +2																		3.0094							
	1								X									X			X				
gi|6323639|ref|NP_013710.1|																	8.6	12.9		8					Monomeric glyoxalase I, catalyzes the detoxification of methylglyoxal (a by-product of glycolysis) via condensation with glutathione to produce S-D-lactoylglutathione; expression regulated by methylglyoxal levels and osmotic stress; Glo1p [Saccharomyces cerevisiae]
K.ASNDPTLLLNHTCLR.V +2																		2.5964							
K.DPDGYSIEVVPHGLIA.- +2																	2.6871	3.1947		3.0926					
K.FSLYFLSFPK.D +2																				2.5707					
K.TCEELESQGVK.F +2																		3.0142							
R.SLEFYQNVLGMK.L +2																	3.9838								
	1																X	X		X					
gi|6325146|ref|NP_015214.1|															9			7.5		8.7					Arginase, responsible for arginine degradation, expression responds to both induction by arginine and nitrogen catabolite repression; disruption enhances freeze tolerance; Car1p [Saccharomyces cerevisiae]
K.DLGIAAFSMYHVDK.Y +2																				3.3622					
K.DSTTGGSSVMIDGVK.A +2															2.8148										
K.RADLVGEATK.L +2																		2.7367							
R.ELSIVLAPFSGGQGK.L +2															3.1101			3.1931		2.6097					
	1														X			X		X					
gi|6324859|ref|NP_014928.1|														24.5				25.2		20.9					Protein of unknown function, localized to the mitochondrial outer membrane; Yor285wp [Saccharomyces cerevisiae]
K.ELIFYCASGK.R +2																		2.889							
K.HDPNVVLVDVR.E +2																		3.1327							
K.NVSNIQSYSFEDM*K.R +2																				3.2021					
K.NVSNIQSYSFEDMK.R +2																		2.7449							
R.EPSEYSIVHIPASINVPYR.S +2														4.0298											
R.SHPDAFALDPLEFEK.Q +2														3.5403						3.5094					
	1													X				X		X					
gi|6324857|ref|NP_014926.1|													11.3				11.3			13					Putative protein of unknown function with some similarity to GPM1/YKL152C, a phosphoglycerate mutase; YOR283W is not an essential gene; Yor283wp [Saccharomyces cerevisiae]
K.DTSINPTGEEQATK.L +2													3.1074				3.0244								
K.NLALVSHGGAIR.M +2													3.1897				2.7405			3.1472					
R.LTGCVEEEVAEASNEGVK.N +2																				4.5345					
R.YMGVIEGMQITEAEK.Y +2																									
	1												X				X			X					
gi|6321842|ref|NP_011918.1|														21.6	21.6					21.6					Subunit VI of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; expression is regulated by oxygen levels; Cox6p [Saccharomyces cerevisiae]
K.EFDEAYDLFEVQR.V +2														4.4669	4.4622					3.6054					
R.VLNNCFSYDLVPAPAVIEK.A +2														2.6616	3.603					3.1781					
	1													X	X					X					
gi|6324429|ref|NP_014498.1|													32.5	17.2						15.4					Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, also known as DMRL synthase); catalyzes synthesis of immediate precursor to riboflavin; Rib4p [Saccharomyces cerevisiae]
K.GLGKPDQVYDGSK.I +2													3.1398							3.0973					
K.PLDVVIPIGVLIK.G +2													3.5693							2.502					
K.VDM*PVIFGLLTCM*TEEQALAR.A +2																									
K.VDM*PVIFGLLTCM*TEEQALAR.A +3													4.0504	3.6536											
R.VIIDALVK.G +1													1.98	2.0186											
	1												X	X						X					
gi|6323917|ref|NP_013988.1|													1.6	3.1					3.1						Regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; Tps3p [Saccharomyces cerevisiae]
K.NAPLLLSEFTGSSSVLK.E +2													5.3004	4.9863					3.0383						
R.FLIENPEYIEK.V +2																									
R.ILEGIIGANFVGFQTK.E +2														2.693					2.6443						

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
	1												X	X					X						
gi|6322053|ref|NP_012128.1|													23			14.3		17.4							Minor isoform of tropomyosin, binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; appears to have distinct and also overlapping functions with Tpm1p; Tpm2p [Saccharomyces cerevisiae]
K.EADLNSEQMGR.R +2																									
K.ELDEIANSLENL.- +2																									
K.KNQDLEQQLEDSEAK.L +2																		4.0479							
K.LESQLSDTK.Q +2																2.5602									
K.NEQLDSEVEKLESQLSDTK.Q +3																									
K.NQDLEQQLEDSEAK.L +2													4.4872			4.1691									
K.QLAEDSNNLR.S +2													2.5414												
R.IVALEEERDEWEK.K +2													2.6213					3.4816							
	1												X			X		X							
gi|6322529|ref|NP_012603.1|											14.2				13.7			17.8							Conserved protein with deoxyribonucleoside triphosphate pyrophosphohydrolase activity, mediates exclusion of noncanonical purines from deoxyribonucleoside triphosphate pools; mutant is sensitive to the base analog 6-N-hydroxylaminopurine; Ham1p [Saccharomyces cerevisiae]
K.EVQSILTQEVDNNNK.T +2											3.644							4.6759							
K.EYLYQNDF.- +1																		1.9257							
K.GKPVFVEDTALR.F +2																		2.5466							
K.NAEAVTTICFADSR.G +2															3.76										
R.FDEFNGLPGAYIK.W +2											3.6659				3.9647										
R.GEYHFFQGITR.G +2																									
	1										X				X			X							
gi|6319849|ref|NP_009930.1|													6.1	11.7				14.6							Protein of unknown function, has sequence and structural similarity to flavodoxins; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; Ycp4p [Saccharomyces cerevisiae]
K.AAGIFVSTSSYGGGQESTVK.A +2																		5.0457							
K.MNAPQKPEDIPVATEK.T +2																		3.0656							
K.TLLEYDAFLFGVPTR.F +2													3.7601	3.68											
R.FGNLPAQWSAFWDK.T +2														4.3804											
R.VEETLPDEVLTK.M +2																									
	1												X	X				X							
gi|6321839|ref|NP_011915.1|														14.4		10.7	11.5								Serine hydrolase that localizes to both the nucleus and cytoplasm; sequence is similar to Fsh2p and Fsh3p; Fsh1p [Saccharomyces cerevisiae]
K.ANVQCDYIDAPVLLEK.K +2														4.828		5.2444	4.5226								
K.DIIRPIVEQITSSLQEASE.- +2														2.8473											
K.DLPFEMDDEK.W +2																2.6413									
K.ISELVPDHPQFK.V +2																	3.3531								
	1													X		X	X								
gi|6325198|ref|NP_015266.1|									30.7						20	20.7									Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; mitochondrial matrix protein involved in the synthesis/assembly of iron-sulfur centers; monothiol glutaredoxin subfamily member along with Grx3p and Grx4p; Grx5p [Saccharomyces cerevisiae]
K.AIEDAIESAPVVLFMK.G +2									3.7703							4.2813									
K.EFSEWPTIPQLYVNK.E +2									2.8463						2.6504										
K.FAAYNVLEDPELR.E +2																									
R.ATIGLLGNQGVDPAK.F +2									3.4535						4.017	3.5562									
	1								X						X	X									
gi|6321809|ref|NP_011885.1|									18.3					8.5		18.3									Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Ap and has similarity to rat S27 ribosomal protein; Rps27bp [Saccharomyces cerevisiae]
gi|6322693|ref|NP_012766.1|									X					X		X									Protein component of the small (40S) ribosomal subunit; nearly identical to Rps27Bp and has similarity to rat S27 ribosomal protein; Rps27ap [Saccharomyces cerevisiae]
K.LSEGTSFR.R +1									1.8583																
K.LSEGTSFR.R +2									2.6461							2.777									
R.SYFLDVK.C +1									2.0072					2.0126											
R.SYFLDVK.C +2														2.6921		2.6458									
	1								X					X		X									
gi|6320966|ref|NP_011046.1|									11.9				17.2			11.1									Integral ER membrane protein that regulates phospholipid metabolism via an interaction with the FFAT motif of Opi1p, also involved in telomeric silencing, disruption causes inositol auxotrophy above 34 degrees C, VAP homolog; Scs2p [Saccharomyces cerevisiae]
K.AVADVWSDLEAEFK.Q +2									4.6959				3.6518			4.5977									
K.ETVEPVVQDSEPK.E +2													2.7149			3.0504									
K.EVPAEPETQPPVQVK.K +2									2.5304																
K.FLVITLPSPYDLNGK.A +2													2.6163												
	1								X				X			X									
gi|6319729|ref|NP_009811.1|													17.7	17.7	17.7										dUTPase, catalyzes hydrolysis of dUTP to dUMP and PPi, thereby preventing incorporation of uracil into DNA during replication; critical for the maintenance of genetic stability; Dut1p [Saccharomyces cerevisiae]
K.IVDDAQNVVVDSLEESAR.G +2													4.7359	5.4083	6.0903										
K.NGIQTGAGVVDR.D +2																									
R.DYTGEVK.V +1																									
R.VAQLILEK.I +1													2.3696	2.2874	2.4013										
gi|6321531|ref|NP_011608.1|													2.6	2.6	2.6										Mitochondrial and cytoplasmic valyl-tRNA synthetase; Vas1p [Saccharomyces cerevisiae]
K.LDNTVAEIEGLEATIENLK.R +2													3.0908	5.0722	3.8832										
K.LDNTVAEIEGLEATIENLK.R +3													3.7267												
K.TGEVIINPLK.E +2													2.6323	3.2353	2.9708										
K.TGEVIINPLKEDGSPK.T +2																									
	2												X	X	X										
gi|42742289|ref|NP_013493.2|							1.5		2.7					2.7											Metalloprotease involved, with homolog Axi1p, in N-terminal processing of pro-a-factor to the mature form; member of the insulin-degrading enzyme family; Ste23p [Saccharomyces cerevisiae]
K.WIFNELQDISNATFK.F +2														2.8508											
K.YEPDLLTQYTDALVPENSR.V +2																									
R.EDLDTLSDWTYDLFK.D +2							3.7721		3.2223																
R.INNFYETFGQVLR.D +2									3.1722					2.8398											
	1						X		X					X											
gi|6322507|ref|NP_012581.1|																						11.5		11.5	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functionally redundant with Hyp2p; undergoes an essential hypusination modification; expressed under anaerobic conditions; Anb1p [Saccharomyces cerevisiae]
K.APEGELGDSM*QAAFDEGK.D +2																						3.4733		3.6254	
K.APEGELGDSMQAAFDEGK.D +2																						3.4543		2.529	
	1																					X		X	
gi|6325140|ref|NP_015208.1|																		16.7						11.8	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase), catalyzes an essential activation step in the isoprenoid biosynthetic pathway; required for viability; Idi1p [Saccharomyces cerevisiae]
K.ENLTVNPNVNEVR.D +2																		3.8103						2.9359	
K.LMNENCIVLDWDDNAIGAGTK.K +2																		4.211						4.1034	
R.KLDHELGIPEDETK.T +2																		3.6514							
	1																	X						X	
gi|6324839|ref|NP_014908.1|																23.6								23.6	Protein involved in microtubule morphogenesis, required for protection from excess free beta-tubulin; proposed to be involved the folding of beta-tubulin; Rbl2p [Saccharomyces cerevisiae]
K.TYQGTEDVSDAR.S +2																2.9495								3.9938	
R.SAITSAQELLDSK.- +2																4.2555								4.042	
	1															X								X	
gi|6325360|ref|NP_015428.1|																						9.4	15.7		20S proteasome beta-type subunit, responsible for the chymotryptic activity of the proteasome; Pre2p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.EGPTIYYVDSDGTR.L +2																						3.2247			
K.GDIFCVGSGQTFAYGVLDSNYK.W +2																							5.0891		
K.ILSNLVYQYK.G +2																							3.1397		
K.WDLSVEDALYLGK.R +2																									
R.ATAGNWVASQTVK.K +2																						4.4451	4.5195		
R.FQGGIIVAVDSR.A +2																									
	1																					X	X		
gi|6320181|ref|NP_010262.1|																					9.2		9.2		NAD-dependent glycerol-3-phosphate dehydrogenase, key enzyme of glycerol synthesis, essential for growth under osmotic stress; expression regulated by high-osmolarity glycerol response pathway; homolog of Gpd2p; Gpd1p [Saccharomyces cerevisiae]
K.NLPDM*IEELDLHED.- +2																					2.7451				
K.NLPDMIEELDLHED.- +2																							2.8911		
K.YLPGITLPDNLVANPDLIDSVK.D +2																									
R.EETYYQESAGVADLITTCAGGR.N +2																					3.7583		3.8676		
	1																				X		X		
gi|6320418|ref|NP_010498.1|																		5.5					4.5		Alpha subunit of chaperonin-containing T-complex, which mediates protein folding in the cytosol; involved in maintenance of actin cytoskeleton; homolog to Drosophila melanogaster and mouse tailless complex polypeptide; Tcp1p [Saccharomyces cerevisiae]
K.IACLDLNLQK.A +2																							3.1237		
K.IIDAGAQVVLTTK.G +2																									
K.IVDEIHAGVLEPTISK.V +2																		3.812							
R.FINEVLSTSVDTLGK.E +2																							4.1641		
R.NQNVLATM*AVANVVK.S +2																									
R.NQNVLATMAVANVVK.S +2																		3.1859							
	1																	X					X		
gi|6323045|ref|NP_013117.1|															9.2								9.2		Methylthioadenosine phosphorylase (MTAP), catalyzes the initial step in the methionine salvage pathway; affects polyamine biosynthesis through regulation of ornithine decarboxylase (Spe1p) activity; regulates ADH2 gene expression; Meu1p [Saccharomyces cerevisiae]
K.FAEYIYQFK.N +2																									
R.DEAEPVTVETVIGNLTNNGR.N +2															3.2893								4.9288		
R.DFVLPQQIIDR.T +2															2.7517								2.5072		
	1														X								X		
gi|6319899|ref|NP_009980.1|													15.3										15.8		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; contains ankyrin (Ank) repeats; YCR051W is not an essential gene; Ycr051wp [Saccharomyces cerevisiae]
K.SGVADVHGVDGVQGEGVIDSK.L +2																									
K.SGVADVHGVDGVQGEGVIDSK.L +3													4.1406												
R.LIVEELGGDFTIR.N +2													2.8048												
R.QLEQIITGDNAEEELER.Y +2																							3.0528		
R.YTLENDPEEGADEATLQR.R +2																							5.2281		
	1												X										X		
gi|6321601|ref|NP_011678.1|											3.5												5.4		Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33p); associates with the poly(A)-binding protein Pab1p, also interacts with eIF4A (Tif1p); homologous to Tif4632p; Tif4631p [Saccharomyces cerevisiae]
K.ASSEENISEAEK.T +2											3.0815												3.1914		
K.ETSDSTSTSTPTPTPSTNDSK.A +2											4.2843												4.624		
K.SDEAEAEVEAEAGDAGTK.I +2																							4.4972		
	1										X												X		
gi|6322420|ref|NP_012494.1|																					4.9	4.9			Essential component of the nuclear pore complex, which mediates nuclear import and export; Nsp1p [Saccharomyces cerevisiae]
K.SAFSFGSKPTGK.E +2																									
K.TEALLSDVVSTSSGAAANNDQK.R +2																					3.693	2.9612			
K.TTNIDINNEDENIQLIK.I +2																					2.609	3.576			
	1																				X	X			
gi|6321818|ref|NP_011894.1|													9.5									11.6			Protein of unknown function that is a member of the PhzF superfamily, although unlike its bacterial homolog, is most likely not involved in phenazine production; possibly involved in a membrane regulation metabolic pathway; Yhi9p [Saccharomyces cerevisiae]
K.IGAVPITINEGLISFK.A +2													2.8095												
K.NTTATSLVQECK.I +2													4.0125												
K.TTDITISEGGR.L +2																						2.7805			
R.AFAPVINVYEDPVCGSGSVALAR.Y +2																						2.7756			
	1												X									X			
gi|6322168|ref|NP_012243.1|																			9.1		11				RNA polymerase II third largest subunit B44, part of central core; similar to prokaryotic alpha subunit; Rpb3p [Saccharomyces cerevisiae]
K.DLVIVSNLM*GR.N +2																			2.8699						
K.NCEYEDPPNEGDPFDYK.A +2																					4.2531				
K.VASILLALTQM*DQDK.V +2																									
K.WGPAAAIEFEYDPWNK.L +2																									
R.LGLIPLQSM*DIEQLEYSR.D +2																			3.3742		2.956				
R.LGLIPLQSMDIEQLEYSR.D +2																									
	1																		X		X				
gi|6322636|ref|NP_012709.1|																		4.5			4.9				WD repeat protein required for ubiquitin-mediated protein degradation, forms complex with Cdc48p, plays a role in controlling cellular ubiquitin concentration; also promotes efficient NHEJ in postdiauxic/stationary phase; Doa1p [Saccharomyces cerevisiae]
K.KVGDVVGAGATGNDK.K +2																		2.8847							
K.LPINVSDNPYTAADNFLAR.Y +2																					4.1581				
K.SPQGTIEAHQFSNSSWK.K +2																		2.6554							
K.YGPLEEYQECEEAAYR.L +2																									
R.WASEDEINELSTQVEK.S +2																					3.2306				
	1																	X			X				
gi|6322156|ref|NP_012231.1|																	9.1				6.5				Regulatory subunit of the cyclic AMP-dependent protein kinase (PKA), a component of a signaling pathway that controls a variety of cellular processes, including metabolism, cell cycle, stress response, stationary phase, and sporulation; Bcy1p [Saccharomyces cerevisiae]
K.QGDQGDYFYVVEK.G +2																									
K.VNSSGPGSSFGELALMYNSPR.A +2																	2.8752								
R.AATVVATSDCLLWALDR.L +2																	2.7214				3.8642				
R.LLGPAVDVLK.L +2																					2.6089				
	1																X				X				
gi|6321995|ref|NP_012071.1|														6.3							6				Exopolyphosphatase, hydrolyzes inorganic polyphosphate (poly P) into Pi residues; located in the cytosol, plasma membrane, and mitochondrial matrix; Ppx1p [Saccharomyces cerevisiae]
K.GSFIVPIIDIPR.E +2																					2.6378				
K.IKEEELFFIEDLK.S +2														2.7033											
K.QNVSQGTELNSYLVDNNDTPK.N +2																									
R.ELVILGDSNVVR.E +2														3.4565							3.77				
	1													X							X				
gi|14627173|ref|NP_012514.2|											2										2				Protein possibly involved in assembly of actin patches; interacts with an actin assembly factor Las17p and with the SH3 domains of Type I myosins Myo3p and Myo5p; localized predominantly to cortical actin patches; Bbc1p [Saccharomyces cerevisiae]
K.NEPYTETEEAEENEK.T +2																					3.2304				
K.SDYEDDLNFEK.D +2											2.9158														
K.SFVAVQGSEVGK.E +2											2.5749														
K.VVAQFPYK.S +1																					1.9669				
	1										X										X				
gi|6321456|ref|NP_011533.1|																	9.6			7.2					Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase) involved in the 4-aminobutyrate and glutamate degradation pathways; required for normal oxidative stress tolerance and nitrogen utilization; Uga1p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.GQDHVWSGLSGADANELAFK.A +2																	2.8675			2.9748					
K.HADIFIEALAK.S +2																	2.6332								
K.YNVVYIIDEVQTGVGATGK.L +2																									
R.GTFIAWDLPTGEK.R +2																									
R.LFASGSTTCSKPIHK.L +2																									
R.M*IIAGAIGQEISDK.K +2																									
R.MIIAGAIGQEISDK.K +2																	3.6348			3.6082					
gi|6323299|ref|NP_013372.1|																	13.4			8					Non-essential hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; interacts with neutral trehalase Nth1p; Dcs1p [Saccharomyces cerevisiae]
K.TITYAIGENHDLWK.R +2																									
K.VMSLLGTIDNK.D +2																	2.9631								
K.WVNNILYEGAESER.V +2																	3.5885			4.0279					
R.FQFVSVLDSNPQTK.V +2																				3.1286					
R.STPVLYNCENEYSCINGIQELK.E +2																	3.1651								
	2																X			X					
gi|6681849|ref|NP_014237.2|															7.5					7.5					Protein component of the large (60S) ribosomal subunit, identical to Rpl42Bp and has similarity to rat L44 ribosomal protein; Rpl42ap [Saccharomyces cerevisiae]
K.ASLFAQGK.R +2																									
K.HFELGGEK.K +1															2.3282					2.5797					
K.HFELGGEK.K +2															2.8581					2.9195					
	1														X					X					
gi|6320720|ref|NP_010801.1|													18.9							12.6					Cytoplasmic glutaredoxin, thioltransferase, glutathione-dependent disulfide oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity, expression induced in response to stress; Grx2p [Saccharomyces cerevisiae]
K.ATLSTLFQELNVPK.S +2													4.2229												
K.EVFVAAK.T +1																				2.2508					
K.HIGGNSDLETLKK.N +2													2.5947												
K.MVSQETVAHVK.D +2																				2.9283					
gi|6321644|ref|NP_011721.1|													11.7							11.7					ATP-binding protein of unknown function; crystal structure resembles that of E.coli pantothenate kinase and other small kinases; Ygr205wp [Saccharomyces cerevisiae]
K.CPLFIFFSGPQGSGK.S +2													4.2475							3.1915					
K.GMTDEQVHAFVDR.Y +2																									
K.SIGYASIDDFYLTHEDQLK.L +2													3.8851							2.5561					
gi|6323725|ref|NP_013796.1|													8.2							13.5					Phosphatidylinositol/phosphatidylcholine transfer protein involved in coordinate regulation of PtdIns and PtdCho metabolism, products of which are regulators in Golgi to plasma membrane transport; functionally homologous to mammalian PITPs; Sec14p [Saccharomyces cerevisiae]
K.FYIINAPFGFSTAFR.L +2													4.1907							3.155					
K.LLEDAGFIER.L +2													3.3059							2.8868					
R.AAGHLVETSCTIMDLK.G +2																				4.4104					
R.KFDVQLAK.E +2																									
gi|6324188|ref|NP_014258.1|													7.5							8.1					Adenine deaminase (adenine aminohydrolase), involved in purine salvage and nitrogen catabolism; Aah1p [Saccharomyces cerevisiae]
K.LQVVQSVSELPLQK.F +2													4.241							4.3594					
K.RNDIILPEGFPK.S +2													2.7495												
R.DQTMLTICPLSNVK.L +2																				3.5274					
gi|6324421|ref|NP_014490.1|													9.1							9.1					NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway; Gre2p [Saccharomyces cerevisiae]
K.AENLTEAFGNNPK.F +2																				3.8453					
K.ETIDDTASQILK.F +2																									
K.FELTAVNPVYVFGPQM*FDK.D +2													2.6019												
K.IPELFGGYIDVR.D +2													2.8077												
K.IVLHTASPFCFDITDSER.D +2																				2.6791					
R.VVLTSSYAAVFDM*AK.E +2																									
	5												X							X					
gi|6323452|ref|NP_013524.1|														7.4					15.9						Dihydroorotase, catalyzes the third enzymatic step in the de novo biosynthesis of pyrimidines, converting carbamoyl-L-aspartate into dihydroorotate; Ura4p [Saccharomyces cerevisiae]
K.CYPAGVTTNSAAGVDPNDFSAFYPIFK.A +3																			3.7093						
K.DLTPDLIHEAAQQHAIR.G +2																			3.1368						
K.GFVSDFGISFYEVK.D +2														3.0326					3.5267						
K.IILEHCTSESAIK.T +2														4.0712											
	1													X					X						
gi|6321517|ref|NP_011594.1|														8.7				9							Twinfilin, highly conserved actin monomer-sequestering protein involved in regulation of the cortical actin cytoskeleton, composed of two cofilin-like regions, localizes actin monomers to sites of rapid filament assembly; Twf1p [Saccharomyces cerevisiae]
K.ISPDSTSVHQTQVAR.S +2																		3.381							
K.LVSQDSASPLSLTFR.V +2														3.6451				3.5621							
K.YFFVSFIPDGSPVR.S +2														2.8706											
	1													X				X							
gi|6323201|ref|NP_013273.1|														12			9								Methyltransferase required for synthesis of diphthamide, which is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); not essential for viability; GFP-Dph5p fusion protein localizes to the cytoplasm; Dph5p [Saccharomyces cerevisiae]
-.M*LYLIGLGLSYK.S +2														4.3365											
K.AYTPDTPAVAISR.L +2																									
K.DVANDQEYFK.P +2																	2.5602								
K.SGTISELANYDSGEPLHSLVILGR.Q +3														4.249											
R.YMSIAQCCEQLLEIEEK.R +2																	3.2792								
	1													X			X								
gi|6322288|ref|NP_012362.1|											27						23.8								Subunit of heterotrimeric Replication Factor A (RF-A), which is a highly conserved single-stranded DNA binding protein involved in DNA replication, repair, and recombination; Rfa3p [Saccharomyces cerevisiae]
K.ENEDLSLNGVVALQR.L +2																									
K.NGSEVEMITLNNIR.V +2																	3.1224								
K.SQPTESQLILQSPTISSK.N +2											3.5402														
R.VDPTEISNVNAPVFR.I +2											4.1361						3.5183								
	1										X						X								
gi|6320303|ref|NP_010383.1|													7			9.1									Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx4p and Grx5p; protects cells from oxidative damage; Grx3p [Saccharomyces cerevisiae]
K.ESLEEDPDFLQHALQS.- +2																4.2189									
K.EYVSLLEDCK.N +2																2.7306									
K.LVNAAPVMFLFMPK.G +2													2.5858												
K.LVNAAPVMLFMK.G +2																									
R.FGFFDILR.D +2													3.1753												
	1												X			X									
gi|6319435|ref|NP_009517.1|													9.7	11.3											Single-domain racemase, possibly non-specific due to the lack of the second domain, which presumably determines specificity; Ybl036cp [Saccharomyces cerevisiae]
K.LKPASDIQILYDHGVR.E +2														3.514											
K.LNGLMTIGSWNVSHEDSK.E +2																									
K.VPNLYSVETIDSLK.K +2																									
R.EFGENYVQELIEK.A +2													3.5717	3.2882											
R.IGTDIFGARPPK.N +2													2.7885												
gi|6322228|ref|NP_012303.1|													26.4	14.1											Thiol peroxidase that functions as a hydroperoxide receptor to sense intracellular hydroperoxide levels and transduce a redox signal to the Yap1p transcription factor; Hyr1p [Saccharomyces cerevisiae]
K.CGFTPQYK.E +2																									
K.ELEALYK.R +1													2.289												
K.IDVNGGNEDPVYK.F +2													3.415												
K.PSSLSETIEELLK.E +2													3.7	3.1325											

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.VVLIVNVASK.C +2													2.7048	3.106											
gi|6322350|ref|NP_012424.1|													4.4	8.5											Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct7p [Saccharomyces cerevisiae]
K.INALNSATEATNLILSVDETITTNK.G +3														3.7392											
K.LIVAGGGATEM*EVSK.C +2																									
K.LIVAGGGATEMEVSK.C +2																									
K.LLDVVHPAAK.T +2													2.9995	3.0228											
K.LPIGDLATQFFADR.N +2													3.6394												
R.QVEETGANIVLSK.L +2														2.9937											
gi|6323088|ref|NP_013160.1|													5.2	5.2											RNA exonuclease, required for U4 snRNA maturation; functions redundantly with Rnh70p in 5.8S rRNA maturation, and with Rnh70p and Rex3p in processing of U5 snRNA and RNase P RNA; member of RNase D family of exonucleases; Rex2p [Saccharomyces cerevisiae]
K.NVGVLAGNSVHM*DR.L +2													3.8277	4.0755											
K.NVGVLAGNSVHMDR.L +2													2.9255	3.0169											
R.IVDVSSIMEVAR.R +2																									
	4												X	X											
gi|14318526|ref|NP_116659.1|									8.8					8.2											Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates; Rpn11p [Saccharomyces cerevisiae]
K.ANIQALIHGLNR.H +2														3.3181											
R.AVAVVVDPIQSVK.G +2									3.547					3.6131											
R.LIDTGALINNLEPR.Q +2									2.9814																
gi|6320100|ref|NP_010180.1|									7.1					9.4											UDP-N-acetylglucosamine pyrophosphorylase, catalyzes the formation of UDP-N-acetylglucosamine (UDP-GlcNAc), which is important in cell wall biosynthesis, protein N-glycosylation, and GPI anchor biosynthesis; Qri1p [Saccharomyces cerevisiae]
K.DQEELLSNLEQISSK.R +2																									
K.DTGVEISPLPPTSYESLIGNSK.K +2									2.7243																
K.EQITFFNQGTLPAFDLTGK.H +2														3.0804											
K.LGTSWLEDAGAIVK.D +2														3.5814											
K.LSYAGENLSQFK.G +2														2.9097											
R.DAHESVGLIATK.N +1									2.0201																
	2								X					X											
gi|6320117|ref|NP_010197.1|							11							12.5											Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YDL086W is not an essential gene; Ydl086wp [Saccharomyces cerevisiae]
- M*LITETFHDVQTSYGTTLR.I +2														2.9942											
R.IDLGEFVDDNTPLEHVC.- +2							3.2629																		
R.TLGLGQNDNSLER.V +2							2.8161																		
R.VTCATCFFPTDIHSR.T +2														4.1498											
	1						X							X											
gi|6319587|ref|NP_009669.1|												11.7	11.7												Nudix hydrolase family member with ADP-ribose pyrophosphatase activity; Ysa1p [Saccharomyces cerevisiae]
R.SSGGVDGIGILTILK.Y +2												4.5724	4.4131												
R.VQNVAQGILM*AK.Q +2													3.2858												
R.VQNVAQGILMAK.Q +2												2.7325													
	1											X	X												
gi|6320205|ref|NP_010285.1|		15.9											16.4												Ran GTPase binding protein; involved in nuclear protein import and RNA export, ubiquitin-mediated protein degradation during the cell cycle; shuttles between the nucleus and cytoplasm; is essential; homolog of human RanBP1; Yrb1p [Saccharomyces cerevisiae]
K.EGDDAPESPDIHFEPVVHLEK.V +2													3.8731												
K.ICANHIIAPEYTLKPNVGSDR.S +3		5.5237																							
K.KEGDDAPESPDIHFEPVVHLEK.V +3													4.7407												
K.TM*EEDEEVLYK.V +2													3.6553												
K.TMEEDEEVLYK.V +2		4.0983																							
	1	X											X												
gi|14318557|ref|NP_116690.1|		13.6	13.6																						Protein component of the large (60S) ribosomal subunit, has similarity to rat L29 ribosomal protein; not essential for translation, but required for proper joining of the large and small ribosomal subunits and for normal translation rate; Rpl29p [Saccharomyces cerevisiae]
K.HALHGTAK.A +2		2.9027	2.969																						
	1	X	X																						
gi|6323287|ref|NP_013359.1|																								4.5	Glycogen synthase, similar to Gsy1p; expression induced by glucose limitation, nitrogen starvation, heat shock, and stationary phase; activity regulated by cAMP-dependent, Snf1p and Pho85p kinases as well as by the Gac1p-Glc7p phosphatase; Gsy2p [Saccharomyces cerevisiae]
K.APITVAQYK.D +2																									
K.ATYQNEVDILDWK.K +2																								2.7021	
K.TVVAFIVM*PAK.N +2																									
R.ELVGEELNDSNMDALAGGK.K +2																								2.7689	
	1																							X	
gi|14318437|ref|NP_116578.1|																							4.1		Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p [Saccharomyces cerevisiae]
K.EATSWETTPMDIAK.G +2																							2.7596		
K.QQSLYLDPEPTFIEER.I +2																							2.7236		
R.TVSQADFPGLEGVAK.N +2																									
R.VADFGVIHR.N +2																									
gi|6321646|ref|NP_011723.1|																							14.6		Protein that interacts with frataxin (Yfh1p); homolog of mammalian electron transfer flavoprotein complex subunit ETF-beta; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; Ygr207cp [Saccharomyces cerevisiae]
K.FSINPFDDIAVEEAIR.I +2																							3.4065		
K.GIDTCSLIDSVGK.E +2																									
K.SLVESTHAVSIGSAK.A +2																									
R.EIDDGEEVIEASLPMVITTDLR.L +2																							3.4858		
gi|6323273|ref|NP_013345.1|																							7.8		Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal methionine from nascent polypeptides; function is partially redundant with that of Map2p; Map1p [Saccharomyces cerevisiae]
K.DGLEGAYDPFPK.F +2																							3.4487		
K.QGIVSIFCDTSCYENNYK.A +2																							2.7361		
gi|6324208|ref|NP_014278.1|																							5.2		Component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; Tom70p [Saccharomyces cerevisiae]
K.FGDIDTATATPTELSTQPAK.E +2																							4.5726		
R.NDSTEYYNYFDK.A +2																							3.152		
gi|6324856|ref|NP_014924.1|																							13.6		Essential protein with similarity to phosducins, which are GTPase inhibitors; lethality of null mutation is functionally complemented by expression of mouse phosducin-like protein MgcPhLP; Plp2p [Saccharomyces cerevisiae]
K.DLSDLEELEDDEDEDFLEAYK.I +2																							2.5607		
R.AIENYPESNCPTLIVYYR.G +2																							3.2626		
gi|6325172|ref|NP_015240.1|																							2.7		COPII vesicle coat protein required for ER transport vesicle budding and autophagosome formation; Sec16p is bound to the periphery of ER membranes and may act to stabilize initial COPII complexes; interacts with Sec23p, Sec24p and Sec31p; Sec16p [Saccharomyces cerevisiae]
K.DSADVTDETMDIEGPGFNDVK.N +2																							2.9525		
K.SDAYDFPLEIISESSK.K +2																							3.5054		
K.TSPSPTGPNPNNSPSPSSPISR.I +2																							2.5798		
	6																						X		
gi|6320478|ref|NP_010558.1|																						6.6			Cytoplasmic glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione into glutathione and D-lactate; Glo2p [Saccharomyces cerevisiae]
K.DEVEFNPFMR.L +2																						2.8805			
K.SWLIDPAEPPEVLPELTEDEK.I +2																									
K.VEVIGGSK.D +1																						1.8542			
R.CIFTGDTLFTAGCGR.F +2																									
R.VYPGHEYTSDNVK.F +2																									
R.WESGGVNYCYLLSDSK.N +2																									

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6320869|ref|NP_010948.1|																						17			GTPase of the Ypt/Rab family, very similar to Ypt32p; involved in the exocytic pathway; mediates intra-Golgi traffic or the budding of post-Golgi vesicles from the trans-Golgi; Ypt31p [Saccharomyces cerevisiae]
K.TFAQENQLLFTETSALNSENVDK.A +2																						3.8918			
R.ENADDNVAVGLIGNK.S +2																						2.7335			
gi|6321753|ref|NP_011829.1|																						10.2			Nucleolar single-strand nucleic acid binding protein; associates with small nuclear RNAs; Sbp1p [Saccharomyces cerevisiae]
K.DTLYINNVPFK.A +2																						3.0356			
K.EEVAEFFGTDADSISLPM*R.K +2																						4.0366			
K.EEVAEFFGTDADSISLPMR.K +2																									
K.TVIDPEDTIFIGNVAHECTEDDLK.Q +2																									
R.GM*AFVTFSGENVDIEAK.A +2																									
gi|6322321|ref|NP_012395.1|																						14			RNA polymerase II subunit B32; forms two subunit dissociable complex with Rpb7p; dispensable under some environmental conditions; involved in export of mRNA to cytoplasm under stress conditions; involved in telomere maintenance; Rpb4p [Saccharomyces cerevisiae]
K.ELESIDVLLEQTTGGNNK.D +2																						3.818			
K.NTMQYLTNFSR.F +2																									
K.STGLHPFEVAQLGSLACDTADEAK.T +3																									
R.DQETVGAVIQLLK.S +2																						3.2812			
gi|6324595|ref|NP_014664.1|																						13.6			hypothetical protein; Yor021cp [Saccharomyces cerevisiae]
K.TAYPNLLISR.R +2																						2.6486			
R.EVGAENLILSSLPESTTEK.D +2																						2.7985			
	5																					X			
gi|116006493|ref|NP_012376.3|																					7				O-mannosylated heat shock protein that is secreted and covalently attached to the cell wall via beta-1,3-glucan and disulfide bridges; required for cell wall stability; induced by heat shock, oxidative stress, and nitrogen limitation; Hsp150p [Saccharomyces cerevisiae]
K.TSGTLEMNLK.G +2																					2.7265				
K.TTAAAVSQIGDGQIQATTK.T +2																					3.335				
R.IGSIVANR.Q +2																									
gi|14318538|ref|NP_116671.1|																					2.7				Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and bud; interacts with Spa2p; YFL016C is not an essential gene; Yfr016cp [Saccharomyces cerevisiae]
K.DILDETNEFLEQLK.I +2																					2.5484				
K.DVTGDQEIDDINISDEFQR.T +2																					3.0996				
gi|6320152|ref|NP_010232.1|																					11.6				RNA binding protein required for maturation of tRNA and snRNA precursors; acts as a molecular chaperone for RNAs transcribed by polymerase III; homologous to human La (SS-B) autoantigen; Lhp1p [Saccharomyces cerevisiae]
K.SYSNDDESNEILSYEGK.K +2																					4.0799				
R.NSFAVIEFTPEVLDR.C +2																					4.3297				
gi|6320598|ref|NP_010678.1|																					4.2				Nuclear protein that acts as a heterodimer with Aos1p to activate Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability; Uba2p [Saccharomyces cerevisiae]
R.ETSLVTIIGEDSYK.K +2																					2.9474				
R.LLFDYDFEDLNDR.T +2																					3.3556				
gi|6320863|ref|NP_010942.1|																					6.6				Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the ternary complex with GTP and tRNAi-Met; Gcd11p [Saccharomyces cerevisiae]
K.VAFTGLEEDGETEEEK.R +2																					3.4099				
R.EFEEGGGLPEQPLNPDFSK.L +2																					3.5637				
gi|6321599|ref|NP_011675.1|																					8.9				Nucleolar protein that binds nuclear localization sequences, required for pre-rRNA processing and ribosome biogenesis; Nsr1p [Saccharomyces cerevisiae]
K.FGDTPSEPSDTLFLGNLSFNADR.D +2																					2.6819				
K.NEETEEPATIFVGR.L +2																					3.8435				
gi|6322485|ref|NP_012559.1|																					16.9				3-hydroxyanthranilic acid dioxygenase, required for biosynthesis of nicotinic acid from tryptophan via kynurenine pathway; Bna1p [Saccharomyces cerevisiae]
K.EAILDFENDVEK.R +2																					2.9137				
R.FADTVGIVVEQDRPGGENDK.I +2																									
R.QVVHESELQMLDLGTQVK.E +2																					3.1856				
gi|6324156|ref|NP_014226.1|																					11.2				Plasma membrane protein involved in G-protein mediated pheromone signaling pathway; overproduction suppresses bem1 mutations; Mdg1p [Saccharomyces cerevisiae]
K.DPSGAFEITLPVTFDSPSSK.F +2																									
K.NADGLSGTTTIIENNVGVNEEK.A +2																					3.5777				
K.VNIDEGVENNFITEEDVIK.Q +2																					4.677				
gi|6324521|ref|NP_014590.1|																					8.1				S-adenosylmethionine decarboxylase, required for the biosynthesis of spermidine and spermine; cells lacking Spe2p require spermine or spermidine for growth in the presence of oxygen but not when grown anaerobically; Spe2p [Saccharomyces cerevisiae]
K.FVCGPEASTTALVEPNEDK.G +2																					3.0707				
K.LLSINESLPDYIK.L +2																					2.9632				
gi|6324731|ref|NP_014800.1|																					3.4				Endopeptidase with trypsin-like activity that cleaves after basic residues; beta-type subunit of 20S proteasome synthesized as a proprotein before being proteolytically processed for assembly into 20S particle; human homolog is subunit Z; Pup1p [Saccharomyces cerevisiae]
R.VVSALQMLK.Q +1																					2.2148				
R.VVSALQMLK.Q +2																					2.7573				
gi|6324798|ref|NP_014867.1|																					11				RNA polymerase subunit ABC14.5, common to RNA polymerases I, II, and III; Rpb8p [Saccharomyces cerevisiae]
R.SLADDYDYVM*YGTAYK.F +2																					3.1697				
R.SLADDYDYVMYGTAYK.F +2																					2.9304				
	11																				X				
gi|6319500|ref|NP_009582.1|																				7.6					2-enoyl thioester reductase, member of the medium chain dehydrogenase/reductase family; localized to in mitochondria, where it has a probable role in fatty acid synthesis; Etr1p [Saccharomyces cerevisiae]
K.SLIYSTHEVEDCTK.V +2																				3.6521					
R.VIPLQANQGTWSNYR.V +2																				4.3534					
gi|6319508|ref|NP_009590.1|																				7.2					Nuclear SAM-dependent mono- and asymmetric arginine dimethylating methyltransferase that modifies hnRNPs, including Npl3p and Hrp1p, thus facilitating nuclear export of these proteins; required for viability of npl3 mutants; Hmt1p [Saccharomyces cerevisiae]
K.ELVELNGFSDK.I +2																				2.809					
R.DHYLVEGGLIFPDK.C +2																				3.7857					
gi|6319569|ref|NP_009651.1|																				7.3					Repressible acid phosphatase (1 of 3) that also mediates extracellular nucleotide-derived phosphate hydrolysis; secretory pathway derived cell surface glycoprotein; induced by phosphate starvation and coordinately regulated by PHO4 and PHO2; Pho5p [Saccharomyces cerevisiae]
K.DIFPFLGGAGPYYSFPGDYGISR.D +2																				3.941					
K.GYSDVCDIFTK.D +2																				3.5408					
R.SWYVPQGAR.V +2																									
gi|6320033|ref|NP_010113.1|																				11.7					Bifunctional enzyme containing both alcohol dehydrogenase and glutathione-dependent formaldehyde dehydrogenase activities, functions in formaldehyde detoxification and formation of long chain and complex alcohols, regulated by Hog1p-Sko1p; Sfa1p [Saccharomyces cerevisiae]
K.EINQAFEDLHNGDCLR.T +2																				3.0592					
K.KPLSVEEITVDAPK.A +2																				3.5461					
K.QYCSQFGATDFVNPK.E +2																				3.9552					
K.VEEFITHR.R +2																									
gi|6322029|ref|NP_012104.1|																				5.6					Invertase, sucrose hydrolyzing enzyme; a secreted, glycosylated form is regulated by glucose repression, and an intracellular, nonglycosylated enzyme is produced constitutively; Suc2p [Saccharomyces cerevisiae]
K.AEPILNISNAGPWSR.F +2																				3.1477					
K.FSLNTEYQANPETELINLK.A +2																									
K.NPVLAANSTQFR.D +2																									
K.NPVLAANSTQFRDPK.V +2																				3.093					
gi|6322585|ref|NP_012659.1|																				5.1					Protein containing an N-terminal epsin-like domain involved in clathrin recruitment and traffic between the Golgi and endosomes; associates with the clathrin adaptor Gga2p; Ent3p [Saccharomyces cerevisiae]
K.ALIELLSDDNK.I +2																				3.1694					
K.ALQLLDYLIK.H +2																				2.7821					

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|6323147|ref|NP_013219.1|																									Acyl-protein thioesterase responsible for depalmitoylation of Gpa1p; the mutant has no gross defects in signaling through the mating pathway; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ylr118cp [Saccharomyces cerevisiae]
K.IGGIVALSGFCSIPGILK.Q +2																				14.5					
K.VDSDGFMNSLNSIEK.T +2																				2.604					
																				3.2378					
gi|6323374|ref|NP_013446.1|																									Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alternate catalytic subunit Gsc2p; binds to regulatory subunit Rho1p; involved in cell wall synthesis and maintenance; localizes to sites of cell wall remodeling; Fks1p [Saccharomyces cerevisiae]
R.ARITGFKRKLVGDESEK.A +2																				1.8					
R.AYPDLQIAYLDEEPPLTEGEEEPR.I +2																				2.6117					
R.GEYIQLIDANQDNYLEECLK.I +2																									
R.YEEQTTNHPVAIVGAR.E +2																				2.5515					
gi|6323402|ref|NP_013474.1|																				7.3					Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; Arc18p [Saccharomyces cerevisiae]
R.GPAYPSNSDYDIIDECLDLFR.A +2																									
R.M*VGNFALLPLNTK.F +2																				3.3933					
R.MVGNFALLPLNTK.F +2																				2.6208					
gi|6324543|ref|NP_014612.1|																				6.4					Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the cell wall; Gas5p [Saccharomyces cerevisiae]
K.LYQDYSVPVFLSEFGCNQVK.S +2																									
R.QIPVGYSAADIVANR.Q +2																									
R.QLAAEYFNCGDEADAR.I +2																				4.1416					
R.VYTVDNSQDHSHCMK.L +2																				2.5361					
gi|6325445|ref|NP_015513.1|																				26.5					RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III; part of central core; similar to bacterial omega subunit; Rpo26p [Saccharomyces cerevisiae]
K.TIVTGGNGPEDFQQHEQIR.R +2																				3.4619					
R.ALQISM*NAPVFVDLEGETDPLR.I +2																				2.7099					
R.ALQISM*NAPVFVDLEGETDPLR.I +3																									
R.ALQISMNAPVFVDLEGETDPLR.I +2																				3.8165					
	11																			X					
gi|6319470|ref|NP_009552.1|																			29.5						One of two nearly identical (see also HTA1) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; Hta2p [Saccharomyces cerevisiae]
gi|6320431|ref|NP_010511.1|																			X						One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p; Hta1p [Saccharomyces cerevisiae]
K.AGLTFPVGR.V +2																			2.6066						
K.LLGNVTIAQGGVLPNIHQNLLPK.K +3																			4.557						
R.HLQLAIR.N +2																			2.8109						
gi|6319630|ref|NP_009712.1|																									RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III; contacts DNA and affects transactivation; Rpb5p [Saccharomyces cerevisiae]
K.NFQTGIFVYQNNITPSAM*K.L +2																			14						
R.ADPVALYLGLK.R +2																			4.7318						
R.GYFITQEEVELPLEDFK.A +2																			3.4686						
gi|6321793|ref|NP_011869.1|																									Essential protein of the mitochondrial intermembrane space, forms a complex with Tim9p (TIM10 complex) that mediates insertion of hydrophobic proteins at the inner membrane, has homology to Mrs5p, which is also involved in this process; Mrs11p [Saccharomyces cerevisiae]
K.CINTSYSEGELNK.N +2																			32.3						
K.IQAAEAELDLVTDMFNK.L +2																			2.8495						
K.IQAAEAELDLVTDMFNK.L +2																			4.2824						
R.CVAKYFETNVQVGENMQK.M +2																									
gi|6323719|ref|NP_013790.1|																			17.9						Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus and cytoplasm; YMR074C is not an essential gene; Ymr074cp [Saccharomyces cerevisiae]
K.DFSEDLNSFDK.Q +2																									
K.ITEAEIVSILNGIAK.Q +2																			2.9615						
K.KLIATNNVTHK.I +2																			3.5796						
	4																		X						
gi|37362671|ref|NP_012726.2|																		9.7							Essential protein of the mitochondrial intermembrane space (IMS); promotes retention of newly imported proteins; may do so by stabilizing client protein folding as part of a disulfide relay system or transferring metal to client proteins; Mia40p [Saccharomyces cerevisiae]
K.TAEEELSSGGEQSPENEDDNNSK.S +2																		3.1295							
K.VAEDGELVVLAEEDNK.S +2																		2.9529							
K.VNTIESAPNVSSAK.E +2																									
gi|6319530|ref|NP_009612.1|																		4.8							Putative cytoplasmic protein of unknown function; Ybr056wp [Saccharomyces cerevisiae]
K.EYDSEFDAISQQLK.K +2																		2.5096							
K.TAVDDIIAFR.K +2																		2.8796							
gi|6320640|ref|NP_010720.1|																		8.7							RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytoplasm; dissociation from mRNAs is promoted by Mtr10p; phosphorylated by Sky1p in the cytoplasm; Npl3p [Saccharomyces cerevisiae]
K.SFANQPLEVVYSKL.L +2																									
R.DFDGTGALEFPSEEILVEALER.L +2																		2.6297							
R.ENSLETTFSSVNTR.D +2																		3.3097							
gi|6321650|ref|NP_011727.1|																		5.6							Essential protein with two zinc fingers, present in the nucleus of growing cells but relocates to the cytoplasm in starved cells via a process mediated by Cpr1p; binds to translation elongation factor eEF-1 (Tef1p); Zpr1p [Saccharomyces cerevisiae]
K.EQNEDLGLSDIKVE.- +2																		2.935							
R.ITLYCDDAADLSR.D +2																		3.1747							
gi|6321704|ref|NP_011780.1|																		4.3							Methionyl-tRNA synthetase, forms a complex with glutamyl-tRNA synthetase (Gus1p) and Arc1p, which increases the catalytic efficiency of both tRNA synthetases; also has a role in nuclear export of tRNAs; Mes1p [Saccharomyces cerevisiae]
K.DINEILSNYVK.E +2																									
R.DLVWGTPVPLEK.Y +2																		2.5944							
R.NYNALFICGTDEYGTATETK.A +2																		3.0449							
gi|6324433|ref|NP_014502.1|																		12.2							Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-dependent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p); Cdc33p [Saccharomyces cerevisiae]
K.GADIDELWLR.T +2																		3.2491							
K.KFEENVSVDDTTATPK.T +2																		5.2996							
	6																	X							
gi|6319553|ref|NP_009635.1|																	4.3								Subunit of the core complex of translation initiation factor 3(eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes; Rpg1p [Saccharomyces cerevisiae]
R.AGNREPPSTPSTLPK.A +2																	2.958								
R.TAGGSSPATPATPATPATPTPSSGPK.K +2																	3.7285								
R.TAGGSSPATPATPATPATPTPSSGPK.K +3																									
gi|6321628|ref|NP_011705.1|																	6.9								Cell wall protein that functions in the transfer of chitin to beta(1-6)glucan, putative chitin transglycosidase; Crh1p [Saccharomyces cerevisiae]
K.TTWYLDGESVR.V +2																									
K.YGSDGLSMTLAK.R +2																	3.228								
K.YTYGDQSGSWESIEADGGSIYGR.Y +2																	2.9438								
gi|6323420|ref|NP_013492.1|																	17.9								Protein component of the small (40S) ribosomal subunit; nearly identical to Rps29Bp and has similarity to rat S29 and E. coli S14 ribosomal proteins; Rps29ap [Saccharomyces cerevisiae]
K.ANDIGFNK.F +1																									
K.ANDIGFNK.F +2																									
R.VCSSHTGLIR.K +1																	2.2961								
R.VCSSHTGLIR.K +2																	2.7732								
	3																X								
gi|6319638|ref|NP_009720.1|																4									Covalently-bound cell wall protein of unknown function; identified as a cell cycle regulated SBF target gene; deletion mutants are highly resistant to treatment with beta-1,3-glucanase; has sequence similarity to YJL171C; Tos1p [Saccharomyces cerevisiae]

Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
K.TGCGEM*DLFEILTAGSDK.L +2																2.5835									
K.TGCGEMDLFEILTAGSDK.L +2																3.2982									
R.TLQYGDASCSCWK.T +2																									
gi|6320273|ref|NP_010353.1|																8.1									Protein of unknown function, green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; Dos2p [Saccharomyces cerevisiae]
K.DDGIEINLPISNETTETAQK.Y +2																									
K.MDLQLDPFDVDEK.T +2																3.2967									
K.TEEICSILQGDK.D +2																2.5864									
gi|6320352|ref|NP_010432.1|																6.9									Dihydrolipoyl transsuccinylase, a component of the mitochondrial alpha-ketoglutarate dehydrogenase complex, which catalyzes a step in the tricarboxylic acid (TCA) cycle, the oxidative decarboxylation of alpha-ketoglutarate to succinyl-CoA; Kgd2p [Saccharomyces cerevisiae]
K.AQEPPVASNSFTPFPR.T +2																3.615									
K.DIPAVNGAIEGDQIVYR.D +2																									
R.NAESLSVLDIENEIVR.L +2																3.6257									
	3															X									
gi|6321575|ref|NP_011652.1|															10.8										Protein containing an N-terminal SH3 domain; binds Las17p, which is a homolog of human Wiskott-Aldrich Syndrome protein involved in actin patch assembly and actin polymerization; Lsb1p [Saccharomyces cerevisiae]
K.ESNVISGDIFELINSK.L +2															3.6655										
K.IGIFPANYVK.P +2															2.752										
gi|6322559|ref|NP_012633.1|															11.4										Ubiquitin C-terminal hydrolase that cleaves ubiquitin-protein fusions to generate monomeric ubiquitin; hydrolyzes the peptide bond at the C-terminus of ubiquitin; also the major processing enzyme for the ubiquitin-like protein Rub1p; Yuh1p [Saccharomyces cerevisiae]
K.AIVLLFPINEDR.K +2															2.7274										
K.SDPTATDLIEQELVR.V +2															4.2152										
gi|6323192|ref|NP_013264.1|															5.2										Smaller subunit of the mitochondrial processing protease (MPP), essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins; Mas1p [Saccharomyces cerevisiae]
K.AVDILSDILTK.S +2															2.6439										
R.MVLAGAGAVDHEK.L +2															2.7933										
gi|6325298|ref|NP_015366.1|															6.2										Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation; Tif5p [Saccharomyces cerevisiae]
K.DDEWAVDMSEEAIR.A +2															2.7471										
K.LQDVLDGFINK.F +2															3.7797										
K.NPETEIIITK.D +2																									
gi|6325309|ref|NP_015377.1|															28										High-mobility group non-histone chromatin protein, functionally redundant with Nhp6Bp; homologous to mammalian high mobility group proteins 1 and 2; acts to recruit transcription factor Rcs1p to certain promoters; Nhp6ap [Saccharomyces cerevisiae]
R.ALSAYM*FFANENR.D +2															3.454										
R.SENPDITFGQVGK.K +2															4.087										
	5														X										
gi|42759861|ref|NP_012891.2|														11											Putative protein of unknown function; similar to uncharacterized proteins from other fungi; Ykl033w-ap [Saccharomyces cerevisiae]
K.LPITLDEYDER.N +2														3.3219											
K.WGTCEFLPGALNLLK.Y +2														4.9405											
gi|6320222|ref|NP_010302.1|														9.2											T subunit of the mitochondrial glycine decarboxylase complex, required for the catabolism of glycine to 5,10-methylene-THF; expression is regulated by levels of levels of 5,10-methylene-THF in the cytoplasm; Gcv1p [Saccharomyces cerevisiae]
K.AVEFAEQLLANPVM*KPIGLAAR.D +3														4.5162											
K.ENDDNEFYIVTNAGCAER.D +2																									
R.SLLALQGPK.A +2																									
R.TNAGLFDVSHMLQSK.L +2														2.8836											
gi|6320726|ref|NP_010806.1|														7											Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p [Saccharomyces cerevisiae]
K.VVILPYFTDIEPDLFPK.Y +2														3.5463											
R.FAPIYEEIANVLASDESVR.D +2														3.5971											
R.FAPIYEEIANVLASDESVR.D +3														4.7001											
gi|6320742|ref|NP_010822.1|														15.2											Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S. cerevisiae Hsp32p, Hsp33p, and Sno4p; member of the DJ-1/ThiJ/PfpI superfamily, which includes human DJ-1 involved in Parkinson's disease; exists as a dimer; Hsp31p [Saccharomyces cerevisiae]
K.SITGFTDVGETILGVDSILK.A +2														3.1371											
R.LVTGVNPASAHSTAVR.S +2														3.5852											
gi|6321905|ref|NP_011981.1|														5.3											Cytoplasmic aspartyl aminopeptidase; cleaves unblocked N-terminal acidic amino acid residues from peptide substrates; forms a 12 subunit homo-oligomeric complex; M18 metalloprotease family member; may interact with ribosomes; Yhr113wp [Saccharomyces cerevisiae]
K.IPTLAIHLDR.D +2																									
K.PLFHSAILETSAK.S +2																									
R.ETQLLPIGGLQEDK.T +2														2.9929											
R.YM*TNSPGLVLVK.R +2														3.3056											
gi|6321929|ref|NP_012005.1|														3.9											Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism; Aro9p [Saccharomyces cerevisiae]
K.ILDLADITTR.A +2														3.5929											
K.SFLTLDTDAR.V +2														2.7709											
R.APSGTSQAIVYSTIK.A +2																									
gi|6322839|ref|NP_012912.1|														14											Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches; Arc19p [Saccharomyces cerevisiae]
R.AEAFYILR.R +2														2.9511											
R.NENEQVLIEPSVNSVR.M +2														4.6737											
gi|6323755|ref|NP_013826.1|														3.2											Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control; Ilv2p [Saccharomyces cerevisiae]
K.VVQTQIAVEGDATTNLGK.M +2																									
R.INEAFEIATSGR.P +2														2.982											
R.PGPVLVDLPK.D +2														2.7481											
gi|6324169|ref|NP_014239.1|														8.5											Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associated growth arrest and upon entry into stationary phase; may be involved in adaptation prior to stationary phase entry; has similarity to Sps100p; Ygp1p [Saccharomyces cerevisiae]
K.NAVGAGYLSPIK.A +2														3.368											
K.WFFDASKPTLISSDSIIR.K +3														3.6689											
gi|6324221|ref|NP_014291.1|														4.1											Putative protein of unknown function with similarity to TFC7 and phosphotranfer enzymes in prokaryotes; a deletion mutant shows alterations in glucose metabolism; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; Ynl108cp [Saccharomyces cerevisiae]
K.TIMIVTHAATK.S +2														2.7183											
K.TIMIVTHAATK.S +2														2.7779											
gi|6325112|ref|NP_015180.1|														6.7											Member of the oxysterol binding protein family, which includes seven yeast homologs; involved in negative regulation of Sec14p-dependent Golgi complex secretory functions, peripheral membrane protein that localizes to the Golgi complex; Kes1p [Saccharomyces cerevisiae]
K.EHCLIDPEVESPELAR.M +2																									
K.LGDFNLIAK.T +2														3.1455											
R.IPAEHLNVKPLEEQHPLESR.K +3														3.9322											
gi|6325449|ref|NP_015517.1|														8.4											Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; transcription is regulated by Hap1p, Hap2p/Hap3p, and heme; Qcr2p [Saccharomyces cerevisiae]
K.DDLPYYVNALADVLYK.T +2																									
K.FNYVAVGDVSNLPYLDEL.- +2																									
K.NAVQNESVSSPIELNFDAVK.D +2																									
K.SAEDQLYAITFR.K +2																									
K.TAFKPHELTESVLPAAR.Y +2														2.9721											
R.FVDESLLSTLPAGK.S +2														3.148											

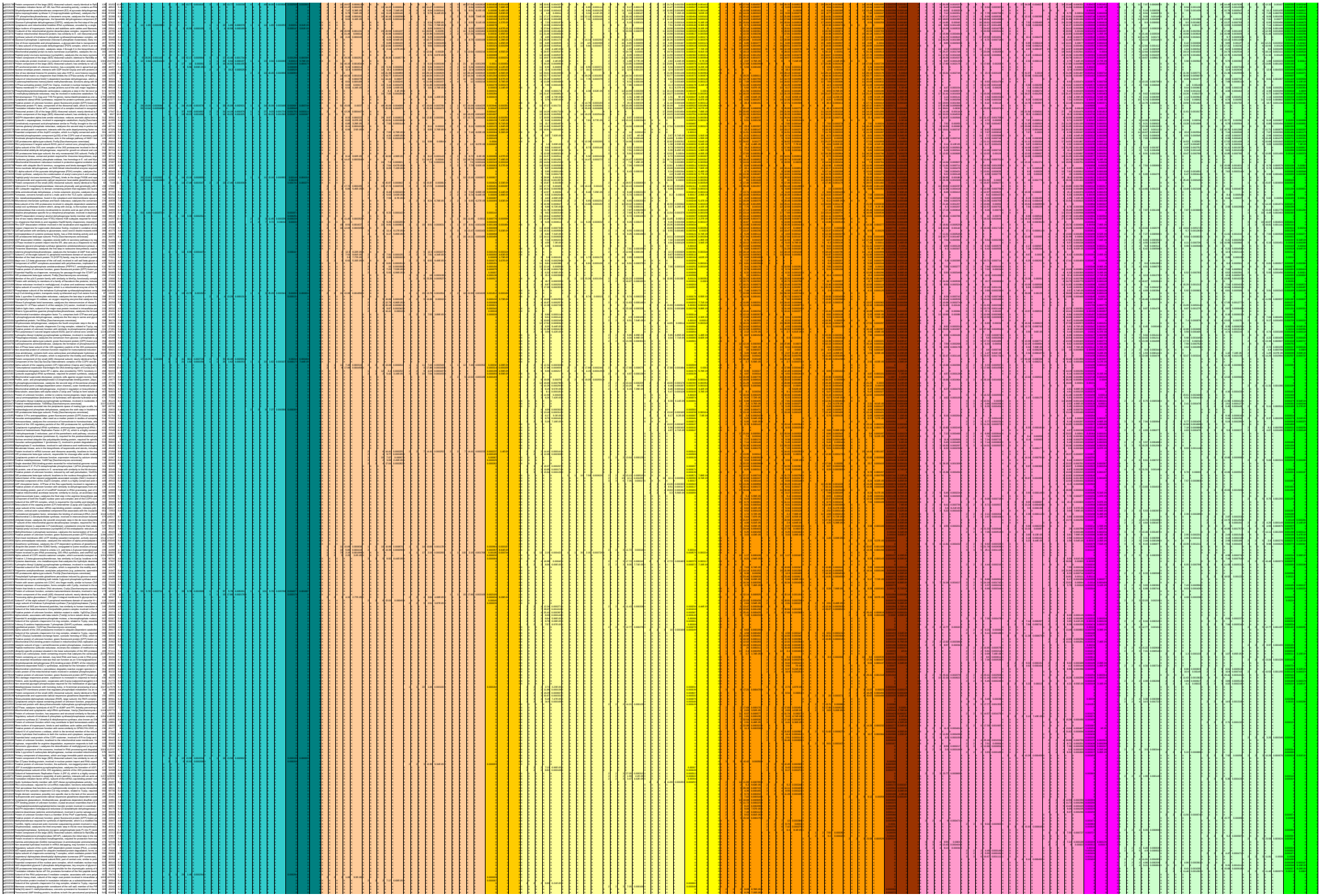
Locus	noDE-1	noDE-2	noDE-3	noDE-4	DE15-1	DE15-2	DE15-3	DE15-4	DE60-1	DE60-2	DE60-3	DE60-4	DE90-1	DE90-2	DE90-3	DE90-4	DE300-1	DE300-2	DE300-3	DE300-4	DE600-1	DE600-2	DE600-3	DE600-4	Description
gi|82795247|ref|NP_010666.2|																									Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and either Lsm1p or 8p): cytoplasmic Lsm1p complex involved in mRNA decay; nuclear Lsm8p complex part of U6 snRNP and possibly involved in processing tRNA, snoRNA, and rRNA; Lsm6p [Saccharomyces cerevisiae]
K.ASTEGSVTTEFLSDIIGK.T +2														32.6											
K.FNSDVFLR.G +2														2.708											
K.LASGLLYSGR.L +2														2.8351											
	13													X											
gi|6319699|ref|NP_009781.1|													8.3												Peroxisomal AMP-binding protein, localizes to both the peroxisomal peripheral membrane and matrix, expression is highly inducible by oleic acid, similar to E. coli long chain acyl-CoA synthetase; Pcs60p [Saccharomyces cerevisiae]
R.GENVTLGYANNPK.A +2																									
R.SCSSALAPATFHK.L +2													3.2404												
R.TGDQGYFDPEGFLVLTGR.I +2													3.0902												
R.TQGSVVVPDGFHPK.L +2													2.7195												
gi|6320695|ref|NP_010775.1|													10.6												3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis from ribulose-5-phosphate, also has an unrelated function in mitochondrial respiration; Rib3p [Saccharomyces cerevisiae]
- M*FTPIDQAIEHFK.Q +2													3.4415												
K.FVIVMDDAGR.E +2																									
K.LSGLSPVAVIGELVNDDEQGTM*M*R.L +2																									
R.ENEGDLICAAENVSTEQMAFLVR.H +2																									
R.LNDCQAFGK.K +2													2.682												
gi|6320976|ref|NP_011055.1|													2.6												Upstream kinase for the SNF1 complex; partially redundant function with Elm1p and Tos3p; members of this family of kinases have functional orthology with LKB1, a mammalian kinase associated with Peutz-Jeghers cancer-susceptibility syndrome; Sak1p [Saccharomyces cerevisiae]
K.DPPRININSSDKSGSK.N +2													3.2967												
R.SRSLTVAELNEEKR.R +2													3.4695												
gi|6321924|ref|NP_012000.1|													6.3												Putative metalloprotease with similarity to the zinc carboxypeptidase family, required for normal cell wall assembly; Ecm14p [Saccharomyces cerevisiae]
R.DLENLLELSYGLSK.A +2													3.8255												
R.SFPSLVAVEHLGR.T +2													3.1294												
gi|6323635|ref|NP_013706.1|													8.1												Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; localized to both lipid particles and mitochondrial outer membrane; Erg6p [Saccharomyces cerevisiae]
K.EVTAALENAAVGLVAGGK.S +2													3.3128												
K.VYAIEATCHAPKL.L +2																									
K.YVQNLANLATFFR.T +2													2.7508												
R.FTGCNVIGLNNNDYQIAK.A +2																									
gi|6324100|ref|NP_014170.1|													6.8												Nitrogen catabolite repression regulator that acts by inhibition of GLN3 transcription in good nitrogen source; altered form of Ure2p creates [URE3] prion; Ure2p [Saccharomyces cerevisiae]
R.APEFVSVNPNAR.V +2																									
R.FFDYPVWLVGDK.L +2													2.8462												
R.VYGVVEM*ALAER.R +2													3.1691												
gi|6324265|ref|NP_014335.1|													7.8												Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation across membranes; member of the DnaJ family; Ydj1p [Saccharomyces cerevisiae]
K.EASAAYEILSDPEK.R +2																									
K.FYDILGVPVTATDVEIK.K +2													2.5091												
K.FYDILGVPVTATDVEIKK.A +2													2.5075												
K.VGIVPGEVIAPGM*R.K +2													3.3523												
	7												X												
gi|6322303|ref|NP_012377.1|											7														Mannose-containing glycoprotein constituent of the cell wall; member of the PIR (proteins with internal repeats) family; Cis3p [Saccharomyces cerevisiae]
K.DGVLTDAK.G +1											1.8889														
R.IGSIVANR.Q +2											2.6289														
	1										X														
gi|6322446|ref|NP_012520.1|									6																Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo; Cct3p [Saccharomyces cerevisiae]
K.IVDM*VSYGIWEPEVIK.Q +2																									
K.IVDMVSYGIWEPEVIK.Q +2									2.9726																
K.TAIESACLLLR.V +2																									
K.VEM*IGDEYFSFLDNCK.E +2																									
K.VEMIGDEYFSFLDNCK.E +2									2.852																
R.VVLLDCPLEYK.K +2																									
	1								X																
SHUFFLED_gi|6324815|ref|NP_014884.1|							1.5																		FALSE POSITIVE
R.YQM*VDIFK.I +1							1.9855																		
R.YQM*VDIFK.I +2							2.6151																		
	1						X																		
gi|6323221|ref|NP_013293.1|						7.2																			Dual function protein involved in translation initiation as a substoichiometric component of eukaryotic translation initiation factor 3 (eIF3) and required for processing of 20S pre-rRNA; binds to eIF3 subunits Rpg1p and Prt1p and 18S rRNA; Hcr1p [Saccharomyces cerevisiae]
K.EQPKKVKK.G +2						2.8386																			
R.ALLDIDTLDEK.T +2						3.8322																			
	1					X																			
SHUFFLED_gi|6322498|ref|NP_012573.1|					1																				FALSE POSITIVE
R.FTGKNKELNVR.V +2					3.1637																				
gi|6321232|ref|NP_011309.1|					1.9																				Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to regulate function; Chc1p [Saccharomyces cerevisiae]
K.AEDPSNYENVIDIAEQAGK.Y +2					2.7431																				
K.FSDLIGPSTLIK.L +2					2.9621																				
K.LASTLVYLGDYQAAVDTAR.K +2																									
K.LNVEQSLACLK.A +2																									
	2				X																				
SHUFFLED_gi|6324479|ref|NP_014548.1|			3.4																						FALSE POSITIVE
K.DEINLGFSSR.Y +1			2.1087																						
SHUFFLED_gi|6325374|ref|NP_015442.1|			0.4																						FALSE POSITIVE
R.KIDEILLAVVK.V +2			4.0388																						
	2		X																						
gi|6320860|ref|NP_010939.1|		1.5																							Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation; Srb4p [Saccharomyces cerevisiae]
K.RANLMLVM*LR.L +2		2.8833																							
	1	X																							

Supporting Table 1B: List of detected Proteins

(pages 89-91)

The number of peptides (columns header ends with _P), number of unique peptide sequences (_uP), number of spectra (_S), sequence coverage (_SC), and normalized spectral abundance factor (_NSAF) are specified for each replicate run in all DE conditions. The average (columns header ends with "AVG") and standard deviations ("STD") calculated for NSAF values across the 4 replicates, as well as the number of times a protein was detected in each set of 4 replicates are listed in the darker-colored columns.

noDE | DE15 | DE60 | DE90 | DE300 | DE600



gi|6324100	Nitrogen catabolite repression regulator that acts by inhibition of GLN3 transcrip	354	40271	6.5
gi|6324265	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; in	409	44671	6.3
gi|6321924	Putative metalloprotease with similarity to the zinc carboxypeptidase family, req	430	49829	5.3
gi|6320976	Upstream kinase for the SNF1 complex; partially redundant function with Elm1p	1142	126872	8.7
gi|6320695	3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for	208	22568	5.8
gi|6320222	T subunit of the mitochondrial glycine decarboxylase complex, required for the c	400	44469	8.8
gi|6322839	Subunit of the ARP2/3 complex, which is required for the motility and integrity of	171	19916	5.4
gi|4275986	Putative protein of unknown function; similar to uncharacterized proteins from ot	236	26170	5.8
gi|8279524	Lsm (Like Sm) protein; part of heteroheptameric complexes (Lsm2p-7p and eith	86	9398	6
gi|6323755	Acetolactate synthase, catalyses the first common step in isoleucine and valine	687	74937	8.5
gi|6325112	Member of the oxysterol binding protein family, which includes seven yeast hom	434	49492	6
gi|6321929	Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine	513	58528	5.5
gi|6320742	Possible chaperone and cysteine protease with similarity to E. coli Hsp31 and S	237	25670	5.5
gi|6320726	Protein disulfide isomerase of the endoplasmic reticulum lumen, function overla	517	58982	4.9
gi|6321905	Cytoplasmic aspartyl aminopeptidase; cleaves unblocked N-terminal acidic ami	490	54174	7
gi|6325449	Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a compon	368	40478	8
gi|6324169	Cell wall-related secretory glycoprotein; induced by nutrient deprivation-associa	354	37328	5.4
gi|6324221	Putative protein of unknown function with similarity to TFC7 and phosphotranfer	270	30748	5.7
gi|6325298	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-act	405	45261	5.1
gi|6323192	Smaller subunit of the mitochondrial processing protease (MPP), essential proc	462	51084	7
gi|6321575	Protein containing an N-terminal SH3 domain; binds Las17p, which is a homolo	241	26139	5.2
gi|6325309	High-mobility group non-histone chromatin protein, functionally redundant with N	93	10802	9.8
gi|6322559	Ubiquitin C-terminal hydrolase that cleaves ubiquitin-protein fusions to generate	236	26385	4.6
gi|6320352	Dihydrolipoyl transsuccinylase, a component of the mitochondrial alpha-ketoglu	463	50431	8.9
gi|6320273	Protein of unknown function, green fluorescent protein (GFP)-fusion protein loca	310	35964	4.6
gi|6319638	Covalently-bound cell wall protein of unknown function; identified as a cell cycle	455	47994	4.7
gi|6319553	Subunit of the core complex of translation initiation factor 3(eIF3), essential for t	964	110344	6.3
gi|6321628	Cell wall protein that functions in the transfer of chitin to beta(1-6)glucan, putativ	507	52758	4.6
gi|6323420	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps	56	6661	10.3
gi|3736267	Essential protein of the mitochondrial intermembrane space (IMS); promotes ret	403	44537	4.6
gi|6319530	Putative cytoplasmic protein of unknown function; Ybr056wp [Saccharomyces c	501	57822	6.5
gi|6321650	Essential protein with two zinc fingers, present in the nucleus of growing cells b	486	55072	4.9
gi|6321704	Methionyl-tRNA synthetase, forms a complex with glutamyl-tRNA synthetase (G	751	85678	6.6
gi|6320640	RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytop	414	45407	5.5
gi|6324433	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible f	213	24254	5.5
gi|6323719	Putative protein of unknown function; green fluorescent protein (GFP)-fusion pro	145	15977	4.9
gi|6321793	Essential protein of the mitochondrial intermembrane space, forms a complex w	93	10305	5.3
gi|6319470	One of two nearly identical (see also HTA1) histone H2A subtypes; core histone	132	13989	10.7
gi|6319630	RNA polymerase subunit ABC27, common to RNA polymerases I, II, and III; co	215	25079	9.1
gi|6323374	Catalytic subunit of 1,3-beta-D-glucan synthase, functionally redundant with alt	1876	214849	7.2
gi|6323402	Subunit of the ARP2/3 complex, which is required for the motility and integrity of	178	20579	8
gi|6325445	RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III; pa	155	17910	4.6
gi|6319500	2-enoyl thioester reductase, member of the medium chain dehydrogenase/redu	380	42067	9
gi|6322029	Invertase, sucrose hydrolyzing enzyme; a secreted, glycosylated form is regulat	532	60639	4.8
gi|6319569	Repressible acid phosphatase (1 of 3) that also mediates extracellular nucleotid	467	52859	4.8
gi|6322585	Protein containing an N-terminal epsin-like domain involved in clathrin recruitme	408	45091	4.8
gi|6323147	Acyl-protein thioesterase responsible for depalmitoylation of Gpa1p; the mutant	227	24700	6.9
gi|6319508	Nuclear SAM-dependent mono- and asymmetric arginine dimethylating methyltr	348	39786	5.5
gi|6320033	Bifunctional enzyme containing both alcohol dehydrogenase and glutathione-de	386	41042	6.8
gi|6324543	Putative 1,3-beta-glucanosyltransferase, has similarity to Gas1p; localizes to the	484	51870	4.6
gi|6324731	Endopeptidase with trypsin-like activity that cleaves after basic residues; beta-ty	261	28268	6.6
gi|1160064	O-mannosylated heat shock protein that is secreted and covalently attached to t	413	41059	5.3
gi|6320598	Nuclear protein that acts as a heterodimer with Aos1p to activate Smt3p (SUMO	636	71259	5.1
gi|6320152	RNA binding protein required for maturation of tRNA and snRNA precursors; ac	275	32104	8.5
gi|6324798	RNA polymerase subunit ABC14.5, common to RNA polymerases I, II, and III; F	146	16511	4.7
gi|1431853	Putative protein of unknown function; green fluorescent protein (GFP)-fusion pro	1233	137698	4.5
gi|6324156	Plasma membrane protein involved in G-protein mediated pheromone signaling	366	40278	5.8
gi|6322485	3-hydroxyanthranilic acid dioxygenase, required for biosynthesis of nicotinic aci	177	20235	5.8
gi|6324521	S-adenosylmethionine decarboxylase, required for the biosynthesis of spermidi	396	46232	5.6
gi|6321599	Nucleolar protein that binds nuclear localization sequences, required for pre-rR	414	44535	4.9
gi|6320863	Gamma subunit of the translation initiation factor eIF2, involved in the identificat	527	57866	6.8
gi|6320478	Cytoplasmic glyoxalase II, catalyzes the hydrolysis of S-D-lactoylglutathione int	274	31327	6.2
gi|6321753	Nucleolar single-strand nucleic acid binding protein; associates with small nucle	294	32990	5.7
gi|6320869	GTPase of the Ypt/Rab family, very similar to Ypt32p; involved in the exocytic p	223	24469	5.1
gi|6322321	RNA polymerase II subunit B32; forms two subunit dissociable complex with Rp	221	25414	4.9
gi|6324595	hypothetical protein; Yor021cp [Saccharomyces cerevisiae]	213	24743	5.1
gi|6324856	Essential protein with similarity to phosducins, which are GTPase inhibitors; leth	286	32793	4.7
gi|6321646	Protein that interacts with frataxin (Yfh1p); homolog of mammalian electron tran	261	28759	8.4
gi|6324208	Component of the TOM (translocase of outer membrane) complex responsible f	617	70123	5.4
gi|1431843	Threonyl-tRNA synthetase, essential cytoplasmic protein; Ths1p [Saccharomyc	734	84520	7
gi|6325172	COPII vesicle coat protein required for ER transport vesicle budding and autoph	2195	241694	5.4
gi|6323273	Methionine aminopeptidase, catalyzes the cotranslational removal of N-terminal	387	43373	7.9
	Total SpC			28210 / 46912 / 32985 / 31547 / 41489
	FDR in SpC (%)			0.085 / 0.124 / 0.212 / 0.165 / 0.058
	FDR in Protein Number (%)			0.54 / 0.44 / 1.42 / 0.49 / 0.34
	SHUFFLED_SpC			12 / 29 / 35 / 26 / 12
SHUFFLE	FALSE POSITIVE	778	89786	5.6
SHUFFLE	FALSE POSITIVE	2489	285902	8.3
SHUFFLE	FALSE POSITIVE	293	34520	9.2
SHUFFLE	FALSE POSITIVE	1121	127439	6.3
SHUFFLE	FALSE POSITIVE	548	62152	8.8
SHUFFLE	FALSE POSITIVE	899	102853	6
SHUFFLE	FALSE POSITIVE	696	77066	9.3
SHUFFLE	FALSE POSITIVE	1703	194050	7
SHUFFLE	FALSE POSITIVE	590	67731	8.2
SHUFFLE	FALSE POSITIVE	430	42778	9.9
SHUFFLE	FALSE POSITIVE	203	22963	9.5
SHUFFLE	FALSE POSITIVE	1418	162188	6.2
SHUFFLE	FALSE POSITIVE	769	87062	7

Supporting Table 2A: Proteins detected in noDE and/or DE15 replicates

Proteins detected in both DE conditions were sorted into two groups of high and low abundances based on their averaged NSAF values measured when DE was turned off (noDE NSAF AVG).
Averages ("AVG") and standard deviations ("STD") were calculated for NSAF values and Peptide counts across the 4 replicates of a DE condition.
t-test p-values were calculated using the TTEST function in MSExcel (NSAF t-test p-Value).

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE15	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE15 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6321631	0.089245	0.03073	4	0.077339	0.010243	4	0.866592	-1.111601	-1.04942	-0.06219	1	133	100	26.5	18	0.506595	0
High Abundance	gi|6322468	0.056902	0.011085	4	0.05035	0.011142	4	0.884855	-1.298001	-1.24487	-0.05313	1	132	99.2481203	20.25	15	0.43633	0
High Abundance	gi|6321968	0.054496	0.010495	4	0.047899	0.007393	4	0.878945	-1.319674	-1.26364	-0.05604	1	131	98.4962406	21.25	18.25	0.347946	0
High Abundance	gi|1038378	0.040924	0.00377	4	0.043424	0.003014	4	1.061089	-1.36227	-1.38802	0.025752	1	130	97.7443609	26.5	23.75	0.342106	0
High Abundance	gi|6319279	0.039967	0.008049	4	0.025545	0.002595	4	0.639152	-1.592694	-1.3983	-0.1944	1	129	96.9924812	28.75	27.25	0.031602	1
High Abundance	gi|6322697	0.037728	0.004085	4	0.026121	0.006807	4	0.692351	-1.58301	-1.42334	-0.15967	1	128	96.2406015	12	11.25	0.03355	1
High Abundance	gi|6323073	0.035041	0.005287	4	0.022525	0.007168	4	0.642818	-1.647335	-1.45542	-0.19191	1	127	95.4887218	26	25	0.033665	1
High Abundance	gi|6322790	0.030639	0.005672	4	0.034894	0.009097	4	1.138875	-1.457249	-1.51373	0.056476	1	126	94.7368421	12.75	8.25	0.463151	0
High Abundance	gi|6321693	0.029306	0.007833	4	0.031889	0.006978	4	1.088139	-1.496359	-1.53304	0.036684	1	125	93.9849624	14	11.75	0.64012	0
High Abundance	gi|6322409	0.028438	0.009301	4	0.023267	0.013377	4	0.818166	-1.63326	-1.5461	-0.08716	1	124	93.2330827	9.75	9.5	0.551706	0
High Abundance	gi|6324486	0.020489	0.004948	4	0.011681	0.001867	4	0.570111	-1.93252	-1.68848	-0.24404	1	123	92.481203	13.75	12.5	0.030958	1
High Abundance	gi|6320255	0.016329	0.005011	4	0.0104	0.002929	4	0.636904	-1.982967	-1.78704	-0.19593	1	122	91.7293233	9.75	7	0.098432	0
High Abundance	gi|6321464	0.016263	0.010451	4	0.006111	0.002921	4	0.375761	-2.213888	-1.7888	-0.42509	1	121	90.9774436	2.5	2.25	0.145574	0
High Abundance	gi|9755341	0.015824	0.002579	4	0.007946	0.002372	4	0.502149	-2.099851	-1.80068	-0.29917	1	120	90.2255639	5	4.5	0.004189	1
High Abundance	gi|6320359	0.013516	0.001583	4	0.008644	0.002345	4	0.639538	-2.063285	-1.86915	-0.19413	1	119	89.4736842	5.75	4.75	0.01692	1
High Abundance	gi|6323138	0.013418	0.003594	4	0.010146	0.002037	4	0.756148	-1.993705	-1.87231	-0.12139	1	118	88.7218045	5.5	5.5	0.177221	0
High Abundance	gi|6323196	0.013086	0.004083	4	0.002458	0.000549	4	0.187834	-2.609418	-1.88319	-0.72623	1	117	87.9699248	4.5	2.75	0.012924	1
High Abundance	gi|6323004	0.012217	0.002947	4	0.014628	0.002432	4	1.197348	-1.834815	-1.91304	0.07822	1	116	87.2180451	23.5	25	0.255346	0
High Abundance	gi|6319314	0.011825	0.003174	4	0.013564	0.00257	4	1.147061	-1.867612	-1.9272	0.059587	1	115	86.4661654	22.25	23.75	0.428527	0
High Abundance	gi|6322978	0.009927	0.003509	4	0.008986	0.002529	4	0.905208	-2.046434	-2.00318	-0.04325	1	114	85.7142857	4.25	5.25	0.679913	0
High Abundance	gi|6323613	0.009356	0.001911	4	0.006978	0.001164	4	0.745832	-2.156269	-2.02891	-0.12736	1	113	84.962406	5.25	4.25	0.087326	0
High Abundance	gi|6320269	0.00911	0.002752	4	0.006795	0.001149	4	0.745884	-2.167811	-2.04048	-0.12733	1	112	84.2105263	5.5	5	0.195239	0
High Abundance	gi|6321408	0.008197	0.001899	4	0.005806	0.00174	4	0.708308	-2.236123	-2.08635	-0.14978	1	111	83.4586466	2.75	2.5	0.11326	0
High Abundance	gi|6319673	0.00789	0.000658	4	0.007257	0.002812	4	0.919772	-2.139243	-2.10292	-0.03632	1	109	81.9548872	11	9.25	0.688169	0
High Abundance	gi|6320148	0.00789	0.001499	4	0.005585	0.000871	4	0.707858	-2.252977	-2.10292	-0.15005	1	110	82.7067669	13.75	14.5	0.046609	1
High Abundance	gi|6324027	0.007695	0.002305	4	0.00986	0.000582	4	1.281352	-2.006123	-2.11379	0.107668	1	108	81.2030075	4.5	5.5	0.155689	0
High Abundance	gi|6320963	0.007322	0.002373	4	0.004691	0.001477	4	0.640672	-2.328735	-2.13537	-0.19336	1	107	80.4511278	3	5.75	0.118374	0
High Abundance	gi|6320122	0.006788	0.004237	3	0.013173	0.0022	4	1.940631	-1.880315	-2.16826	0.287943	1	106	79.6992481	1	1	0.103301	0
High Abundance	gi|6324670	0.006571	0.001895	4	0.006075	0.000608	4	0.924517	-2.216454	-2.18237	-0.03409	1	105	78.9473684	5.25	4.5	0.646743	0
High Abundance	gi|6323615	0.006483	0.001929	4	0.003455	0.000191	4	0.532932	-2.461552	-2.18822	-0.27333	1	104	78.1954887	7.25	6.5	0.050972	0
High Abundance	gi|6322271	0.006476	0.002661	4	0.00266	0.000556	4	0.410747	-2.575118	-2.18869	-0.38643	1	103	77.443609	2.25	2.25	0.06128	0
High Abundance	gi|6319505	0.006391	0.001517	4	0.003014	0.000493	4	0.471601	-2.520857	-2.19443	-0.32643	1	102	76.6917293	9.75	8.5	0.016379	1
High Abundance	gi|6320215	0.006169	0.001503	4	0.002788	0.000534	4	0.451937	-2.554707	-2.20979	-0.34492	1	101	75.9398496	8.75	7.75	0.015275	1
High Abundance	gi|6320128	0.006127	0.002945	4	0.004199	0.002589	4	0.685327	-2.376854	-2.21275	-0.1641	1	100	75.1879699	1.75	1.5	0.36397	0
High Abundance	gi|6323294	0.006126	0.002746	4	0.00433	0.001762	3	0.706823	-2.363512	-2.21282	-0.15069	1	99	74.4360902	2.5	2.666667	0.341668	0
High Abundance	gi|6321025	0.00602	0.002137	4	0.002421	0.000787	4	0.402159	-2.616005	-2.2204	-0.3956	1	98	73.6842105	8.25	6.25	0.036711	1
High Abundance	gi|6320590	0.005993	0.002091	4	0.009025	0.00176	4	1.505924	-2.044553	-2.22236	0.177803	1	97	72.9323308	3	3.75	0.069623	0
High Abundance	gi|6322583	0.005947	0.002258	4	0.007611	0.004239	4	1.279805	-2.118558	-2.2257	0.107144	1	96	72.1804511	5.75	4.25	0.522093	0
High Abundance	gi|6324085	0.005945	0	1	0.00047	0.000105	3	0.079058	-3.327902	-2.22585	-1.10205	1	95	71.4285714	1	2		
High Abundance	gi|6322794	0.005885	0.001154	4	0.006681	0.002522	4	1.135259	-2.175159	-2.23025	0.055095	1	94	70.6766917	3.25	3	0.594995	0
High Abundance	gi|6320655	0.005876	0.001226	4	0.007277	0.001379	4	1.238428	-2.138048	-2.23092	0.092871	1	93	69.924812	5.25	5.25	0.180328	0
High Abundance	gi|6320304	0.005749	0.002138	4	0.002464	0.000649	4	0.428596	-2.608359	-2.24041	-0.36795	1	92	69.1729323	7.5	6.5	0.049103	1
High Abundance	gi|6321184	0.005739	0.002451	4	0.005776	0.000815	4	1.006447	-2.238373	-2.24116	0.002791	1	91	68.4210526	11.25	16.5	0.97828	0
High Abundance	gi|6320949	0.005297	0.00123	4	0.003822	0.000518	4	0.72154	-2.417709	-2.27597	-0.14174	1	90	67.6691729	5	3.25	0.091067	0
High Abundance	gi|6324120	0.005255	0.001045	4	0.005697	0.000499	4	1.08411	-2.244354	-2.27943	0.035073	1	89	66.9172932	15	18.5	0.484726	0
High Abundance	gi|6319972	0.005174	0.001091	4	0.005931	0.000372	4	1.146308	-2.226872	-2.28617	0.059301	1	88	66.1654135	15	18.5	0.264621	0
High Abundance	gi|6319483	0.004895	0.001423	4	0.005783	0.001262	4	1.18141	-2.237847	-2.31025	0.0724	1	87	65.4135338	7	11	0.387299	0
High Abundance	gi|6321524	0.004766	0.001734	4	0.002311	0.000513	4	0.484893	-2.6362	-2.32185	-0.31435	1	86	64.6616541	3	2.5	0.061102	0
High Abundance	gi|6324534	0.00454	0.001142	4	0.011258	0.005556	4	2.479736	-1.948539	-2.34294	0.394405	1	85	63.9097744	3.75	3.75	0.09188	0
High Abundance	gi|6323077	0.004456	0.000773	4	0.002888	0.001409	4	0.648115	-2.539403	-2.35105	-0.18835	1	84	63.1578947	5	5	0.112792	0
High Abundance	gi|6323072	0.004322	0.001604	4	0.005163	0.001953	4	1.194586	-2.287098	-2.36432	0.077217	1	83	62.406015	5.25	5.25	0.531405	0
High Abundance	gi|6319559	0.004142	0.000987	4	0.002026	0.000334	4	0.489136	-2.693361	-2.38279	-0.31057	1	82	61.6541353	4.75	3.75	0.018123	1
High Abundance	gi|6322984	0.004123	0.000792	4	0.003897	0.000581	4	0.945186	-2.40927	-2.38479	-0.02448	1	81	60.9022556	7.75	7.75	0.662451	0
High Abundance	gi|6321754	0.004062	0.000734	4	0.003865	0.000587	4	0.951502	-2.412851	-2.39126	-0.02159	1	80	60.1503759	6.75	7	0.690674	0
High Abundance	gi|8655890	0.004039	0.0022	4	0.008954	0.002397	4	1.41124	-2.244125	-2.39373	0.149601	1	78	58.6466165	8.75	8.25	0.023566	1
High Abundance	gi|6324151	0.004039	0.00087	4	0.0057	0.001649	4	2.216885	-2.047983	-2.39373	0.345743	1	79	59.3984962	6.5	8	0.140691	0
High Abundance	gi|6323104	0.003953	0.001466	3	0.001272	0.000876	3	0.321781	-2.895513	-2.40307	-0.49244	1	77	57.8947368	5.66666667	1.666667	0.066086	0
High Abundance	gi|6323090	0.003925	0.000624	4	0.011395	0.002545	4	2.903185	-1.943286	-2.40616	0.462875	1	76	57.1428571	1.75	1.75	0.007818	1
High Abundance	gi|6320228	0.003915	0.000904	4	0.001556	0.000217	4	0.397446	-2.80799	-2.40727	-0.40072	1	75	56.3909774	6.75	5.25	0.011295	1
High Abundance	gi|1038379	0.003833	0.001506	4	0.008377	0.000579	4	2.185494	-2.076911	-2.41646	0.33955	1	74	55.6390977	5.25	4.75	0.005404	1
High Abundance	gi|6325196	0.003811	0.001209	4	0.005702	0.000571	4	1.496195	-2.243973	-2.41896	0.174988	1	73	54.887218	17.25	18	0.043873	1
High Abundance	gi|6323763	0.003676	0.000858	4	0.003601	0.001281	4	0.979597	-2.443577	-2.43462	-0.00895	1	72	54.1353383	8.25	8.75	0.925783	0
High Abundance	gi|6319396	0.003464	0.001319	4	0.004156	0.001025	4	1.199769	-2.381324	-2.46042	0.079098	1	71	53.3834586	5.25	4.75	0.440711	0
High Abundance	gi|6320950	0.00335	0.001239	4	0.003725	0.000744	4	1.11194	-2.428874	-2.47496	0.046081	1	70	52.6315789	4.25	5	0.626374	0
High Abundance	gi|6323163	0.003242	0.002212	4	0.003243	0.000916	4	1.000308	-2.489053	-2.48919	0.000134	1	69	51.8796992	5.5	3.25	0.999284	0
High Abundance	gi|6323371	0.003123	0.001026	4	0.002603	0.00066	4	0.833493	-2.584526	-2.50543	-0.0791	1	68	51.1278195	4.25	5	0.43269	0
High Abundance	gi|6321977	0.003107	0.000583	4	0.005518	0.001139	4	1.77599	-2.258218	-2.50766	0.24944	1	67	50.3759398	8.5	12	0.016004	1
High Abundance	gi|6319315	0.003028	0.000564	4	0.003334	0.00047	4	1.101057	-2.477034	-2.51884	0.04181	1	66	49.6240602	6	2.75	0.437164	0
High Abundance	gi|6323057	0.003025	0.00049	4	0.000959	0.000129	4	0.317025	-3.018181	-2.51927	-0.49891	1	65	48.8721805	4	1.5	0.002365	1
High Abundance	gi|6321315	0.00302	0.001813	4	0.001536	0.000295	4	0.508609	-2.813609	-2.51999	-0.29362	1	64	48.1203008	6	2.25	0.200113	0
High Abundance	gi|6320679	0.003006	0.001789	4	0.002197	0.000624	4	0.730872	-2.65817	-2.52201	-0.13616	1	63	47.3684211	3.5	3	0.44419	0
High Abundance	gi|1431847	0.003005	0.000901	4	0.002283	0.000233	4	0.759734	-2.641494	-2.52216	-0.11934	1	62	46.6165414	8	8.25	0.20773	0
High Abundance	gi|6322605	0.002896	0.001109	4	0.002932	0.001313	4	1.012431	-2.532836	-2.5382	0.005365	1	61	45.8646617	6.5	8	0.967796	0
High Abundance	gi|6321772	0.002821	0.00075	4	0.00538	0.002613	4	1.907125	-2.269218	-2.5496	0.280379	1	60	45.112782	4.25	5.75	0.143187	0
High Abundance	gi|6322120	0.002803	0.000508	4	0.00319	0.00123	4	1.138066	-2.496209	-2.55238	0.056168	1	59	44.3609023	3.5	3	0.591897	0
High Abundance	gi|6324445	0.002779	0.000717	4	0.004853	0.000845	4	1.746312	-2.31399	-2.55611	0.242122	1	58	43.6090226	3.75	4.75	0.010066	1
High Abundance	gi|6322564	0.002737	0.000717	4	0.002277	0.000506	4	0.831933	-2.642637	-2.56273	-0.07991	1	57	42.8571429	3.75	4.75	0.338949	0
High Abundance	gi|6320073	0.002687	0.000748	4	0.003946	0.000252	4	1.468552	-2.403843	-2.57073	0.166889	1	56	42.1052632	1	1	0.037502	1
High Abundance	gi|6322847	0.002661	0.000926	3	0.000947	0.001173	4	0.355881	-3.02365	-2.57496	-0.44869	1	55	41.3533835	3.66666667	3	0.0838	0
High Abundance	gi|6323387	0.002605	0.000784	4	0.003611	0.000489	4	1.38618	-2.442373	-2.58419	0.14182	1	54	40.6015038	10	11.5	0.08112	0
High Abundance	gi|6321249	0.002598	0.000535	4	0.003999	0.001349	4	1.539261	-2.398049	-2.58536	0.187312	1	52	39.0977444	2	2	0.127324	0
High Abundance	gi|6320978	0.002598	0.000535	4	0.003999	0.001349	4	1.539261	-2.398049	-2.58536	0.187312	1	53	39.8496241	2	2	0.127324	0
High Abundance	gi|6321786	0.002568	0.000861	3	0.001616	0.001419	2	0.629283	-2.791559	-2.5904	-0.20115	1	51	38.3458647	3	3	0.508903	0
High Abundance	gi|6323474	0.002537	0.000832	4	0.000587	0.000264	4	0.231376	-3.231362	-2.59568	-0.63568	1	50	37.593985	7.5	4.75	0.014093	1
High Abundance	gi|6323386	0.002527	0.001322	4	0.002532	0.000669	4	1.001979	-2.596536	-2.59739	0.000858	1	49	36.8421053	5.5	9.25	0.995082	0
High Abundance	gi|6323577	0.00252	0.000846	4	0.000596	0.000355	4	0.236508	-3.224754	-2.5986	-0.62615	1	48	36.0902256	7.25	5	0.013595	1
High Abundance	gi|6325126	0.002511	0.000965	4	0.001481	0.000449	4	0.589805	-2.829445	-2.60015	-0.22929	1	47	35.3383459	4.5	4.25	0.121048	0
High Abundance	gi|3736268	0.002496	0.000657	4	0.002054	0.000395	4	0.822917	-2.6874	-2.60276	-0.08464	1	46	34.5864662	3.75	4.5	0.30179	0
High Abundance	gi|6320065	0.002434	0.001331	4	0.003663	0.002142	4	1.50493	-2.436163	-2.61368	0.177516	1	45	33.8345865	2.25	2.5	0.374387	0
High Abundance	gi|6321335	0.002424	0.000352	4	0.003767	0.001205	4	1.554043	-2.424004	-2.61547	0.191463	1	44	33.0827068	3.25	3	0.108649	0
High Abundance	gi|6322668	0.002273	0.000458	4	0.00195	0.000503	4	0.857897	-2.709965	-2.6434	-0.06656	1	43	32.3308271	4	2.5	0.379951	0
High Abundance	gi|6321362	0.00223	0.000632	4	0.003195	0.000932	4	1.432735	-2.495529	-2.6517	0.156166	1	42	31.5789474	5.75	4.75	0.144073	0
High Abundance	gi|6322138	0.002207	0.000866	4	0.00343	0.000221	4	1.554146	-2.464706	-2.6562	0.191492	1	41	30.8270677	3.5	4.75	0.062532	0
High Abundance	gi|6322284	0.002206	0.0005	4	0.00195	0.000503	4	0.883953	-2.709965	-2.65639	-0.05357	1	40	30.075188	3.75	2.5	0.498592	0
High Abundance	gi|6320142	0.002178	0	1	0.002105	0	1	0.966483	-2.676748	-2.66194	-0.01481	1	39	29.3233083	1	1		
High Abundance	gi|6325058	0.002175	0.00062	4	0.002602	0.000788	4	1.196322	-2.584693	-2.66254	0.077848	1	38	28.5714286	5.25	3.75	0.429553	0
High Abundance	gi|6321648	0.002154	0.000306	4	0.003439	0.001156	4	1.596565	-2.463568	-2.66675	0.203186	1	37	27.8195489	4	4.75	0.109744	0
High Abundance	gi|6323376	0.002105	0.000235	4	0.000636	0.000352	4	0.302138	-3.196543	-2.67675	-0.51979	1	36	27.0676692	3	3	0.000792	1
High Abundance	gi|6323840	0.002039	0.000504	4	0.00415	0.000517	4	2.035311	-2.381952	-2.69058	0.308631	1	35	26.3157895	14.75	18.75	0.00111	1
High Abundance	gi|1160064	0.002009	0.000242	4	0.000889	0.000194	4	0.442509	-3.051098	-2.69702	-0.35408	1	34	25.5639098	2.75	3	0.000439	1
High Abundance	gi|6320801	0.001985	0.000514	4	0.0021	0.000785	4	1.057935	-2.677781	-2.70224	0.024459	1	33	24.8120301	1	1.5	0.816987	0
High Abundance	gi|6319666	0.001922	0.000523	4	0.001036	0.000303	4	0.539022	-2.98464	-2.71625	-0.26839	1	32	24.0601504	4.25	2.75	0.033966	1
High Abundance	gi|6321291	0.0019	0.000958	4	0.001964	0.000737	4	1.033684	-2.706859	-2.72125	0.014388	1	31	23.3082707	3.5	3.25	0.91935	0
High Abundance	gi|6319965	0.001871	0	1	0.000142	0	1	0.075895	-3.847712	-2.72793	-1.11979	1	30	22.556391	1	2		
High Abundance	gi|6325016	0.001829	0.000394	4	0.003743	0.000524	4	2.046473	-2.42678	-2.73779	0.311006	1	29	21.8045113	12.5	17.75	0.001439	1
High Abundance	gi|6325176	0.001797	0.000376	4	0.001025	0.0003	4	0.570395	-2.989276	-2.74545	-0.24382	1	28	21.0526316	4	2.75	0.019665	1
High Abundance	gi|6325389	0.001781	0.001314	4	0.001305	0.000598	4	0.732734	-2.884389	-2.74934	-0.13505	1	27	20.3007519	2.25	1.75	0.544663	0
High Abundance	gi|6324452	0.001776	0.000794	4	0.003808	0.000759	4	2.144144	-2.419303	-2.75056	0.331254	2	110	100	2	2.75	0.010111	1
High Abundance	gi|6320905	0.001754	0.000703	4	0.002185	0.000257	4	1.245724	-2.660549	-2.75597	0.095422	1	26	19.5488722	2.25	2.75	0.316791	0
High Abundance	gi|6321407	0.001753	0.000111	3	0.000364	0.000185	3	0.207644	-3.438899	-2.75622	-0.68268	1	24	18.0451128	1.33333333	2	0.001028	1
High Abundance	gi|6321587	0.001753	0.000111	3	0.000447	0	1	0.254991	-3.349692	-2.75622	-0.59347	1	25	18.7969925	1.33333333	2		
High Abundance	gi|6324756	0.001742	0.000275	2	0.000826	2.33E-05	2	0.474168	-3.08302	-2.75895	-0.32407	1	23	17.2932331	2	1	0.131139	0

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE15	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE15 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6323357	0.001671	0.000267	3	0.001007	0	1	0.602633	-2.996971	-2.77702	-0.21995	1	22	16.5413534	1	1		
High Abundance	gi|6324262	0.001621	0.000738	4	0.001343	0.000499	4	0.828501	-2.871924	-2.79022	-0.08171	1	21	15.7894737	2.75	3	0.557914	0
High Abundance	gi|6320882	0.001527	0.000325	4	0.00178	0.000348	4	1.165684	-2.74958	-2.81616	0.066581	1	20	15.037594	7.75	7	0.329094	0
High Abundance	gi|6323288	0.001526	0.000417	4	0.00234	0.000395	4	1.533421	-2.630784	-2.81645	0.185661	1	19	14.2857143	11	15.5	0.029942	1
High Abundance	gi|6324194	0.00149	0.001016	3	0.000827	0	1	0.555034	-3.082494	-2.82681	-0.25568	1	18	13.5338346	1	1		
High Abundance	gi|6324637	0.001484	0.000866	4	0.000561	0.00024	4	0.378032	-3.251037	-2.82857	-0.42247	1	17	12.7819549	7.25	4	0.120059	0
High Abundance	gi|6321679	0.001482	0.000783	4	0.001293	0.000253	4	0.87247	-2.888401	-2.82915	-0.05925	1	16	12.0300752	9.25	18.75	0.671587	0
High Abundance	gi|6320781	0.001401	0.000375	4	0.001766	0.000439	4	1.260528	-2.753009	-2.85356	0.100553	1	15	11.2781955	4	4.5	0.253146	0
High Abundance	gi|1431847	0.001378	0.000471	3	0.000779	9.42E-05	4	0.565312	-3.108463	-2.86075	-0.24771	1	14	10.5263158	2.33333333	4	0.154868	0
High Abundance	gi|6325300	0.001286	0.000395	3	0.000414	0.000231	2	0.321928	-3.383	-2.89076	-0.49224	1	13	9.77443609	3	2	0.05285	0
High Abundance	gi|6325006	0.001251	0.000943	3	0.002776	0.000822	4	2.219025	-2.556581	-2.90274	0.346162	2	109	99.0909091	2.66666667	3.25	0.088016	0
High Abundance	gi|6324945	0.00122	0.000932	4	0.002277	0.000392	4	1.866393	-2.642637	-2.91364	0.271003	2	108	98.1818182	3	4	0.104073	0
High Abundance	gi|6324260	0.001209	0.000628	4	0.001156	0.000279	4	0.956162	-2.937042	-2.91757	-0.01947	1	12	9.02255639	2.75	3.75	0.884364	0
High Abundance	gi|6319307	0.001205	0.000648	4	0.001782	0.000235	4	1.478838	-2.749092	-2.91901	0.169921	1	11	8.27067669	3.75	6	0.173483	0
High Abundance	gi|6320121	0.001197	0.000549	4	0.001335	0.000522	4	1.115288	-2.874519	-2.92191	0.047387	1	10	7.51879699	4.5	4.75	0.728214	0
High Abundance	gi|6323567	0.001187	0.000626	3	0.002284	0.00198	4	1.924179	-2.641304	-2.92555	0.284245	2	107	97.2727273	2.33333333	4.5	0.360518	0
High Abundance	gi|6324533	0.001167	0.000461	3	0.003495	0.00044	4	2.994859	-2.456553	-2.93293	0.476376	2	106	96.3636364	2.66666667	4.5	0.001894	1
High Abundance	gi|1431855	0.001152	0.000263	4	0.000449	0.0001	4	0.389757	-3.347754	-2.93855	-0.40921	1	9	6.76691729	4.25	1	0.008282	1
High Abundance	gi|6322325	0.00111	0.000241	2	0.013942	0.005088	4	12.56036	-1.855675	-2.95468	1.099002	2	105	95.4545455	3.5	5	0.014795	1
High Abundance	gi|6324463	0.001107	0.000456	4	0.001474	0.000491	4	1.331527	-2.831503	-2.95585	0.12435	1	8	6.01503759	3.5	3.75	0.31634	0
High Abundance	gi|6323087	0.00108	0.000228	4	0.001923	0.000301	4	1.780556	-2.716021	-2.96658	0.250556	2	104	94.5454545	7.75	6.5	0.005052	1
High Abundance	gi|6319585	0.001056	0.000481	3	0.001193	0.000746	4	1.129735	-2.92336	-2.97634	0.052977	1	7	5.26315789	1.66666667	2.5	0.780445	0
High Abundance	gi|6324808	0.00104	0.000511	3	0.002054	0.000969	4	1.975	-2.6874	-2.98297	0.295567	2	103	93.6363636	3.33333333	2	0.13794	0
High Abundance	gi|6319378	0.001033	0.000173	2	0.0011	0.000832	3	1.06486	-2.958607	-2.9859	0.027292	1	6	4.5112782	1.5	1.333333	0.903344	0

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value >= 0.05 (% of Protein
136	36.07%	97.6439	3.779412	0.59243598	87.9031	3.808824	0.649954	0.00718	0.0064635				6.44669118	5.69813948	6.37622549	5.746362	37	28.46%

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE15	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE15 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6319806	0.001028	0.000724	4	0.002186	0.000609	4	2.126459	-2.66035	-2.98801	0.327657	2	102	92.7272727	4.25	6.5	0.051021	0
Low Abundance	gi|6322599	0.001004	0.000515	4	0.002063	0.001287	4	2.054781	-2.685501	-2.99827	0.312766	2	101	91.8181818	4	7.5	0.2025	0
Low Abundance	gi|6323481	0.000987	0.000667	4	0.002469	0.001876	4	2.50152	-2.607479	-3.00568	0.398204	2	100	90.9090909	2.5	4.5	0.215396	0
Low Abundance	gi|6325114	0.000969	0.00038	3	0.003986	0.000994	4	4.113519	-2.399463	-3.01368	0.614214	2	99	90	3.66666667	2	0.004948	1
Low Abundance	gi|6322910	0.000964	0.000475	4	0.01171	0.003959	4	12.1473	-1.931443	-3.01592	1.08448	2	98	89.0909091	2.75	5	0.011624	1
Low Abundance	gi|6324707	0.00096	0.000258	4	0.002588	0.000569	4	2.695833	-2.587036	-3.01773	0.430693	2	97	88.1818182	14.5	23.75	0.005731	1
Low Abundance	gi|6324298	0.000959	0	1	0.000867	4.56E-05	3	0.904067	-3.061981	-3.01818	-0.0438	2	96	87.2727273	2	2.666667		
Low Abundance	gi|6320226	0.000944	0.000578	4	0.001432	0.000125	4	1.516949	-2.844057	-3.02503	0.180971	2	94	85.4545455	7	8	0.189527	0
Low Abundance	gi|6322505	0.000944	0.000237	4	0.001618	0.000461	4	1.713983	-2.791021	-3.02503	0.234007	2	95	86.3636364	11	14.5	0.053534	0
Low Abundance	gi|6324923	0.00094	0.000201	4	0.002234	0.000381	4	2.376596	-2.650917	-3.02687	0.375955	2	93	84.5454545	1.5	2	0.002546	1
Low Abundance	gi|6321474	0.00093	0.000834	2	0.001812	0.000169	3	1.948387	-2.741842	-3.03152	0.289675	2	92	83.6363636	1	1.666667	0.370275	0
Low Abundance	gi|6325331	0.000911	0.000531	4	0.000898	0.00014	4	0.98573	-3.046724	-3.04048	-0.00624	2	91	82.7272727	5.75	11	0.964661	0
Low Abundance	gi|6323729	0.000886	0.000288	4	0.000434	0.000291	4	0.489842	-3.36251	-3.05257	-0.30994	2	90	81.8181818	1	1.75	0.069342	0
Low Abundance	gi|6321987	0.000884	0.000403	3	0.000897	0.000275	4	1.014706	-3.047208	-3.05355	0.00634	2	89	80.9090909	1.66666667	3	0.966204	0
Low Abundance	gi|6323848	0.000853	5.09E-05	2	0.002666	0.000944	4	3.12544	-2.57414	-3.06905	0.494911	2	88	80	3.5	3	0.030753	1
Low Abundance	gi|6323324	0.00085	0.000512	4	0.002502	0.000276	4	2.943529	-2.601713	-3.07058	0.468868	2	87	79.0909091	2.75	3.25	0.003045	1
Low Abundance	gi|6323391	0.000799	0	1	0.00019	0.000109	4	0.237797	-3.721246	-3.09745	-0.62379	2	86	78.1818182	2	2.75		
Low Abundance	gi|6324233	0.000787	0.00044	4	0.002634	0.000442	4	3.346887	-2.579384	-3.10403	0.524641	2	85	77.2727273	3.75	4.75	0.001029	1
Low Abundance	gi|6321973	0.000785	0.000258	4	0.002393	0.001341	4	3.048408	-2.621057	-3.10513	0.484073	2	84	76.3636364	5.25	8	0.093896	0
Low Abundance	gi|6322058	0.000758	0.000585	4	0.000681	0.000115	3	0.898417	-3.166853	-3.12033	-0.04652	2	83	75.4545455	2	3	0.814309	0
Low Abundance	gi|6321563	0.000731	0.000277	4	0.001115	0.00034	4	1.525308	-2.952725	-3.13608	0.183357	2	82	74.5454545	4.5	6	0.132913	0
Low Abundance	gi|6322002	0.000706	0.000269	4	0.00083	0.000157	4	1.175637	-3.080922	-3.1512	0.070273	2	81	73.6363636	4	6.5	0.463666	0
Low Abundance	gi|6323861	0.000695	0.000159	4	0.000681	0.000167	4	0.979856	-3.166853	-3.15802	-0.00884	2	80	72.7272727	8	11.75	0.906899	0
Low Abundance	gi|6325036	0.000678	0.000535	4	0.002445	0.002427	4	3.606195	-2.611721	-3.16877	0.557049	2	79	71.8181818	3	4.5	0.242539	0
Low Abundance	gi|6322565	0.000592	0.000323	4	0.001306	0.000491	4	2.206081	-2.884057	-3.22768	0.343621	2	78	70.9090909	3.75	5.75	0.057528	0
Low Abundance	gi|6324907	0.000581	0.000172	3	0.001369	0.000544	4	2.356282	-2.863597	-3.23582	0.372227	2	77	70	2.66666667	3.75	0.056865	0
Low Abundance	gi|6323464	0.000559	0.000383	4	0.002027	0.000251	4	3.626118	-2.693146	-3.25259	0.559442	2	76	69.0909091	5.25	8	0.001201	1
Low Abundance	gi|6323208	0.000546	0.000284	3	0.00071	0.000146	4	1.300366	-3.148742	-3.26281	0.114066	2	75	68.1818182	2	3.5	0.431556	0
Low Abundance	gi|6325178	0.000537	0.000263	4	0.000975	0.000188	4	1.815642	-3.010995	-3.27003	0.25903	2	73	66.3636364	3.25	3.25	0.038624	1
Low Abundance	gi|6319668	0.000537	0.000263	4	0.000975	0.000188	4	1.815642	-3.010995	-3.27003	0.25903	2	74	67.2727273	3.25	3.25	0.038624	1
Low Abundance	gi|6320846	0.000525	0	1	0.000729	0.000163	4	1.388571	-3.137272	-3.27984	0.142568	2	72	65.4545455	2	2		
Low Abundance	gi|6325229	0.000513	0.000187	2	0.001779	0.000825	4	3.467836	-2.749824	-3.28988	0.540059	2	71	64.5454545	1.5	8.75	0.050174	0
Low Abundance	gi|6322608	0.00049	0.000107	4	0.000744	0.00013	4	1.518367	-3.128427	-3.3098	0.181377	2	70	63.6363636	2.75	4	0.024777	1
Low Abundance	gi|6322912	0.000485	7.25E-05	4	0.001151	0.000242	4	2.373196	-2.938925	-3.31426	0.375334	2	69	62.7272727	4.5	11.5	0.008737	1
Low Abundance	gi|6319603	0.000456	0.000356	3	0.001326	0.000379	4	2.907895	-2.877456	-3.34104	0.463579	2	67	60.9090909	2	3	0.029468	1
Low Abundance	gi|6321522	0.000456	0.000248	3	0.000772	0.000399	4	1.692982	-3.112383	-3.34104	0.228652	2	68	61.8181818	5.66666667	12.75	0.255078	0
Low Abundance	gi|6323585	0.000454	0.000193	4	0.001876	0.000256	4	4.132159	-2.726767	-3.34294	0.616177	2	66	60	4.25	7.5	0.000171	1
Low Abundance	gi|6323619	0.000447	0	1	0.000155	0.000103	2	0.346756	-3.809668	-3.34969	-0.45998	1	5	3.7593985	1	2		
Low Abundance	gi|6325167	0.000444	0.000337	4	0.002327	0.000618	4	5.240991	-2.633204	-3.35262	0.719413	2	65	59.0909091	2.75	4.5	0.003831	1
Low Abundance	gi|6325403	0.00044	7.87E-05	4	0.000712	0.000281	4	1.618182	-3.14752	-3.35655	0.209027	2	64	58.1818182	4.75	10.5	0.146386	0
Low Abundance	gi|6319901	0.000432	0.000118	4	0.001377	0.000436	4	3.1875	-2.861066	-3.36452	0.50345	2	63	57.2727273	5	7	0.018984	1
Low Abundance	gi|6322783	0.000431	3E-05	2	0.000492	9.88E-05	4	1.141531	-3.308035	-3.36552	0.057488	2	62	56.3636364	2	2	0.319382	0
Low Abundance	gi|6323470	0.000426	7.07E-05	2	0.000536	0.000253	4	1.258216	-3.270835	-3.37059	0.099755	2	61	55.4545455	2.5	3.75	0.466782	0
Low Abundance	gi|6319726	0.000424	0.000227	3	0.000706	0.000393	4	1.665094	-3.151195	-3.37263	0.221439	2	60	54.5454545	2.66666667	3.5	0.287577	0
Low Abundance	gi|6323554	0.000418	0	1	0.000263	0.000124	4	0.629187	-3.580044	-3.37882	-0.20122	2	59	53.6363636	1	1.75		
Low Abundance	gi|6324951	0.000404	0.000247	4	0.001768	0.000311	4	4.376238	-2.752518	-3.39362	0.641101	2	58	52.7272727	5	10.5	0.000578	1
Low Abundance	gi|6320362	0.000395	0.000193	4	0.001431	0.000542	4	3.622785	-2.84436	-3.4034	0.559043	2	57	51.8181818	3.75	4.75	0.025421	1
Low Abundance	gi|6325326	0.000385	8.27E-05	3	0.000939	0.000371	4	2.438961	-3.027334	-3.41454	0.387205	2	56	50.9090909	2.33333333	4	0.054376	0
Low Abundance	gi|6320936	0.000379	8.39E-05	4	0.001603	0.0004	4	4.229551	-2.795066	-3.42136	0.626294	2	55	50	6.5	14.75	0.007328	1
Low Abundance	gi|6321013	0.000356	3.69E-05	4	0.000853	0.000105	4	2.396067	-3.069051	-3.44855	0.379499	2	54	49.0909091	4.75	9	0.00121	1
Low Abundance	gi|6322666	0.000324	0.000143	4	0.000619	7.76E-05	4	1.910494	-3.208309	-3.48945	0.281146	2	53	48.1818182	12.5	24.25	0.017205	1
Low Abundance	gi|6322732	0.00032	0	1	0.000205	0	1	0.640625	-3.688246	-3.49485	-0.1934	2	52	47.2727273	2	2		
Low Abundance	gi|6325290	0.00031	6.31E-05	3	0.000078	0	1	0.251613	-4.107905	-3.50864	-0.59927	2	51	46.3636364	1	2		
Low Abundance	gi|6320016	0.000304	0.000202	4	0.000775	0.000182	4	2.549342	-3.110698	-3.51713	0.406428	2	49	44.5454545	1	2.333333	0.013649	1
Low Abundance	gi|6320710	0.000304	0	1	0.000111	8.08E-05	3	0.365132	-3.954677	-3.51713	-0.43755	2	50	45.4545455	6	11.75		
Low Abundance	gi|6319625	0.000275	7.4E-05	2	0.000128	5.7E-05	4	0.465455	-3.89279	-3.56067	-0.33212	2	48	43.6363636	2.5	2.75	0.159599	0
Low Abundance	gi|1431857	0.000271	0.000214	4	0.000625	0.000273	4	2.306273	-3.20412	-3.56703	0.362911	2	47	42.7272727	2	5.5	0.090297	0
Low Abundance	gi|6322434	0.00026	0.00021	4	0.000992	0.000324	4	3.815385	-3.003488	-3.58503	0.581538	2	45	40.9090909	2	4.5	0.012045	1
Low Abundance	gi|6325166	0.00026	2.01E-05	2	0.000947	0.000312	3	3.642308	-3.02365	-3.58503	0.561377	2	46	41.8181818	1	1.666667	0.061287	0
Low Abundance	gi|6321721	0.000256	0.000161	3	0.000572	0.000298	4	2.234375	-3.242604	-3.59176	0.349156	2	44	40	2.66666667	3.25	0.135853	0
Low Abundance	gi|6321673	0.000252	3.78E-05	3	0.000464	5.6E-05	4	1.84127	-3.333482	-3.5986	0.265117	2	43	39.0909091	3.33333333	3	0.001865	1
Low Abundance	gi|6323209	0.000235	0.0001	2	0.000178	0	1	0.757447	-3.74958	-3.62893	-0.12065	2	42	38.1818182	1.5	2		
Low Abundance	gi|6319471	0.000226	0	1	0.000776	0.000599	2	3.433628	-3.110138	-3.64589	0.535753	1	4	3.0075188	2	1.5		
Low Abundance	gi|6322476	0.00022	0	1	0.00039	3.34E-05	4	1.772727	-3.408935	-3.65758	0.248642	2	41	37.2727273	1	5.5		
Low Abundance	gi|6325292	0.000216	0.000151	3	0.000136	4.49E-05	2	0.62963	-3.866461	-3.66555	-0.20091	1	3	2.2556391	2.66666667	2.5	0.464247	0
Low Abundance	gi|6319395	0.000199	8.67E-05	4	0.001206	0.000244	4	6.060302	-2.918653	-3.70115	0.782494	2	40	36.3636364	5.75	15.25	0.001934	1
Low Abundance	gi|6322012	0.000188	0.000191	2	0.000793	0.000331	4	4.218085	-3.100727	-3.72584	0.625115	2	39	35.4545455	3.5	4.5	0.053768	0
Low Abundance	gi|6322722	0.000164	0	1	0.000299	2.17E-05	4	1.823171	-3.524329	-3.78516	0.260827	2	38	34.5454545	2	3.25		
Low Abundance	gi|6322294	0.000153	2.12E-05	2	0.000184	0.000166	2	1.202614	-3.735182	-3.81531	0.080126	1	2	1.5037594	2.5	2.5	0.836478	0
Low Abundance	gi|6321643	0.000147	7.26E-05	2	0.000305	8.95E-05	4	2.07483	-3.5157	-3.83268	0.316983	2	1	0.7518797	4	9	0.116707	0
Low Abundance	gi|6324250	0.000147	5.91E-05	2	0.000204	4.67E-05	2	1.387755	-3.69037	-3.83268	0.142313	1	37	33.6363636	2	2	0.401073	0
Low Abundance	gi|6320077	0.000146	0.000116	3	0.000487	8.59E-05	4	3.335616	-3.312471	-3.83565	0.523176	2	34	30.9090909	2	3.75	0.016161	1
Low Abundance	gi|8279524	0.000146	5.56E-05	3	0.000404	9.99E-05	4	0.452055	-4.180456	-3.83565	-0.34481	2	35	31.8181818	2	6.5	0.008166	1
Low Abundance	gi|6321837	0.000146	0.00016	2	0.000066	3.37E-05	4	2.767123	-3.393619	-3.83565	0.442029	2	36	32.7272727	2.33333333	2	0.606291	0
Low Abundance	gi|6322815	0.000139	6.58E-07	2	0.000185	0.000118	4	1.330935	-3.732828	-3.85699	0.124157	2	33	30	2	3.75	0.489714	0
Low Abundance	gi|6324804	0.000136	5.52E-05	4	0.000313	5.86E-05	4	2.301471	-3.504456	-3.86646	0.362005	2	32	29.0909091	3.25	5.75	0.004592	1
Low Abundance	gi|6322581	0.00013	7.32E-05	3	0.000777	5.26E-05	4	5.976923	-3.109579	-3.88606	0.776478	2	31	28.1818182	3.33333333	7.75	0.000439	1
Low Abundance	gi|6321594	0.000126	7.39E-05	2	0.000549	0.000235	4	4.357143	-3.260428	-3.89963	0.639202	2	30	27.2727273	2	6.5	0.031971	1
Low Abundance	gi|6323967	0.000125	0	1	0.000249	0.000101	4	1.992	-3.603801	-3.90309	0.299289	2	29	26.3636364	2	2.75		
Low Abundance	gi|1038376	0.00012	6.64E-05	3	0.000347	8.05E-05	4	2.891667	-3.459671	-3.92082	0.461148	2	28	25.4545455	3	6.5	0.010073	1
Low Abundance	gi|6320432	0.000119	5.14E-05	3	0.00097	0.000402	4	8.151261	-3.013228	-3.92445	0.911225	2	27	24.5454545	2.33333333	4.25	0.022773	1
Low Abundance	gi|6320560	0.000117	4.23E-05	2	0.001016	0.00033	4	8.683761	-2.993106	-3.93181	0.938708	2	26	23.6363636	2	5.75	0.010872	1
Low Abundance	gi|6320839	0.000115	0	1	0.000445	0.000125	4	3.869565	-3.35164	-3.9393	0.587662	2	25	22.7272727	2	4.5		
Low Abundance	gi|6323768	0.000108	0.000128	3	0.000768	0.000258	4	6.712963	-3.139662	-3.96658	0.826914	2	23	20.9090909	1.66666667	9	0.008376	1
Low Abundance	gi|6321619	0.000108	9.65E-06	2	0.000725	3.2E-05	4	7.111111	-3.114639	-3.96658	0.851937	2	24	21.8181818	2	4.5	6.02E-06	1
Low Abundance	gi|6319597	0.000107	4.78E-05	2	0.000541	0.000121	4	5.056075	-3.266803	-3.97062	0.703813	2	21	19.0909091	3	5.5	0.003307	1
Low Abundance	gi|6324321	0.000107	0	1	0.000543	0.000186	4	5.074766	-3.2652	-3.97062	0.705416	2	22	20	2	6.25		
Low Abundance	gi|6325025	0.000105	4.23E-05	4	0.000474	9.59E-05	4	1.609524	-3.772113	-3.97881	0.206697	2	19	17.2727273	1.5	4.5	0.001896	1
Low Abundance	gi|6321203	0.000105	9.66E-05	2	0.000169	7.05E-05	4	4.514286	-3.324222	-3.97881	0.654589	2	20	18.1818182	5.75	21.5	0.513598	0
Low Abundance	gi|6320789	0.000097	0	1	0.00017	7.63E-05	3	1.752577	-3.769551	-4.01323	0.243677	2	18	16.3636364	2	3		
Low Abundance	gi|6324601	0.000095	5.71E-05	4	0.000431	0.000173	4	4.536842	-3.365523	-4.02228	0.656754	2	17	15.4545455	2.5	4.75	0.025012	1
Low Abundance	gi|6319552	0.000089	0	1	0.000243	4.12E-05	4	2.730337	-3.614394	-4.05061	0.436216	2	16	14.5454545	2	2		
Low Abundance	gi|6321236	0.000086	4.02E-05	3	0.000624	0.000183	4	7.255814	-3.204815	-4.0655	0.860686	2	15	13.6363636	2.66666667	5.75	0.007744	1
Low Abundance	gi|6320548	0.00008	0	1	0.000065	2.42E-05	4	0.8125	-4.187087	-4.09691	-0.09018	2	14	12.7272727	3	2.25		
Low Abundance	gi|6321498	0.000079	3.16E-05	3	0.000222	7.11E-05	4	2.810127	-3.653647	-4.10237	0.448726	2	13	11.8181818	4	8	0.020236	1
Low Abundance	gi|6323509	0.000076	0	1	0.000756	0.000175	4	9.947368	-3.121478	-4.11919	0.997708	2	12	10.9090909	3	5		
Low Abundance	gi|1431856	0.000059	0	1	0.00065	0.000133	4	11.01695	-3.187087	-4.22915	1.042061	2	11	10	2	6		
Low Abundance	gi|6319695	0.000052	1.58E-05	2	0.000136	5.96E-05	4	2.615385	-3.866461	-4.284	0.417536	2	10	9.09090909	3	5	0.063727	0

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE15	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE15 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6324709	0.000051	0	1	0.000317	0.000132	4	6.215686	-3.498941	-4.29243	0.793489	2	9	8.18181818	2	2		
Low Abundance	gi|6321376	0.00005	2E-05	2	0.000128	5.06E-05	4	2.56	-3.89279	-4.30103	0.40824	2	8	7.27272727	2.5	3.75	0.054163	0
Low Abundance	gi|6321429	0.000048	0	1	0.000149	8.32E-05	4	3.104167	-3.826814	-4.31876	0.491945	2	6	5.45454545	2	4		
Low Abundance	gi|6321859	0.000048	0	1	0.000195	9.94E-05	4	4.0625	-3.709965	-4.31876	0.608793	2	7	6.36363636	2	6.75		
Low Abundance	gi|6320019	0.000033	0	1	0.000311	0.000155	4	9.424242	-3.50724	-4.48149	0.974246	2	4	3.63636364	2	4.25		
Low Abundance	gi|6320137	0.000033	0	1	0.000459	0.000152	4	13.90909	-3.338187	-4.48149	1.143299	2	5	4.54545455	2	2		
Low Abundance	gi|6320071	0.000032	0	1	0.000322	0.000137	4	10.0625	-3.492144	-4.49485	1.002706	2	3	2.72727273	2	4.75		
Low Abundance	gi|6319809	0.000028	0	1	0.000468	0.000125	4	16.71429	-3.329754	-4.55284	1.223088	2	2	1.81818182	2	3.75		
Low Abundance	gi|6323335	0.000018	0	1	0.000222	7.88E-05	4	12.33333	-3.653647	-4.74473	1.09108	2	1	0.90909091	2	5.25		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6324709	X	X	X	X	X	X	X	X	X	X	2	2	2	7.32	5.09E-05	X	X	X	X	X
gi|6321376	X	X	X	X	X	3	3	6	3.06	3.55E-05	2	2	8	2.04	6.37E-05	X	X	X	X	X
gi|6321429	X	X	X	X	X	X	X	X	X	X	2	2	4	3.72	4.82E-05	X	X	X	X	X
gi|6321859	X	X	X	X	X	X	X	X	X	X	2	2	2	8.53	4.85E-05	X	X	X	X	X
gi|6320019	X	X	X	X	X	2	2	2	6.07	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320137	X	X	X	X	X	2	2	2	5.61	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320071	X	X	X	X	X	2	2	2	5.91	3.16E-05	X	X	X	X	X	X	X	X	X	X
gi|6319809	X	X	X	X	X	2	2	2	4.6	2.79E-05	X	X	X	X	X	X	X	X	X	X
gi|6323335	X	X	X	X	X	2	2	2	3.34	1.79E-05	X	X	X	X	X	X	X	X	X	X

Locus	DE15-1_P	DE15-1_uP	DE15-1_S	DE15-1_SC	DE15-1_NSAF	DE15-2_P	DE15-2_uP	DE15-2_S	DE15-2_SC	DE15-2_NSAF	DE15-3_P	DE15-3_uP	DE15-3_S	DE15-3_SC	DE15-3_NSAF	DE15-4_P	DE15-4_uP	DE15-4_S	DE15-4_SC	DE15-4_NSAF
gi|6324709	2	2	9	9.49	0.000188	2	2	20	10.03	0.000479	3	3	16	13.01	0.000369	1	1	11	4.88	0.000234
gi|6321376	4	4	28	4.75	0.000183	4	4	20	4.67	0.00015	3	3	9	3.57	6.49E-05	4	4	17	4.58	0.000113
gi|6321429	5	5	10	8.73	9.87E-05	7	7	11	9.5	0.000125	8	8	25	14.38	0.000273	7	7	10	10.01	0.000101
gi|6321859	5	5	6	17.05	0.000119	4	4	13	12.92	0.000297	5	5	12	16.28	0.000264	2	2	5	8.01	0.000102
gi|6320019	5	5	16	17.52	0.000287	5	5	26	17.29	0.000537	3	3	11	11.21	0.000218	4	4	11	14.49	0.000202
gi|6320137	3	3	21	8.41	0.000377	3	3	25	8.88	0.000517	1	1	15	3.5	0.000298	1	1	35	3.5	0.000643
gi|6320071	5	5	16	17.05	0.00028	5	5	26	16.82	0.000523	4	4	14	13.18	0.00027	5	5	12	16.36	0.000214
gi|6319809	4	4	25	13.6	0.000384	4	4	20	13.6	0.000354	4	4	37	13.6	0.000629	3	3	32	10.8	0.000503
gi|6323335	4	4	12	7.33	0.000119	6	6	22	9.51	0.00025	5	5	28	9	0.000306	6	6	21	10.28	0.000212

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG	noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Protein
107	28.38%	4.1354	2.691589	1.20854829	10.5115	3.766355	0.667005	0.000386	0.0009824	3.15809969	2.16312406	5.63161994	4.294609	40	50.63%

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	DE15 Peptides AVG
DE15-only	gi|6325097	0	0	0	0.00009	4.23E-05	4	4.75
DE15-only	gi|3736267	0	0	0	0.000242	5.32E-05	4	4.25
DE15-only	gi|9755335	0	0	0	0.000129	5.84E-05	4	4.5
DE15-only	gi|6321412	0	0	0	0.000272	6.11E-05	4	4.5
DE15-only	gi|6323056	0	0	0	0.000117	5.39E-05	4	4
DE15-only	gi|6320242	0	0	0	0.000143	3.19E-05	4	2
DE15-only	gi|6320764	0	0	0	0.000135	0.000106	4	2.75
DE15-only	gi|6319326	0	0	0	0.000478	0.000173	4	3
DE15-only	gi|1431849	0	0	0	0.000319	7.48E-05	4	4.25
DE15-only	gi|6319564	0	0	0	0.000393	0.000142	4	3
DE15-only	gi|6325151	0	0	0	0.000761	0.000229	4	4.75
DE15-only	gi|6323873	0	0	0	0.000407	0.00014	4	5
DE15-only	gi|6323179	0	0	0	0.000383	0.000183	4	3.25
DE15-only	gi|6322331	0	0	0	0.000126	5.06E-05	4	12
DE15-only	gi|6322531	0	0	0	0.001164	0.000743	4	3
DE15-only	gi|6323332	0	0	0	0.000331	7.9E-05	4	2.5
DE15-only	gi|6323570	0	0	0	0.000088	3.36E-05	4	3.25
DE15-only	gi|6324580	0	0	0	0.000786	0.00022	4	4.5
DE15-only	gi|6323882	0	0	0	0.000694	0.000158	4	4.5
DE15-only	gi|6324225	0	0	0	0.000174	4.94E-05	4	4.25
DE15-only	gi|6322765	0	0	0	0.000689	0.000235	4	4
DE15-only	gi|6322639	0	0	0	0.000066	1.72E-05	4	5
DE15-only	gi|6324109	0	0	0	0.000124	2.66E-05	4	2.75
DE15-only	gi|6321332	0	0	0	0.002629	0.001161	4	3
DE15-only	gi|6324371	0	0	0	0.000209	5.31E-05	4	3.5
DE15-only	gi|6323530	0	0	0	0.000748	0.00039	4	2.25
DE15-only	gi|6320662	0	0	0	0.000745	0.000258	4	2.25
DE15-only	gi|3736262	0	0	0	0.000118	7.46E-05	4	2.75
DE15-only	gi|6323089	0	0	0	0.000215	6.69E-05	4	1.75
DE15-only	gi|6325421	0	0	0	0.000233	7.88E-05	4	4
DE15-only	gi|6324258	0	0	0	0.00009	3.48E-05	4	2.5
DE15-only	gi|3736260	0	0	0	0.000835	0.000382	4	2
DE15-only	gi|6322707	0	0	0	0.00016	2.85E-05	4	2.25
DE15-only	gi|6324594	0	0	0	0.001204	0.000174	4	3.25
DE15-only	gi|6324291	0	0	0	0.000286	6.67E-05	4	2.25
DE15-only	gi|6324982	0	0	0	0.000202	3.78E-05	4	3
DE15-only	gi|6320079	0	0	0	0.000463	0.000255	4	2.5
DE15-only	gi|6321814	0	0	0	0.000086	4.07E-05	4	2
DE15-only	gi|6320066	0	0	0	0.001168	0.000456	4	1
DE15-only	gi|6322845	0	0	0	0.00032	4.08E-05	4	1.25
DE15-only	gi|6320935	0	0	0	0.000158	3.74E-05	3	2.333333
DE15-only	gi|6320030	0	0	0	0.000062	3.32E-05	3	3.666667
DE15-only	gi|6322569	0	0	0	0.000023	1.45E-05	3	2
DE15-only	gi|6324378	0	0	0	0.000094	5.71E-05	3	3.333333
DE15-only	gi|6325439	0	0	0	0.000056	3.6E-05	3	2.333333
DE15-only	gi|6319370	0	0	0	0.000071	2.25E-05	3	2
DE15-only	gi|6320788	0	0	0	0.000078	2.93E-05	3	2.333333
DE15-only	gi|6324682	0	0	0	0.000102	3.83E-05	3	2
DE15-only	gi|6320896	0	0	0	0.000186	0.000109	3	2.666667
DE15-only	gi|6319602	0	0	0	0.000216	6.37E-05	3	1.666667
DE15-only	gi|6323746	0	0	0	0.000103	1.28E-05	3	2.333333
DE15-only	gi|6323891	0	0	0	0.000279	0.000173	3	2
DE15-only	gi|6321430	0	0	0	0.00003	1.14E-05	3	2.666667
DE15-only	gi|6324899	0	0	0	0.000123	1.94E-05	3	2
DE15-only	gi|6319509	0	0	0	0.000387	7.49E-05	3	2.333333
DE15-only	gi|6321898	0	0	0	0.000343	0.000242	3	1
DE15-only	gi|6320078	0	0	0	0.000451	0.000267	3	2
DE15-only	gi|6322770	0	0	0	0.000092	4.63E-05	3	2
DE15-only	gi|6322843	0	0	0	0.000237	1.4E-05	3	2
DE15-only	gi|6320718	0	0	0	0.000964	0.000187	3	1
DE15-only	gi|6324886	0	0	0	0.00105	0.000744	3	1
DE15-only	gi|6319931	0	0	0	0.000147	2.48E-05	2	4.5
DE15-only	gi|1431850	0	0	0	0.000102	5.67E-05	2	4
DE15-only	gi|6324088	0	0	0	0.000041	1.37E-05	2	2
DE15-only	gi|6319351	0	0	0	0.000121	1.65E-05	2	2
DE15-only	gi|6319698	0	0	0	0.000324	0.000294	2	2.5
DE15-only	gi|6323562	0	0	0	0.000248	4.55E-05	2	2
DE15-only	gi|6320527	0	0	0	0.000133	7.43E-05	2	2.5
DE15-only	gi|6319568	0	0	0	0.000073	5.71E-05	2	2
DE15-only	gi|6323739	0	0	0	0.000026	1.86E-06	2	2
DE15-only	gi|6320175	0	0	0	0.000064	5.36E-06	2	2
DE15-only	gi|6320798	0	0	0	0.000063	5.27E-06	2	2
DE15-only	gi|6321398	0	0	0	0.000086	2.44E-05	2	2
DE15-only	gi|6324993	0	0	0	0.00005	1.99E-05	2	2
DE15-only	gi|6321290	0	0	0	0.000065	3.63E-06	2	2
DE15-only	gi|6321718	0	0	0	0.000127	5.03E-05	2	3
DE15-only	gi|6319646	0	0	0	0.00009	1.73E-05	2	2
DE15-only	gi|6323331	0	0	0	0.000073	3.07E-05	2	2
DE15-only	gi|6320249	0	0	0	0.000132	3.73E-06	2	2
DE15-only	gi|4274231	0	0	0	0.000314	0.000205	2	2
DE15-only	gi|6325337	0	0	0	0.000199	4.58E-05	2	1.5
DE15-only	gi|6321807	0	0	0	0.000093	8.59E-05	2	2.5
DE15-only	gi|6322754	0	0	0	0.000357	8.64E-05	2	1.5
DE15-only	gi|6321411	0	0	0	0.000034	9.28E-06	2	2
DE15-only	gi|6320332	0	0	0	0.000017	0	1	2
DE15-only	gi|6323246	0	0	0	0.000069	0	1	2
DE15-only	gi|6324702	0	0	0	0.000031	0	1	2
DE15-only	gi|6320576	0	0	0	0.000284	0	1	1
DE15-only	gi|2033676	0	0	0	0.000015	0	1	2
DE15-only	gi|6320006	0	0	0	0.000049	0	1	3
DE15-only	gi|6324783	0	0	0	0.000103	0	1	2
DE15-only	gi|6323974	0	0	0	0.0004	0	1	1
DE15-only	gi|6320061	0	0	0	0.000009	0	1	2
DE15-only	gi|6322097	0	0	0	0.000072	0	1	2
DE15-only	gi|6319413	0	0	0	0.000055	0	1	2
DE15-only	gi|6319793	0	0	0	0.000087	0	1	3
DE15-only	gi|6323681	0	0	0	0.000309	0	1	2
DE15-only	gi|2780871	0	0	0	0.000058	0	1	2
DE15-only	gi|6319430	0	0	0	0.000489	0	1	2
DE15-only	gi|6324772	0	0	0	0.000151	0	1	2
DE15-only	gi|6323958	0	0	0	0.000156	0	1	3
DE15-only	gi|6323669	0	0	0	0.000075	0	1	2
DE15-only	gi|6320372	0	0	0	0.00007	0	1	2
DE15-only	gi|6323547	0	0	0	0.000136	0	1	3
DE15-only	gi|6320899	0	0	0	0.000527	0	1	2
DE15-only	gi|6324669	0	0	0	0.000069	0	1	2
DE15-only	gi|6321829	0	0	0	0.000621	0	1	2
DE15-only	gi|6321606	0	0	0	0.000342	0	1	2
DE15-only	gi|6320607	0	0	0	0.00016	0	1	2
DE15-only	gi|6324761	0	0	0	0.000039	0	1	2
DE15-only	gi|6321796	0	0	0	0.000169	0	1	2
DE15-only	gi|6322459	0	0	0	0.000165	0	1	2
DE15-only	gi|6322244	0	0	0	0.00067	0	1	1

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE15 NSAF AVG	DE15 NSAF STD	DE15 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE15	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE15 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE15-only	gi|6324515	0	0	0	0.000025	0	1									2		
DE15-only	gi|1038379	0	0	0	0.000262	0	1									2		
DE15-only	gi|6320056	0	0	0	0.000032	0	1									2		
DE15-only	gi|6323871	0	0	0	0.000084	0	1									3		
DE15-only	gi|6321457	0	0	0	0.00045	0	1									2		
DE15-only	gi|6323537	0	0	0	0.000039	0	1									2		
DE15-only	gi|4274228	0	0	0	0.000182	0	1									1		
DE15-only	gi|6320117	0	0	0	0.000093	0	1									2		
DE15-only	gi|6321232	0	0	0	0.000009	0	1									2		
DE15-only	gi|6323221	0	0	0	0.000067	0	1									2		
Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD		
123	32.63%				3.2529	2.504065	1.243831	0	0.0002645						2.54403794	1.266751		

Group	Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE15-1_P	DE15-1_uP	DE15-1_S	DE15-1_SC	DE15-1_NSAF	DE15-2_P	DE15-2_uP	DE15-2_S	DE15-2_SC	DE15-2_NSAF	DE15-3_P	DE15-3_uP	DE15-3_S	DE15-3_SC	DE15-3_NSAF	DE15-4_P	DE15-4_uP	DE15-4_S	DE15-4_SC	DE15-4_NSAF
DE15-only	gi|6324515	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	3.09	2.49E-05	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|1038379	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	17.04	0.000262	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|6320056	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	2.25	3.2E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|6323871	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	9.92	8.44E-05	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|6321457	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	22.03	0.00045	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|6323537	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	2.91	3.87E-05	X	X	X	X	X
DE15-only	gi|4274228	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	22	1.46	0.000182	X	X	X	X	X
DE15-only	gi|6320117	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	10.99	9.34E-05	X	X	X	X	X
DE15-only	gi|6321232	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	1.88	9.3E-06	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE15-only	gi|6323221	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.17	6.68E-05	X	X	X	X	X	X	X	X	X	X

Group	Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE15-1_P	DE15-1_uP	DE15-1_S	DE15-1_SC	DE15-1_NSAF	DE15-2_P	DE15-2_uP	DE15-2_S	DE15-2_SC	DE15-2_NSAF	DE15-3_P	DE15-3_uP	DE15-3_S	DE15-3_SC	DE15-3_NSAF	DE15-4_P	DE15-4_uP	DE15-4_S	DE15-4_SC	DE15-4_NSAF
noDE-only	gi|6325407	1	1	55	5.78	0.003711	1	1	39	5.78	0.001569	1	1	97	5.78	0.005261	1	1	101	5.78	0.005768	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6319424	1	1	12	0.94	0.000101	X	X	X	X	X	1	1	29	0.94	0.000197	1	1	13	0.94	0.000093	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6323886	2	2	17	24.76	0.00189	3	3	41	38.1	0.002718	2	2	30	30.48	0.002681	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6322082	X	X	X	X	X	1	1	21	1.62	0.000158	1	1	25	1.62	0.000253	1	1	10	1.62	0.000107	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|1431855	X	X	X	X	X	1	1	13	13.56	0.001534	1	1	18	13.56	0.002862	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6319814	1	1	13	13.64	0.00138	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6323980	X	X	X	X	X	1	1	13	3.33	0.000251	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6320861	X	X	X	X	X	X	X	X	X	X	2	2	4	13.29	0.000131	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6324776	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	7.27	0.000359	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6320205	X	X	X	X	X	2	2	6	15.92	0.000208	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	gi|6320860	X	X	X	X	X	1	1	29	1.46	0.000294	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD																									
11	2.92%	1.1631	1.909091	1.1361818				0.001057					1.39393939	0.55413961																											

Supporting Table 2B: Proteins detected in noDE and/or DE60 replicates

Proteins detected in both DE conditions were sorted into two groups of high and low abundances based on their averaged NSAF values measured when DE was turned off (noDE NSAF AVG).
Averages ("AVG") and standard deviations ("STD") were calculated for NSAF values and Peptide counts across the 4 replicates of a DE condition.
t-test p-values were calculated using the TTEST function in MSExcel (NSAF t-test p-Value).

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6321631	0.089245	0.0307299	4	0.072575	0.017572	4	0.813211	-0.089797	-1.139213	-1.049416	1	151	100	26.5	17	0.391455	0
High Abundance	gi|6322468	0.056902	0.0110847	4	0.044188	0.015349	4	0.776563	-0.109823	-1.354696	-1.244872	1	150	99.33774834	20.25	14.5	0.232379	0
High Abundance	gi|6321968	0.054496	0.0104952	4	0.049435	0.008424	4	0.907131	-0.04233	-1.305965	-1.263635	1	149	98.67549669	21.25	19.25	0.481734	0
High Abundance	gi|1038378	0.040924	0.0037701	4	0.032653	0.005564	4	0.797894	-0.098055	-1.486077	-1.388022	1	148	98.01324503	26.5	24.5	0.054576	0
High Abundance	gi|6319279	0.039967	0.0080495	4	0.021187	0.005028	4	0.530112	-0.275632	-1.673931	-1.398298	1	147	97.35099338	28.75	26.75	0.010634	1
High Abundance	gi|6322697	0.037728	0.004085	4	0.015494	0.002994	4	0.410676	-0.3865	-1.809836	-1.423336	1	146	96.68874172	12	12.25	0.000194	1
High Abundance	gi|6323073	0.035041	0.0052874	4	0.020047	0.002215	4	0.572101	-0.242527	-1.697951	-1.455424	1	145	96.02649007	26	25.25	0.006285	1
High Abundance	gi|6322790	0.030639	0.0056721	4	0.0377	0.008912	4	1.230458	0.0900668	-1.423659	-1.513725	1	144	95.36423841	12.75	9.5	0.237988	0
High Abundance	gi|6321693	0.029306	0.0078327	4	0.029881	0.009648	4	1.019621	0.0084386	-1.524605	-1.533043	1	143	94.70198675	14	12.25	0.929351	0
High Abundance	gi|6322409	0.028438	0.0093006	4	0.027123	0.012244	4	0.953759	-0.020561	-1.566662	-1.546101	1	142	94.0397351	9.75	9.75	0.870175	0
High Abundance	gi|6324486	0.020489	0.0049482	4	0.011734	0.007041	4	0.572698	-0.242075	-1.930554	-1.688479	1	141	93.37748344	13.75	11.75	0.093519	0
High Abundance	gi|6320255	0.016329	0.005011	4	0.006979	0.002549	4	0.427399	-0.369166	-2.156207	-1.78704	1	140	92.71523179	9.75	7.25	0.024824	1
High Abundance	gi|6321464	0.016263	0.0104511	4	0.002396	0.000999	4	0.147328	-0.831714	-2.620513	-1.788799	1	139	92.05298013	2.5	3.25	0.07608	0
High Abundance	gi|9755341	0.015824	0.0025789	4	0.007448	0.002528	4	0.470677	-0.327277	-2.12796	-1.800684	1	138	91.39072848	5	4.25	0.003548	1
High Abundance	gi|6320359	0.013516	0.0015829	4	0.007537	0.00166	4	0.557635	-0.25365	-2.122801	-1.869152	1	137	90.72847682	5.75	5.5	0.002001	1
High Abundance	gi|6323138	0.013418	0.0035944	4	0.009114	0.00432	4	0.679237	-0.167979	-2.040291	-1.872312	1	136	90.06622517	5.5	6.25	0.178168	0
High Abundance	gi|6323196	0.013086	0.0040826	4	0.003989	0.000694	4	0.30483	-0.515943	-2.399136	-1.883193	1	135	89.40397351	4.5	3	0.019433	1
High Abundance	gi|6323004	0.012217	0.0029473	4	0.013672	0.003149	4	1.119096	0.0488675	-1.864168	-1.913035	1	134	88.74172185	23.5	27.75	0.525086	0
High Abundance	gi|6319314	0.011825	0.0031741	4	0.012535	0.003757	4	1.060042	0.0253232	-1.901876	-1.927199	1	133	88.0794702	22.25	27.75	0.782666	0
High Abundance	gi|6322978	0.009927	0.0035095	4	0.007705	0.001427	4	0.776166	-0.110045	-2.113227	-2.003182	1	132	87.41721854	4.25	5.25	0.306379	0
High Abundance	gi|6323613	0.009356	0.0019107	4	0.010024	0.004222	4	1.071398	0.0299508	-1.998959	-2.02891	1	131	86.75496689	5.25	4.75	0.787084	0
High Abundance	gi|6320269	0.00911	0.0027517	4	0.005398	0.000951	4	0.592536	-0.227285	-2.267767	-2.040482	1	130	86.09271523	5.5	5	0.068167	0
High Abundance	gi|6321408	0.008197	0.0018995	4	0.004905	0.002689	4	0.59839	-0.223016	-2.309361	-2.086345	1	129	85.43046358	2.75	3.75	0.097774	0
High Abundance	gi|6319673	0.00789	0.0006584	4	0.00565	0.001514	4	0.716096	-0.145029	-2.247952	-2.102923	1	127	84.10596026	13.75	16	0.051987	0
High Abundance	gi|6320148	0.00789	0.001499	4	0.007604	0.001033	4	0.963752	-0.016035	-2.118958	-2.102923	1	128	84.76821192	11	9.5	0.76478	0
High Abundance	gi|6324027	0.007695	0.0023053	4	0.009424	0.001167	4	1.224691	0.0880267	-2.025765	-2.113791	1	126	83.44370861	4.5	6	0.24514	0
High Abundance	gi|6320963	0.007322	0.0023735	4	0.004182	0.001643	4	0.571155	-0.243246	-2.378616	-2.13537	1	125	82.78145695	3	5.25	0.078146	0
High Abundance	gi|6320122	0.006788	0.0042374	3	0.005841	0.004421	3	0.860489	-0.065255	-2.233513	-2.168258	1	124	82.1192053	1	1	0.802072	0
High Abundance	gi|6324670	0.006571	0.0018952	4	0.005063	0.000702	4	0.770507	-0.113224	-2.295592	-2.182369	1	123	81.45695364	5.25	5	0.213357	0
High Abundance	gi|6323615	0.006483	0.0019291	4	0.004078	0.001306	4	0.62903	-0.201329	-2.389553	-2.188224	1	122	80.79470199	7.25	7	0.090902	0
High Abundance	gi|6322271	0.006476	0.0026614	4	0.002125	0.000757	4	0.328135	-0.483948	-2.672641	-2.188693	1	121	80.13245033	2.25	2	0.041989	1
High Abundance	gi|6319505	0.006391	0.0015172	4	0.003306	0.000468	4	0.51729	-0.286266	-2.480697	-2.194431	1	120	79.47019868	9.75	9.25	0.022005	1
High Abundance	gi|6320215	0.006169	0.0015034	4	0.003187	0.00049	4	0.516615	-0.286833	-2.496618	-2.209785	1	119	78.80794702	8.75	8.5	0.023331	1
High Abundance	gi|6320128	0.006127	0.0029448	4	0.005591	0.005058	4	0.912518	-0.039758	-2.252511	-2.212752	1	118	78.14569536	1.75	1.25	0.861947	0
High Abundance	gi|6323294	0.006126	0.0027463	4	0.004392	0.000292	4	0.716944	-0.144515	-2.357338	-2.212823	1	117	77.48344371	2.5	2.5	0.296345	0
High Abundance	gi|6321025	0.00602	0.0021373	4	0.003207	0.000575	4	0.532724	-0.273498	-2.493901	-2.220404	1	116	76.82119205	8.25	9	0.074114	0
High Abundance	gi|6320590	0.005993	0.002091	4	0.010789	0.004236	4	1.800267	0.2553369	-1.967019	-2.222356	1	115	76.1589404	3	3.5	0.106035	0
High Abundance	gi|6322583	0.005947	0.002258	4	0.005617	0.001193	4	0.94451	-0.024794	-2.250496	-2.225702	1	114	75.49668874	5.75	5	0.807149	0
High Abundance	gi|6324085	0.005945	0	1	0.000731	8.27E-05	3	0.12296	-0.910234	-3.136083	-2.225848	1	113	74.83443709	1	2.333333		
High Abundance	gi|6322794	0.005885	0.0011539	4	0.005132	0.001751	4	0.872048	-0.05946	-2.289713	-2.230254	1	112	74.17218543	3.25	4.5	0.504233	0
High Abundance	gi|6320655	0.005876	0.001226	4	0.007262	0.006234	4	1.235875	0.0919745	-2.138944	-2.230918	1	111	73.50993377	5.25	5.25	0.690133	0
High Abundance	gi|6320304	0.005749	0.0021378	4	0.002968	0.000385	4	0.516264	-0.287128	-2.527536	-2.240408	1	110	72.84768212	7.5	8.5	0.078124	0
High Abundance	gi|6321184	0.005739	0.0024514	4	0.006952	0.00061	4	1.211361	0.0832735	-2.15789	-2.241164	1	109	72.18543046	11.25	18.25	0.400305	0
High Abundance	gi|6320949	0.005297	0.0012303	4	0.004077	0.001468	4	0.769681	-0.113689	-2.389659	-2.27597	1	108	71.52317881	5	4	0.251165	0
High Abundance	gi|6324120	0.005255	0.0010446	4	0.007493	0.001011	4	1.42588	0.154083	-2.125344	-2.279427	1	107	70.86092715	15	17.5	0.02172	1
High Abundance	gi|6319972	0.005174	0.0010909	4	0.007419	0.000936	4	1.4339	0.1565189	-2.129655	-2.286174	1	106	70.1986755	15	17	0.021109	1
High Abundance	gi|6319483	0.004895	0.0014228	4	0.007526	0.001898	4	1.537487	0.1868115	-2.123436	-2.310247	1	105	69.53642384	7	9.25	0.07185	0
High Abundance	gi|6321524	0.004766	0.0017336	4	0.001749	0.0002	4	0.366974	-0.435364	-2.75721	-2.321846	1	104	68.87417219	3	2.5	0.039097	1
High Abundance	gi|6324534	0.00454	0.0011418	4	0.008388	0.002234	4	1.847577	0.2666026	-2.076342	-2.342944	1	103	68.21192053	3.75	3.75	0.032344	1
High Abundance	gi|6323077	0.004456	0.0007734	4	0.002978	0.001717	4	0.668312	-0.17502	-2.526075	-2.351055	1	102	67.54966887	5	4.75	0.189	0
High Abundance	gi|6323072	0.004322	0.0016035	4	0.00619	0.002193	4	1.432207	0.1560059	-2.208309	-2.364315	1	101	66.88741722	5.25	5.75	0.222558	0
High Abundance	gi|6319559	0.004142	0.000987	4	0.002683	0.000661	4	0.647755	-0.188589	-2.571379	-2.38279	1	100	66.22516556	4.75	4	0.055306	0
High Abundance	gi|6322984	0.004123	0.0007924	4	0.003271	0.001073	4	0.793354	-0.100533	-2.485319	-2.384787	1	99	65.56291391	7.75	8	0.252322	0
High Abundance	gi|6321754	0.004062	0.0007343	4	0.003244	0.001108	4	0.798621	-0.097659	-2.488919	-2.39126	1	98	64.90066225	6.75	7.75	0.271565	0
High Abundance	gi|8655890	0.004039	0.0022002	4	0.00701	0.001828	4	1.02971	0.0127151	-2.381011	-2.393726	1	96	63.57615894	6.5	7.75	0.084637	0
High Abundance	gi|6324151	0.004039	0.0008696	4	0.004159	0.000776	4	1.735578	0.2394442	-2.154282	-2.393726	1	97	64.2384106	8.75	7.75	0.844147	0
High Abundance	gi|6323104	0.003953	0.0014655	3	0.001266	0.000882	4	0.320263	-0.494493	-2.897566	-2.403073	1	95	62.91390728	5.666666667	3.75	0.06484	0
High Abundance	gi|6323090	0.003925	0.0006235	4	0.008253	0.002351	4	2.102675	0.3227722	-2.083388	-2.40616	1	94	62.25165563	1.75	2.5	0.030597	1
High Abundance	gi|6320228	0.003915	0.0009042	4	0.001651	0.000714	4	0.421711	-0.374985	-2.782253	-2.407268	1	93	61.58940397	6.75	6	0.008547	1
High Abundance	gi|1038379	0.003833	0.0015058	4	0.002761	0.000362	4	0.720324	-0.142472	-2.558934	-2.416461	1	92	60.92715232	5.25	5.25	0.251485	0
High Abundance	gi|6325196	0.003811	0.0012089	4	0.005728	0.000148	4	1.503018	0.1769641	-2.241997	-2.418961	1	91	60.26490066	17.25	21.25	0.049314	1
High Abundance	gi|6323763	0.003676	0.0008584	4	0.00471	0.000398	4	1.281284	0.1076454	-2.326979	-2.434624	1	90	59.60264901	8.25	8.75	0.090579	0
High Abundance	gi|6319396	0.003464	0.0013192	4	0.004465	0.002617	4	1.288972	0.1102436	-2.350179	-2.460422	1	89	58.94039735	5.25	5.25	0.528549	0
High Abundance	gi|6320950	0.00335	0.0012392	4	0.003499	0.000438	4	1.044478	0.0188991	-2.456056	-2.474955	1	88	58.2781457	4.25	6	0.832748	0
High Abundance	gi|6323163	0.003242	0.0022117	4	0.003798	0.0014	4	1.171499	0.0687419	-2.420445	-2.489187	1	87	57.61589404	5.5	4	0.688466	0
High Abundance	gi|6323371	0.003123	0.0010263	4	0.001886	0.000296	4	0.603907	-0.21903	-2.724458	-2.505428	1	86	56.95364238	4.25	5	0.091018	0
High Abundance	gi|6321977	0.003107	0.0005829	4	0.004577	0.000945	4	1.473125	0.1682397	-2.339419	-2.507659	1	85	56.29139073	8.5	14	0.045554	1
High Abundance	gi|6319315	0.003028	0.0005642	4	0.003164	0.000558	4	1.044914	0.0190806	-2.499764	-2.518844	1	84	55.62913907	6	3.5	0.743924	0
High Abundance	gi|6323057	0.003025	0.0004902	4	0.001146	0.000278	4	0.378843	-0.421541	-2.940815	-2.519275	1	83	54.96688742	4	2.75	0.001398	1
High Abundance	gi|6321315	0.00302	0.0018134	4	0.002245	0.000314	4	0.743377	-0.128791	-2.648784	-2.519993	1	82	54.30463576	6	2.75	0.458752	0
High Abundance	gi|6320679	0.003006	0.0017893	4	0.002123	0.000578	4	0.706254	-0.151039	-2.67305	-2.522011	1	81	53.64238411	3.5	3.75	0.405872	0
High Abundance	gi|1431847	0.003005	0.0009009	4	0.002253	0.000641	4	0.74975	-0.125083	-2.647239	-2.522156	1	80	52.98013245	8	9	0.227484	0
High Abundance	gi|6322605	0.002896	0.0011085	4	0.003551	0.000838	4	1.226174	0.0885521	-2.449649	-2.538201	1	79	52.31788079	6.5	7	0.384754	0
High Abundance	gi|6321772	0.002821	0.00075	4	0.004403	0.001475	4	1.560794	0.1933456	-2.356251	-2.549597	1	78	51.65562914	4.25	5.5	0.12099	0
High Abundance	gi|6322120	0.002803	0.0005083	4	0.003879	0.001359	4	1.383874	0.1410967	-2.41128	-2.552377	1	77	50.99337748	3.5	3	0.215456	0
High Abundance	gi|6324445	0.002779	0.0007174	4	0.003884	0.001573	4	1.397625	0.1453907	-2.410721	-2.556111	1	76	50.33112583	3.75	5.5	0.267448	0
High Abundance	gi|6322564	0.002737	0.0007168	4	0.002711	0.000656	4	0.990501	-0.004145	-2.56687	-2.562725	1	75	49.66887417	3.75	6.75	0.959062	0
High Abundance	gi|6320073	0.002687	0.0007479	4	0.003522	0.001964	4	1.310755	0.1175217	-2.453211	-2.570732	1	74	49.00662252	1	1.25	0.472934	0
High Abundance	gi|6322847	0.002661	0.0009261	3	0.002519	0.001722	3	0.946637	-0.023817	-2.598772	-2.574955	1	73	48.34437086	3.666666667	2.666667	0.907714	0
High Abundance	gi|6323387	0.002605	0.0007836	4	0.00379	0.000406	4	1.454894	0.1628315	-2.421361	-2.584192	1	72	47.68211921	10	11.25	0.048502	1
High Abundance	gi|6321249	0.002598	0.0005352	4	0.002199	0.001331	4	0.84642	-0.072414	-2.657775	-2.585361	1	70	46.35761589	2	2	0.607724	0
High Abundance	gi|6320978	0.002598	0.0005352	4	0.002199	0.001331	4	0.84642	-0.072414	-2.657775	-2.585361	1	71	47.01986755	2	2	0.607724	0
High Abundance	gi|6321786	0.002568	0.0008615	3	0.003329	0.001412	2	1.29634	0.1127188	-2.477686	-2.590405	1	69	45.69536424	3	3	0.584306	0
High Abundance	gi|6323474	0.002537	0.000832	4	0.001208	0.000785	4	0.476153	-0.322254	-2.917933	-2.59568	1	68	45.03311258	7.5	6.25	0.05931	0
High Abundance	gi|6323386	0.002527	0.0013219	4	0.003493	0.000515	4	1.382271	0.1405933	-2.456801	-2.597395	1	67	44.37086093	5.5	12.5	0.246853	0
High Abundance	gi|6323577	0.00252	0.0008462	4	0.001081	0.000769	4	0.428968	-0.367575	-2.966174	-2.598599	1	66	43.70860927	7.25	6.25	0.045777	1
High Abundance	gi|6325126	0.002511	0.0009648	4	0.001799	0.000638	4	0.716448	-0.144816	-2.744969	-2.600153	1	65	43.04635762	4.5	5	0.271357	0
High Abundance	gi|3736268	0.002496	0.0006565	4	0.003017	0.000665	4	1.208734	0.0823307	-2.520425	-2.602755	1	64	42.38410596	3.75	6	0.307578	0
High Abundance	gi|6320065	0.002434	0.0013313	4	0.002251	0.001088	4	0.924815	-0.033945	-2.647625	-2.613679	1	63	41.7218543	2.25	2.5	0.83933	0
High Abundance	gi|6321335	0.002424	0.0003522	4	0.002239	0.00137	4	0.92368	-0.034479	-2.649946	-2.615467	1	62	41.05960265	3.25	2.75	0.808436	0
High Abundance	gi|6322668	0.002273	0.0004578	4	0.002596	0.001562	4	1.142103	0.0577053	-2.585695	-2.643401	1	61	40.39735099	4	3.75	0.714324	0
High Abundance	gi|6321362	0.00223	0.0006323	4	0.003311	0.000814	4	1.484753	0.1716543	-2.480041	-2.651695	1	60	39.73509934	5.75	5.5	0.08356	0
High Abundance	gi|6322138	0.002207	0.000866	4	0.004533	0.001351	4	2.053919	0.3125834	-2.343614	-2.656198	1	59	39.07284768	3.5	5.25	0.032999	1
High Abundance	gi|6322284	0.002206	0.0004999	4	0.002576	0.00158	4	1.167724	0.0673404	-2.589054	-2.656394	1	58	38.41059603	3.75	3.75	0.680444	0
High Abundance	gi|6325058	0.002175	0.0006199	4	0.00302	0.000649	4	1.388506	0.1425477	-2.519993	-2.662541	1	57	37.74834437	5.25	5	0.108792	0
High Abundance	gi|6321648	0.002154	0.0003065	4	0.004412	0.001371	4	2.048282	0.3113898	-2.355364	-2.666754	1	56	37.08609272	4	6	0.04269	1
High Abundance	gi|6323376	0.002105	0.0002353	4	0.000827	0.000472	4	0.392874	-0.405747	-3.082494	-2.676748	1	55	36.42384106	3	3	0.006569	1
High Abundance	gi|6323840	0.002039	0.0005044	4	0.004207	0.000509	4	2.063266	0.3145553	-2.376027	-2.690583	1	54	35.7615894	14.75	18.5	0.00092	1
High Abundance	gi|1160064	0.002009	0.0002418	4	0.000667	0.000398	4	0.332006	-0.478854	-3.175874	-2.69702	1	53	35.09933775	2.75	2.5	0.002298	1
High Abundance	gi|6320801	0.001985	0.0005144	4	0.001955	0.001498	4	0.984887	-0.006614	-2.708853	-2.702239	1	52	34.43708609	1	1.25	0.971753	0
High Abundance	gi|6319666	0.001922	0.0005228	4	0.00109	4.87E-05	4	0.567118	-0.246327	-2.962574	-2.716247	1	51	33.77483444	4.25	4.5	0.04922	1
High Abundance	gi|6321291	0.0019	0.0009582	4	0.004395	0.001079	4	2.313158	0.3642053	-2.357041	-2.721246	1	50	33.11258278	3.5	4.75	0.01381	1
High Abundance	gi|6319965	0.001871	0	1	0.000259	0.000156	3	0.138429	-0.858774	-3.5867	-2.727926	1	49	32.45033113	1	2.333333		
High Abundance	gi|6325016	0.001829	0.000394	4	0.003704	0.000556	4	2.02515	0.3064573	-2.431329	-2.737786	1	48	31.78807947	12.5	17.5	0.002119	1
High Abundance	gi|6325176	0.001797	0.0003761	4	0.000926	0.000166	4	0.515303	-0.287937	-3.033389	-2.745452	1	47	31.12582781	4	4	0.012448	1
High Abundance	gi|6325389	0.001781	0.0013141	4	0.002933	0.001204	3	1.646828	0.2166481	-2.532688	-2.749336	1	46	30.46357616	2.25	2.333333	0.285692	0
High Abundance	gi|6324452	0.001776	0.0007938	4	0.004155	0.00138	4	2.339527	0.3691281	-2.381429	-2.750557	1	45	29.8013245	2	3	0.032183	1
High Abundance	gi|6320905	0.001754	0.0007026	4	0.001871	0.000298	4	1.066705	0.0280442	-2.727926	-2.75597	1	44	29.13907285	2.25	3.5	0.774497	0
High Abundance	gi|6321407	0.001753	0.0001109	3	0.001318	0.000864	3	0.751854	-0.123867	-2.880085	-2.756218	1	42	27.81456954	1.333333333	3.333333	0.475355	0

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6321587	0.001753	0.0001109	3	0.001658	7.69E-05	2	0.945807	-0.024197	-2.780415	-2.756218	1	43	28.47682119	1.333333333	3.5	0.34216	0
High Abundance	gi|6324756	0.001742	0.0002751	2	0.001194	0.000545	2	0.685419	-0.164044	-2.922996	-2.758952	1	41	27.15231788	2	1.5	0.36872	0
High Abundance	gi|6323357	0.001671	0.0002665	3	0.002761	0.000369	3	1.652304	0.21809	-2.558934	-2.777024	1	40	26.49006623	1	1	0.017296	1
High Abundance	gi|6324262	0.001621	0.0007381	4	0.002835	0.001376	4	1.74892	0.24277	-2.547447	-2.790217	1	39	25.82781457	2.75	4.5	0.185695	0
High Abundance	gi|6320882	0.001527	0.0003252	4	0.001927	0.000609	4	1.261952	0.1010427	-2.715118	-2.816161	1	38	25.16556291	7.75	8.75	0.303921	0
High Abundance	gi|6323288	0.001526	0.000417	4	0.003105	0.00019	4	2.034731	0.3085071	-2.507938	-2.816445	1	37	24.50331126	11	18	0.001946	1
High Abundance	gi|6324194	0.00149	0.0010164	3	0.001104	0.000291	2	0.74094	-0.130217	-2.957031	-2.826814	1	36	23.8410596	1	2	0.587188	0
High Abundance	gi|6324637	0.001484	0.0008663	4	0.001101	0.000888	3	0.741914	-0.129647	-2.958213	-2.828566	1	35	23.17880795	7.25	7	0.595847	0
High Abundance	gi|6321679	0.001482	0.0007832	4	0.001911	0.000734	4	1.289474	0.1104125	-2.718739	-2.829152	1	34	22.51655629	9.25	21.75	0.455152	0
High Abundance	gi|6320781	0.001401	0.0003751	4	0.003241	0.001431	4	2.313348	0.3642409	-2.489321	-2.853562	1	33	21.85430464	4	4.75	0.078573	0
High Abundance	gi|6319814	0.00138	0	1	0.001144	0.000302	2	0.828986	-0.081453	-2.941574	-2.860121	1	32	21.19205298	1	2		
High Abundance	gi|1431847	0.001378	0.0004714	3	0.001258	0.000454	4	0.912917	-0.039569	-2.900319	-2.860751	1	31	20.52980132	2.333333333	4.25	0.750036	0
High Abundance	gi|6325300	0.001286	0.0003953	3	0.002069	0.000594	3	1.608865	0.2065195	-2.68424	-2.890759	1	30	19.86754967	3	2	0.140671	0
High Abundance	gi|6325006	0.001251	0.0009425	3	0.002814	0.001114	4	2.2494	0.3520668	-2.550676	-2.902743	1	29	19.20529801	2.666666667	3.5	0.10287	0
High Abundance	gi|6324945	0.00122	0.0009316	4	0.002511	0.001383	4	2.058197	0.3134869	-2.600153	-2.91364	1	28	18.54304636	3	5	0.179283	0
High Abundance	gi|6324260	0.001209	0.0006283	4	0.001709	0.000537	4	1.413565	0.1503158	-2.767258	-2.917574	1	27	17.8807947	2.75	3.75	0.272878	0
High Abundance	gi|6319307	0.001205	0.0006478	4	0.002165	0.000437	4	1.79668	0.2544709	-2.664542	-2.919013	1	26	17.21854305	3.75	6.75	0.055087	0
High Abundance	gi|6320121	0.001197	0.0005492	4	0.001935	0.000227	4	1.616541	0.2085868	-2.713319	-2.921906	1	25	16.55629139	4.5	5	0.068054	0
High Abundance	gi|6323567	0.001187	0.0006256	3	0.001238	0.000956	4	1.042965	0.0182699	-2.907279	-2.925549	1	24	15.89403974	2.333333333	4	0.936337	0
High Abundance	gi|6324533	0.001167	0.0004606	3	0.005702	0.001894	4	4.886033	0.6889564	-2.243973	-2.932929	2	95	100	2.666666667	5.5	0.013961	1
High Abundance	gi|1431855	0.001152	0.0002631	4	0.000853	0.00034	4	0.740451	-0.130503	-3.069051	-2.938548	1	23	15.23178808	4.25	2.5	0.216717	0
High Abundance	gi|6322325	0.00111	0.0002411	2	0.009124	0.002815	4	8.21982	0.9148623	-2.039815	-2.954677	2	94	98.94736842	3.5	5	0.010149	1
High Abundance	gi|6324463	0.001107	0.0004562	4	0.001371	0.000253	4	1.238482	0.0928898	-2.862963	-2.955852	1	22	14.56953642	3.5	5	0.360928	0
High Abundance	gi|6323087	0.00108	0.0002282	4	0.001703	0.000438	4	1.576852	0.1977909	-2.768785	-2.966576	1	21	13.90728477	7.75	8	0.058028	0
High Abundance	gi|6319585	0.001056	0.0004812	3	0.001858	0.000777	4	1.75947	0.2453818	-2.730954	-2.976336	1	20	13.24503311	1.666666667	3.25	0.154941	0
High Abundance	gi|6324808	0.00104	0.0005113	3	0.001006	0.000675	3	0.967308	-0.014435	-2.997402	-2.982967	1	19	12.58278146	3.333333333	2.333333	0.948325	0
High Abundance	gi|6319378	0.001033	0.0001728	2	0.000976	0.000339	3	0.944821	-0.024651	-3.01055	-2.9859	1	18	11.9205298	1.5	3	0.823317	0
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**	**Number of Proteins with p-Value < 0.05**	**Proteins with p-Value < 0.05 (% of Protein)**
136	**30.91%**	**97.5641**	**3.7794118**	**0.592435981**	**83.6634**	**3.845588**	**0.453442**	**0.007174**	**0.0061517**				**6.446691176**	**5.698139477**	**7.013480392**	**5.90617**	**35**	**26.32%**
Low Abundance	gi|6319806	0.001028	0.0007237	4	0.002536	0.000524	4	2.466926	0.3921561	-2.595851	-2.988007	2	93	97.89473684	4.25	9.75	0.017213	1
Low Abundance	gi|6322599	0.001004	0.0005152	4	0.002647	0.001456	4	2.636454	0.4210202	-2.577246	-2.998266	2	92	96.84210526	4	8.25	0.105261	0
Low Abundance	gi|6323481	0.000987	0.0006673	4	0.001438	0.0008	4	1.45694	0.1634417	-2.842241	-3.005683	1	17	11.25827815	2.5	4.75	0.420892	0
Low Abundance	gi|6325114	0.000969	0.0003805	3	0.002735	0.00078	4	2.822497	0.4506336	-2.563043	-3.013676	2	91	95.78947368	3.666666667	2.25	0.013312	1
Low Abundance	gi|6322910	0.000964	0.0004746	4	0.006033	0.001245	4	6.258299	0.7964563	-2.219467	-3.015923	2	90	94.73684211	2.75	5	0.001858	1
Low Abundance	gi|6324707	0.00096	0.0002577	4	0.003032	0.001006	4	3.158333	0.499458	-2.518271	-3.017729	2	89	93.68421053	14.5	24.5	0.022361	1
Low Abundance	gi|6324298	0.000959	0	1	0.001534	0.000564	2	1.599583	0.2040068	-2.814175	-3.018181	1	16	10.59602649	2	2.5		
Low Abundance	gi|6320226	0.000944	0.0005776	4	0.001542	0.000399	4	1.633475	0.2131124	-2.811916	-3.025028	1	15	9.933774834	7	9.5	0.145274	0
Low Abundance	gi|6322505	0.000944	0.0002374	4	0.002329	0.000596	4	2.467161	0.3921975	-2.632831	-3.025028	2	88	92.63157895	11	15.5	0.012932	1
Low Abundance	gi|6324923	0.00094	0.0002014	4	0.001428	0.000469	4	1.519149	0.1816004	-2.845272	-3.026872	1	14	9.271523179	1.5	2	0.127766	0
Low Abundance	gi|6325331	0.000911	0.0005313	4	0.001108	0.000189	4	1.216246	0.0850214	-2.95546	-3.040482	1	13	8.609271523	5.75	10.25	0.525548	0
Low Abundance	gi|6323729	0.000886	0.0002884	4	0.000427	0.000272	2	0.481941	-0.317006	-3.369572	-3.052566	1	12	7.947019868	1	4	0.184712	0
Low Abundance	gi|6321987	0.000884	0.0004026	3	0.001676	8.83E-05	4	1.895928	0.2778217	-2.775726	-3.053548	1	11	7.284768212	1.666666667	4.5	0.071568	0
Low Abundance	gi|6323848	0.000853	5.087E-05	2	0.002745	0.001158	4	3.218054	0.5075933	-2.561458	-3.069051	2	87	91.57894737	3.5	3	0.046545	1
Low Abundance	gi|6323324	0.00085	0.0005116	4	0.002199	0.000814	4	2.587059	0.4128063	-2.657775	-3.070581	2	86	90.52631579	2.75	3.75	0.037291	1
Low Abundance	gi|6323391	0.000799	0	1	0.000177	3.71E-05	3	0.221527	-0.654574	-3.752027	-3.097453	1	10	6.622516556	2	3		
Low Abundance	gi|6324233	0.000787	0.00044	4	0.002894	0.000968	4	3.677255	0.5655238	-2.538501	-3.104025	2	85	89.47368421	3.75	5.75	0.015174	1
Low Abundance	gi|6321973	0.000785	0.0002581	4	0.002171	0.00021	4	2.765605	0.4417902	-2.66334	-3.10513	2	84	88.42105263	5.25	8.75	0.0002	1
Low Abundance	gi|6322058	0.000758	0.0005851	4	0.000975	0.000267	4	1.28628	0.1093354	-3.010995	-3.120331	1	9	5.960264901	2	3.25	0.533959	0
Low Abundance	gi|6321563	0.000731	0.0002768	4	0.001145	0.000106	4	1.566347	0.1948881	-2.941195	-3.136083	1	8	5.298013245	4.5	7	0.051216	0
Low Abundance	gi|6322002	0.000706	0.0002692	4	0.001613	0.000508	4	2.284703	0.3588297	-2.792366	-3.151195	2	83	87.36842105	4	6	0.02872	1
Low Abundance	gi|6323861	0.000695	0.0001588	4	0.001153	0.000288	4	1.658993	0.2198445	-2.938171	-3.158015	1	7	4.635761589	8	16.5	0.041744	1
Low Abundance	gi|6325036	0.000678	0.0005354	4	0.00304	0.002169	4	4.483776	0.6516439	-2.517126	-3.16877	2	82	86.31578947	3	5	0.114869	0
Low Abundance	gi|6322565	0.000592	0.0003229	4	0.00126	0.000686	4	2.128378	0.3280488	-2.899629	-3.227678	2	81	85.26315789	3.75	7	0.147933	0
Low Abundance	gi|6324907	0.000581	0.0001725	3	0.001278	0.000152	4	2.199656	0.3423547	-2.893469	-3.235824	2	80	84.21052632	2.666666667	5	0.0048	1
Low Abundance	gi|6323464	0.000559	0.0003827	4	0.002303	0.00073	4	4.119857	0.6148821	-2.637706	-3.252588	2	79	83.15789474	5.25	11.25	0.010225	1
Low Abundance	gi|6323208	0.000546	0.0002841	3	0.001104	0.000594	4	2.021978	0.3057764	-2.957031	-3.262807	2	78	82.10526316	2	3.25	0.167312	0
Low Abundance	gi|6325178	0.000537	0.0002627	4	0.001354	0.000364	4	2.521415	0.4016444	-2.868381	-3.270026	2	76	80	3.25	4.25	0.01283	1
Low Abundance	gi|6319668	0.000537	0.0002627	4	0.001354	0.000364	4	2.521415	0.4016444	-2.868381	-3.270026	2	77	81.05263158	3.25	4.25	0.01283	1
Low Abundance	gi|6320846	0.000525	0	1	0.001535	0.000211	4	2.92381	0.4659491	-2.813892	-3.279841	2	75	78.94736842	2	2.25		
Low Abundance	gi|6325229	0.000513	0.0001867	2	0.00251	0.001586	4	4.892788	0.6895564	-2.600326	-3.289883	2	74	77.89473684	1.5	8.5	0.084702	0
Low Abundance	gi|6322608	0.00049	0.0001071	4	0.001332	0.000316	4	2.718367	0.4343081	-2.875496	-3.309804	2	73	76.84210526	2.75	5	0.008992	1
Low Abundance	gi|6322912	0.000485	7.247E-05	4	0.002175	0.000671	4	4.484536	0.6517175	-2.662541	-3.314258	2	72	75.78947368	4.5	13	0.014467	1
Low Abundance	gi|6319603	0.000456	0.0003563	3	0.002863	0.000605	4	6.278509	0.7978565	-2.543179	-3.341035	2	70	73.68421053	5.666666667	15.75	0.001362	1
Low Abundance	gi|6321522	0.000456	0.0002485	3	0.001	0.000526	4	2.192982	0.3410352	-3	-3.341035	2	71	74.73684211	2	3.25	0.136055	0
Low Abundance	gi|6323585	0.000454	0.0001934	4	0.001625	0.00061	4	3.579295	0.5537975	-2.789147	-3.342944	2	69	72.63157895	4.25	8	0.025968	1
Low Abundance	gi|6323619	0.000447	0	1	0.000381	0.000346	2	0.852349	-0.069383	-3.419075	-3.349692	1	6	3.973509934	1	2		
Low Abundance	gi|6325167	0.000444	0.0003366	4	0.00237	0.000939	4	5.337838	0.7273654	-2.625252	-3.352617	2	68	71.57894737	2.75	5.25	0.020385	1
Low Abundance	gi|6325403	0.00044	7.871E-05	4	0.001231	0.000388	4	2.797727	0.4468054	-2.909742	-3.356547	2	67	70.52631579	4.75	12.25	0.024232	1
Low Abundance	gi|6319901	0.000432	0.0001175	4	0.001956	0.000456	4	4.527778	0.6558851	-2.708631	-3.364516	2	66	69.47368421	5	7.5	0.005051	1
Low Abundance	gi|6322783	0.000431	3.004E-05	2	0.001459	0.000588	4	3.385151	0.529578	-2.835945	-3.365523	2	65	68.42105263	2	3	0.039191	1
Low Abundance	gi|6323470	0.000426	7.068E-05	2	0.000939	0.000533	4	2.204225	0.343256	-3.027334	-3.37059	2	64	67.36842105	2.5	5.5	0.149094	0
Low Abundance	gi|6319726	0.000424	0.0002274	3	0.000742	0.000578	4	1.75	0.243038	-3.129596	-3.372634	2	63	66.31578947	2.666666667	4	0.372075	0
Low Abundance	gi|6323554	0.000418	0	1	0.000179	0.000114	2	0.42823	-0.368323	-3.747147	-3.378824	1	5	3.311258278	1	2.5		
Low Abundance	gi|6324951	0.000404	0.0002468	4	0.002435	0.000498	4	6.027228	0.7801176	-2.613501	-3.393619	2	62	65.26315789	5	13	0.001293	1
Low Abundance	gi|6320362	0.000395	0.0001931	4	0.002167	0.000711	4	5.486076	0.7392618	-2.664141	-3.403403	2	61	64.21052632	3.75	5.75	0.012385	1
Low Abundance	gi|6325326	0.000385	8.272E-05	3	0.001355	0.000164	4	3.519481	0.5464786	-2.868061	-3.414539	2	60	63.15789474	2.333333333	3.5	0.00025	1
Low Abundance	gi|6320936	0.000379	8.388E-05	4	0.002526	0.000719	4	6.664908	0.8237941	-2.597567	-3.421361	2	59	62.10526316	6.5	18.5	0.008884	1
Low Abundance	gi|6324776	0.000359	0	1	0.000302	0	1	0.841226	-0.075088	-3.519993	-3.444906	1	4	2.649006623	2	1		
Low Abundance	gi|6321013	0.000356	3.694E-05	4	0.001435	0.000453	4	4.030899	0.6054019	-2.843148	-3.44855	2	58	61.05263158	4.75	9.75	0.017203	1
Low Abundance	gi|6322666	0.000324	0.0001428	4	0.001022	0.000247	4	3.154321	0.4989059	-2.990549	-3.489455	2	57	60	12.5	27.25	0.005054	1
Low Abundance	gi|6322732	0.00032	0	1	0.000514	0.000137	4	1.60625	0.2058131	-3.289037	-3.49485	2	56	58.94736842	2	2		
Low Abundance	gi|6325290	0.00031	6.308E-05	3	0.000146	9.36E-05	2	0.470968	-0.327009	-3.835647	-3.508638	1	3	1.986754967	1	2.5	0.191203	0
Low Abundance	gi|6320016	0.000304	0.0002023	4	0.00133	5.82E-05	4	4.375	0.6409781	-2.876148	-3.517126	2	2	1.324503311	6	15.25	0.00118	1
Low Abundance	gi|6320710	0.000304	0	1	0.000276	0.000154	4	0.907895	-0.041965	-3.559091	-3.517126	1	55	57.89473684	1	3.75		
Low Abundance	gi|6319625	0.000275	7.403E-05	2	0.000325	0.00022	3	1.181818	0.0725507	-3.488117	-3.560667	2	54	56.84210526	2.5	3.333333	0.740889	0
Low Abundance	gi|1431857	0.000271	0.000214	4	0.001282	0.000289	4	4.730627	0.6749187	-2.892112	-3.567031	2	53	55.78947368	2	8	0.001794	1
Low Abundance	gi|6322434	0.00026	0.0002101	4	0.001112	0.000201	4	4.276923	0.6311314	-2.953895	-3.585027	2	51	53.68421053	2	5.5	0.001102	1
Low Abundance	gi|6325166	0.00026	2.008E-05	2	0.00031	0.000132	3	1.192308	0.0763883	-3.508638	-3.585027	2	52	54.73684211	1	3.333333	0.578646	0
Low Abundance	gi|6321721	0.000256	0.0001613	3	0.000741	5.43E-05	4	2.894531	0.4615782	-3.130182	-3.59176	2	50	52.63157895	2.666666667	4.25	0.02711	1
Low Abundance	gi|6321673	0.000252	3.779E-05	3	0.000635	8.96E-05	4	2.519841	0.4013732	-3.197226	-3.598599	2	49	51.57894737	3.333333333	3.5	0.001217	1
Low Abundance	gi|6323980	0.000251	0	1	0.000307	0.000283	2	1.223108	0.0874647	-3.512862	-3.600326	2	48	50.52631579	1	3.5		
Low Abundance	gi|6323209	0.000235	0.0001001	2	0.000289	0.000184	4	1.229787	0.08983	-3.539102	-3.628932	2	47	49.47368421	1.5	3.5	0.66455	0
Low Abundance	gi|6319471	0.000226	0	1	0.002137	2.27E-05	2	9.455752	0.9756961	-2.670195	-3.645892	2	46	48.42105263	2	1		
Low Abundance	gi|6322476	0.00022	0	1	0.000807	0.000502	4	3.668182	0.5644509	-3.093126	-3.657577	2	45	47.36842105	1	6.25		
Low Abundance	gi|6325292	0.000216	0.0001511	3	0.000442	0.000199	2	2.046296	0.3109685	-3.354578	-3.665546	2	44	46.31578947	2.666666667	2.5	0.317584	0
Low Abundance	gi|6319395	0.000199	8.669E-05	4	0.001229	0.000211	4	6.175879	0.7906988	-2.910448	-3.701147	2	43	45.26315789	5.75	18	0.000838	1
Low Abundance	gi|6322012	0.000188	0.0001907	2	0.001454	0.000301	4	7.734043	0.8884066	-2.837436	-3.725842	2	42	44.21052632	3.5	6.25	0.006013	1
Low Abundance	gi|6322722	0.000164	0	1	0.000301	0.000215	3	1.835366	0.2637226	-3.521434	-3.785156	2	41	43.15789474	2	3.666667		
Low Abundance	gi|6322294	0.000153	2.118E-05	2	0.000433	0.000223	4	2.830065	0.4517965	-3.363512	-3.815309	2	40	42.10526316	2.5	4.25	0.085623	0
Low Abundance	gi|6321643	0.000147	7.262E-05	2	0.00055	0.000216	4	3.741497	0.5730454	-3.259637	-3.832683	2	38	40	4	8.75	0.029216	1
Low Abundance	gi|6324250	0.000147	5.914E-05	2	0.000386	8.15E-05	3	2.62585	0.41927	-3.413413	-3.832683	2	39	41.05263158	2	3.333333	0.034889	1
Low Abundance	gi|6320077	0.000146	0.000116	3	0.000789	0.000411	4	5.40411	0.7327241	-3.102923	-3.835647	2	35	36.84210526	2	8	0.046687	1
Low Abundance	gi|8279524	0.000146	5.559E-05	3	0.001016	0.000144	4	1.171233	0.0686433	-3.767004	-3.835647	2	36	37.89473684	2.333333333	4	0.00035	1
Low Abundance	gi|6321837	0.000146	0.00016	2	0.000171	0.000124	4	6.958904	0.8425409	-2.993106	-3.835647	2	37	38.94736842	2	4	0.867931	0
Low Abundance	gi|6322815	0.000139	6.576E-07	2	0.000482	0.000377	4	3.467626	0.5400322	-3.316953	-3.856985	2	34	35.78947368	2	5	0.166266	0
Low Abundance	gi|6324804	0.000136	5.518E-05	4	0.00082	0.000437	4	6.029412	0.7802749	-3.086186	-3.866461	2	33	34.73684211	3.25	8.25	0.050681	0
Low Abundance	gi|6320861	0.000131	0	1	0.000176	6.55E-05	2	1.343511	0.1282414	-3.754487	-3.882729	2	32	33.68421053	2	2		
Low Abundance	gi|6322581	0.00013	7.319E-05	3	0.001183	0.00076	4	0.238462	-0.622582	-4.508638	-3.886057	1	1	0.662251656	3.333333333	9.75	0.068668	0
Low Abundance	gi|6319424	0.00013	5.777E-05	3	0.000031	9.7E-06	3	9.1	0.9590414	-2.927015	-3.886057	2	31	32.63157895	1	2.333333	0.093145	0
Low Abundance	gi|6321594	0.000126	7.388E-05	2	0.001043	0.000439	4	8.277778	0.9179138	-2.981716	-3.899629	2	30	31.57894737	2	8.5	0.02216	1
Low Abundance	gi|6323967	0.000125	0	1	0.000595	0.000185	4	4.76	0.677607	-3.225483	-3.90309	2	29	30.52631579	2	4.25		
Low Abundance	gi|1038376	0.00012	6.64E-05	3	0.000707	0.000157	4	5.891667	0.7702382	-3.150581	-3.920819	2	28	29.47368421	3	8.25	0.002059	1
Low Abundance	gi|6320432	0.000119	5.143E-05	3	0.001999	0.001074	4	16.79832	1.2252658	-2.699187	-3.924453	2	27	28.42105263	2.333333333	6.75	0.039224	1
Low Abundance	gi|6320560	0.000117	4.226E-05	2	0.001673	0.000958	4	14.29915	1.1553101	-2.776504	-3.931814	2	26	27.36842105	2	6.75	0.047241	1
Low Abundance	gi|6320839	0.000115	0	1	0.000819	0.000428	4	7.121739	0.8525861	-3.086716	-3.939302	2	25	26.31578947	2	6		
Low Abundance	gi|6323768	0.000108	0.0001282	3	0.001311	0.00045	4	13.36111	1.1258426	-2.840734	-3.966576	2	23	24.21052632	1.666666667	11.25	0.009219	1
Low Abundance	gi|6321619	0.000108	9.652E-06	2	0.001443	0.000627	4	12.13889	1.0841789	-2.882397	-3.966576	2	24	25.26315789	2	5.25	0.023656	1
Low Abundance	gi|6319597	0.000107	4.781E-05	2	0.001023	0.00017	4	9.560748	0.9804919	-2.990124	-3.970616	2	21	22.10526316	3	10	0.000777	1
Low Abundance	gi|6324321	0.000107	0	1	0.001313	0.000227	4	12.27103	1.0888809	-2.881735	-3.970616	2	22	23.15789474	2	6.5		
Low Abundance	gi|6325025	0.000105	4.233E-05	4	0.000768	0.000274	4	3.371429	0.527814	-3.450997	-3.978811	2	19	20	5.75	27.5	0.015549	1

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6321203	0.000105	9.663E-05	2	0.000354	8.5E-05	4	7.314286	0.8641719	-3.114639	-3.978811	2	20	21.05263158	1.5	8	0.100919	0
Low Abundance	gi|6320789	0.000097	0	1	0.000605	0.000411	4	6.237113	0.7949836	-3.218245	-4.013228	2	18	18.94736842	2	4.75		
Low Abundance	gi|6324601	0.000095	5.708E-05	4	0.000975	0.000208	4	10.26316	1.011281	-3.010995	-4.022276	2	17	17.89473684	2.5	8.75	0.002277	1
Low Abundance	gi|6319552	0.000089	0	1	0.000379	8.23E-06	4	4.258427	0.6292492	-3.421361	-4.05061	2	16	16.84210526	2	2.75		
Low Abundance	gi|6321236	0.000086	4.019E-05	3	0.001067	0.000381	4	12.40698	1.093666	-2.971836	-4.065502	2	15	15.78947368	2.666666667	6.75	0.013524	1
Low Abundance	gi|6320548	0.00008	0	1	0.000155	4.48E-05	3	1.9375	0.2872417	-3.809668	-4.09691	2	14	14.73684211	3	4		
Low Abundance	gi|6321498	0.000079	3.164E-05	3	0.000401	0.000278	4	5.075949	0.7055173	-3.396856	-4.102373	2	13	13.68421053	4	13	0.103074	0
Low Abundance	gi|6323509	0.000076	0	1	0.000954	0.000241	4	12.55263	1.0987348	-3.020452	-4.119186	2	12	12.63157895	3	5.75		
Low Abundance	gi|1431856	0.000059	0	1	0.000887	0.000513	4	15.0339	1.1770716	-3.052076	-4.229148	2	11	11.57894737	2	6.5		
Low Abundance	gi|6319695	0.000052	1.578E-05	2	0.000189	0.000115	4	3.634615	0.5604585	-3.723538	-4.283997	2	10	10.52631579	3	7.25	0.095597	0
Low Abundance	gi|6324709	0.000051	0	1	0.000661	0.000337	4	12.96078	1.1126313	-3.179799	-4.29243	2	9	9.473684211	2	3.75		
Low Abundance	gi|6321376	0.00005	1.998E-05	2	0.000158	9.27E-05	4	3.16	0.4996871	-3.801343	-4.30103	2	8	8.421052632	2.5	5.75	0.099523	0
Low Abundance	gi|6321429	0.000048	0	1	0.000377	0.000223	4	7.854167	0.8951001	-3.423659	-4.318759	2	6	6.315789474	2	5.75		
Low Abundance	gi|6321859	0.000048	0	1	0.000769	0.000394	3	16.02083	1.2046851	-3.114074	-4.318759	2	7	7.368421053	2	7		
Low Abundance	gi|6320019	0.000033	0	1	0.000677	0.000103	4	20.51515	1.3120747	-3.169411	-4.481486	2	4	4.210526316	2	4		
Low Abundance	gi|6320137	0.000033	0	1	0.000564	0.000328	4	17.09091	1.2327652	-3.248721	-4.481486	2	5	5.263157895	2	4.25		
Low Abundance	gi|6320071	0.000032	0	1	0.000606	0.000103	4	18.9375	1.2773226	-3.217527	-4.49485	2	3	3.157894737	2	3.5		
Low Abundance	gi|6319809	0.000028	0	1	0.000754	0.000481	4	26.92857	1.4302133	-3.122629	-4.552842	2	2	2.105263158	2	5		
Low Abundance	gi|6323335	0.000018	0	1	0.000507	0.00021	4	28.16667	1.4497355	-3.294992	-4.744727	2	1	1.052631579	2	6.75		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6321203	X	X	X	X	X	1	1	20	1.87	0.000174	X	X	X	X	X	2	2	3	5.86	3.7E-05
gi|6320789	X	X	X	X	X	X	X	X	X	X	2	2	4	8.01	9.7E-05	X	X	X	X	X
gi|6324601	2	2	2	3.9	3.96E-05	3	3	7	7.81	8.27E-05	3	3	11	7.81	0.000175	2	2	5	4.41	8.39E-05
gi|6319552	X	X	X	X	X	2	2	6	5.56	8.93E-05	X	X	X	X	X	X	X	X	X	X
gi|6321236	2	2	3	5.2	7E-05	2	2	4	5.4	5.57E-05	4	4	7	11.2	0.000131	X	X	X	X	X
gi|6320548	X	X	X	X	X	3	3	7	5.44	8.03E-05	X	X	X	X	X	X	X	X	X	X
gi|6321498	X	X	X	X	X	4	4	9	4.79	4.61E-05	3	3	12	2.8	8.29E-05	5	5	15	5.38	0.000109
gi|6323509	X	X	X	X	X	X	X	X	X	X	3	3	4	7.74	7.64E-05	X	X	X	X	X
gi|1431856	X	X	X	X	X	X	X	X	X	X	2	2	3	5.61	5.85E-05	X	X	X	X	X
gi|6319695	X	X	X	X	X	4	4	7	3.98	4.13E-05	2	2	8	2.03	6.36E-05	X	X	X	X	X
gi|6324709	X	X	X	X	X	X	X	X	X	X	2	2	2	7.32	5.09E-05	X	X	X	X	X
gi|6321376	X	X	X	X	X	3	3	6	3.06	3.55E-05	2	2	8	2.04	6.37E-05	X	X	X	X	X
gi|6321429	X	X	X	X	X	X	X	X	X	X	2	2	4	3.72	4.82E-05	X	X	X	X	X
gi|6321859	X	X	X	X	X	X	X	X	X	X	2	2	2	8.53	4.85E-05	X	X	X	X	X
gi|6320019	X	X	X	X	X	2	2	2	6.07	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320137	X	X	X	X	X	2	2	2	5.61	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320071	X	X	X	X	X	2	2	2	5.91	3.16E-05	X	X	X	X	X	X	X	X	X	X
gi|6319809	X	X	X	X	X	2	2	2	4.6	2.79E-05	X	X	X	X	X	X	X	X	X	X
gi|6323335	X	X	X	X	X	2	2	2	3.34	1.79E-05	X	X	X	X	X	X	X	X	X	X

Locus	DE60-1_P	DE60-1_uP	DE60-1_S	DE60-1_SC	DE60-1_NSAF	DE60-2_P	DE60-2_uP	DE60-2_S	DE60-2_SC	DE60-2_NSAF	DE60-3_P	DE60-3_uP	DE60-3_S	DE60-3_SC	DE60-3_NSAF	DE60-4_P	DE60-4_uP	DE60-4_S	DE60-4_SC	DE60-4_NSAF
gi|6321203	7	7	22	12.84	0.000455	6	6	16	10.47	0.000247	11	11	22	20.57	0.000349	8	8	20	12.84	0.000365
gi|6320789	7	7	27	21.71	0.001157	3	3	9	10.85	0.000288	4	4	9	14.21	0.000296	5	5	18	14.73	0.00068
gi|6324601	11	11	34	27.5	0.000958	9	9	60	18.68	0.001263	7	7	42	15.96	0.000908	8	8	31	17.49	0.000769
gi|6319552	3	3	11	8.55	0.00039	3	3	14	8.55	0.000371	3	3	14	8.55	0.000381	2	2	12	5.34	0.000375
gi|6321236	7	7	39	21.4	0.001294	5	5	20	11.6	0.000496	8	8	49	22.2	0.001249	7	7	42	20.2	0.001228
gi|6320548	5	5	7	13.51	0.000191	X	X	X	X	X	2	2	5	4.61	0.000105	5	5	7	10.21	0.000169
gi|6321498	20	20	58	22.53	0.000708	7	7	14	6.55	0.000128	10	10	22	9.5	0.000206	15	15	52	16.79	0.00056
gi|6323509	7	7	33	20.57	0.001115	3	3	33	8.76	0.000834	7	7	26	19.76	0.000675	6	6	40	17.72	0.001191
gi|1431856	9	9	42	29.73	0.001448	6	6	21	16.84	0.000541	5	5	14	16.63	0.000371	6	6	39	16.01	0.001185
gi|6319695	9	9	23	11.36	0.000323	3	3	4	3.81	4.2E-05	8	8	18	8.56	0.000194	9	9	16	11.1	0.000198
gi|6324709	6	6	22	26.02	0.000989	2	2	7	9.49	0.000235	3	3	25	14.63	0.000863	4	4	14	17.07	0.000555
gi|6321376	8	8	18	9.34	0.000253	2	2	3	2.8	3.16E-05	7	7	17	7.56	0.000184	6	6	13	6.62	0.000161
gi|6321429	9	9	30	13.86	0.000639	2	2	6	3.59	9.55E-05	6	6	22	11.55	0.00036	6	6	22	9.63	0.000413
gi|6321859	10	10	28	37.21	0.0012	X	X	X	X	X	4	4	13	11.63	0.000428	7	7	18	20.16	0.00068
gi|6320019	5	5	20	16.59	0.000775	4	4	26	14.72	0.000753	4	4	19	14.25	0.000566	3	3	18	10.75	0.000615
gi|6320137	6	6	23	19.86	0.000891	2	2	4	5.61	0.000116	5	5	19	15.42	0.000566	4	4	20	13.32	0.000683
gi|6320071	4	4	17	13.41	0.000641	4	4	26	14.32	0.000733	4	4	19	13.86	0.00055	2	2	15	7.73	0.000498
gi|6319809	7	7	28	21.4	0.000929	2	2	3	3.8	7.44E-05	4	4	32	12.4	0.000815	7	7	41	18.6	0.001199
gi|6323335	11	11	37	19.28	0.000789	5	5	23	8.23	0.000367	5	5	20	8.1	0.000328	6	6	29	10.41	0.000545

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Protein)
110	25.00%	4.1295	2.6545455	1.222393228	13.2176	3.736364	0.645056	0.000375	0.0012016				3.117424242	2.148485689	6.784090909	4.948618	50	61.73%

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE60-only	gi|6325097	0	0	0	0.000241	0.00012	4									6		
DE60-only	gi|3736267	0	0	0	0.000505	0.000327	4									5.25		
DE60-only	gi|9755335	0	0	0	0.000353	0.000193	4									6.75		
DE60-only	gi|6321412	0	0	0	0.000481	0.000298	4									6.25		
DE60-only	gi|6323056	0	0	0	0.000263	0.000125	4									4.75		
DE60-only	gi|6320242	0	0	0	0.0003	7.48E-05	4									2.25		
DE60-only	gi|6320764	0	0	0	0.000428	0.000452	4									4.25		
DE60-only	gi|6319326	0	0	0	0.000467	0.00016	4									3.75		
DE60-only	gi|1431849	0	0	0	0.000411	0.000151	4									4.75		
DE60-only	gi|6319564	0	0	0	0.00076	0.000429	4									3.25		
DE60-only	gi|6325151	0	0	0	0.000954	0.000162	4									7		
DE60-only	gi|6323873	0	0	0	0.000654	0.00016	4									6.5		
DE60-only	gi|6323179	0	0	0	0.001335	0.000519	4									4.5		
DE60-only	gi|6322331	0	0	0	0.000279	0.00017	4									16.75		
DE60-only	gi|6322531	0	0	0	0.000945	0.000701	4									4.25		
DE60-only	gi|6323332	0	0	0	0.000668	8.47E-05	4									4		
DE60-only	gi|6323570	0	0	0	0.000265	0.000178	4									4.75		
DE60-only	gi|6324580	0	0	0	0.000756	0.000205	4									5		
DE60-only	gi|6323882	0	0	0	0.001018	0.000566	4									5		
DE60-only	gi|6324225	0	0	0	0.000292	0.000209	4									4.5		
DE60-only	gi|6322765	0	0	0	0.000897	0.00058	4									5		
DE60-only	gi|6320935	0	0	0	0.000454	9.52E-05	4									4.25		
DE60-only	gi|6321332	0	0	0	0.001831	0.000557	4									3		
DE60-only	gi|6319370	0	0	0	0.000282	7.38E-05	4									3.75		
DE60-only	gi|6319931	0	0	0	0.000402	0.000215	4									4.75		
DE60-only	gi|6325421	0	0	0	0.000347	0.000239	4									3.5		
DE60-only	gi|6324258	0	0	0	0.000322	0.000146	4									3.25		
DE60-only	gi|6324682	0	0	0	0.000088	3.83E-05	4									2		
DE60-only	gi|6320896	0	0	0	0.000464	0.000102	4									3.5		
DE60-only	gi|1431850	0	0	0	0.000445	0.000132	4									3.75		
DE60-only	gi|6323746	0	0	0	0.000772	0.000376	4									5.5		
DE60-only	gi|6319351	0	0	0	0.000498	0.000121	4									1.75		
DE60-only	gi|6319698	0	0	0	0.000618	0.000261	4									5		
DE60-only	gi|6324594	0	0	0	0.001572	0.000674	4									3.25		
DE60-only	gi|6324291	0	0	0	0.000325	0.000146	4									3		
DE60-only	gi|6324702	0	0	0	0.000197	0.0001	4									4		
DE60-only	gi|6321427	0	0	0	0.000182	4.02E-05	4									2		
DE60-only	gi|6319509	0	0	0	0.000643	0.000347	4									2.5		
DE60-only	gi|6320078	0	0	0	0.001311	0.00033	4									1.25		
DE60-only	gi|6320941	0	0	0	0.000523	0.000228	4									2.25		
DE60-only	gi|6319646	0	0	0	0.000184	4.62E-05	4									1.75		
DE60-only	gi|4274231	0	0	0	0.000516	0.0002	4									2		
DE60-only	gi|6322639	0	0	0	0.000248	0.000143	3									6.333333		
DE60-only	gi|6324109	0	0	0	0.000441	7.74E-05	3									4.333333		
DE60-only	gi|6324371	0	0	0	0.000375	0.00015	3									3.333333		
DE60-only	gi|6323530	0	0	0	0.001077	0.000603	3									5		
DE60-only	gi|6320662	0	0	0	0.001712	0.000775	3									4		
DE60-only	gi|3736262	0	0	0	0.000425	0.000105	3									4.333333		
DE60-only	gi|6323089	0	0	0	0.000341	0.00019	3									4.666667		
DE60-only	gi|6320030	0	0	0	0.00007	2.96E-05	3									6		
DE60-only	gi|6322569	0	0	0	0.000059	4.04E-05	3									2.333333		
DE60-only	gi|6324378	0	0	0	0.000241	0.000158	3									2.666667		
DE60-only	gi|6325439	0	0	0	0.000127	9.15E-05	3									3.666667		
DE60-only	gi|6320788	0	0	0	0.000313	0.000314	3									3.333333		
DE60-only	gi|6324088	0	0	0	0.000138	5.18E-05	3									2		
DE60-only	gi|3736260	0	0	0	0.000928	0.000545	3									3		
DE60-only	gi|6320332	0	0	0	0.000077	7.72E-05	3									4		
DE60-only	gi|6323562	0	0	0	0.000633	8.81E-05	3									3.333333		
DE60-only	gi|6323246	0	0	0	0.000382	0.000214	3									3.333333		
DE60-only	gi|6324982	0	0	0	0.000336	0.000122	3									3		
DE60-only	gi|6323891	0	0	0	0.000178	3.24E-05	3									2.333333		
DE60-only	gi|6320576	0	0	0	0.00058	0.000262	3									3		
DE60-only	gi|2033676	0	0	0	0.000047	3.23E-06	3									2.333333		
DE60-only	gi|6324911	0	0	0	0.00012	6.87E-05	3									2.333333		
DE60-only	gi|6322896	0	0	0	0.000207	0.000112	3									2.666667		
DE60-only	gi|6320079	0	0	0	0.000481	0.000381	3									3		
DE60-only	gi|6320527	0	0	0	0.000231	0.000121	3									3		
DE60-only	gi|6324899	0	0	0	0.000328	0.000122	3									4		
DE60-only	gi|6320006	0	0	0	0.000059	1.91E-05	3									2		
DE60-only	gi|6323974	0	0	0	0.00032	5.84E-05	3									2.333333		
DE60-only	gi|6324950	0	0	0	0.000101	1.96E-05	3									2.333333		
DE60-only	gi|6321574	0	0	0	0.000303	4.93E-05	3									2		
DE60-only	gi|6321814	0	0	0	0.000287	0.000207	3									3		
DE60-only	gi|6321898	0	0	0	0.000714	0.000582	3									1.333333		
DE60-only	gi|6320798	0	0	0	0.000311	0.000241	3									3.666667		
DE60-only	gi|3736264	0	0	0	0.000171	6.49E-05	3									2		
DE60-only	gi|6321398	0	0	0	0.000212	0.000134	3									2.333333		
DE60-only	gi|6324993	0	0	0	0.00017	2.95E-05	3									2.333333		
DE60-only	gi|6321290	0	0	0	0.000248	5.47E-05	3									2.666667		
DE60-only	gi|6323182	0	0	0	0.00009	4.43E-05	3									2.666667		
DE60-only	gi|6321718	0	0	0	0.000394	0.00023	3									2.666667		
DE60-only	gi|6324772	0	0	0	0.000291	0.000161	3									2		
DE60-only	gi|6320899	0	0	0	0.00121	0.000352	3									2		
DE60-only	gi|8279525	0	0	0	0.000393	0.000352	3									2		
DE60-only	gi|6324273	0	0	0	0.000197	0.000102	3									2		
DE60-only	gi|6320917	0	0	0	0.000103	3.42E-05	3									2.333333		
DE60-only	gi|6325319	0	0	0	0.000375	0.000117	3									2		
DE60-only	gi|6322707	0	0	0	0.000617	0.000306	2									2.5		
DE60-only	gi|6319602	0	0	0	0.000322	0.000171	2									3.5		
DE60-only	gi|6324783	0	0	0	0.000159	1.55E-05	2									3		
DE60-only	gi|6320061	0	0	0	0.000032	9.18E-06	2									2		
DE60-only	gi|6322097	0	0	0	0.000213	7.82E-05	2									3.5		
DE60-only	gi|6324328	0	0	0	0.000132	5.77E-05	2									2.5		
DE60-only	gi|6319413	0	0	0	0.0003	0.000131	2									3		
DE60-only	gi|6321401	0	0	0	0.00031	0.000105	2									2.5		
DE60-only	gi|6323681	0	0	0	0.000484	0.000352	2									3		
DE60-only	gi|2780871	0	0	0	0.000121	6.74E-05	2									2.5		
DE60-only	gi|6319430	0	0	0	0.000625	0.000284	2									2.5		
DE60-only	gi|6320983	0	0	0	0.000208	1.85E-05	2									2		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6325097	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736267	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|9755335	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321412	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323056	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320242	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320764	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319326	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319564	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325151	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323873	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323179	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322331	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322531	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323570	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324580	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323882	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324225	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322765	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320935	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319370	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319931	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325421	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324258	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324682	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431850	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323746	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319351	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319698	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324594	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324291	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324702	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321427	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319509	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320078	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320941	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319646	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|4274231	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322639	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324109	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324371	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323530	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320662	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736262	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323089	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320030	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322569	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324378	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325439	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320788	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324088	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736260	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323562	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323246	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324982	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323891	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320576	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|2033676	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324911	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320079	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320527	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324899	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320006	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323974	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324950	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321574	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321814	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321898	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320798	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736264	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321398	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324993	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321290	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323182	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321718	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324772	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320899	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|8279525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324273	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320917	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325319	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322707	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319602	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324783	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320061	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322097	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324328	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319413	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321401	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323681	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|2780871	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319430	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320983	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Locus	DE60-1_P	DE60-1_uP	DE60-1_S	DE60-1_SC	DE60-1_NSAF	DE60-2_P	DE60-2_uP	DE60-2_S	DE60-2_SC	DE60-2_NSAF	DE60-3_P	DE60-3_uP	DE60-3_S	DE60-3_SC	DE60-3_NSAF	DE60-4_P	DE60-4_uP	DE60-4_S	DE60-4_SC	DE60-4_NSAF
gi|6325097	7	7	27	9.91	0.000411	6	6	21	9.08	0.000239	7	7	13	10.09	0.000152	4	4	12	5.14	0.000161
gi|3736267	8	8	23	25.12	0.000913	2	2	5	5.98	0.000148	5	5	12	15.79	0.000366	6	6	17	18.9	0.000595
gi|9755335	10	10	31	15.83	0.00055	3	3	16	4.06	0.000212	5	5	12	7.91	0.000164	9	9	31	14.55	0.000485
gi|6321412	11	11	37	22.49	0.000868	1	1	12	2.26	0.000211	4	4	16	9.05	0.000288	9	9	27	19.52	0.000558
gi|6323056	7	7	16	16.41	0.000449	3	3	9	6.77	0.000189	3	3	10	7.78	0.000216	6	6	8	13.2	0.000198
gi|6320242	3	3	14	7.45	0.000393	2	2	10	4.74	0.00021	2	2	14	5.41	0.000302	2	2	12	5.41	0.000297
gi|6320764	8	8	32	27.02	0.00107	2	2	3	6.25	7.5E-05	3	3	6	9.07	0.000154	4	4	14	10.89	0.000413
gi|6319326	5	5	13	25.82	0.000705	3	3	9	12.75	0.000365	4	4	10	16.01	0.000416	3	3	8	14.38	0.000382
gi|1431849	4	4	14	12.72	0.000462	3	3	9	8.15	0.000222	6	6	15	14.71	0.00038	6	6	20	16.9	0.000581
gi|6319564	3	3	19	18.22	0.001222	2	2	4	12.79	0.000192	4	4	18	23.26	0.000889	4	4	13	22.09	0.000737
gi|6325151	9	9	34	19.19	0.000814	5	5	66	11.11	0.001181	7	7	52	13.85	0.000956	7	7	41	12.99	0.000865
gi|6323873	7	7	27	19.24	0.000853	6	6	28	14.67	0.000661	6	6	19	14.48	0.000461	7	7	23	19.05	0.000641
gi|6323179	4	4	25	24.54	0.001519	5	5	22	27.11	0.000999	4	4	18	24.18	0.00084	5	5	37	27.11	0.001981
gi|6322331	23	23	63	15.67	0.000472	7	7	18	4.34	0.000101	16	16	31	10.25	0.000178	21	21	55	13.69	0.000363
gi|6322531	5	5	35	25.54	0.001786	3	3	9	14.46	0.000343	4	4	10	16.62	0.000392	5	5	28	23.38	0.00126
gi|6323332	4	4	10	25.41	0.00068	3	3	12	18.03	0.00061	4	4	15	21.72	0.000783	5	5	10	30.33	0.000599
gi|6323570	8	8	18	21.58	0.000511	2	2	4	3.94	8.5E-05	4	4	11	9.93	0.00024	5	5	9	11.3	0.000225
gi|6324580	7	7	22	25.14	0.001055	5	5	20	19.08	0.000717	3	3	18	12.72	0.000663	5	5	14	19.94	0.000592
gi|6323882	7	7	28	32.21	0.00174	2	2	9	8.99	0.000418	6	6	16	26.97	0.000763	5	5	21	24.72	0.00115
gi|6324225	5	5	21	13.73	0.000563	3	3	3	5.65	6.01E-05	5	5	15	13.09	0.000309	5	5	10	13.57	0.000236
gi|6322765	6	6	30	29.04	0.00149	3	3	5	14.37	0.000186	5	5	18	23.95	0.000687	6	6	28	26.65	0.001226
gi|6320935	5	5	16	13.61	0.000523	3	3	15	8.88	0.000367	3	3	15	9.66	0.000377	6	6	19	15.19	0.000548
gi|6321332	3	3	19	34.9	0.002115	3	3	12	25.5	0.000999	3	3	24	34.9	0.002052	3	3	22	34.9	0.002159
gi|6319370	4	4	9	9.36	0.000274	3	3	8	7.34	0.000182	4	4	15	9.72	0.000351	4	4	12	9.54	0.000322
gi|6319931	6	6	23	14.53	0.000644	3	3	9	7.43	0.000189	5	5	12	10.81	0.000258	5	5	21	11.66	0.000519
gi|6325421	5	5	13	14.22	0.000495	2	2	4	6.65	0.000114	3	3	6	9.17	0.000175	4	4	18	11.47	0.000604
gi|6324258	4	4	12	12.66	0.000413	2	2	5	6.64	0.000129	3	3	11	8.51	0.000291	4	4	15	12.66	0.000455
gi|6324682	2	2	4	4.8	0.00011	2	2	2	3.31	4.11E-05	2	2	6	4.8	0.000127	2	2	3	5.79	7.26E-05
gi|6320896	4	4	11	17.17	0.000614	3	3	10	12.12	0.000418	4	4	10	16.16	0.000429	3	3	8	13.13	0.000394
gi|1431850	5	5	15	15.23	0.000499	2	2	10	7.01	0.000249	4	4	21	11.82	0.000536	4	4	17	11.82	0.000498
gi|6323746	7	7	21	29.29	0.001173	3	3	7	14.14	0.000292	5	5	16	21.21	0.000686	7	7	19	26.26	0.000935
gi|6319351	2	2	15	6.85	0.000533	1	1	15	4.5	0.000398	2	2	24	6.85	0.000655	2	2	13	6.85	0.000407
gi|6319698	7	7	12	28.69	0.000544	2	2	12	9.84	0.000407	5	5	15	19.67	0.000522	6	6	25	24.59	0.000999
gi|6324594	4	4	15	53.77	0.002347	2	2	9	29.25	0.001053	3	3	16	44.34	0.001923	4	4	7	53.77	0.000965
gi|6324291	6	6	11	25.28	0.000507	2	2	11	7.78	0.000379	2	2	6	7.78	0.000212	2	2	5	8.61	0.000203
gi|6324702	3	3	6	8.58	0.000174	2	2	3	4.38	6.52E-05	6	6	12	14.89	0.000268	5	5	11	13.13	0.000282
gi|6321427	2	2	3	9.92	0.000197	2	2	3	8.73	0.000148	2	2	3	9.52	0.000152	2	2	4	8.73	0.000232
gi|6319509	3	3	15	19.74	0.001091	2	2	5	14.47	0.000272	2	2	9	14.47	0.000503	3	3	11	19.74	0.000705
gi|6320078	2	2	10	17.72	0.00105	1	1	13	10.13	0.00102	1	1	21	10.13	0.001693	1	1	16	10.13	0.001481
gi|6320941	2	2	8	16.59	0.000647	2	2	3	13.66	0.000182	3	3	10	19.02	0.000621	2	2	9	16.59	0.000642
gi|6319646	2	2	8	3.9	0.000191	1	1	10	1.73	0.000179	2	2	13	2.89	0.000239	2	2	6	2.89	0.000127
gi|4274231	2	2	6	17.88	0.000659	2	2	3	17.88	0.000246	2	2	8	17.88	0.000675	2	2	5	17.88	0.000484
gi|6322639	9	9	25	16.02	0.000405	X	X	X	X	X	5	5	10	6.84	0.000124	5	5	15	8.4	0.000214
gi|6324109	5	5	13	16.86	0.000498	X	X	X	X	X	4	4	12	14.09	0.000353	4	4	14	14.09	0.000473
gi|6324371	4	4	13	16.16	0.000545	X	X	X	X	X	2	2	10	8.59	0.000322	4	4	7	15.15	0.000258
gi|6323530	5	5	21	30.97	0.001541	X	X	X	X	X	3	3	7	15.93	0.000395	7	7	20	41.59	0.001294
gi|6320662	4	4	24	37.43	0.002129	X	X	X	X	X	4	4	12	31.55	0.000818	4	4	28	28.34	0.002189
gi|3736262	4	4	9	11.43	0.000305	X	X	X	X	X	5	5	19	12.04	0.000494	4	4	16	11.02	0.000477
gi|6323089	6	6	19	15.8	0.00053	X	X	X	X	X	2	2	7	4.2	0.00015	6	6	14	13.28	0.000344
gi|6320030	6	6	11	4.38	8.51E-05	X	X	X	X	X	4	4	6	2.89	3.56E-05	8	8	13	5.45	8.86E-05
gi|6322569	2	2	7	4.11	0.000104	X	X	X	X	X	3	3	4	4.2	4.56E-05	2	2	2	3.4	2.62E-05
gi|6324378	3	3	10	10.99	0.000372	X	X	X	X	X	3	3	10	8.97	0.000286	2	2	2	8.07	6.56E-05
gi|6325439	5	5	10	9.77	0.000216	X	X	X	X	X	2	2	2	3.91	3.32E-05	4	4	7	8.59	0.000133
gi|6320788	5	5	19	13.62	0.000671	X	X	X	X	X	2	2	3	7.45	8.13E-05	3	3	6	8.51	0.000187
gi|6324088	2	2	6	7.33	0.000197	X	X	X	X	X	2	2	4	5.15	0.000101	2	2	4	5.15	0.000116
gi|3736260	3	3	15	20.59	0.001464	X	X	X	X	X	3	3	5	20.59	0.000375	3	3	11	20.59	0.000946
gi|6320332	3	3	4	2.83	4.18E-05	X	X	X	X	X	2	2	3	1.83	2.41E-05	7	7	18	5.54	0.000166
gi|6323562	4	4	6	28.57	0.000547	X	X	X	X	X	3	3	9	19.78	0.00063	3	3	9	19.78	0.000723
gi|6323246	5	5	12	18.06	0.000537	X	X	X	X	X	2	2	4	8.09	0.000137	3	3	12	11.59	0.000473
gi|6324982	3	3	8	11.08	0.000408	X	X	X	X	X	2	2	5	8.31	0.000196	4	4	9	12	0.000405
gi|6323891	2	2	4	7.86	0.000163	X	X	X	X	X	2	2	5	7.86	0.000157	3	3	6	11.3	0.000216
gi|6320576	4	4	16	21.47	0.000851	X	X	X	X	X	2	2	8	13.14	0.000327	3	3	12	18.27	0.000562
gi|2033676	3	3	5	1.99	4.73E-05	X	X	X	X	X	2	2	6	1.31	4.36E-05	2	2	6	1.31	5E-05
gi|6324911	2	2	4	3.76	6.93E-05	X	X	X	X	X	3	3	7	4.18	9.31E-05	2	2	13	2.92	0.000198
gi|6322896	X	X	X	X	X	2	2	4	14.76	0.000183	4	4	7	20.3	0.000329	2	2	2	11.44	0.000108
gi|6320079	4	4	17	19.55	0.000904	X	X	X	X	X	2	2	4	8.97	0.000163	3	3	8	12.82	0.000375
gi|6320527	3	3	6	9.19	0.000261	2	2	3	7.61	9.77E-05	4	4	10	13.12	0.000334	X	X	X	X	X
gi|6324899	3	3	12	11.62	0.000437	X	X	X	X	X	4	4	7	14.04	0.000196	5	5	11	17.54	0.000353
gi|6320006	2	2	6	2.67	7.82E-05	X	X	X	X	X	2	2	4	2.67	4E-05	2	2	5	2.67	5.74E-05
gi|6323974	X	X	X	X	X	2	2	5	12.39	0.000265	3	3	7	14.96	0.000381	2	2	5	12.82	0.000312
gi|6324950	2	2	3	5.01	9.59E-05	X	X	X	X	X	3	3	5	7.51	0.000123	2	2	3	5.39	8.45E-05
gi|6321574	2	2	5	12.02	0.000321	X	X	X	X	X	2	2	5	5.81	0.000247	2	2	6	12.02	0.00034
gi|6321814	5	5	11	21.57	0.000511	2	2	3	5.32	0.000104	X	X	X	X	X	2	2	6	6.72	0.000246
gi|6321898	2	2	25	14.04	0.001213	X	X	X	X	X	1	1	2	7.6	7.45E-05	1	1	20	7.6	0.000855
gi|6320798	6	6	14	23.62	0.000583	X	X	X	X	X	2	2	4	7.04	0.000128	3	3	6	12.81	0.00022
gi|3736264	2	2	3	5.95	0.000118	X	X	X	X	X	2	2	5	6.43	0.000152	2	2	7	5.24	0.000244
gi|6321398	3	3	7	12.57	0.00034	2	2	2	8.48	7.25E-05	2	2	6	8.48	0.000224	X	X	X	X	X
gi|6324993	2	2	6	5.53	0.000204	X	X	X	X	X	2	2	6	5.74	0.000157	3	3	5	8.2	0.00015
gi|6321290	4	4	7	13.83	0.000309	2	2	7	6.65	0.000231	2	2	6	6.65	0.000203	X	X	X	X	X
gi|6323182	3	3	4	6.88	9.72E-05	X	X	X	X	X	3	3	7	7.03	0.000131	2	2	2	3.37	4.28E-05
gi|6321718	4	4	13	16.32	0.000559	X	X	X	X	X	2	2	4	8.55	0.000132	2	2	13	8.55	0.000492
gi|6324772	2	2	11	6.81	0.000388	2	2	4	6.81	0.000106	2	2	14	6.81	0.000379	X	X	X	X	X
gi|6320899	X	X	X	X	X	2	2	12	23.26	0.001154	3	3	9	30.23	0.000889	1	1	14	13.95	0.001587
gi|8279525	2	2	12	16.06	0.000799	X	X	X	X	X	2	2	4	10.44	0.000205	2	2	3	16.06	0.000176
gi|6324273	2	2	5	10.25	0.000293	X	X	X	X	X	2	2	2	10.25	9E-05	2	2	4	8.48	0.000207
gi|6320917	2	2	3	6.15	9.57E-05	X	X	X	X	X	2	2	3	6.15	7.35E-05	3	3	5	8.46	0.000141
gi|6325319	2	2	4	18.99	0.00042	X	X	X	X	X	2	2	3	17.72	0.000242	2	2	5	17.72	0.000463
gi|6322707	3	3	11	21.46	0.000833	X	X	X	X	X	X	X	X	X	X	2	2	6	15.98	0.000401
gi|6319602	2	2	6	4.85	0.000201	X	X	X	X	X	X	X	X	X	X	5	5	15	12.53	0.000443
gi|6324783	X	X	X	X	X	X	X	X	X	X	2	2	5	6.76	0.000148	4	4	5	14.69	0.00017
gi|6320061	2	2	4	1.9	3.83E-05	X	X	X	X	X	X	X	X	X	X	2	2	3	1.38	2.53E-05
gi|6322097	3	3	6	9.97	0.000268	X	X	X	X	X	X	X	X	X	X	4	4	4	15.09	0.000158
gi|6324328	3	3	5	7.93	0.000173	X	X	X	X	X	X	X	X	X	X	2	2	3	4.8	9.16E-05
gi|6319413	4	4	10	16.31	0.000392	X	X	X	X	X	X	X	X	X	X	2	2	6	6.86	0.000207
gi|6321401	3	3	5	21.76	0.000384	X	X	X	X	X	2	2	4	7.87	0.000236	X	X	X	X	X
gi|6323681	3	3	11	16.06	0.000733	X	X	X	X	X	X	X	X	X	X	3	3	4	16.06	0.000235
gi|2780871	2	2	2	6.83	7.31E-05	X	X	X	X	X	3	3	6	9.25	0.000168	X	X	X	X	X
gi|6319430	3	3	12	14.11	0.000826	X	X	X	X	X	X	X	X	X	X	2	2	7	14.11	0.000425
gi|6320983	2	2	6	7.32	0.000221	X	X	X	X	X	X	X	X	X	X	2	2	6	7.32	0.000195

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE60-only	gi|6322426	0	0	0	0.000101	3.94E-05	2									2		
DE60-only	gi|6323958	0	0	0	0.000252	0.000195	2									3		
DE60-only	gi|6320235	0	0	0	0.000264	0.0001	2									2		
DE60-only	gi|6324669	0	0	0	0.000203	7.71E-05	2									2.5		
DE60-only	gi|6321829	0	0	0	0.00062	0.000152	2									2.5		
DE60-only	gi|6321606	0	0	0	0.000258	9.89E-05	2									3.5		
DE60-only	gi|6322116	0	0	0	0.000125	2.32E-05	2									2		
DE60-only	gi|6321004	0	0	0	0.00016	0.00012	2									2.5		
DE60-only	gi|6322633	0	0	0	0.000387	0.000349	2									2.5		
DE60-only	gi|6322667	0	0	0	0.000079	1.49E-05	2									2		
DE60-only	gi|6323752	0	0	0	0.000083	8.82E-06	2									2		
DE60-only	gi|6325337	0	0	0	0.000176	5.79E-05	2									2.5		
DE60-only	gi|6324696	0	0	0	0.00069	0.000141	2									2		
DE60-only	gi|1431848	0	0	0	0.000155	3.78E-05	2									2.5		
DE60-only	gi|1431857	0	0	0	0.000238	0.000104	2									2		
DE60-only	gi|1431852	0	0	0	0.000087	7.8E-06	2									2		
DE60-only	gi|6320849	0	0	0	0.000571	7.89E-05	2									1.5		
DE60-only	gi|6325220	0	0	0	0.000993	8.74E-05	2									1.5		
DE60-only	gi|6324886	0	0	0	0.000575	0.000216	2									1		
DE60-only	gi|6324511	0	0	0	0.000072	7.19E-06	2									2		
DE60-only	gi|6325273	0	0	0	0.000239	4.44E-05	2									2		
DE60-only	gi|6321430	0	0	0	0.000064	0	1									3		
DE60-only	gi|6319568	0	0	0	0.000497	0	1									4		
DE60-only	gi|6323739	0	0	0	0.000405	0	1									5		
DE60-only	gi|6320175	0	0	0	0.00013	0	1									3		
DE60-only	gi|6319793	0	0	0	0.000047	0	1									2		
DE60-only	gi|6320066	0	0	0	0.000434	0	1									2		
DE60-only	gi|6319725	0	0	0	0.00015	0	1									2		
DE60-only	gi|6320930	0	0	0	0.000155	0	1									3		
DE60-only	gi|6322770	0	0	0	0.000112	0	1									2		
DE60-only	gi|6323331	0	0	0	0.000296	0	1									2		
DE60-only	gi|6323669	0	0	0	0.000176	0	1									3		
DE60-only	gi|6320372	0	0	0	0.000066	0	1									2		
DE60-only	gi|6323547	0	0	0	0.000398	0	1									4		
DE60-only	gi|6321896	0	0	0	0.000203	0	1									2		
DE60-only	gi|6324716	0	0	0	0.000353	0	1									3		
DE60-only	gi|6320249	0	0	0	0.000253	0	1									3		
DE60-only	gi|6324761	0	0	0	0.000114	0	1									2		
DE60-only	gi|6322049	0	0	0	0.000094	0	1									3		
DE60-only	gi|6324318	0	0	0	0.000413	0	1									3		
DE60-only	gi|6324725	0	0	0	0.000054	0	1									2		
DE60-only	gi|6324535	0	0	0	0.000301	0	1									2		
DE60-only	gi|6322845	0	0	0	0.000309	0	1									2		
DE60-only	gi|6321807	0	0	0	0.000138	0	1									2		
DE60-only	gi|6321217	0	0	0	0.00023	0	1									2		
DE60-only	gi|6324283	0	0	0	0.000074	0	1									2		
DE60-only	gi|6321776	0	0	0	0.000091	0	1									2		
DE60-only	gi|6322746	0	0	0	0.000161	0	1									3		
DE60-only	gi|6320440	0	0	0	0.000072	0	1									2		
DE60-only	gi|1431857	0	0	0	0.000107	0	1									2		
DE60-only	gi|6324475	0	0	0	0.000102	0	1									2		
DE60-only	gi|6319321	0	0	0	0.000047	0	1									2		
DE60-only	gi|6322843	0	0	0	0.000141	0	1									2		
DE60-only	gi|6322459	0	0	0	0.000309	0	1									2		
DE60-only	gi|6322244	0	0	0	0.000129	0	1									2		
DE60-only	gi|1038375	0	0	0	0.000207	0	1									3		
DE60-only	gi|6323383	0	0	0	0.000171	0	1									2		
DE60-only	gi|6319527	0	0	0	0.000139	0	1									3		
DE60-only	gi|6322525	0	0	0	0.00017	0	1									3		
DE60-only	gi|6320009	0	0	0	0.000323	0	1									2		
DE60-only	gi|6324195	0	0	0	0.000117	0	1									2		
DE60-only	gi|6320809	0	0	0	0.000464	0	1									2		
DE60-only	gi|6322261	0	0	0	0.000056	0	1									2		
DE60-only	gi|6322754	0	0	0	0.00016	0	1									2		
DE60-only	gi|6323229	0	0	0	0.001019	0	1									2		
DE60-only	gi|6321195	0	0	0	0.000367	0	1									2		
DE60-only	gi|6323511	0	0	0	0.000149	0	1									2		
DE60-only	gi|6320777	0	0	0	0.00006	0	1									2		
DE60-only	gi|6320393	0	0	0	0.000061	0	1									2		
DE60-only	gi|6320240	0	0	0	0.00009	0	1									2		
DE60-only	gi|6323286	0	0	0	0.000278	0	1									2		
DE60-only	gi|6321692	0	0	0	0.000169	0	1									2		
DE60-only	gi|4274228	0	0	0	0.000032	0	1									2		
DE60-only	gi|6320966	0	0	0	0.000136	0	1									2		
DE60-only	gi|6321809	0	0	0	0.000607	0	1									2		
DE60-only	gi|6325198	0	0	0	0.000332	0	1									3		
DE60-only	gi|6320914	0	0	0	0.000075	0	1									3		
DE60-only	gi|6325017	0	0	0	0.000166	0	1									2		
DE60-only	gi|6322529	0	0	0	0.000129	0	1									2		
DE60-only	gi|6320100	0	0	0	0.00007	0	1									2		
DE60-only	gi|1431852	0	0	0	0.000108	0	1									2		
DE60-only	gi|6322288	0	0	0	0.000313	0	1									2		
DE60-only	gi|1462717	0	0	0	0.000022	0	1									2		
DE60-only	gi|6321601	0	0	0	0.00004	0	1									2		
DE60-only	gi|6319587	0	0	0	0.000253	0	1									2		
DE60-only	gi|6322446	0	0	0	0.000062	0	1									2		
DE60-only	gi|6322303	0	0	0	0.000168	0	1									2		
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**		
186	**42.27%**				**6.3281**	**2.33871**	**1.180154**		**0.0003402**						**2.938172043**	**1.549237**		

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE60 NSAF AVG	DE60 NSAF STD	DE60 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE60	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE60 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
noDE-only	gi|6325407	0.004077	0.0018869	4	0	0	0								1			
noDE-only	gi|6323886	0.00243	0.0004677	3	0	0	0								2.333333333			
noDE-only	gi|6322082	0.000173	7.442E-05	3	0	0	0								1			
noDE-only	gi|1431855	0.002198	0.0009394	2	0	0	0								1			
noDE-only	gi|6321474	0.00093	0.0008341	2	0	0	0								1			
noDE-only	gi|6320142	0.002178	0	1	0	0	0								1			
noDE-only	gi|6320860	0.000294	0	1	0	0	0								1			
noDE-only	gi|6320205	0.000208	0	1	0	0	0								2			
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**		
8	**1.82%**	**1.2488**	**2.125**	**1.125991626**				**0.001561**					**1.291666667**	**0.547360187**				

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE60-1_P	DE60-1_uP	DE60-1_S	DE60-1_SC	DE60-1_NSAF	DE60-2_P	DE60-2_uP	DE60-2_S	DE60-2_SC	DE60-2_NSAF	DE60-3_P	DE60-3_uP	DE60-3_S	DE60-3_SC	DE60-3_NSAF	DE60-4_P	DE60-4_uP	DE60-4_S	DE60-4_SC	DE60-4_NSAF
gi|6322426	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	4.55	7.3E-05	X	X	X	X	X	X	X	X	X	X	2	2	6	4.84	0.000129
gi|6323958	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	12	12.16	0.00039	X	X	X	X	X	X	X	X	X	X	2	2	4	7.06	0.000115
gi|6320235	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	19.7	0.000335	X	X	X	X	X	2	2	3	16.67	0.000193	X	X	X	X	X
gi|6324669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	16.67	0.000257	X	X	X	X	X	2	2	3	11.63	0.000148	X	X	X	X	X
gi|6321829	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	12.28	0.000728	X	X	X	X	X	X	X	X	X	X	3	3	4	21.93	0.000513
gi|6321606	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	6	23.18	0.000328	3	3	3	16.31	0.000188
gi|6322116	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.61	0.000141	X	X	X	X	X	2	2	4	4.9	0.000109	X	X	X	X	X
gi|6321004	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	10.65	0.000245	X	X	X	X	X	2	2	2	6.51	7.54E-05	X	X	X	X	X
gi|6322633	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	12	17.52	0.000634	X	X	X	X	X	X	X	X	X	X	2	2	3	14.65	0.00014
gi|6322667	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.85	8.95E-05	2	2	2	5.85	6.85E-05
gi|6323752	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.04	8.96E-05	2	2	3	4.04	7.71E-05
gi|6325337	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	9.39	0.000217	2	2	5	4.15	0.000135	X	X	X	X	X	X	X	X	X	X
gi|6324696	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	19.05	0.00079	2	2	6	19.05	0.000591	X	X	X	X	X	X	X	X	X	X
gi|1431848	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	8.1	0.000181	X	X	X	X	X	X	X	X	X	X	2	2	4	5.47	0.000128
gi|1431857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	13.16	0.000312	X	X	X	X	X	X	X	X	X	X	2	2	3	13.16	0.000165
gi|1431852	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.17	9.3E-05	X	X	X	X	X	X	X	X	X	X	2	2	3	6.17	8.2E-05
gi|6320849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	10	7.58	0.000626	2	2	8	13.13	0.000515	X	X	X	X	X
gi|6325220	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	13	12.1	0.001055	1	1	10	12.1	0.000931
gi|6324886	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	13	2.15	0.000422	1	1	30	2.15	0.000728	X	X	X	X	X	X	X	X	X	X
gi|6324511	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.06	6.69E-05	X	X	X	X	X	2	2	3	8.06	7.71E-05	X	X	X	X	X
gi|6325273	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	12.24	0.000271	X	X	X	X	X	2	2	4	11.43	0.000208	X	X	X	X	X
gi|6321430	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	6.1	6.37E-05
gi|6319568	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	14	13.7	0.000497	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323739	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	15	16.91	0.000405	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320175	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	11	0.00013	X	X	X	X	X
gi|6319793	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.63	4.66E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320066	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	15.35	0.000434
gi|6319725	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	4.35	0.00015	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320930	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	7.81	0.000155	X	X	X	X	X
gi|6322770	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	8.67	0.000112
gi|6323331	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	9.15	0.000296	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	11.28	0.000176	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320372	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.32	6.56E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323547	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	6	23.2	0.000398	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.87	0.000203	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324716	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	17.93	0.000353	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320249	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	10.06	0.000253	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324761	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.86	0.000114	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322049	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	3	8.35	9.44E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324318	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	21.99	0.000413	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324725	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	3.59	5.42E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324535	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	13.39	0.000301	X	X	X	X	X
gi|6322845	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	12.31	0.000309	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321807	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	4.87	0.000138	X	X	X	X	X
gi|6321217	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	14.93	0.00023	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324283	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.26	7.42E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321776	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	9.38	9.14E-05
gi|6322746	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	8.75	0.000161	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320440	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.19	7.18E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	10.22	0.000107
gi|6324475	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.56	0.000102
gi|6319321	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.67	4.71E-05
gi|6322843	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	14.41	0.000141	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322459	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	12.09	0.000309	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322244	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	13.64	0.000129	X	X	X	X	X
gi|1038375	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	18.07	0.000207	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323383	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	10.65	0.000171	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319527	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	3	15.64	0.000139	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	7.35	0.00017	X	X	X	X	X
gi|6320009	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	13.26	0.000323
gi|6324195	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	8.51	0.000117
gi|6320809	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	20.63	0.000464
gi|6322261	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.3	5.56E-05
gi|6322754	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	11.72	0.00016	X	X	X	X	X
gi|6323229	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	7	28.07	0.001019	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321195	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	25.41	0.000367	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323511	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.09	0.000149	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320777	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.64	5.96E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320393	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.79	6.08E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320240	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.57	8.97E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323286	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	7	12.77	0.000278	X	X	X	X	X
gi|6321692	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	10	0.000169
gi|4274228	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2.73	3.23E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320966	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	11.89	0.000136	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321809	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	18.29	0.000607	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325198	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	3	30.67	0.000332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320914	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	5.18	7.47E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325017	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	14.5	0.000166	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322529	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	14.21	0.000129	X	X	X	X	X
gi|6320100	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.13	6.96E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431852	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.82	0.000108	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322288	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	27.05	0.000313	X	X	X	X	X
gi|1462717	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	1.99	2.2E-05	X	X	X	X	X
gi|6321601	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.47	4.02E-05	X	X	X	X	X
gi|6319587	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.69	0.000253
gi|6322446	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.99	6.21E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322303	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.05	0.000168	X	X	X	X	X
gi|6325407	1	1	55	5.78	0.003711	1	1	39	5.78	0.001569	1	1	97	5.78	0.005261	1	1	101	5.78	0.005768	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323886	2	2	17	24.76	0.00189	3	3	41	38.1	0.002718	2	2	30	30.48	0.002681	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322082	X	X	X	X	X	1	1	21	1.62	0.000158	1	1	25	1.62	0.000253	1	1	10	1.62	0.000107	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431855	X	X	X	X	X	1	1	13	13.56	0.001534	1	1	18	13.56	0.002862	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321474	X	X	X	X	X	1	1	19	13.79	0.00152	X	X	X	X	X	1	1	3	25.29	0.000341	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320142	X	X	X	X	X	X	X	X	X	X	1	1	13	17.86	0.002178	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320860	X	X	X	X	X	1	1	29	1.46	0.000294	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320205	X	X	X	X	X	2	2	6	15.92	0.000208	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Supporting Table 2C: Proteins detected in noDE and/or DE90 replicates

Proteins detected in both DE conditions were sorted into two groups of high and low abundances based on their averaged NSAF values measured when DE was turned off (noDE NSAF AVG).
Averages ("AVG") and standard deviations ("STD") were calculated for NSAF values and Peptide counts across the 4 replicates of a DE condition.
t-test p-values were calculated using the TTEST function in MSExcel (NSAF t-test p-Value).

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6321631	0.089245	0.03073	4	0.049066	0.020317	4	0.54979	-1.309219	-1.04942	-0.2598	1	155	100	26.5	23	0.078862	0
High Abundance	gi|6322468	0.056902	0.011085	4	0.026724	0.01394	4	0.46965	-1.573099	-1.24487	-0.32823	1	154	99.3548387	20.25	19	0.015859	1
High Abundance	gi|6321968	0.054496	0.010495	4	0.038258	0.008834	4	0.702033	-1.417278	-1.26364	-0.15364	1	153	98.7096774	21.25	24	0.056943	0
High Abundance	gi|1038378	0.040924	0.00377	4	0.032923	0.004103	4	0.804491	-1.482501	-1.38802	-0.09448	1	152	98.0645161	26.5	31	0.028582	1
High Abundance	gi|6319279	0.039967	0.008049	4	0.015633	0.002258	4	0.391148	-1.805958	-1.3983	-0.40766	1	151	97.4193548	28.75	38.5	0.006665	1
High Abundance	gi|6322697	0.037728	0.004085	4	0.010066	0.001006	4	0.266804	-1.997143	-1.42334	-0.57381	1	150	96.7741935	12	12.75	0.000523	1
High Abundance	gi|6323073	0.035041	0.005287	4	0.01262	0.000848	4	0.36015	-1.898941	-1.45542	-0.44352	1	149	96.1290323	26	28.5	0.002951	1
High Abundance	gi|6322790	0.030639	0.005672	4	0.034563	0.012421	4	1.128072	-1.461389	-1.51373	0.052337	1	148	95.483871	12.75	15.25	0.594854	0
High Abundance	gi|6321693	0.029306	0.007833	4	0.023558	0.008265	4	0.803863	-1.627862	-1.53304	-0.09482	1	147	94.8387097	14	18.25	0.351832	0
High Abundance	gi|6322409	0.028438	0.009301	4	0.017402	0.014825	4	0.611928	-1.759401	-1.5461	-0.2133	1	146	94.1935484	9.75	13.5	0.262412	0
High Abundance	gi|6324486	0.020489	0.004948	4	0.008341	0.001307	4	0.407096	-2.078782	-1.68848	-0.3903	1	145	93.5483871	13.75	14	0.013137	1
High Abundance	gi|6320255	0.016329	0.005011	4	0.023843	0.01801	4	1.460163	-1.622639	-1.78704	0.164401	1	144	92.9032258	9.75	11	0.472995	0
High Abundance	gi|6321464	0.016263	0.010451	4	0.003312	0.000507	4	0.203652	-2.47991	-1.7888	-0.69111	1	143	92.2580645	2.5	3.75	0.089228	0
High Abundance	gi|9755341	0.015824	0.002579	4	0.004842	0.000938	4	0.305991	-2.314975	-1.80068	-0.51429	1	142	91.6129032	5	5.5	0.00167	1
High Abundance	gi|6320359	0.013516	0.001583	4	0.005246	0.000452	4	0.388133	-2.280172	-1.86915	-0.41102	1	141	90.9677419	5.75	6	0.001074	1
High Abundance	gi|6323138	0.013418	0.003594	4	0.00608	0.000531	4	0.453123	-2.216096	-1.87231	-0.34378	1	140	90.3225806	5.5	5.5	0.025189	1
High Abundance	gi|6323196	0.013086	0.004083	4	0.005117	0.001102	4	0.391029	-2.290985	-1.88319	-0.40779	1	139	89.6774194	4.5	4.5	0.025792	1
High Abundance	gi|6323004	0.012217	0.002947	4	0.008685	0.000866	4	0.710895	-2.06123	-1.91304	-0.14819	1	138	89.0322581	23.5	32.5	0.092154	0
High Abundance	gi|6319314	0.011825	0.003174	4	0.007634	0.001275	4	0.645581	-2.117248	-1.9272	-0.19005	1	137	88.3870968	22.25	30.25	0.071329	0
High Abundance	gi|6322978	0.009927	0.003509	4	0.006149	0.000625	4	0.619422	-2.211196	-2.00318	-0.20801	1	136	87.7419355	4.25	5.25	0.118778	0
High Abundance	gi|6323613	0.009356	0.001911	4	0.00681	0.000572	4	0.727875	-2.166853	-2.02891	-0.13794	1	135	87.0967742	5.25	9.25	0.071178	0
High Abundance	gi|6320269	0.00911	0.002752	4	0.004043	0.000629	4	0.443798	-2.393296	-2.04048	-0.35281	1	134	86.4516129	5.5	4.5	0.031473	1
High Abundance	gi|6321408	0.008197	0.001899	4	0.005515	0.001251	4	0.672807	-2.258454	-2.08635	-0.17211	1	133	85.8064516	2.75	5.5	0.063045	0
High Abundance	gi|6319673	0.00789	0.000658	4	0.008057	0.00055	4	1.021166	-2.093827	-2.10292	0.009096	1	131	84.516129	13.75	20	0.710458	0
High Abundance	gi|6320148	0.00789	0.001499	4	0.006094	0.000374	4	0.77237	-2.215098	-2.10292	-0.11217	1	132	85.1612903	11	13.25	0.092953	0
High Abundance	gi|6324027	0.007695	0.002305	4	0.005778	0.000405	4	0.750877	-2.238222	-2.11379	-0.12443	1	130	83.8709677	4.5	6.75	0.194709	0
High Abundance	gi|6320963	0.007322	0.002373	4	0.003572	0.001349	4	0.487845	-2.447089	-2.13537	-0.31172	1	129	83.2258065	3	6	0.042681	1
High Abundance	gi|6320122	0.006788	0.004237	3	0.006621	0.001679	4	1.012941	-3.064997	-3.07058	0.005584	1	128	82.5806452	1	1	0.953423	0
High Abundance	gi|6324670	0.006571	0.001895	4	0.002556	0.001156	4	0.975398	-2.179076	-2.16826	-0.01082	1	127	81.9354839	5.25	6.25	0.015479	1
High Abundance	gi|6323615	0.006483	0.001929	4	0.004083	0.000645	4	0.388982	-2.592439	-2.18237	-0.41007	1	126	81.2903226	7.25	8	0.083647	0
High Abundance	gi|6322271	0.006476	0.002661	4	0.003076	0.000646	4	0.629801	-2.389021	-2.18822	-0.2008	1	125	80.6451613	2.25	3.25	0.080174	0
High Abundance	gi|6319505	0.006391	0.001517	4	0.005135	0.000962	4	0.474985	-2.512014	-2.18869	-0.32332	1	124	80	9.75	14.5	0.220034	0
High Abundance	gi|6320215	0.006169	0.001503	4	0.00488	0.000883	4	0.803474	-2.28946	-2.19443	-0.09503	1	123	79.3548387	8.75	13.5	0.201174	0
High Abundance	gi|6320128	0.006127	0.002945	4	0.004489	0.002137	4	0.791052	-2.31158	-2.20979	-0.10179	1	122	78.7096774	1.75	1.75	0.405629	0
High Abundance	gi|6323294	0.006126	0.002746	4	0.0044	0.000454	4	0.732659	-2.34785	-2.21275	-0.1351	1	121	78.0645161	2.5	2.75	0.298883	0
High Abundance	gi|6321025	0.00602	0.002137	4	0.004731	0.001149	4	0.71825	-2.356547	-2.21282	-0.14372	1	120	77.4193548	8.25	10.75	0.340932	0
High Abundance	gi|6320590	0.005993	0.002091	4	0.006683	0.001233	4	0.78588	-2.325047	-2.2204	-0.10464	1	119	76.7741935	3	4.25	0.594618	0
High Abundance	gi|6322583	0.005947	0.002258	4	0.004868	0.001239	4	1.115134	-2.175029	-2.22236	0.047327	1	118	76.1290323	5.75	6	0.443081	0
High Abundance	gi|6324085	0.005945	0	1	0.001179	0.000456	4	3.219512	-3.277366	-3.78516	0.50779	2	96	100	1	3		
High Abundance	gi|6322794	0.005885	0.001154	4	0.00255	0.000583	4	0.818564	-2.312649	-2.2257	-0.08695	1	117	75.483871	3.25	5.5	0.005033	1
High Abundance	gi|6320655	0.005876	0.001226	4	0.004552	0.00076	4	0.198318	-2.928486	-2.22585	-0.70264	1	116	74.8387097	5.25	7.25	0.125775	0
High Abundance	gi|6320304	0.005749	0.002138	4	0.004228	0.001125	4	0.433305	-2.59346	-2.23025	-0.36321	1	115	74.1935484	7.5	9.75	0.268696	0
High Abundance	gi|6321184	0.005739	0.002451	4	0.005561	0.001025	4	0.774677	-2.341798	-2.23092	-0.11088	1	114	73.5483871	11.25	22.25	0.900171	0
High Abundance	gi|6320949	0.005297	0.00123	4	0.002383	0.000152	4	0.735432	-2.373865	-2.24041	-0.13346	1	113	72.9032258	5	5	0.017012	1
High Abundance	gi|6324120	0.005255	0.001045	4	0.005459	0.000759	4	0.968984	-2.254847	-2.24116	-0.01368	1	112	72.2580645	15	20.75	0.763555	0
High Abundance	gi|6319972	0.005174	0.001091	4	0.005336	0.000614	4	0.449877	-2.622876	-2.27597	-0.34691	1	111	71.6129032	15	20.75	0.806437	0
High Abundance	gi|6319483	0.004895	0.001423	4	0.006946	0.001097	4	1.03882	-2.262887	-2.27943	0.01654	1	110	70.9677419	7	12	0.065396	0
High Abundance	gi|6321524	0.004766	0.001734	4	0.001384	0.000197	4	1.03131	-2.272784	-2.28617	0.013389	1	109	70.3225806	3	3	0.029025	1
High Abundance	gi|6324534	0.00454	0.001142	4	0.007231	0.001329	4	1.418999	-2.158265	-2.31025	0.151982	1	108	69.6774194	3.75	3.75	0.022551	1
High Abundance	gi|6323077	0.004456	0.000773	4	0.003181	0.000461	4	0.29039	-2.858864	-2.32185	-0.53702	1	107	69.0322581	5	7	0.037563	1
High Abundance	gi|6323072	0.004322	0.001604	4	0.004743	0.002203	4	1.592731	-2.140802	-2.34294	0.202143	1	106	68.3870968	5.25	4.75	0.769059	0
High Abundance	gi|6319559	0.004142	0.000987	4	0.00255	0.000732	4	0.713869	-2.497436	-2.35105	-0.14638	1	105	67.7419355	4.75	6	0.044387	1
High Abundance	gi|6322984	0.004123	0.000792	4	0.005141	0.000664	4	1.097409	-2.323947	-2.36432	0.040368	1	104	67.0967742	7.75	14.25	0.098113	0
High Abundance	gi|6321754	0.004062	0.000734	4	0.004901	0.000672	4	0.615645	-2.59346	-2.38279	-0.21067	1	103	66.4516129	6.75	12.5	0.143049	0
High Abundance	gi|8655890	0.004039	0.0022	4	0.008662	0.001904	4	1.246908	-2.288952	-2.38479	0.095834	1	101	65.1612903	6.5	10.75	0.019666	1
High Abundance	gi|6324151	0.004039	0.00087	4	0.005184	0.001559	4	1.206548	-2.309715	-2.39126	0.081545	1	102	65.8064516	8.75	10.25	0.259456	0
High Abundance	gi|6323104	0.003953	0.001466	3	0.001772	0.000449	4	0.56821	-3.342944	-3.09745	-0.24549	1	100	64.516129	5.66666667	6.75	0.11478	0
High Abundance	gi|6323090	0.003925	0.000624	4	0.006277	0.000993	4	1.283486	-2.285335	-2.39373	0.108391	1	99	63.8709677	1.75	3	0.01	1
High Abundance	gi|6320228	0.003915	0.000904	4	0.002742	0.000641	4	2.14459	-2.062382	-2.39373	0.331344	1	98	63.2258065	6.75	7	0.08357	0
High Abundance	gi|1038379	0.003833	0.001506	4	0.004896	0.001897	4	0.448267	-2.751536	-2.40307	-0.34846	1	97	62.5806452	5.25	7.75	0.415377	0
High Abundance	gi|6325196	0.003811	0.001209	4	0.007146	0.00069	4	1.599236	-2.202248	-2.40616	0.203912	1	96	61.9354839	17.25	29.75	0.005569	1
High Abundance	gi|6323763	0.003676	0.000858	4	0.003151	0.000975	4	0.700383	-2.561933	-2.40727	-0.15466	1	95	61.2903226	8.25	9	0.449873	0
High Abundance	gi|6319396	0.003464	0.001319	4	0.001677	0.000408	4	1.277328	-2.310159	-2.41646	0.106303	1	94	60.6451613	5.25	6.5	0.068188	0
High Abundance	gi|6320950	0.00335	0.001239	4	0.002189	0.000212	4	1.875098	-2.145937	-2.41896	0.273024	1	93	60	4.25	7	0.156816	0
High Abundance	gi|6323163	0.003242	0.002212	4	0.003268	0.001088	4	0.857182	-2.501552	-2.43462	-0.06693	1	92	59.3548387	5.5	5.25	0.98383	0
High Abundance	gi|6323371	0.003123	0.001026	4	0.00161	0.000242	4	0.484122	-2.775467	-2.46042	-0.31504	1	91	58.7096774	4.25	6.25	0.056534	0
High Abundance	gi|6321977	0.003107	0.000583	4	0.004485	0.000543	4	0.653433	-2.659754	-2.47496	-0.1848	1	90	58.0645161	8.5	21.5	0.013539	1
High Abundance	gi|6319315	0.003028	0.000564	4	0.003063	0.000468	4	1.00802	-2.485718	-2.48919	0.003469	1	89	57.4193548	6	6.5	0.926528	0
High Abundance	gi|6323057	0.003025	0.00049	4	0.00211	0.000256	4	0.51553	-2.793174	-2.50543	-0.28775	1	88	56.7741935	4	5.5	0.024685	1
High Abundance	gi|6321315	0.00302	0.001813	4	0.002981	0.000943	4	1.443515	-2.348238	-2.50766	0.159421	1	87	56.1290323	6	6.5	0.971427	0
High Abundance	gi|6320679	0.003006	0.001789	4	0.00327	0.000668	4	1.011559	-2.513853	-2.51884	0.004991	1	86	55.483871	3.5	5	0.796546	0
High Abundance	gi|1431847	0.003005	0.000901	4	0.002978	0.000124	4	0.697521	-2.675718	-2.51927	-0.15644	1	85	54.8387097	8	12.75	0.956458	0
High Abundance	gi|6322605	0.002896	0.001109	4	0.002675	0.000891	4	0.987086	-2.525638	-2.51999	-0.00564	1	84	54.1935484	6.5	8.75	0.766779	0
High Abundance	gi|6321772	0.002821	0.00075	4	0.002564	0.000611	4	1.087824	-2.485452	-2.52201	0.036559	1	83	53.5483871	4.25	6.25	0.614703	0
High Abundance	gi|6322120	0.002803	0.000508	4	0.004044	0.000902	4	0.991015	-2.526075	-2.52216	-0.00392	1	82	52.9032258	3.5	5.25	0.064725	0
High Abundance	gi|6324445	0.002779	0.000717	4	0.002756	0.000618	4	0.923688	-2.572676	-2.5382	-0.03447	1	81	52.2580645	3.75	6	0.96212	0
High Abundance	gi|6322564	0.002737	0.000717	4	0.003201	0.001068	4	0.908898	-2.591082	-2.5496	-0.04149	1	80	51.6129032	3.75	6.5	0.501771	0
High Abundance	gi|6320073	0.002687	0.000748	4	0.003171	0	1	50.14286	-2.852633	-4.55284	1.700209	2	95	98.9583333	1	2		
High Abundance	gi|6322847	0.002661	0.000926	3	0.004286	0.00191	4	2.733164	-2.66736	-3.10403	0.436666	2	94	97.9166667	3.66666667	3.75	0.203809	0
High Abundance	gi|6323387	0.002605	0.000784	4	0.004674	0.001063	4	1.44274	-2.393189	-2.55238	0.159188	1	79	50.9677419	10	14.25	0.022644	1
High Abundance	gi|6321249	0.002598	0.000535	4	0.001359	0.000475	4	0.991724	-2.559721	-2.55611	-0.00361	1	77	49.6774194	2	2.25	0.013682	1
High Abundance	gi|6320978	0.002598	0.000535	4	0.001366	0.000544	4	1.169529	-2.494714	-2.56273	0.068011	1	78	50.3225806	2	2.25	0.017966	1
High Abundance	gi|6321786	0.002568	0.000861	3	0.004229	0.001911	4	3.492994	-2.561933	-3.10513	0.543198	2	93	96.875	3	3.5	0.191883	0
High Abundance	gi|6323474	0.002537	0.000832	4	0.002451	0.000761	4	1.180127	-2.498804	-2.57073	0.071929	1	76	49.0322581	7.5	9.5	0.884489	0
High Abundance	gi|6323386	0.002527	0.001322	4	0.003855	0.000985	4	1.610673	-2.367948	-2.57496	0.207007	1	75	48.3870968	5.5	12.75	0.162271	0
High Abundance	gi|6323577	0.00252	0.000846	4	0.002381	0.000645	4	1.794242	-2.330311	-2.58419	0.253881	1	74	47.7419355	7.25	8.75	0.802406	0
High Abundance	gi|6325126	0.002511	0.000965	4	0.002149	0.000233	4	0.525789	-2.864549	-2.58536	-0.27919	1	73	47.0967742	4.5	6.75	0.514384	0
High Abundance	gi|3736268	0.002496	0.000657	4	0.003194	0.000893	4	0.523095	-2.866781	-2.58536	-0.28142	1	72	46.4516129	3.75	7.75	0.258182	0
High Abundance	gi|6320065	0.002434	0.001331	4	0.004056	0.000583	4	1.646807	-2.373762	-2.5904	0.216643	1	71	45.8064516	2.25	4.5	0.087556	0
High Abundance	gi|6323886	0.00243	0.000468	3	0.002176	0.00142	3	9	-3.142668	-4.09691	0.954243	2	92	95.8333333	2.33333333	2	0.792044	0
High Abundance	gi|6321335	0.002424	0.000352	4	0.001066	0.000378	4	0.966102	-2.610657	-2.59568	-0.01498	1	70	45.1612903	3.25	4	0.00193	1
High Abundance	gi|6322668	0.002273	0.000458	4	0.003573	0.000534	4	1.525524	-2.413976	-2.59739	0.183419	1	69	44.516129	4	4.75	0.01055	1
High Abundance	gi|6321362	0.00223	0.000632	4	0.002387	0.00078	4	0.944841	-2.623241	-2.5986	-0.02464	1	68	43.8709677	5.75	6	0.765256	0
High Abundance	gi|6322138	0.002207	0.000866	4	0.003267	0.000889	4	0.855834	-2.667764	-2.60015	-0.06761	1	67	43.2258065	3.5	7.75	0.138778	0
High Abundance	gi|6322284	0.002206	0.0005	4	0.002899	0.000337	4	1.279647	-2.495665	-2.60276	0.10709	1	66	42.5806452	3.75	4	0.06706	0
High Abundance	gi|6320142	0.002178	0	1	0.001058	0.000188	2	38.96875	-2.904134	-4.49485	1.590716	2	91	94.7916667	1	2		
High Abundance	gi|6325058	0.002175	0.00062	4	0.001999	0.000458	4	1.666393	-2.391902	-2.61368	0.221777	1	65	41.9354839	5.25	5.25	0.663968	0
High Abundance	gi|6321648	0.002154	0.000306	4	0.00288	0.001168	4	0.895473	-2.662341	-2.61439	-0.04795	1	64	41.2903226	4	5	0.306118	0
High Abundance	gi|6323376	0.002105	0.000235	4	0.001598	0.000425	4	0.439769	-2.972243	-2.61547	-0.35678	1	63	40.6451613	3	4.5	0.095152	0
High Abundance	gi|6323840	0.002039	0.000504	4	0.002814	0.000655	4	1.571931	-2.446967	-2.6434	0.196434	1	62	40	14.75	19.5	0.11321	0
High Abundance	gi|1160064	0.002009	0.000242	4	0.001499	0.00036	4	1.070404	-2.622148	-2.6517	0.029548	1	61	39.3548387	2.75	3.75	0.06332	0
High Abundance	gi|6320801	0.001985	0.000514	4	0.001805	0.000489	4	1.48029	-2.485851	-2.6562	0.170347	1	60	38.7096774	1	4.75	0.629308	0
High Abundance	gi|6319666	0.001922	0.000523	4	0.001738	0.0003	4	1.314143	-2.537752	-2.65639	0.118643	1	59	38.0645161	4.25	8	0.568827	0
High Abundance	gi|6321291	0.0019	0.000958	4	0.00461	0.00108	4	0.485767	-2.975514	-2.66194	-0.31357	1	58	37.4193548	3.5	6.75	0.009704	1
High Abundance	gi|6319965	0.001871	0	1	0.000794	0.000186	4	9.54902	-2.83535	-3.81531	0.979959	2	90	93.75	1	3		
High Abundance	gi|6325016	0.001829	0.000394	4	0.002824	0.00065	4	0.91908	-2.699187	-2.66254	-0.03665	1	57	36.7741935	12.5	18.75	0.047837	1
High Abundance	gi|6325176	0.001797	0.000376	4	0.001593	0.000333	4	1.337047	-2.540608	-2.66675	0.126147	1	56	36.1290323	4	7.25	0.448353	0
High Abundance	gi|6325389	0.001781	0.001314	4	0.002736	0.000503	4	0.759145	-2.796423	-2.67675	-0.11968	1	55	35.483871	2.25	2.5	0.248621	0
High Abundance	gi|6324452	0.001776	0.000794	4	0.002282	0.000581	4	1.380088	-2.550676	-2.69058	0.139907	1	54	34.8387097	2	2.75	0.346792	0
High Abundance	gi|6320905	0.001754	0.000703	4	0.001116	0.000536	4	0.746142	-2.824198	-2.69702	-0.12718	1	53	34.1935484	2.25	3.75	0.202202	0
High Abundance	gi|6321407	0.001753	0.000111	3	0.002067	0.000896	4	1.572559	-2.923724	-3.12033	0.196607	1	51	32.9032258	1.33333333	3.75	0.53609	0
High Abundance	gi|6321587	0.001753	0.000111	3	0.002016	0.000918	4	1.719562	-2.900665	-3.13608	0.235418	1	52	33.5483871	1.33333333	3.5	0.608697	0
High Abundance	gi|6324756	0.001742	0.000275	2	0.0014	0.000549	4	1.292479	-3.333482	-3.44491	0.111424	1	50	32.2580645	2	2.25	0.36933	0
High Abundance	gi|6323357	0.001671	0.000267	3	0.002822	0.000447	4	3.681303	-2.585194	-3.1512	0.566002	2	89	92.7083333	1	1.75	0.008633	1

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6324262	0.001621	0.000738	4	0.003629	0.001208	4	0.90932	-2.743523	-2.70224	-0.04128	1	49	31.6129032	2.75	6.75	0.036726	1
High Abundance	gi|6320882	0.001527	0.000325	4	0.00206	0.000533	4	0.904266	-2.75995	-2.71625	-0.0437	1	48	30.9677419	7.75	12.75	0.148951	0
High Abundance	gi|6323288	0.001526	0.000417	4	0.002747	0.000337	4	2.426316	-2.336299	-2.72125	0.384947	1	47	30.3225806	11	23	0.004322	1
High Abundance	gi|6324194	0.00149	0.001016	3	0.001881	0.000629	4	2.310791	-2.794254	-3.15802	0.363761	2	88	91.6666667	1	2	0.596924	0
High Abundance	gi|6324637	0.001484	0.000866	4	0.002509	0.000672	4	0.424372	-3.100179	-2.72793	-0.37225	1	46	29.6774194	7.25	14	0.113787	0
High Abundance	gi|6321679	0.001482	0.000783	4	0.002907	0.000307	4	1.544013	-2.549135	-2.73779	0.188651	1	45	29.0322581	9.25	26.75	0.028651	1
High Abundance	gi|6320781	0.001401	0.000375	4	0.003116	0.001263	4	0.886477	-2.797784	-2.74545	-0.05233	1	44	28.3870968	4	5.5	0.067864	0
High Abundance	gi|6319814	0.00138	0	1	0.001476	0.00058	4	5.442177	-3.09691	-3.83268	0.735773	2	87	90.625	1	4		
High Abundance	gi|1431847	0.001378	0.000471	3	0.00132	0.00036	4	8.597345	-2.234406	-3.16877	0.934364	2	86	89.5833333	2.33333333	4.5	0.868244	0
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High Abundance	gi|6323567	0.001187	0.000626	3	0.004448	0.001159	4	4.772809	-2.573814	-3.25259	0.678774	2	83	86.4583333	2.33333333	5.75	0.005814	1
High Abundance	gi|6324533	0.001167	0.000461	3	0.003141	0.000302	4	2.168498	-2.926648	-3.26281	0.336159	2	82	85.4166667	2.66666667	4.75	0.005769	1
High Abundance	gi|1431855	0.001152	0.000263	4	0.001718	0.000713	4	1.150029	-2.695509	-2.75622	0.060709	1	39	25.1612903	4.25	5	0.214063	0
High Abundance	gi|6322325	0.00111	0.000241	2	0.006326	0.000658	4	5.884831	-2.678816	-3.44855	0.769734	2	81	84.375	3.5	3.5	0.000155	1
High Abundance	gi|6324463	0.001107	0.000456	4	0.002314	0.000974	4	0.803674	-2.853872	-2.75895	-0.09492	1	38	24.516129	3.5	6	0.084267	0
High Abundance	gi|6323087	0.00108	0.000228	4	0.001523	0.000267	4	1.688809	-2.549443	-2.77702	0.227581	1	37	23.8709677	7.75	10.5	0.045921	1
High Abundance	gi|6319585	0.001056	0.000481	3	0.0012	0.000208	4	1.394786	-3.125518	-3.27003	0.144508	1	36	23.2258065	1.66666667	3	0.664844	0
High Abundance	gi|6324808	0.00104	0.000511	3	0.000682	0.000492	4	1.662942	-3.049149	-3.27003	0.220877	1	35	22.5806452	3.33333333	2	0.400691	0
High Abundance	gi|6319378	0.001033	0.000173	2	0.001819	0.001325	3	10.84615	-3.248721	-4.284	1.035276	2	80	83.3333333	1.5	2.333333	0.412487	0

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG	noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Protein
138	25.10%	98.0249	3.753623	0.6371881	73.0823	3.948529	0.329306	0.007103	0.0052958	6.37741546	5.68594823	8.86111111	7.396195	41	30.83%

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6319806	0.001028	0.000724	4	0.002413	0.000187	4	2.238742	-2.440213	-2.79022	0.350004	1	34	21.9354839	4.25	14.5	0.027524	1
Low Abundance	gi|6322599	0.001004	0.000515	4	0.00498	0.001983	4	1.34905	-2.686133	-2.81616	0.130028	1	33	21.2903226	4	12.25	0.024086	1
Low Abundance	gi|6323481	0.000987	0.000667	4	0.004414	0.001137	4	1.800131	-2.561141	-2.81645	0.255304	1	32	20.6451613	2.5	5.75	0.003793	1
Low Abundance	gi|6325114	0.000969	0.00038	3	0.001789	0.000616	4	2.47619	-2.886057	-3.27984	0.393784	2	79	82.2916667	3.66666667	2.25	0.083343	0
Low Abundance	gi|6322910	0.000964	0.000475	4	0.00478	0.00019	4	1.262416	-2.725611	-2.82681	0.101203	1	31	20	2.75	3.5	0.00013	1
Low Abundance	gi|6324707	0.00096	0.000258	4	0.003458	0.000281	4	1.690701	-2.600499	-2.82857	0.228067	1	30	19.3548387	14.5	29.75	1.29E-05	1
[illegible]																		

[illegible]

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6321236	0.000086	4.02E-05	3	0.001471	0.000308	4	5.12987	-2.704433	-3.41454	0.710106	2	14	14.5833333	2.66666667	11	0.002524	1
Low Abundance	gi|6320548	0.00008	0	1	0.00072	0.00021	4	16.38462	-2.717378	-3.93181	1.214436	2	13	13.5416667	3	9		
Low Abundance	gi|6321498	0.000079	3.16E-05	3	0.000907	0.000109	4	7.986807	-2.518988	-3.42136	0.902373	2	12	12.5	4	20.5	0.000242	1
Low Abundance	gi|6323509	0.000076	0	1	0.001133	0.000299	4	13.52174	-2.80827	-3.9393	1.131033	2	11	11.4583333	3	7.25		
Low Abundance	gi|1431856	0.000059	0	1	0.001656	0.000331	4	15.60185	-2.7734	-3.96658	1.193176	2	10	10.4166667	2	10		
Low Abundance	gi|6319695	0.000052	1.58E-05	2	0.000564	3.41E-05	4	8.329787	-2.805208	-3.72584	0.920634	2	9	9.375	3	11.75	1.67E-05	1
Low Abundance	gi|6324709	0.000051	0	1	0.001156	0.000387	4	15.89815	-2.76523	-3.96658	1.201347	2	8	8.33333333	2	7.5		
Low Abundance	gi|6321376	0.00005	2E-05	2	0.000389	3.52E-05	4	0.323699	-4.251812	-3.76195	-0.48986	1	1	0.64516129	2.5	8.5	0.000217	1
Low Abundance	gi|6321429	0.000048	0	1	0.000759	9.98E-05	4	12.37383	-2.878112	-3.97062	1.092504	2	7	7.29166667	2	12.25		
Low Abundance	gi|6321859	0.000048	0	1	0.001962	0.000481	4	9.570093	-2.9897	-3.97062	0.980916	2	6	6.25	2	9.75		
Low Abundance	gi|6320019	0.000033	0	1	0.001279	0.000177	4	4.285714	-3.346787	-3.97881	0.632023	2	5	5.20833333	2	6.75		
Low Abundance	gi|6320137	0.000033	0	1	0.001154	0.000318	4	13.71429	-2.841638	-3.97881	1.137173	2	4	4.16666667	2	7.25		
Low Abundance	gi|6320071	0.000032	0	1	0.001247	0.000218	4	10.35052	-2.998266	-4.01323	1.014962	2	3	3.125	2	7		
Low Abundance	gi|6319809	0.000028	0	1	0.001404	0.000406	4	14.25263	-2.868381	-4.02228	1.153895	2	2	2.08333333	2	8.5		
Low Abundance	gi|6323335	0.000018	0	1	0.000932	5.83E-05	4	2.966292	-3.578396	-4.05061	0.472214	2	1	1.04166667	2	11		
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**	**Number of Proteins with p-Value < 0.05**	**Proteins with p-Value < 0.05 (% of Protein**
113	**20.58%**	**4.2606**	**2.637168**	**1.21788713**	**17.7375**	**3.876106**	**0.425373**	**0.000377**	**0.0015697**				**3.070059**	**2.14039609**	**9.45427729**	**6.99759**	**67**	**80.72%**
DE90-only	gi|6325097	0	0	0	0.000399	2.98E-05	4									9.25		
DE90-only	gi|3736267	0	0	0	0.001177	0.000319	4									10		
DE90-only	gi|9755335	0	0	0	0.000651	0.000171	4									11.5		
DE90-only	gi|6321412	0	0	0	0.001036	0.000413	4									10.25		
DE90-only	gi|6323056	0	0	0	0.000786	0.000284	4									9		
DE90-only	gi|6320242	0	0	0	0.000629	0.000155	4									6.5		
DE90-only	gi|6320764	0	0	0	0.000849	0.000322	4									5.75		
DE90-only	gi|6319326	0	0	0	0.00099	0.000232	4									6		
DE90-only	gi|1431849	0	0	0	0.000777	0.000106	4									6.25		
DE90-only	gi|6319564	0	0	0	0.001266	0.000466	4									4.5		
DE90-only	gi|6325151	0	0	0	0.000885	4.96E-05	4									10.5		
DE90-only	gi|6323873	0	0	0	0.000965	0.000288	4									8.25		
DE90-only	gi|6323179	0	0	0	0.001883	0.000344	4									4.5		
DE90-only	gi|6322331	0	0	0	0.000575	0.000202	4									22.5		
DE90-only	gi|6322531	0	0	0	0.00237	0.000456	4									7.75		
DE90-only	gi|6323332	0	0	0	0.001224	0.000329	4									7.75		
DE90-only	gi|6323570	0	0	0	0.000409	7.29E-05	4									7		
DE90-only	gi|6324580	0	0	0	0.00077	0.00019	4									6.75		
DE90-only	gi|6323882	0	0	0	0.001396	0.000823	4									7.25		
DE90-only	gi|6324225	0	0	0	0.000688	0.000172	4									8.5		
DE90-only	gi|6322765	0	0	0	0.001586	0.0004	4									8.5		
DE90-only	gi|6322639	0	0	0	0.00047	0.00011	4									9.25		
DE90-only	gi|6324109	0	0	0	0.000689	0.000207	4									6		
DE90-only	gi|6320935	0	0	0	0.000368	0.00018	4									4.25		
DE90-only	gi|6321332	0	0	0	0.002488	0.000474	4									4.25		
DE90-only	gi|6324371	0	0	0	0.000492	0.000124	4									5		
DE90-only	gi|6323530	0	0	0	0.001462	0.00023	4									5.75		
DE90-only	gi|6320662	0	0	0	0.002069	0.000403	4									5.75		
DE90-only	gi|3736262	0	0	0	0.000852	0.000312	4									8		
DE90-only	gi|6323089	0	0	0	0.000986	0.00026	4									10.75		
DE90-only	gi|6320030	0	0	0	0.000105	3.16E-05	4									5.5		
DE90-only	gi|6322569	0	0	0	0.000133	5.71E-05	4									4.75		
DE90-only	gi|6324378	0	0	0	0.000326	0.000113	4									4		
DE90-only	gi|6325439	0	0	0	0.000261	8.96E-05	4									5.5		
DE90-only	gi|6319370	0	0	0	0.000673	0.000348	4									6		
DE90-only	gi|6320788	0	0	0	0.001382	0.000489	4									7		
DE90-only	gi|6319931	0	0	0	0.000676	0.000124	4									6.75		
DE90-only	gi|6325421	0	0	0	0.000372	0.00025	4									4.5		
DE90-only	gi|6324258	0	0	0	0.000358	0.000143	4									4.25		
DE90-only	gi|6324682	0	0	0	0.000288	3.32E-05	4									4.25		
DE90-only	gi|6320896	0	0	0	0.000797	0.000132	4									6		
DE90-only	gi|1431850	0	0	0	0.00058	0.000102	4									5.75		
DE90-only	gi|6324088	0	0	0	0.00052	0.000183	4									5.25		
DE90-only	gi|3736260	0	0	0	0.000653	0.000216	4									2.5		
DE90-only	gi|6322707	0	0	0	0.000576	0.000488	4									3.25		
DE90-only	gi|6319602	0	0	0	0.000476	0.000186	4									4.25		
DE90-only	gi|6323746	0	0	0	0.000989	0.000212	4									5.5		
DE90-only	gi|6319351	0	0	0	0.000417	0.000132	4									2		
DE90-only	gi|6319698	0	0	0	0.000764	0.000204	4									5		
DE90-only	gi|6320332	0	0	0	0.000308	6.44E-05	4									12.75		
DE90-only	gi|6323562	0	0	0	0.000528	0.000155	4									4		
DE90-only	gi|6323246	0	0	0	0.000909	0.000253	4									4.75		
DE90-only	gi|6324594	0	0	0	0.001346	0.000617	4									2.75		
DE90-only	gi|6324291	0	0	0	0.000664	0.000117	4									4.25		
DE90-only	gi|6324982	0	0	0	0.000609	0.000145	4									3.5		
DE90-only	gi|6323891	0	0	0	0.000338	0.000127	4									4		
DE90-only	gi|6321430	0	0	0	0.000106	5.3E-05	4									3		
DE90-only	gi|6324702	0	0	0	0.00019	6.85E-05	4									4		
DE90-only	gi|6320576	0	0	0	0.000798	0.000248	4									3.75		
DE90-only	gi|2033676	0	0	0	0.000062	1.86E-05	4									4		
DE90-only	gi|6324911	0	0	0	0.000283	5.72E-05	4									6.5		
DE90-only	gi|6322896	0	0	0	0.000331	0.000105	4									3		
DE90-only	gi|6320079	0	0	0	0.000597	0.00026	4									4.25		
DE90-only	gi|6324899	0	0	0	0.000435	9.37E-05	4									4.5		
DE90-only	gi|6323739	0	0	0	0.000256	8.94E-05	4									5.75		
DE90-only	gi|6320175	0	0	0	0.000325	4.36E-05	4									3		
DE90-only	gi|6320006	0	0	0	0.000189	5.94E-05	4									6.5		
DE90-only	gi|6324783	0	0	0	0.000327	0.00014	4									3.5		
DE90-only	gi|6323974	0	0	0	0.001001	0.000553	4									4.5		
DE90-only	gi|6320061	0	0	0	0.000065	2.59E-05	4									4.25		
DE90-only	gi|6321427	0	0	0	0.000493	0.000128	4									3.5		
DE90-only	gi|6324950	0	0	0	0.000179	9.8E-05	4									2.5		
DE90-only	gi|6321814	0	0	0	0.000572	0.00025	4									3.25		
DE90-only	gi|6319509	0	0	0	0.000895	0.00024	4									3		
DE90-only	gi|6321898	0	0	0	0.000445	0.000238	4									2		
DE90-only	gi|6322097	0	0	0	0.000763	0.000234	4									5.75		
DE90-only	gi|3736264	0	0	0	0.000288	8.66E-05	4									3.75		
DE90-only	gi|6324328	0	0	0	0.000413	0.000124	4									4.75		
DE90-only	gi|6324993	0	0	0	0.00045	0.000191	4									4.75		
DE90-only	gi|6319793	0	0	0	0.000193	7.76E-05	4									4		
DE90-only	gi|6320941	0	0	0	0.001253	0.000516	4									2.75		
DE90-only	gi|6323182	0	0	0	0.000189	8.61E-05	4									3.75		
DE90-only	gi|6321401	0	0	0	0.000541	0.00013	4									2.25		
DE90-only	gi|6321718	0	0	0	0.000347	0.000101	4									2.75		
DE90-only	gi|6319430	0	0	0	0.00061	0.000334	4									3		
DE90-only	gi|6320983	0	0	0	0.000305	0.000163	4									3.5		
DE90-only	gi|6322426	0	0	0	0.000124	2.46E-05	4									3.5		
DE90-only	gi|6319725	0	0	0	0.000429	0.00011	4									4.75		
DE90-only	gi|6320930	0	0	0	0.000163	7.11E-05	4									3		
DE90-only	gi|6322770	0	0	0	0.00036	0.000149	4									3.75		
DE90-only	gi|6323958	0	0	0	0.000238	4.95E-05	4									4		
DE90-only	gi|6323669	0	0	0	0.000182	1.82E-05	4									2.5		
DE90-only	gi|6323547	0	0	0	0.000275	3.93E-05	4									2.25		
DE90-only	gi|6320235	0	0	0	0.000546	0.000191	4									2		
DE90-only	gi|6321896	0	0	0	0.000487	0.000294	4									3		
DE90-only	gi|6324716	0	0	0	0.000473	0.000141	4									4.5		
DE90-only	gi|6320279	0	0	0	0.000124	4.04E-05	4									3.25		
DE90-only	gi|6324669	0	0	0	0.000356	0.000206	4									3		
DE90-only	gi|6320607	0	0	0	0.00049	0.000232	4									2		
DE90-only	gi|6322116	0	0	0	0.000207	0.000113	4									2.5		
DE90-only	gi|6322633	0	0	0	0.000551	0.000348	4									3.25		
DE90-only	gi|6324758	0	0	0	0.000477	0.000192	4									4		
DE90-only	gi|6321816	0	0	0	0.000122	3.73E-05	4									2.75		
DE90-only	gi|6320724	0	0	0	0.000445	0.000228	4									4.5		
DE90-only	gi|6319685	0	0	0	0.000052	2.23E-05	4									3.25		
DE90-only	gi|6321796	0	0	0	0.0007	0.00035	4									2.75		
DE90-only	gi|8279525	0	0	0	0.000263	3.13E-05	4									2.75		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6321236	2	2	3	5.2	7E-05	2	2	4	5.4	5.57E-05	4	4	7	11.2	0.000131	X	X	X	X	X
gi|6320548	X	X	X	X	X	3	3	7	5.44	8.03E-05	X	X	X	X	X	X	X	X	X	X
gi|6321498	X	X	X	X	X	4	4	9	4.79	4.61E-05	3	3	12	2.8	8.29E-05	5	5	15	5.38	0.000109
gi|6323509	X	X	X	X	X	X	X	X	X	X	3	3	4	7.74	7.64E-05	X	X	X	X	X
gi|1431856	X	X	X	X	X	X	X	X	X	X	2	2	3	5.61	5.85E-05	X	X	X	X	X
gi|6319695	X	X	X	X	X	4	4	7	3.98	4.13E-05	2	2	8	2.03	6.36E-05	X	X	X	X	X
gi|6324709	X	X	X	X	X	X	X	X	X	X	2	2	2	7.32	5.09E-05	X	X	X	X	X
gi|6321376	X	X	X	X	X	3	3	6	3.06	3.55E-05	2	2	8	2.04	6.37E-05	X	X	X	X	X
gi|6321429	X	X	X	X	X	X	X	X	X	X	2	2	4	3.72	4.82E-05	X	X	X	X	X
gi|6321859	X	X	X	X	X	X	X	X	X	X	2	2	2	8.53	4.85E-05	X	X	X	X	X
gi|6320019	X	X	X	X	X	2	2	2	6.07	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320137	X	X	X	X	X	2	2	2	5.61	3.25E-05	X	X	X	X	X	X	X	X	X	X
gi|6320071	X	X	X	X	X	2	2	2	5.91	3.16E-05	X	X	X	X	X	X	X	X	X	X
gi|6319809	X	X	X	X	X	2	2	2	4.6	2.79E-05	X	X	X	X	X	X	X	X	X	X
gi|6323335	X	X	X	X	X	2	2	2	3.34	1.79E-05	X	X	X	X	X	X	X	X	X	X
gi|6325097	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736267	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|9755335	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321412	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323056	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320242	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320764	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319326	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319564	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325151	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323873	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323179	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322331	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322531	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323570	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324580	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323882	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324225	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322765	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322639	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324109	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320935	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324371	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323530	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320662	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736262	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323089	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320030	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322569	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324378	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325439	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319370	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320788	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319931	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325421	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324258	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324682	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431850	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324088	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736260	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322707	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319602	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323746	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319351	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319698	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320332	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323562	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323246	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324594	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324291	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324982	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323891	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321430	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324702	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320576	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|2033676	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324911	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320079	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324899	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323739	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320175	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320006	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324783	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323974	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320061	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321427	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324950	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321814	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319509	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321898	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322097	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736264	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324328	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324993	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319793	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320941	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323182	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321401	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321718	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319430	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320983	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322426	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319725	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320930	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322770	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323958	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323547	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320235	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324716	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320279	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320607	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322116	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322633	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324758	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321816	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320724	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319685	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321796	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|8279525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Locus	DE90-1_P	DE90-1_uP	DE90-1_S	DE90-1_SC	DE90-1_NSAF	DE90-2_P	DE90-2_uP	DE90-2_S	DE90-2_SC	DE90-2_NSAF	DE90-3_P	DE90-3_uP	DE90-3_S	DE90-3_SC	DE90-3_NSAF	DE90-4_P	DE90-4_uP	DE90-4_S	DE90-4_SC	DE90-4_NSAF
gi|6321236	14	14	64	35.2	0.001657	13	13	53	36.8	0.001767	9	9	29	26.4	0.001077	8	8	37	25	0.001382
gi|6320548	8	8	46	15.65	0.000981	12	12	29	26.36	0.000796	9	9	19	20.1	0.000581	7	7	17	12.85	0.000523
gi|6321498	25	25	108	27.17	0.00103	21	21	72	23.12	0.000884	19	19	69	20.25	0.000944	17	17	56	20.4	0.00077
gi|6323509	11	11	57	30.55	0.001503	6	6	30	18.74	0.001018	6	6	32	17.52	0.00121	6	6	21	19.14	0.000799
gi|1431856	9	9	47	29.52	0.001265	12	12	53	40.75	0.001837	9	9	52	21.83	0.002008	10	10	39	26.82	0.001514
gi|6319695	13	13	48	16.36	0.000527	14	14	43	16.02	0.000607	10	10	35	10.76	0.000551	10	10	36	12.54	0.00057
gi|6324709	8	8	17	34.96	0.000596	8	8	30	35.5	0.001355	8	8	29	35.5	0.00146	6	6	24	27.1	0.001215
gi|6321376	9	9	32	10.02	0.000352	9	9	26	8.74	0.000368	8	8	27	7.05	0.000426	8	8	26	8.83	0.000412
gi|6321429	16	16	48	28.63	0.000798	13	13	41	26.32	0.000877	11	11	30	20.41	0.000715	9	9	27	15.28	0.000647
gi|6321859	11	11	63	40.57	0.002108	11	11	54	37.73	0.002326	9	9	45	29.2	0.00216	8	8	26	23.77	0.001255
gi|6320019	7	7	42	25	0.00127	6	6	34	20.79	0.001324	7	7	34	22.2	0.001475	7	7	24	25.7	0.001047
gi|6320137	8	8	29	25.47	0.000877	8	8	29	25	0.001129	6	6	37	17.52	0.001606	7	7	23	21.96	0.001004
gi|6320071	8	8	44	28.18	0.001295	7	7	35	22.5	0.001326	7	7	34	22.73	0.001435	6	6	22	20.68	0.000934
gi|6319809	8	8	55	24.8	0.001424	8	8	32	25.8	0.001067	8	8	53	21	0.001969	10	10	31	27.4	0.001158
gi|6323335	13	13	57	21.47	0.000949	12	12	47	20.57	0.001007	9	9	37	15.81	0.000883	10	10	37	16.45	0.000888
gi|6325097	8	8	36	8.9	0.000428	11	11	26	12.02	0.000398	7	7	21	7.89	0.000358	11	11	24	15.05	0.000411
gi|3736267	9	9	25	28.71	0.000774	13	13	35	45.22	0.001396	9	9	33	28.47	0.001466	9	9	24	28.47	0.001072
gi|9755335	13	13	37	16.26	0.000512	14	14	47	19.04	0.000838	10	10	38	16.47	0.000755	9	9	25	13.8	0.000499
gi|6321412	9	9	54	19.94	0.000989	13	13	69	29.99	0.001627	6	6	26	13.72	0.000683	13	13	32	28.15	0.000845
gi|6323056	12	12	29	28.76	0.000635	10	10	41	22	0.001156	8	8	27	21.66	0.000848	6	6	16	14.72	0.000506
gi|6320242	8	8	34	19.63	0.000745	8	8	26	16.58	0.000733	7	7	20	17.09	0.000629	3	3	13	6.94	0.000411
gi|6320764	6	6	22	17.14	0.000574	6	6	37	17.14	0.001243	5	5	16	17.14	0.000599	6	6	26	19.35	0.000979
gi|6319326	6	6	16	25.82	0.000677	6	6	20	27.78	0.001089	5	5	16	23.2	0.000971	7	7	20	34.31	0.001221
gi|1431849	7	7	30	20.48	0.000772	7	7	28	21.87	0.000928	4	4	19	13.52	0.000702	7	7	19	19.09	0.000705
gi|6319564	6	6	22	32.56	0.001104	6	6	30	39.15	0.001938	3	3	12	18.6	0.000864	3	3	16	18.22	0.001158
gi|6325151	15	15	44	28.14	0.000822	10	10	37	22.08	0.00089	9	9	33	17.6	0.000884	8	8	35	15.44	0.000943
gi|6323873	9	9	39	20.76	0.000962	9	9	31	24.38	0.000984	8	8	37	18.48	0.001309	7	7	17	18.48	0.000605
gi|6323179	5	5	35	29.3	0.00166	3	3	28	20.88	0.00171	5	5	26	27.84	0.001769	5	5	35	29.3	0.002394
gi|6322331	18	18	64	10.75	0.000374	27	27	96	16.12	0.000723	24	24	92	15	0.000772	21	21	51	13.64	0.00043
gi|6322531	9	9	58	45.54	0.00231	10	10	56	46.77	0.002872	6	6	44	29.85	0.002514	6	6	31	28.31	0.001781
gi|6323332	7	7	17	34.02	0.000902	8	8	16	44.67	0.001093	9	9	22	50.41	0.001675	7	7	16	44.26	0.001225
gi|6323570	7	7	14	17.29	0.00031	7	7	14	19.86	0.0004	8	8	15	21.4	0.000477	6	6	14	15.58	0.000448
gi|6324580	7	7	15	21.1	0.000561	8	8	21	28.9	0.001012	5	5	13	19.08	0.000698	7	7	15	28.9	0.00081
gi|6323882	6	6	23	20.6	0.001115	8	8	19	36.7	0.001186	7	7	10	35.96	0.000696	8	8	37	33.33	0.002588
gi|6324225	10	10	29	23.42	0.000607	8	8	35	20.19	0.000942	8	8	19	19.06	0.00057	8	8	21	19.22	0.000634
gi|6322765	9	9	29	35.33	0.001124	9	9	42	40.42	0.002096	8	8	29	34.43	0.001613	8	8	27	39.82	0.00151
gi|6322639	10	10	37	13.67	0.000468	8	8	22	9.28	0.000358	8	8	24	9.57	0.000435	11	11	34	16.11	0.00062
gi|6324109	5	5	13	16.86	0.000389	7	7	19	20.32	0.000731	7	7	20	20.79	0.000858	5	5	18	15.7	0.000776
gi|6320935	5	5	7	13.02	0.000179	4	4	17	10.06	0.000559	2	2	7	5.92	0.000256	6	6	13	16.17	0.000479
gi|6321332	3	3	28	32.89	0.002433	6	6	27	49.66	0.00302	3	3	21	36.24	0.002618	5	5	15	46.31	0.00188
gi|6324371	5	5	15	21.46	0.00049	7	7	15	24.24	0.000631	5	5	11	14.14	0.000516	3	3	7	10.61	0.00033
gi|6323530	7	7	25	44.69	0.001432	6	6	23	33.63	0.001696	5	5	19	26.55	0.001561	5	5	14	26.55	0.001157
gi|6320662	6	6	33	39.04	0.002285	8	8	27	42.78	0.002407	5	5	21	38.5	0.002086	4	4	15	31.55	0.001498
gi|3736262	9	9	26	22.24	0.000687	10	10	32	31.02	0.001089	8	8	30	22.45	0.001137	5	5	13	14.08	0.000495
gi|6323089	11	11	58	27.06	0.001262	13	13	41	34.79	0.001149	10	10	26	25.88	0.000812	9	9	23	22.02	0.000722
gi|6320030	7	7	15	4.48	9.05E-05	9	9	18	5.97	0.00014	2	2	8	1.59	6.93E-05	4	4	14	2.98	0.000122
gi|6322569	7	7	16	11.45	0.000185	6	6	12	9.57	0.000179	3	3	5	3.94	8.31E-05	3	3	5	5.19	8.35E-05
gi|6324378	5	5	9	18.83	0.000261	3	3	10	9.64	0.000374	2	2	5	6.95	0.000208	6	6	11	21.52	0.000461
gi|6325439	8	8	21	13.93	0.000354	4	4	14	7.42	0.000304	6	6	10	11.46	0.000242	4	4	6	6.77	0.000146
gi|6319370	8	8	40	17.43	0.00095	7	7	28	16.51	0.000856	6	6	21	14.5	0.000716	3	3	5	7.16	0.000171
gi|6320788	9	9	59	26.17	0.001625	6	6	52	17.02	0.001844	6	6	34	16.6	0.001344	7	7	18	18.3	0.000715
gi|6319931	7	7	26	17.23	0.000569	6	6	30	17.4	0.000845	6	6	22	14.19	0.00069	8	8	19	21.96	0.000599
gi|6325421	6	6	9	17.43	0.000267	2	2	4	6.65	0.000153	3	3	8	8.94	0.000341	7	7	17	18.81	0.000728
gi|6324258	4	4	6	10.58	0.000161	5	5	11	11	0.00038	3	3	10	9.34	0.000385	5	5	13	13.49	0.000504
gi|6324682	6	6	15	14.24	0.000322	4	4	10	9.93	0.000276	4	4	10	8.77	0.000307	3	3	8	7.62	0.000247
gi|6320896	7	7	16	35.02	0.000697	5	5	12	21.89	0.000673	4	4	15	14.81	0.000938	8	8	14	36.36	0.00088
gi|1431850	5	5	21	14.03	0.000545	6	6	14	17.84	0.000468	6	6	16	16.83	0.000596	6	6	19	18.04	0.000711
gi|6324088	6	6	26	15.64	0.000667	6	6	16	15.64	0.000528	6	6	17	16.83	0.000625	3	3	7	8.91	0.000259
gi|3736260	2	2	5	20.59	0.000381	3	3	6	28.82	0.000588	3	3	8	20.59	0.000874	2	2	7	20.59	0.000769
gi|6322707	2	2	4	12.33	0.000236	3	3	7	17.81	0.000533	2	2	3	15.98	0.000254	6	6	15	40.18	0.001279
gi|6319602	5	5	10	13.74	0.000262	3	3	13	7.07	0.000438	5	5	19	15.35	0.000713	4	4	13	11.92	0.00049
gi|6323746	5	5	25	20.88	0.00109	5	5	12	20.88	0.000673	6	6	18	22.22	0.001126	6	6	17	27.95	0.001069
gi|6319351	2	2	10	6.85	0.000277	2	2	11	6.85	0.000393	2	2	15	6.85	0.000597	2	2	10	6.85	0.0004
gi|6319698	5	5	14	19.95	0.000495	6	6	16	29.51	0.000729	4	4	17	18.03	0.000863	5	5	19	19.95	0.000969
gi|6320332	16	16	37	13.66	0.000302	15	15	36	12.28	0.000378	10	10	28	8.69	0.000327	10	10	19	8.94	0.000223
gi|6323562	3	3	5	18.13	0.000356	5	5	8	28.02	0.000733	4	4	5	30.22	0.00051	4	4	5	31.32	0.000513
gi|6323246	5	5	33	16.44	0.001152	4	4	24	14.56	0.001078	5	5	16	18.87	0.000801	5	5	12	27.76	0.000604
gi|6324594	2	2	5	29.25	0.000611	2	2	8	25.47	0.001258	3	3	8	44.34	0.001402	4	4	12	53.77	0.002114
gi|6324291	3	3	21	12.78	0.000755	4	4	12	14.72	0.000556	5	5	15	22.78	0.000774	5	5	11	20.28	0.000571
gi|6324982	2	2	10	7.08	0.000398	5	5	14	24.62	0.000718	3	3	12	7.69	0.000686	4	4	11	15.69	0.000632
gi|6323891	4	4	5	11.06	0.000159	5	5	9	14.25	0.000369	4	4	8	14.5	0.000365	3	3	10	11.06	0.000459
gi|6321430	4	4	7	5.56	9.87E-05	4	4	10	8.17	0.000182	2	2	3	4.47	6.07E-05	2	2	4	3.27	8.14E-05
gi|6324702	5	5	9	11.56	0.000204	5	5	9	14.01	0.000263	3	3	3	8.93	9.76E-05	3	3	6	8.41	0.000196
gi|6320576	3	3	14	16.03	0.000581	4	4	12	21.15	0.000641	4	4	19	21.47	0.001131	4	4	14	21.47	0.000838
gi|2033676	4	4	9	1.99	6.64E-05	5	5	9	3.13	8.55E-05	3	3	4	1.14	4.23E-05	4	4	5	1.99	5.32E-05
gi|6324911	7	7	19	9.92	0.000257	8	8	19	11.06	0.000331	6	6	17	8.25	0.00033	5	5	11	7.93	0.000214
gi|6322896	3	3	4	20.3	0.000191	3	3	5	17.71	0.000308	3	3	6	20.3	0.000411	3	3	6	17.71	0.000413
gi|6320079	2	2	5	7.69	0.000207	7	7	14	34.94	0.000748	3	3	12	12.82	0.000714	5	5	12	23.4	0.000718
gi|6324899	6	6	14	23.9	0.000397	3	3	11	12.72	0.000402	5	5	9	22.15	0.000367	4	4	14	16.45	0.000573
gi|6323739	5	5	7	12.2	0.000147	5	5	10	13.17	0.000271	6	6	8	16.26	0.000242	7	7	12	16.59	0.000364
gi|6320175	3	3	9	11.51	0.000298	3	3	9	11.51	0.000384	3	3	7	11.76	0.000333	3	3	6	11.25	0.000287
gi|6320006	5	5	11	6.21	0.000112	8	8	19	9.74	0.000249	7	7	15	8.72	0.000219	6	6	12	8.01	0.000176
gi|6324783	3	3	11	10.96	0.000332	3	3	5	9.32	0.000194	4	4	12	14.22	0.00052	4	4	6	13.52	0.000261
gi|6323974	6	6	32	34.62	0.00177	5	5	9	34.62	0.000641	4	4	13	21.37	0.001032	3	3	7	17.52	0.000559
gi|6320061	3	3	6	2.6	4.48E-05	6	6	8	5.77	7.7E-05	5	5	9	4.04	9.65E-05	3	3	4	2.54	4.31E-05
gi|6321427	5	5	12	24.6	0.000616	3	3	6	17.86	0.000397	3	3	8	16.27	0.00059	3	3	5	15.48	0.000371
gi|6324950	3	3	5	7.13	0.000125	2	2	5	5.39	0.000161	3	3	9	7.51	0.000322	2	2	3	4.82	0.000108
gi|6321814	3	3	10	9.8	0.000363	3	3	20	14.01	0.000934	2	2	9	6.72	0.000468	5	5	10	17.09	0.000523
gi|6319509	3	3	15	18.42	0.000852	3	3	15	19.74	0.001097	4	4	13	25	0.001059	2	2	7	14.47	0.000573
gi|6321898	2	2	5	14.04	0.000189	3	3	8	19.59	0.00039	2	2	8	14.04	0.000434	1	1	14	7.6	0.000764
gi|6322097	7	7	17	22.1	0.000593	6	6	19	19.41	0.000854	5	5	21	16.17	0.001051	5	5	11	16.44	0.000554
gi|3736264	2	2	7	4.76	0.000216	4	4	8	12.86	0.000317	5	5	9	17.14	0.000398	4	4	5	12.62	0.000222
gi|6324328	5	5	18	13.36	0.000487	5	5	10	14.61	0.000348	5	5	14	13.78	0.000543	4	4	7	9.39	0.000273
gi|6324993	6	6	19	19.06	0.000504	5	5	19	16.39	0.000649	5	5	12	13.32	0.000457	3	3	5	7.58	0.000191
gi|6319793	2	2	12	3.23	0.000218	5	5	7	9.13	0.000164	5	5	11	9.41	0.000287	4	4	4	7.58	0.000105
gi|6320941	3	3	30	21.46	0.001895	3	3	16	23.41	0.001301	2	2	13	16.59	0.001178	3	3	7	21.95	0.000638
gi|6323182	4	4	10	7.76	0.00019	6	6	12	12.59	0.000293	3	3	7	4.83	0.00019	2	2	3	7.17	8.2E-05
gi|6321401	2	2	10	17.13	0.000599	2	2	8	17.13	0.000617	2	2	7	17.13	0.000602	3	3	4	25.46	0.000346
gi|6321718	3	3	7	13.47	0.000235	3	3	10	13.47	0.000432	3	3	9	13.47	0.000433	2	2	6	8.55	0.00029
gi|6319430	3	3	9	17.84	0.000483	3	3	16	17.84	0.001107	4	4	5	17.84	0.000385	2	2	6	9.54	0.000465
gi|6320983	3	3	8	9.76	0.00023	4	4	10	11.53	0.00037	2	2	3	6.87	0.000124	5	5	12	17.29	0.000497
gi|6322426	5	5	8	10.12	0.000152	3	3	4	5.43	9.78E-05	3	3	5	6.3	0.000136	3	3	4	7.48	0.00011
gi|6319725	6	6	25	13.59	0.000586	4	4	14	7.97	0.000423	4	4	10	9.42	0.000336	5	5	11	11.41	0.000372
gi|6320930	3	3	7	8.68	0.000157	4	4	7	11.28	0.000203	3	3	7	9.03	0.000226	2	2	2	5.38	6.49E-05
gi|6322770	4	4	11	14.54	0.000363	5	5	13	19.64	0.000553	3	3	7	10.97	0.000332	3	3	4	11.99	0.000191
gi|6323958	5	5	7	9.41	0.000178	5	5	8	10.59	0.000261	4	4	8	7.65	0.000291	2	2	6	7.65	0.00022
gi|6323669	3	3	7	9.79	0.000193	2	2	5	5.74	0.000177	2	2	4	5.11	0.000158	3	3	5	9.57	0.000199
gi|6323547	2	2	6	10	0.000311	2	2	4	10	0.000267	2	2	3	10.4	0.000223	3	3	4	13.6	0.000299
gi|6320235	2	2	6	22.73	0.000392	2	2	9	22.73	0.000758	2	2	7	19.7	0.000657	2	2	4	19.7	0.000377
gi|6321896	4	4	17	16.21	0.000673	3	3	15	13.46	0.000765	3	3	7	13.46	0.000398	2	2	2	10.09	0.000114
gi|6324716	4	4	8	19.15	0.000315	6	6	11	31.61	0.000557	5	5	11	25.53	0.000621	3	3	7	14.59	0.000397
gi|6320279	5	5	12	7.48	0.000173	3	3	4	4.58	7.44E-05	2	2	6	2.9	0.000124	3	3	6	4.13	0.000125
gi|6324669	2	2	4	10.85	0.000201	5	5	10	24.42	0.000646	2	2	3	12.02	0.000216	3	3	5	13.57	0.000362
gi|6320607	2	2	4	10.41	0.000234	2	2	5	10.41	0.000377	2	2	7	10.41	0.000588	2	2	9	10.86	0.000761
gi|6322116	4	4	7	13.86	0.000193	2	2	10	6.61	0.000355	2	2	5	5.33	0.000198	2	2	2	5.76	7.96E-05
gi|6322633	2	2	9	16.24	0.000371	6	6	20	38.85	0.001062	2	2	8	16.24	0.000473	3	3	5	17.52	0.000297
gi|6324758	3	3	12	12.15	0.000393	6	6	18	27.85	0.00076	3	3	9	10.13	0.000423	4	4	7	15.19	0.000331
gi|6321816	2	2	6	3.02	7.82E-05	4	4	10	6.04	0.000168	2	2	7	2.82	0.000131	3	3	6	4.33	0.000113
gi|6320724	6	6	13	15	0.000337	7	7	21	17	0.0007	2	2	15	4.8	0.000557	3	3	5	7.6	0.000187
gi|6319685	4	4	8	3.05	5.64E-05	3	3	9	2.07	8.18E-05	3	3	4	2.23	4.05E-05	3	3	3	1.91	3.05E-05
gi|6321796	3	3	14	15.88	0.000778	3	3	16	15.88	0.001145	3	3	7	15.88	0.000558	2	2	4	9.87	0.000321
gi|8279525	3	3	5	21.29	0.00026	3	3	4	20.88	0.000268	2	2	3	15.26	0.000224	3	3	4	21.29	0.0003

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE90-only	gi|6324273	0	0	0	0.000421	9.07E-05	4									3.25		
DE90-only	gi|1431848	0	0	0	0.000321	2.05E-05	4									2.5		
DE90-only	gi|6321217	0	0	0	0.000317	0.000105	4									2.5		
DE90-only	gi|6324474	0	0	0	0.000114	0.000109	4									2.75		
DE90-only	gi|6322174	0	0	0	0.000194	7.42E-05	4									2.5		
DE90-only	gi|1431857	0	0	0	0.000368	0.000165	4									2		
DE90-only	gi|6321854	0	0	0	0.000412	0.000176	4									3.5		
DE90-only	gi|6325103	0	0	0	0.00016	4.91E-05	4									2		
DE90-only	gi|6320009	0	0	0	0.000874	0.000337	4									2.5		
DE90-only	gi|6324195	0	0	0	0.000261	9.93E-05	4									2.25		
DE90-only	gi|6321806	0	0	0	0.000138	6.75E-05	4									2		
DE90-only	gi|6323237	0	0	0	0.00032	0.000115	4									2.5		
DE90-only	gi|6324363	0	0	0	0.000367	0.000248	4									2.25		
DE90-only	gi|6319711	0	0	0	0.000213	0.000116	4									2.5		
DE90-only	gi|6320276	0	0	0	0.00081	0.000515	4									2.25		
DE90-only	gi|6319568	0	0	0	0.00022	6.99E-05	3									2		
DE90-only	gi|6321574	0	0	0	0.00067	0.000278	3									3		
DE90-only	gi|6320798	0	0	0	0.000304	0.000155	3									3		
DE90-only	gi|6320078	0	0	0	0.001546	0.000359	3									2.666667		
DE90-only	gi|6319413	0	0	0	0.000286	8.03E-05	3									3		
DE90-only	gi|6321398	0	0	0	0.00019	7.83E-05	3									2.666667		
DE90-only	gi|6321290	0	0	0	0.000292	0.000168	3									4.333333		
DE90-only	gi|6320066	0	0	0	0.000294	0.000111	3									2		
DE90-only	gi|6323681	0	0	0	0.000772	0.00013	3									2.666667		
DE90-only	gi|2780871	0	0	0	0.000196	0.000115	3									2.666667		
DE90-only	gi|6319646	0	0	0	0.000191	7.05E-05	3									3		
DE90-only	gi|6323331	0	0	0	0.000242	0.000119	3									2		
DE90-only	gi|6324772	0	0	0	0.000331	2.37E-05	3									2		
DE90-only	gi|6320372	0	0	0	0.000194	8.88E-05	3									2.666667		
DE90-only	gi|6320899	0	0	0	0.001582	0.000325	3									2.333333		
DE90-only	gi|6321829	0	0	0	0.000683	0.000193	3									2		
DE90-only	gi|6324761	0	0	0	0.00016	9.48E-05	3									3		
DE90-only	gi|6321004	0	0	0	0.000228	3.62E-05	3									2.666667		
DE90-only	gi|6322049	0	0	0	0.00026	0.000223	3									3.666667		
DE90-only	gi|6324318	0	0	0	0.000557	0.000155	3									3.333333		
DE90-only	gi|6324725	0	0	0	0.000049	1.83E-05	3									2.333333		
DE90-only	gi|6322667	0	0	0	0.000254	0.000124	3									3.333333		
DE90-only	gi|6322127	0	0	0	0.000754	0.000333	3									2.666667		
DE90-only	gi|6325337	0	0	0	0.000183	3.05E-05	3									3		
DE90-only	gi|6321807	0	0	0	0.000161	7.2E-05	3									2		
DE90-only	gi|6324696	0	0	0	0.000623	3.63E-05	3									2.333333		
DE90-only	gi|6320917	0	0	0	0.000139	6.51E-05	3									2.666667		
DE90-only	gi|6324283	0	0	0	0.000086	3.52E-05	3									2.666667		
DE90-only	gi|6321776	0	0	0	0.000359	0.000134	3									2.333333		
DE90-only	gi|1431852	0	0	0	0.000162	7.15E-05	3									1.666667		
DE90-only	gi|1431857	0	0	0	0.000262	0.000106	3									2		
DE90-only	gi|6323932	0	0	0	0.000182	3.78E-05	3									2.666667		
DE90-only	gi|6323955	0	0	0	0.000147	8.6E-06	3									2.333333		
DE90-only	gi|6324508	0	0	0	0.000395	0.000257	3									3.333333		
DE90-only	gi|6323864	0	0	0	0.000151	2.48E-05	3									2		
DE90-only	gi|6322459	0	0	0	0.000201	9.8E-05	3									2.666667		
DE90-only	gi|1038379	0	0	0	0.000418	0.000131	3									2		
DE90-only	gi|1038375	0	0	0	0.000346	0.000107	3									2.333333		
DE90-only	gi|6323383	0	0	0	0.000365	4.74E-05	3									2		
DE90-only	gi|6320849	0	0	0	0.000744	2.13E-05	3									3		
DE90-only	gi|6322525	0	0	0	0.000125	3.65E-05	3									2.666667		
DE90-only	gi|6320809	0	0	0	0.002476	0.000715	3									3		
DE90-only	gi|6322261	0	0	0	0.000129	3.51E-05	3									3.333333		
DE90-only	gi|6322155	0	0	0	0.000312	7.8E-05	3									2.333333		
DE90-only	gi|6579194	0	0	0	0.000087	4.23E-05	3									3		
DE90-only	gi|6323460	0	0	0	0.00012	7.02E-06	3									3.333333		
DE90-only	gi|6323278	0	0	0	0.00011	9.2E-05	3									2.666667		
DE90-only	gi|6319558	0	0	0	0.000074	1.5E-05	3									2.666667		
DE90-only	gi|6322828	0	0	0	0.000533	6.72E-05	3									3.333333		
DE90-only	gi|6323843	0	0	0	0.000051	2.83E-06	3									2.666667		
DE90-only	gi|6320893	0	0	0	0.000142	6.89E-05	3									2.333333		
DE90-only	gi|6324938	0	0	0	0.000405	4.59E-05	3									3		
DE90-only	gi|6319721	0	0	0	0.000572	9.86E-05	3									2.666667		
DE90-only	gi|6322638	0	0	0	0.000075	5.88E-06	3									2		
DE90-only	gi|6323537	0	0	0	0.000086	5.06E-05	3									2		
DE90-only	gi|6323229	0	0	0	0.000937	0.000253	3									2.333333		
DE90-only	gi|6321195	0	0	0	0.000472	0.000131	3									2		
DE90-only	gi|6322452	0	0	0	0.000153	2.64E-05	3									2.333333		
DE90-only	gi|6319577	0	0	0	0.000407	7.57E-05	3									3.333333		
DE90-only	gi|6323975	0	0	0	0.000235	0.000137	3									2.666667		
DE90-only	gi|6325386	0	0	0	0.000394	0.000135	3									2		
DE90-only	gi|6319729	0	0	0	0.00042	0.00023	3									2		
DE90-only	gi|6321531	0	0	0	0.000044	7.78E-06	3									2		
DE90-only	gi|6320527	0	0	0	0.000134	3.3E-06	2									2.5		
DE90-only	gi|6320249	0	0	0	0.0003	0.000137	2									3.5		
DE90-only	gi|6323752	0	0	0	0.000262	1.79E-06	2									3		
DE90-only	gi|6324535	0	0	0	0.00022	8.63E-07	2									2		
DE90-only	gi|6322746	0	0	0	0.000062	1.58E-05	2									2		
DE90-only	gi|6324475	0	0	0	0.000202	4.14E-05	2									3		
DE90-only	gi|6322843	0	0	0	0.00077	0.00059	2									2		
DE90-only	gi|6322244	0	0	0	0.000479	0.000123	2									2		
DE90-only	gi|6324515	0	0	0	0.000108	5.33E-05	2									2		
DE90-only	gi|6325220	0	0	0	0.001132	0.001251	2									2.5		
DE90-only	gi|6320510	0	0	0	0.000387	2.29E-05	2									3.5		
DE90-only	gi|6325375	0	0	0	0.00016	3.34E-06	2									3		
DE90-only	gi|6322634	0	0	0	0.00004	9.83E-07	2									3		
DE90-only	gi|6320056	0	0	0	0.000137	4.15E-05	2									1		
DE90-only	gi|6323871	0	0	0	0.000096	6.59E-05	2									2.5		
DE90-only	gi|6324074	0	0	0	0.000387	6.88E-05	2									2		
DE90-only	gi|6321940	0	0	0	0.00012	5.71E-05	2									2.5		
DE90-only	gi|6321457	0	0	0	0.000573	0.000189	2									2		
DE90-only	gi|6325273	0	0	0	0.000284	2.76E-05	2									2		
DE90-only	gi|6323511	0	0	0	0.0002	4.59E-05	2									2		
DE90-only	gi|6323717	0	0	0	0.000324	5.75E-05	2									2		
DE90-only	gi|6320980	0	0	0	0.000196	0.000101	2									2		
DE90-only	gi|6320881	0	0	0	0.000332	0.000171	2									2.5		
DE90-only	gi|1431853	0	0	0	0.00033	1E-04	2									1		
DE90-only	gi|6322393	0	0	0	0.000358	0.000112	2									3		
DE90-only	gi|6321632	0	0	0	0.000129	1.04E-05	2									2		
DE90-only	gi|6320966	0	0	0	0.000354	0.000175	2									2.5		
DE90-only	gi|6321809	0	0	0	0.000533	0.000109	2									1.5		
DE90-only	gi|6325198	0	0	0	0.000435	8.95E-05	2									2		
DE90-only	gi|6319849	0	0	0	0.000423	0.000217	2									1.5		
DE90-only	gi|6323917	0	0	0	0.000091	6.2E-05	2									1.5		
DE90-only	gi|6324429	0	0	0	0.000367	0.00024	2									3		
DE90-only	gi|6324206	0	0	0	0.000074	1.32E-05	2									2.5		
DE90-only	gi|6322053	0	0	0	0.000277	6.34E-05	2									2.5		
DE90-only	gi|6321842	0	0	0	0.000595	4.55E-05	2									2		
DE90-only	gi|6321839	0	0	0	0.000398	1.93E-05	2									2		
DE90-only	gi|6323088	0	0	0	0.000172	0.000107	2									2		
DE90-only	gi|6322228	0	0	0	0.000562	0.000216	2									3		
DE90-only	gi|6322350	0	0	0	0.000143	3.08E-05	2									2.5		
DE90-only	gi|6319435	0	0	0	0.000198	4.9E-06	2									2		
DE90-only	gi|6320303	0	0	0	0.000454	0.000192	2									2		
DE90-only	gi|6321606	0	0	0	0.000215	0	1									2		
DE90-only	gi|4274231	0	0	0	0.000442	0	1									2		
DE90-only	gi|6320440	0	0	0	0.000056	0	1									2		
DE90-only	gi|6319321	0	0	0	0.00006	0	1									2		
DE90-only	gi|6319527	0	0	0	0.000157	0	1									2		
DE90-only	gi|6324727	0	0	0	0.000037	0	1									2		
DE90-only	gi|6319591	0	0	0	0.000054	0	1									2		
DE90-only	gi|6320718	0	0	0	0.001109	0	1									2		
DE90-only	gi|6322754	0	0	0	0.000156	0	1									2		
DE90-only	gi|6319926	0	0	0	0.000073	0	1									2		
DE90-only	gi|6321411	0	0	0	0.00009	0	1									2		
DE90-only	gi|6321692	0	0	0	0.000199	0	1									2		
DE90-only	gi|6324343	0	0	0	0.000017	0	1									3		

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE90-only	gi|6321865	0	0	0	0.00007	0	1									2		
DE90-only	gi|6322919	0	0	0	0.000092	0	1									2		
DE90-only	gi|6322119	0	0	0	0.000251	0	1									2		
DE90-only	gi|9755326	0	0	0	0.001318	0	1									2		
DE90-only	gi|4274228	0	0	0	0.000049	0	1									2		
DE90-only	gi|6322529	0	0	0	0.00066	0	1									2		
DE90-only	gi|6324857	0	0	0	0.000338	0	1									2		
DE90-only	gi|6321301	0	0	0	0.000113	0	1									2		
DE90-only	gi|6324859	0	0	0	0.000839	0	1									2		
DE90-only	gi|6325146	0	0	0	0.000167	0	1									2		
DE90-only	gi|6320117	0	0	0	0.000305	0	1									2		
DE90-only	gi|6320100	0	0	0	0.000105	0	1									3		
DE90-only	gi|1431852	0	0	0	0.000272	0	1									2		
DE90-only	gi|6319587	0	0	0	0.000785	0	1									2		
DE90-only	gi|6320720	0	0	0	0.000905	0	1									2		
DE90-only	gi|6321644	0	0	0	0.000223	0	1									2		
DE90-only	gi|6323725	0	0	0	0.000298	0	1									2		
DE90-only	gi|6324421	0	0	0	0.000076	0	1									2		
DE90-only	gi|6324188	0	0	0	0.000112	0	1									2		
DE90-only	gi|6321818	0	0	0	0.000088	0	1									2		
DE90-only	gi|6319899	0	0	0	0.000175	0	1									2		
DE90-only	gi|6323201	0	0	0	0.000389	0	1									2		
DE90-only	gi|6321517	0	0	0	0.0001	0	1									2		
DE90-only	gi|6323452	0	0	0	0.000275	0	1									2		
DE90-only	gi|6321995	0	0	0	0.000084	0	1									2		
DE90-only	gi|6681849	0	0	0	0.00035	0	1									1		
DE90-only	gi|6323045	0	0	0	0.00022	0	1									2		
DE90-only	gi|6324839	0	0	0	0.000529	0	1									2		
DE90-only	gi|6323635	0	0	0	0.000068	0	1									2		
DE90-only	gi|6319699	0	0	0	0.000072	0	1									3		
DE90-only	gi|6324100	0	0	0	0.00011	0	1									2		
DE90-only	gi|6324265	0	0	0	0.000127	0	1									3		
DE90-only	gi|6321924	0	0	0	0.00009	0	1									2		
DE90-only	gi|6320976	0	0	0	0.000023	0	1									2		
DE90-only	gi|6320695	0	0	0	0.000249	0	1									2		
DE90-only	gi|6320222	0	0	0	0.000125	0	1									2		
DE90-only	gi|6322839	0	0	0	0.00039	0	1									2		
DE90-only	gi|4275986	0	0	0	0.000283	0	1									2		
DE90-only	gi|8279524	0	0	0	0.000388	0	1									2		
DE90-only	gi|6323755	0	0	0	0.000049	0	1									2		
DE90-only	gi|6325112	0	0	0	0.000077	0	1									2		
DE90-only	gi|6321929	0	0	0	0.000097	0	1									2		
DE90-only	gi|6320742	0	0	0	0.000281	0	1									2		
DE90-only	gi|6320726	0	0	0	0.000129	0	1									2		
DE90-only	gi|6321905	0	0	0	0.000068	0	1									2		
DE90-only	gi|6325449	0	0	0	0.000181	0	1									2		
DE90-only	gi|6324169	0	0	0	0.000188	0	1									2		
DE90-only	gi|6324221	0	0	0	0.000123	0	1									2		
DE90-only	gi|6325298	0	0	0	0.000229	0	1									2		
DE90-only	gi|6323192	0	0	0	0.000161	0	1									2		
DE90-only	gi|6321575	0	0	0	0.000308	0	1									2		
DE90-only	gi|6325309	0	0	0	0.000999	0	1									2		
DE90-only	gi|6322559	0	0	0	0.000157	0	1									2		
DE90-only	gi|6320352	0	0	0	0.000161	0	1									2		
DE90-only	gi|6320273	0	0	0	0.00012	0	1									2		
DE90-only	gi|6319638	0	0	0	0.000123	0	1									2		

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD
295	53.73%				12.5055	2.80678	1.206539		0.0004239						3.33276836	2.215299

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE90 NSAF AVG	DE90 NSAF STD	DE90 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE90	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE90 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
noDE-only	gi|6325407	0.004077	0.001887	4	0	0	0								1			
noDE-only	gi|1431855	0.002198	0.000939	2	0	0	0								1			
noDE-only	gi|6320860	0.000294	0	1	0	0	0								1			

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD
3	0.55%	0.6569	2.333333	1.52752523				0.00219					1	0		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6321865	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322919	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322119	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|9755326	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|4274228	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322529	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321301	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324859	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325146	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320117	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320100	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431852	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319587	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320720	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321644	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323725	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324421	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324188	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321818	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319899	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323201	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321517	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323452	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321995	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6681849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323045	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324839	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323635	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319699	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324100	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324265	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321924	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320976	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320695	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320222	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322839	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|4275986	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|8279524	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323755	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325112	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321929	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320742	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320726	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321905	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325449	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324169	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324221	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325298	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323192	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321575	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325309	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322559	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320352	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320273	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319638	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325407	1	1	55	5.78	0.003711	1	1	39	5.78	0.001569	1	1	97	5.78	0.005261	1	1	101	5.78	0.005768
gi|1431855	X	X	X	X	X	1	1	13	13.56	0.001534	1	1	18	13.56	0.002862	X	X	X	X	X
gi|6320860	X	X	X	X	X	1	1	29	1.46	0.000294	X	X	X	X	X	X	X	X	X	X

Locus	DE90-1_P	DE90-1_uP	DE90-1_S	DE90-1_SC	DE90-1_NSAF	DE90-2_P	DE90-2_uP	DE90-2_S	DE90-2_SC	DE90-2_NSAF	DE90-3_P	DE90-3_uP	DE90-3_S	DE90-3_SC	DE90-3_NSAF	DE90-4_P	DE90-4_uP	DE90-4_S	DE90-4_SC	DE90-4_NSAF
gi|6321865	X	X	X	X	X	2	2	3	3.92	7E-05	X	X	X	X	X	X	X	X	X	X
gi|6322919	X	X	X	X	X	2	2	2	6.37	9.24E-05	X	X	X	X	X	X	X	X	X	X
gi|6322119	X	X	X	X	X	2	2	4	10.9	0.000251	X	X	X	X	X	X	X	X	X	X
gi|9755326	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	29.41	0.001318
gi|4274228	X	X	X	X	X	2	2	3	2.73	4.87E-05	X	X	X	X	X	X	X	X	X	X
gi|6322529	X	X	X	X	X	X	X	X	X	X	2	2	7	13.71	0.00066	X	X	X	X	X
gi|6324857	2	2	6	11.3	0.000338	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321301	X	X	X	X	X	2	2	6	2.81	0.000113	X	X	X	X	X	X	X	X	X	X
gi|6324859	X	X	X	X	X	2	2	7	24.46	0.000839	X	X	X	X	X	X	X	X	X	X
gi|6325146	X	X	X	X	X	X	X	X	X	X	2	2	3	9.01	0.000167	X	X	X	X	X
gi|6320117	X	X	X	X	X	2	2	5	12.45	0.000305	X	X	X	X	X	X	X	X	X	X
gi|6320100	X	X	X	X	X	3	3	3	9.43	0.000105	X	X	X	X	X	X	X	X	X	X
gi|1431852	X	X	X	X	X	2	2	5	8.17	0.000272	X	X	X	X	X	X	X	X	X	X
gi|6319587	2	2	14	11.69	0.000785	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320720	2	2	10	18.88	0.000905	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321644	2	2	5	11.72	0.000223	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323725	2	2	7	8.22	0.000298	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324421	2	2	2	9.06	7.57E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324188	2	2	3	7.49	0.000112	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321818	2	2	2	9.52	8.81E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319899	2	2	3	15.32	0.000175	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323201	X	X	X	X	X	2	2	7	12	0.000389	X	X	X	X	X	X	X	X	X	X
gi|6321517	X	X	X	X	X	2	2	2	8.73	0.0001	X	X	X	X	X	X	X	X	X	X
gi|6323452	X	X	X	X	X	2	2	6	7.42	0.000275	X	X	X	X	X	X	X	X	X	X
gi|6321995	X	X	X	X	X	2	2	2	6.3	8.4E-05	X	X	X	X	X	X	X	X	X	X
gi|6681849	X	X	X	X	X	X	X	X	X	X	1	1	2	7.55	0.00035	X	X	X	X	X
gi|6323045	X	X	X	X	X	X	X	X	X	X	2	2	4	9.2	0.00022	X	X	X	X	X
gi|6324839	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	23.58	0.000529
gi|6323635	2	2	2	8.09	6.76E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319699	3	3	3	8.29	7.15E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324100	2	2	3	6.78	0.00011	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324265	3	3	4	7.82	0.000127	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321924	2	2	3	6.28	9.03E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320976	2	2	2	2.63	2.27E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320695	2	2	4	10.58	0.000249	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320222	X	X	X	X	X	2	2	3	9.25	0.000125	X	X	X	X	X	X	X	X	X	X
gi|6322839	X	X	X	X	X	2	2	4	14.04	0.00039	X	X	X	X	X	X	X	X	X	X
gi|4275986	X	X	X	X	X	2	2	4	11.02	0.000283	X	X	X	X	X	X	X	X	X	X
gi|8279524	X	X	X	X	X	2	2	2	32.56	0.000388	X	X	X	X	X	X	X	X	X	X
gi|6323755	X	X	X	X	X	2	2	2	3.2	4.85E-05	X	X	X	X	X	X	X	X	X	X
gi|6325112	X	X	X	X	X	2	2	2	6.68	7.68E-05	X	X	X	X	X	X	X	X	X	X
gi|6321929	X	X	X	X	X	2	2	3	3.9	9.75E-05	X	X	X	X	X	X	X	X	X	X
gi|6320742	X	X	X	X	X	2	2	4	15.19	0.000281	X	X	X	X	X	X	X	X	X	X
gi|6320726	X	X	X	X	X	2	2	4	6.96	0.000129	X	X	X	X	X	X	X	X	X	X
gi|6321905	X	X	X	X	X	2	2	2	5.31	6.8E-05	X	X	X	X	X	X	X	X	X	X
gi|6325449	X	X	X	X	X	2	2	4	8.42	0.000181	X	X	X	X	X	X	X	X	X	X
gi|6324169	X	X	X	X	X	2	2	4	8.47	0.000188	X	X	X	X	X	X	X	X	X	X
gi|6324221	X	X	X	X	X	2	2	2	4.07	0.000123	X	X	X	X	X	X	X	X	X	X
gi|6325298	X	X	X	X	X	X	X	X	X	X	2	2	5	6.17	0.000229	X	X	X	X	X
gi|6323192	X	X	X	X	X	X	X	X	X	X	2	2	4	5.19	0.000161	X	X	X	X	X
gi|6321575	X	X	X	X	X	X	X	X	X	X	2	2	4	10.79	0.000308	X	X	X	X	X
gi|6325309	X	X	X	X	X	X	X	X	X	X	2	2	5	27.96	0.000999	X	X	X	X	X
gi|6322559	X	X	X	X	X	X	X	X	X	X	2	2	2	11.44	0.000157	X	X	X	X	X
gi|6320352	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.91	0.000161
gi|6320273	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.06	0.00012
gi|6319638	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.96	0.000123
gi|6325407	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431855	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320860	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Supporting Table 2D: Proteins detected in noDE and/or DE300 replicates

Proteins detected in both DE conditions were sorted into two groups of high and low abundances based on their averaged NSAF values measured when DE was turned off (noDE NSAF AVG).
Averages ("AVG") and standard deviations ("STD") were calculated for NSAF values and Peptide counts across the 4 replicates of a DE condition.
t-test p-values were calculated using the TTEST function in MSExcel (NSAF t-test p-Value).

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6321631	0.089245	0.0307299	4	0.06039	0.023811	4	0.676677	-1.219035	-1.049416	-0.169619	1	155	100	26.5	22	0.191217	0
High Abundance	gi|6322468	0.056902	0.0110847	4	0.041101	0.012681	4	0.722312	-1.386148	-1.244872	-0.141275	1	154	99.35483871	20.25	18.5	0.110593	0
High Abundance	gi|6321968	0.054496	0.0104952	4	0.045148	0.014147	4	0.828464	-1.345361	-1.263635	-0.081726	1	153	98.70967742	21.25	21.5	0.332634	0
High Abundance	gi|1038378	0.040924	0.0037701	4	0.023848	0.008956	4	0.582739	-1.622548	-1.388022	-0.234526	1	152	98.06451613	26.5	26.5	0.024259	1
High Abundance	gi|6319279	0.039967	0.0080495	4	0.013801	0.002355	4	0.34531	-1.860089	-1.398298	-0.461791	1	151	97.41935484	28.75	27.5	0.005138	1
High Abundance	gi|6322697	0.037728	0.004085	4	0.012924	0.002656	4	0.342557	-1.888603	-1.423336	-0.465267	1	150	96.77419355	12	13.5	0.000132	1
High Abundance	gi|6323073	0.035041	0.0052874	4	0.018835	0.002891	4	0.537513	-1.725034	-1.455424	-0.269611	1	149	96.12903226	26	27.5	0.003733	1
High Abundance	gi|6322790	0.030639	0.0056721	4	0.026014	0.010375	4	0.849049	-1.584793	-1.513725	-0.071067	1	148	95.48387097	12.75	15	0.471991	0
High Abundance	gi|6321693	0.029306	0.0078327	4	0.016265	0.005885	4	0.555006	-1.788746	-1.533043	-0.255702	1	147	94.83870968	14	14	0.040234	1
High Abundance	gi|6322409	0.028438	0.0093006	4	0.026274	0.009224	4	0.923905	-1.580474	-1.546101	-0.034373	1	146	94.19354839	9.75	12.5	0.752301	0
High Abundance	gi|6324486	0.020489	0.0049482	4	0.011939	0.005655	4	0.582703	-1.923032	-1.688479	-0.234553	1	145	93.5483871	13.75	12.25	0.063929	0
High Abundance	gi|6320255	0.016329	0.005011	4	0.010385	0.008856	4	0.635985	-1.983593	-1.78704	-0.196553	1	144	92.90322581	9.75	7.25	0.298055	0
High Abundance	gi|6321464	0.016263	0.0104511	4	0.003109	0.000664	4	0.19117	-2.507379	-1.788799	-0.71858	1	143	92.25806452	2.5	3.5	0.08609	0
High Abundance	gi|9755341	0.015824	0.0025789	4	0.003722	0.001815	4	0.235212	-2.429224	-1.800684	-0.62854	1	142	91.61290323	5	3.75	0.000426	1
High Abundance	gi|6320359	0.013516	0.0015829	4	0.007066	0.004702	4	0.522788	-2.150826	-1.869152	-0.281675	1	141	90.96774194	5.75	4.5	0.065443	0
High Abundance	gi|6323138	0.013418	0.0035944	4	0.007481	0.002318	4	0.557535	-2.12604	-1.872312	-0.253728	1	140	90.32258065	5.5	5.5	0.038037	1
High Abundance	gi|6323196	0.013086	0.0040826	4	0.005736	0.000713	4	0.438331	-2.241391	-1.883193	-0.358198	1	139	89.67741935	4.5	3.75	0.03471	1
High Abundance	gi|6323004	0.012217	0.0029473	4	0.007559	0.001022	4	0.618728	-2.121536	-1.913035	-0.2085	1	138	89.03225806	23.5	23.25	0.04453	1
High Abundance	gi|6319314	0.011825	0.0031741	4	0.006978	0.001046	4	0.590106	-2.156269	-1.927199	-0.22907	1	137	88.38709677	22.25	22.25	0.049358	1
High Abundance	gi|6322978	0.009927	0.0035095	4	0.006266	0.003676	4	0.631208	-2.20301	-2.003182	-0.199828	1	136	87.74193548	4.25	4	0.199796	0
High Abundance	gi|6323613	0.009356	0.0019107	4	0.006763	0.002088	4	0.722852	-2.169861	-2.02891	-0.140951	1	135	87.09677419	5.25	5.5	0.11688	0
High Abundance	gi|6320269	0.00911	0.0027517	4	0.001776	0.00096	3	0.194951	-2.750557	-2.040482	-0.710075	1	134	86.4516129	5.5	3.666667	0.008324	1
High Abundance	gi|6321408	0.008197	0.0018995	4	0.007728	0.002177	4	0.942784	-2.111933	-2.086345	-0.025588	1	133	85.80645161	2.75	4.5	0.756802	0
High Abundance	gi|6319673	0.00789	0.0006584	4	0.005278	0.000638	4	0.668948	-2.277531	-2.102923	-0.174608	1	131	84.51612903	13.75	13.5	0.001266	1
High Abundance	gi|6320148	0.00789	0.001499	4	0.006028	0.000468	4	0.764005	-2.219827	-2.102923	-0.116904	1	132	85.16129032	11	9.25	0.084349	0
High Abundance	gi|6324027	0.007695	0.0023053	4	0.00759	0.003523	4	0.986355	-2.119758	-2.113791	-0.005967	1	130	83.87096774	4.5	4.25	0.962331	0
High Abundance	gi|6320963	0.007322	0.0023735	4	0.005004	0.001998	4	0.68342	-2.300683	-2.13537	-0.165312	1	129	83.22580645	3	5.75	0.187228	0
High Abundance	gi|6320122	0.006788	0.0042374	3	0.002977	0.001839	3	0.438568	-2.526221	-2.168258	-0.357963	1	128	82.58064516	1	1	0.256869	0
High Abundance	gi|6324670	0.006571	0.0018952	4	0.002675	0.000731	4	0.407092	-2.572676	-2.182369	-0.390308	1	127	81.93548387	5.25	4.25	0.019675	1
High Abundance	gi|6323615	0.006483	0.0019291	4	0.003655	0.002259	4	0.563782	-2.437113	-2.188224	-0.248889	1	126	81.29032258	7.25	5.75	0.106818	0
High Abundance	gi|6322271	0.006476	0.0026614	4	0.004095	0.001309	4	0.632335	-2.387746	-2.188693	-0.199053	1	125	80.64516129	2.25	2.5	0.177554	0
High Abundance	gi|6319505	0.006391	0.0015172	4	0.00303	0.000581	4	0.474104	-2.518557	-2.194431	-0.324126	1	124	80	9.75	9	0.015484	1
High Abundance	gi|6320215	0.006169	0.0015034	4	0.00331	0.000717	4	0.536554	-2.480172	-2.209785	-0.270387	1	123	79.35483871	8.75	9.25	0.023627	1
High Abundance	gi|6320128	0.006127	0.0029448	4	0.00301	0.002167	4	0.491268	-2.521434	-2.212752	-0.308681	1	122	78.70967742	1.75	1.75	0.143418	0
High Abundance	gi|6323294	0.006126	0.0027463	4	0.005798	0.003536	4	0.946458	-2.236722	-2.212823	-0.023899	1	121	78.06451613	2.5	2.25	0.888434	0
High Abundance	gi|6321025	0.00602	0.0021373	4	0.003624	0.000658	4	0.601993	-2.440812	-2.220404	-0.220408	1	120	77.41935484	8.25	8	0.107187	0
High Abundance	gi|6320590	0.005993	0.002091	4	0.007304	0.000832	4	1.218755	-2.136439	-2.222356	0.085916	1	119	76.77419355	3	4.5	0.309672	0
High Abundance	gi|6322583	0.005947	0.002258	4	0.007281	0.002709	4	1.224315	-2.137809	-2.225702	0.087893	1	118	76.12903226	5.75	4.25	0.478893	0
High Abundance	gi|6324085	0.005945	0	1	0.002255	0.00123	3	0.37931	-2.646853	-2.225848	-0.421005	1	117	75.48387097	1	2.666667		
High Abundance	gi|6322794	0.005885	0.0011539	4	0.003187	0.00149	4	0.541546	-2.496618	-2.230254	-0.266364	1	116	74.83870968	3.25	3.5	0.030689	1
High Abundance	gi|6320655	0.005876	0.001226	4	0.005506	0.001753	4	0.937032	-2.259164	-2.230918	-0.028246	1	115	74.19354839	5.25	6.5	0.742593	0
High Abundance	gi|6320304	0.005749	0.0021378	4	0.003112	0.000874	4	0.541312	-2.50696	-2.240408	-0.266553	1	114	73.5483871	7.5	6.75	0.084797	0
High Abundance	gi|6321184	0.005739	0.0024514	4	0.005175	0.001119	4	0.901725	-2.28609	-2.241164	-0.044926	1	113	72.90322581	11.25	16.5	0.696072	0
High Abundance	gi|6320949	0.005297	0.0012303	4	0.003296	0.001499	4	0.622239	-2.482013	-2.27597	-0.206043	1	112	72.25806452	5	5	0.086242	0
High Abundance	gi|6324120	0.005255	0.0010446	4	0.004808	0.000609	4	0.914938	-2.318036	-2.279427	-0.038608	1	111	71.61290323	15	15.75	0.493621	0
High Abundance	gi|6319972	0.005174	0.0010909	4	0.004504	0.000682	4	0.870506	-2.346402	-2.286174	-0.060228	1	110	70.96774194	15	15	0.345233	0
High Abundance	gi|6319483	0.004895	0.0014228	4	0.007991	0.00212	4	1.632482	-2.097399	-2.310247	0.212848	1	109	70.32258065	7	11	0.057418	0
High Abundance	gi|6321524	0.004766	0.0017336	4	0.003212	0.001061	4	0.67394	-2.493224	-2.321846	-0.171379	1	108	69.67741935	3	3.5	0.18721	0
High Abundance	gi|6324534	0.00454	0.0011418	4	0.006237	0.004253	4	1.373789	-2.205024	-2.342944	0.13792	1	107	69.03225806	3.75	3.25	0.490627	0
High Abundance	gi|6323077	0.004456	0.0007734	4	0.001938	0.00068	4	0.434919	-2.712646	-2.351055	-0.361591	1	106	68.38709677	5	4.25	0.002867	1
High Abundance	gi|6323072	0.004322	0.0016035	4	0.004902	0.002746	4	1.134197	-2.309627	-2.364315	0.054689	1	105	67.74193548	5.25	4.25	0.730753	0
High Abundance	gi|6319559	0.004142	0.000987	4	0.002966	0.001623	4	0.716079	-2.527829	-2.38279	-0.145039	1	104	67.09677419	4.75	4.25	0.271197	0
High Abundance	gi|6322984	0.004123	0.0007924	4	0.003089	0.001454	4	0.749212	-2.510182	-2.384787	-0.125395	1	103	66.4516129	7.75	9.25	0.270992	0
High Abundance	gi|6321754	0.004062	0.0007343	4	0.002862	0.001337	4	0.704579	-2.54333	-2.39126	-0.15207	1	102	65.80645161	6.75	8.5	0.180705	0
High Abundance	gi|8655890	0.004039	0.0022002	4	0.004631	0.000638	4	0.93637	-2.422278	-2.393726	-0.028552	1	100	64.51612903	6.5	6.5	0.636248	0
High Abundance	gi|6324151	0.004039	0.0008696	4	0.003782	0.00121	4	1.146571	-2.334325	-2.393726	0.059401	1	101	65.16129032	8.75	8	0.74296	0
High Abundance	gi|6323104	0.003953	0.0014655	3	0.001892	0.000673	4	0.478624	-2.723079	-2.403073	-0.320006	1	99	63.87096774	5.666666667	3.25	0.120621	0
High Abundance	gi|6323090	0.003925	0.0006235	4	0.004091	0.000712	3	1.042293	-2.388171	-2.40616	0.01799	1	98	63.22580645	1.75	2	0.764416	0
High Abundance	gi|6320228	0.003915	0.0009042	4	0.002348	0.00113	4	0.599745	-2.629302	-2.407268	-0.222034	1	97	62.58064516	6.75	4.5	0.075677	0
High Abundance	gi|1038379	0.003833	0.0015058	4	0.005561	0.000824	4	1.450822	-2.254847	-2.416461	0.161614	1	96	61.93548387	5.25	4.25	0.104483	0
High Abundance	gi|6325196	0.003811	0.0012089	4	0.005241	0.00064	4	1.37523	-2.280586	-2.418961	0.138375	1	95	61.29032258	17.25	17.75	0.09613	0
High Abundance	gi|6323763	0.003676	0.0008584	4	0.004375	0.001052	4	1.190152	-2.359022	-2.434624	0.075603	1	94	60.64516129	8.25	7.75	0.345127	0
High Abundance	gi|6319396	0.003464	0.0013192	4	0.00172	0.000697	4	0.496536	-2.764472	-2.460422	-0.304049	1	93	60	5.25	4.75	0.071612	0
High Abundance	gi|6320950	0.00335	0.0012392	4	0.002197	0.000776	4	0.655821	-2.65817	-2.474955	-0.183215	1	92	59.35483871	4.25	6	0.175199	0
High Abundance	gi|6323163	0.003242	0.0022117	4	0.002273	0.000541	4	0.70111	-2.643401	-2.489187	-0.154214	1	91	58.70967742	5.5	3.75	0.451028	0
High Abundance	gi|6323371	0.003123	0.0010263	4	0.001532	0.000468	3	0.490554	-2.814741	-2.505428	-0.309313	1	90	58.06451613	4.25	4.666667	0.046824	1
High Abundance	gi|6321977	0.003107	0.0005829	4	0.003121	0.00094	4	1.004506	-2.505706	-2.507659	0.001953	1	89	57.41935484	8.5	13.75	0.980911	0
High Abundance	gi|6319315	0.003028	0.0005642	4	0.005004	0.002872	4	1.652576	-2.300683	-2.518844	0.218161	1	88	56.77419355	6	6	0.263778	0
High Abundance	gi|6323057	0.003025	0.0004902	4	0.003442	0.001372	4	1.137851	-2.463189	-2.519275	0.056085	1	87	56.12903226	4	3.5	0.599464	0
High Abundance	gi|6321315	0.00302	0.0018134	4	0.004854	0.002416	4	1.607285	-2.3139	-2.519993	0.206093	1	86	55.48387097	6	6.5	0.273587	0
High Abundance	gi|6320679	0.003006	0.0017893	4	0.00433	0.001459	4	1.440452	-2.363512	-2.522011	0.158499	1	85	54.83870968	3.5	4.25	0.296913	0
High Abundance	gi|1431847	0.003005	0.0009009	4	0.00419	0.001297	4	1.394343	-2.377786	-2.522156	0.14437	1	84	54.19354839	8	10.75	0.189868	0
High Abundance	gi|6322605	0.002896	0.0011085	4	0.00299	0.001176	4	1.032459	-2.524329	-2.538201	0.013873	1	83	53.5483871	6.5	5.25	0.91148	0
High Abundance	gi|6321772	0.002821	0.00075	4	0.002809	0.0014	4	0.995746	-2.551448	-2.549597	-0.001851	1	82	52.90322581	4.25	3.75	0.988749	0
High Abundance	gi|6322120	0.002803	0.0005083	4	0.005953	0.001428	4	2.123796	-2.225264	-2.552377	0.327113	1	81	52.25806452	3.5	4	0.016227	1
High Abundance	gi|6324445	0.002779	0.0007174	4	0.002266	7.67E-05	3	0.815401	-2.64474	-2.556111	-0.088629	1	80	51.61290323	3.75	5	0.248269	0
High Abundance	gi|6322564	0.002737	0.0007168	4	0.004192	0.001935	4	1.531604	-2.377579	-2.562725	0.185146	1	79	50.96774194	3.75	4.25	0.234666	0
High Abundance	gi|6320073	0.002687	0.0007479	4	0.005669	0	1	2.109788	-2.246494	-2.570732	0.324239	1	78	50.32258065	1	1		
High Abundance	gi|6322847	0.002661	0.0009261	3	0.004323	0.002324	4	1.624577	-2.364215	-2.574955	0.21074	1	77	49.67741935	3.666666667	3.75	0.261584	0
High Abundance	gi|6323387	0.002605	0.0007836	4	0.005891	0.001952	4	2.26142	-2.229811	-2.584192	0.354381	1	76	49.03225806	10	13.5	0.036083	1
High Abundance	gi|6321249	0.002598	0.0005352	4	0.001738	0.000596	2	0.627406	-2.787812	-2.585361	-0.202452	1	74	47.74193548	2	3	0.235671	0
High Abundance	gi|6320978	0.002598	0.0005352	4	0.00163	0.000444	2	0.668976	-2.75995	-2.585361	-0.174589	1	75	48.38709677	2	2.5	0.116159	0
High Abundance	gi|6321786	0.002568	0.0008615	3	0.00423	0.002451	3	1.647196	-2.37366	-2.590405	0.216745	1	73	47.09677419	3	3.333333	0.363401	0
High Abundance	gi|6323474	0.002537	0.000832	4	0.002644	0.001475	4	1.042176	-2.577739	-2.59568	0.017941	1	72	46.4516129	7.5	6	0.904519	0
High Abundance	gi|6323386	0.002527	0.0013219	4	0.003058	0.001278	4	1.210131	-2.514563	-2.597395	0.082832	1	71	45.80645161	5.5	8.75	0.584891	0
High Abundance	gi|6323577	0.00252	0.0008462	4	0.003068	0.001265	3	1.21746	-2.513145	-2.598599	0.085455	1	70	45.16129032	7.25	7.333333	0.558368	0
High Abundance	gi|6325126	0.002511	0.0009648	4	0.002425	0.000427	4	0.965751	-2.615288	-2.600153	-0.015135	1	69	44.51612903	4.5	5.25	0.87861	0
High Abundance	gi|3736268	0.002496	0.0006565	4	0.003443	0.001725	4	1.379407	-2.463063	-2.602755	0.139692	1	68	43.87096774	3.75	5	0.364691	0
High Abundance	gi|6320065	0.002434	0.0013313	4	0.004214	0.001146	4	1.731306	-2.375305	-2.613679	0.238374	1	67	43.22580645	2.25	3	0.090118	0
High Abundance	gi|6323886	0.00243	0.0004677	3	0.004148	0.003097	2	1.706996	-2.382161	-2.614394	0.232232	1	66	42.58064516	2.333333333	3	0.575692	0
High Abundance	gi|6321335	0.002424	0.0003522	4	0.001189	0.000171	4	0.490512	-2.924818	-2.615467	-0.309351	1	65	41.93548387	3.25	2.75	0.002439	1
High Abundance	gi|6322668	0.002273	0.0004578	4	0.003795	0.001308	4	1.6696	-2.420788	-2.643401	0.222612	1	64	41.29032258	4	4.75	0.098078	0
High Abundance	gi|6321362	0.00223	0.0006323	4	0.002453	0.000428	4	1.1	-2.610302	-2.651695	0.041393	1	63	40.64516129	5.75	5.25	0.584255	0
High Abundance	gi|6322138	0.002207	0.000866	4	0.004937	0.003006	4	2.236973	-2.306537	-2.656198	0.349661	1	62	40	3.5	5.75	0.16624	0
High Abundance	gi|6322284	0.002206	0.0004999	4	0.003581	0.001351	4	1.6233	-2.445996	-2.656394	0.210399	1	61	39.35483871	3.75	4.25	0.132485	0
High Abundance	gi|6325058	0.002175	0.0006199	4	0.00232	0.000462	4	1.066667	-2.634512	-2.662541	0.028029	1	60	38.70967742	5.25	5	0.722602	0
High Abundance	gi|6321648	0.002154	0.0003065	4	0.0014	0.000264	4	0.649954	-2.853872	-2.666754	-0.187118	1	59	38.06451613	4	2.25	0.010158	1
High Abundance	gi|6323376	0.002105	0.0002353	4	0.001427	0.000718	3	0.67791	-2.845576	-2.676748	-0.168828	1	58	37.41935484	3	3	0.238633	0
High Abundance	gi|6323840	0.002039	0.0005044	4	0.002705	0.001042	4	1.326631	-2.567833	-2.690583	0.12275	1	57	36.77419355	14.75	15.5	0.309253	0
High Abundance	gi|1160064	0.002009	0.0002418	4	0.001427	0.000718	3	0.710304	-2.845576	-2.69702	-0.148556	1	56	36.12903226	2.75	3	0.293069	0
High Abundance	gi|6320801	0.001985	0.0005144	4	0.002357	0.001246	3	1.187406	-2.62764	-2.702239	0.074599	1	55	35.48387097	1	2.333333	0.665954	0
High Abundance	gi|6319666	0.001922	0.0005228	4	0.00194	0.00086	4	1.009365	-2.712198	-2.716247	0.004048	1	54	34.83870968	4.25	4	0.973708	0
High Abundance	gi|6321291	0.0019	0.0009582	4	0.003445	0.001366	4	1.813158	-2.462811	-2.721246	0.258436	1	53	34.19354839	3.5	3.75	0.118989	0
High Abundance	gi|6319965	0.001871	0	1	0.000906	0	1	0.484233	-3.042872	-2.727926	-0.314946	1	52	33.5483871	1	3		
High Abundance	gi|6325016	0.001829	0.000394	4	0.002383	0.000861	4	1.302898	-2.622876	-2.737786	0.11491	1	51	32.90322581	12.5	14.25	0.304046	0
High Abundance	gi|6325176	0.001797	0.0003761	4	0.001676	0.000814	4	0.932666	-2.775726	-2.745452	-0.030274	1	50	32.25806452	4	3.5	0.799427	0
High Abundance	gi|6325389	0.001781	0.0013141	4	0.004697	0.001872	4	2.637282	-2.328179	-2.749336	0.421157	1	49	31.61290323	2.25	2	0.048	1

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6324452	0.001776	0.0007938	4	0.001934	0.000519	4	1.088964	-2.713544	-2.750557	0.037014	1	48	30.96774194	2	2	0.752937	0
High Abundance	gi|6320905	0.001754	0.0007026	4	0.00102	0.000605	4	0.581528	-2.9914	-2.75597	-0.235429	1	47	30.32258065	2.25	2.25	0.165707	0
High Abundance	gi|6321407	0.001753	0.0001109	3	0.003106	0.00179	3	1.77182	-2.507799	-2.756218	0.24842	1	45	29.03225806	1.333333333	3.666667	0.320525	0
High Abundance	gi|6321587	0.001753	0.0001109	3	0.003219	0.001813	3	1.836281	-2.492279	-2.756218	0.263939	1	46	29.67741935	1.333333333	3.666667	0.296219	0
High Abundance	gi|6324756	0.001742	0.0002751	2	0.005077	0	1	2.914466	-2.294393	-2.758952	0.464559	1	44	28.38709677	2	1		
High Abundance	gi|6323357	0.001671	0.0002665	3	0.004726	0.001211	3	2.828247	-2.325506	-2.777024	0.451517	1	43	27.74193548	1	2.666667	0.043066	1
High Abundance	gi|6324262	0.001621	0.0007381	4	0.002838	0.001331	4	1.750771	-2.546988	-2.790217	0.243229	1	42	27.09677419	2.75	3.75	0.174392	0
High Abundance	gi|6320882	0.001527	0.0003252	4	0.002236	0.000844	4	1.464309	-2.650528	-2.816161	0.165633	1	41	26.4516129	7.75	7	0.194536	0
High Abundance	gi|6323288	0.001526	0.000417	4	0.003581	0.001562	4	2.346658	-2.445996	-2.816445	0.37045	1	40	25.80645161	11	15.25	0.074145	0
High Abundance	gi|6324194	0.00149	0.0010164	3	0.002621	0.001075	2	1.75906	-2.581533	-2.826814	0.245281	1	39	25.16129032	1	2.5	0.352448	0
High Abundance	gi|6324637	0.001484	0.0008663	4	0.003488	0.001214	4	2.350404	-2.457424	-2.828566	0.371143	1	38	24.51612903	7.25	9.25	0.040006	1
High Abundance	gi|6321679	0.001482	0.0007832	4	0.00341	0.000557	4	2.300945	-2.467246	-2.829152	0.361906	1	37	23.87096774	9.25	21.5	0.008654	1
High Abundance	gi|6320781	0.001401	0.0003751	4	0.00167	0.001039	3	1.192006	-2.777284	-2.853562	0.076278	1	36	23.22580645	4	3.333333	0.703353	0
High Abundance	gi|6319814	0.00138	0	1	0.002852	0.002309	4	2.066667	-2.54485	-2.860121	0.31527	1	35	22.58064516	1	2.75		
High Abundance	gi|1431847	0.001378	0.0004714	3	0.001494	0.000818	4	1.08418	-2.825649	-2.860751	0.035101	1	34	21.93548387	2.333333333	4	0.82332	0
High Abundance	gi|6325300	0.001286	0.0003953	3	0.001327	0.000297	2	1.031882	-2.877129	-2.890759	0.01363	1	33	21.29032258	3	2.5	0.904816	0
High Abundance	gi|6325006	0.001251	0.0009425	3	0.003259	0.001501	3	2.605116	-2.486916	-2.902743	0.415827	1	32	20.64516129	2.666666667	2.666667	0.134431	0
High Abundance	gi|6324945	0.00122	0.0009316	4	0.002476	0.000484	4	2.029508	-2.606249	-2.91364	0.307391	1	31	20	3	4	0.067694	0
High Abundance	gi|6324260	0.001209	0.0006283	4	0.001968	0.000745	4	1.627792	-2.705975	-2.917574	0.211599	1	30	19.35483871	2.75	2.75	0.171566	0
High Abundance	gi|6319307	0.001205	0.0006478	4	0.001409	0.000957	4	1.169295	-2.851089	-2.919013	0.067924	1	29	18.70967742	3.75	4	0.738388	0
High Abundance	gi|6320121	0.001197	0.0005492	4	0.001781	0.000263	4	1.487886	-2.749336	-2.921906	0.17257	1	28	18.06451613	4.5	2.75	0.122524	0
High Abundance	gi|6323567	0.001187	0.0006256	3	0.002138	0.000618	4	1.801179	-2.669992	-2.925549	0.255557	1	27	17.41935484	2.333333333	4	0.109499	0
High Abundance	gi|6324533	0.001167	0.0004606	3	0.003212	0.000998	4	2.752356	-2.493224	-2.932929	0.439705	1	26	16.77419355	2.666666667	3.75	0.018937	1
High Abundance	gi|1431855	0.001152	0.0002631	4	0.001788	0.000541	4	1.552083	-2.747632	-2.938548	0.190915	1	25	16.12903226	4.25	2.75	0.096468	0
High Abundance	gi|6322325	0.00111	0.0002411	2	0.005819	0.002011	3	5.242342	-2.235152	-2.954677	0.719525	2	93	100	3.5	2.333333	0.05304	0
High Abundance	gi|6324463	0.001107	0.0004562	4	0.001777	0.000584	2	1.605239	-2.750313	-2.955852	0.20554	1	24	15.48387097	3.5	3.5	0.31484	0
High Abundance	gi|6323087	0.00108	0.0002282	4	0.001491	0.000443	4	1.380556	-2.826522	-2.966576	0.140054	1	23	14.83870968	7.75	6.5	0.16642	0
High Abundance	gi|6319585	0.001056	0.0004812	3	0.002375	0.001731	4	2.249053	-2.624336	-2.976336	0.352	1	22	14.19354839	1.666666667	2.75	0.227947	0
High Abundance	gi|6324808	0.00104	0.0005113	3	0.00232	0.000946	2	2.230769	-2.634512	-2.982967	0.348455	1	21	13.5483871	3.333333333	2.5	0.272262	0
High Abundance	gi|6319378	0.001033	0.0001728	2	0.001738	0.000652	3	1.682478	-2.75995	-2.9859	0.225949	1	20	12.90322581	1.5	2	0.195728	0
High Abundance	gi|6319806	0.001028	0.0007237	4	0.002943	0.000425	4	2.86284	-2.53121	-2.988007	0.456797	1	19	12.25806452	4.25	10.75	0.006504	1
High Abundance	gi|6322599	0.001004	0.0005152	4	0.001328	0.000794	4	1.322709	-2.876802	-2.998266	0.121464	1	18	11.61290323	4	4.75	0.523346	0
High Abundance	gi|6323481	0.000987	0.0006673	4	0.001765	0.000637	4	1.788247	-2.753255	-3.005683	0.252428	1	17	10.96774194	2.5	3.25	0.142682	0
High Abundance	gi|6325114	0.000969	0.0003805	3	0.002488	0.002118	2	2.567595	-2.60415	-3.013676	0.409527	1	16	10.32258065	3.666666667	2.5	0.493187	0
High Abundance	gi|6322910	0.000964	0.0004746	4	0.003951	0.000158	2	4.098548	-2.403293	-3.015923	0.61263	2	92	98.92473118	2.75	2.5	0.000388	1
High Abundance	gi|6324707	0.00096	0.0002577	4	0.002346	0.001033	4	2.44375	-2.629672	-3.017729	0.388057	1	15	9.677419355	14.5	18.75	0.07112	0
High Abundance	gi|6324298	0.000959	0	1	0.002312	0.000742	4	2.410845	-2.636012	-3.018181	0.382169	1	14	9.032258065	2	2.5		
High Abundance	gi|6320226	0.000944	0.0005776	4	0.002206	0.000129	4	2.336864	-2.656394	-3.025028	0.368634	1	13	8.387096774	7	9.5	0.019499	1
High Abundance	gi|6322505	0.000944	0.0002374	4	0.002736	0.000919	4	2.898305	-2.562884	-3.025028	0.462144	2	91	97.84946237	11	14	0.026079	1
High Abundance	gi|6324923	0.00094	0.0002014	4	0.000754	0.000501	4	0.802128	-3.122629	-3.026872	-0.095757	1	12	7.741935484	1.5	2.75	0.528304	0
High Abundance	gi|6321474	0.00093	0.0008341	2	0.001266	0.000119	2	1.36129	-2.897566	-3.031517	0.133951	1	11	7.096774194	1	2	0.670811	0
High Abundance	gi|6325331	0.000911	0.0005313	4	0.0018	0.000434	4	1.975851	-2.744727	-3.040482	0.295754	1	10	6.451612903	5.75	9.5	0.042586	1
High Abundance	gi|6323729	0.000886	0.0002884	4	0.000934	0.000409	4	1.054176	-3.029653	-3.052566	0.022913	1	9	5.806451613	1	3.25	0.85379	0
High Abundance	gi|6321987	0.000884	0.0004026	3	0.002716	0.001458	4	3.072398	-2.56607	-3.053548	0.487478	2	90	96.77419355	1.666666667	3	0.082251	0
High Abundance	gi|6323848	0.000853	5.087E-05	2	0.004343	0.000643	2	5.091442	-2.36221	-3.069051	0.706841	2	89	95.69892473	3.5	3.5	0.080858	0
High Abundance	gi|6323324	0.00085	0.0005116	4	0.001364	0.000627	4	1.604706	-2.865186	-3.070581	0.205395	1	8	5.161290323	2.75	4	0.252866	0
High Abundance	gi|6323391	0.000799	0	1	0.000554	0.000333	3	0.693367	-3.25649	-3.097453	-0.159037	1	7	4.516129032	2	4		

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Proteins in Group)
154	28.89%	99.3883	3.7207792	0.681182682	79.2676	3.675325	0.694357	0.006454	0.0051472				6.168290043	5.537146549	6.69534632	5.713867	32	21.77%

Low Abundance	gi|6324233	0.000787	0.00044	4	0.003582	0.00174	4	4.551461	-2.445874	-3.104025	0.658151	2	88	94.62365591	3.75	4.75	0.044803	1
Low Abundance	gi|6321973	0.000785	0.0002581	4	0.002252	0.000844	4	2.86879	-2.647432	-3.10513	0.457699	2	87	93.5483871	5.25	7.25	0.034855	1
Low Abundance	gi|6322058	0.000758	0.0005851	4	0.001434	0.000905	4	1.891821	-2.843451	-3.120331	0.27688	1	6	3.870967742	2	3	0.263494	0
Low Abundance	gi|6321563	0.000731	0.0002768	4	0.001185	0.000343	4	1.621067	-2.926282	-3.136083	0.209801	1	5	3.225806452	4.5	7.5	0.087423	0
Low Abundance	gi|6322002	0.000706	0.0002692	4	0.002277	0.000746	4	3.225212	-2.642637	-3.151195	0.508558	2	86	92.47311828	4	7	0.018691	1
Low Abundance	gi|6323861	0.000695	0.0001588	4	0.001841	0.000427	4	2.648921	-2.734946	-3.158015	0.423069	2	85	91.39784946	8	17	0.008331	1
Low Abundance	gi|6325036	0.000678	0.0005354	4	0.001592	0.000779	4	2.348083	-2.798057	-3.16877	0.370713	2	84	90.32258065	3	3.25	0.107282	0
Low Abundance	gi|6322565	0.000592	0.0003229	4	0.002013	0.001306	4	3.400338	-2.696156	-3.227678	0.531522	2	83	89.24731183	3.75	6.5	0.115171	0
Low Abundance	gi|6324907	0.000581	0.0001725	3	0.000977	0.000633	3	1.681583	-3.010105	-3.235824	0.225718	1	4	2.580645161	2.666666667	3.666667	0.393577	0
Low Abundance	gi|6323464	0.000559	0.0003827	4	0.003303	0.000902	4	5.908766	-2.481091	-3.252588	0.771497	2	82	88.17204301	5.25	10.75	0.004827	1
Low Abundance	gi|6323208	0.000546	0.0002841	3	0.001339	0.000702	4	2.452381	-2.873219	-3.262807	0.389588	2	81	87.09677419	2	2.5	0.10724	0
Low Abundance	gi|6325178	0.000537	0.0002627	4	0.001317	0.000593	4	2.452514	-2.880414	-3.270026	0.389611	2	79	84.94623656	3.25	3	0.071707	0
Low Abundance	gi|6319668	0.000537	0.0002627	4	0.001317	0.000593	4	2.452514	-2.880414	-3.270026	0.389611	2	80	86.02150538	3.25	3	0.071707	0
Low Abundance	gi|6320846	0.000525	0	1	0.000822	0	1	1.565714	-3.085128	-3.279841	0.194713	1	3	1.935483871	2	2		
Low Abundance	gi|6325229	0.000513	0.0001867	2	0.003625	0.000613	4	7.066277	-2.440692	-3.289883	0.849191	2	78	83.87096774	1.5	9.25	0.000913	1
Low Abundance	gi|6322608	0.00049	0.0001071	4	0.001404	0.000242	4	2.865306	-2.852633	-3.309804	0.457171	2	77	82.79569892	2.75	5.75	0.002057	1
Low Abundance	gi|6322912	0.000485	7.247E-05	4	0.003115	0.001163	4	6.42268	-2.506542	-3.314258	0.807716	2	76	81.72043011	4.5	9.75	0.019992	1
Low Abundance	gi|6319603	0.000456	0.0003563	3	0.002901	0.000777	4	6.361842	-2.537452	-3.341035	0.803583	2	74	79.56989247	5.666666667	10.5	0.00384	1
Low Abundance	gi|6321522	0.000456	0.0002485	3	0.00186	0.000403	2	4.078947	-2.730487	-3.341035	0.610548	2	75	80.64516129	2	3	0.076575	0
Low Abundance	gi|6323585	0.000454	0.0001934	4	0.002098	0.000947	4	4.621145	-2.678195	-3.342944	0.66475	2	73	78.49462366	4.25	8.75	0.037528	1
Low Abundance	gi|6325167	0.000444	0.0003366	4	0.002562	0.00046	4	5.77027	-2.591421	-3.352617	0.761196	2	72	77.41935484	2.75	3.5	0.00046	1
Low Abundance	gi|6325403	0.00044	7.871E-05	4	0.001532	0.000739	4	3.481818	-2.814741	-3.356547	0.541806	2	71	76.34408602	4.75	9.75	0.058847	0
Low Abundance	gi|6319901	0.000432	0.0001175	4	0.001949	0.000778	4	4.511574	-2.710188	-3.364516	0.654328	2	70	75.2688172	5	8.75	0.0284	1
Low Abundance	gi|6322783	0.000431	3.004E-05	2	0.001737	0.000763	3	4.030162	-2.7602	-3.365523	0.605323	2	69	74.19354839	2	3	0.09718	0
Low Abundance	gi|6323470	0.000426	7.068E-05	2	0.001765	0.000525	4	4.143192	-2.753255	-3.37059	0.617335	2	68	73.11827957	2.5	7.5	0.013004	1
Low Abundance	gi|6319726	0.000424	0.0002274	3	0.000906	0.000283	4	2.136792	-3.042872	-3.372634	0.329762	2	67	72.04301075	2.666666667	5	0.055341	0
Low Abundance	gi|6323554	0.000418	0	1	0.000376	0.000227	4	0.899522	-3.424812	-3.378824	-0.045988	1	2	1.290322581	1	3		
Low Abundance	gi|6324951	0.000404	0.0002468	4	0.003447	0.002198	4	8.532178	-2.462559	-3.393619	0.93106	2	66	70.96774194	5	12	0.068677	0
Low Abundance	gi|6320362	0.000395	0.0001931	4	0.001501	0.00077	4	3.8	-2.823619	-3.403403	0.579784	2	65	69.89247312	3.75	6.75	0.059929	0
Low Abundance	gi|6325326	0.000385	8.272E-05	3	0.002033	0.000993	4	5.280519	-2.691863	-3.414539	0.722677	2	64	68.8172043	2.333333333	5.5	0.044325	1
Low Abundance	gi|6320936	0.000379	8.388E-05	4	0.002813	0.000608	4	7.422164	-2.55083	-3.421361	0.870531	2	63	67.74193548	6.5	18	0.003655	1
Low Abundance	gi|6324776	0.000359	0	1	0.000701	0	1	1.952646	-3.154282	-3.444906	0.290624	2	62	66.66666667	2	1		
Low Abundance	gi|6321013	0.000356	3.694E-05	4	0.001612	0.00036	4	4.52809	-2.792635	-3.44855	0.655915	2	61	65.59139785	4.75	8	0.005729	1
Low Abundance	gi|6322666	0.000324	0.0001428	4	0.001574	0.000385	4	4.858025	-2.802995	-3.489455	0.68646	2	60	64.51612903	12.5	31.25	0.0043	1
Low Abundance	gi|6322732	0.00032	0	1	0.000362	0	1	1.13125	-3.441291	-3.49485	0.053559	1	1	0.64516129	2	2		
Low Abundance	gi|6325290	0.00031	6.308E-05	3	0.000806	0.000602	4	2.6	-3.093665	-3.508638	0.414973	2	59	63.44086022	1	3.75	0.198257	0
Low Abundance	gi|6320016	0.000304	0.0002023	4	0.001351	0.000327	4	4.444079	-2.869345	-3.517126	0.647782	2	57	61.29032258	6	15.5	0.002814	1
Low Abundance	gi|6320710	0.000304	0	1	0.000756	0.000362	4	2.486842	-3.121478	-3.517126	0.395648	2	58	62.3655914	1	3.5		
Low Abundance	gi|6319625	0.000275	7.403E-05	2	0.001178	0.000347	4	4.283636	-2.928855	-3.560667	0.631813	2	56	60.21505376	2.5	4	0.010746	1
Low Abundance	gi|1431857	0.000271	0.000214	4	0.002135	0.000662	4	7.878229	-2.670602	-3.567031	0.896429	2	55	59.13978495	2	7.5	0.007728	1
Low Abundance	gi|6322434	0.00026	0.0002101	4	0.000819	9.84E-05	4	3.15	-3.086716	-3.585027	0.498311	2	53	56.98924731	2	5	0.007301	1
Low Abundance	gi|6325166	0.00026	2.008E-05	2	0.000688	0.000508	4	2.646154	-3.162412	-3.585027	0.422615	2	54	58.06451613	1	4	0.190052	0
Low Abundance	gi|6321721	0.000256	0.0001613	3	0.00105	0.000377	4	4.101563	-2.978811	-3.59176	0.612949	2	52	55.91397849	2.666666667	3	0.01739	1
Low Abundance	gi|6321673	0.000252	3.779E-05	3	0.001322	0.00048	4	5.246032	-2.878769	-3.598599	0.719831	2	51	54.83870968	3.333333333	4.75	0.020519	1
Low Abundance	gi|6323980	0.000251	0	1	0.000981	0.000592	4	3.908367	-3.008331	-3.600326	0.591995	2	50	53.76344086	1	4		
Low Abundance	gi|6323209	0.000235	0.0001001	2	0.001201	0.000573	4	5.110638	-2.920457	-3.628932	0.708475	2	49	52.68817204	1.5	5.25	0.039954	1
Low Abundance	gi|6319471	0.000226	0	1	0.003811	0.001305	3	16.86283	-2.418961	-3.645892	1.226931	2	48	51.61290323	2	2.333333		
Low Abundance	gi|6322476	0.00022	0	1	0.001306	0.000208	4	5.936364	-2.884057	-3.657577	0.77352	2	47	50.53763441	1	7.25		
Low Abundance	gi|6325292	0.000216	0.0001511	3	0.000999	0.000185	4	4.625	-3.000435	-3.665546	0.665112	2	46	49.46236559	2.666666667	3.5	0.001764	1
Low Abundance	gi|6319395	0.000199	8.669E-05	4	0.001613	0.000409	4	8.105528	-2.792366	-3.701147	0.908781	2	45	48.38709677	5.75	18.75	0.004974	1
Low Abundance	gi|6322012	0.000188	0.0001907	2	0.002331	0.000592	4	12.39894	-2.632458	-3.725842	1.093384	2	44	47.31182796	3.5	6.75	0.003078	1
Low Abundance	gi|6322082	0.000173	7.442E-05	3	0.000189	3.17E-05	2	1.092486	-3.723538	-3.761954	0.038416	2	43	46.23655914	1	3.5	0.759954	0
Low Abundance	gi|6322722	0.000164	0	1	0.000288	0.000122	4	1.756098	-3.540608	-3.785156	0.244549	2	42	45.16129032	2	2.75		
Low Abundance	gi|6322294	0.000153	2.118E-05	2	0.001768	0.000907	4	11.55556	-2.752518	-3.815309	1.062791	2	41	44.08602151	2.5	4.75	0.037712	1
Low Abundance	gi|6321643	0.000147	7.262E-05	2	0.001202	0.000533	4	8.176871	-2.920096	-3.832683	0.912587	2	39	41.93548387	4	10.25	0.026653	1
Low Abundance	gi|6324250	0.000147	5.914E-05	2	0.001018	0.000745	3	6.92517	-2.992252	-3.832683	0.84043	2	40	43.01075269	2	3.666667	0.178865	0
Low Abundance	gi|6320077	0.000146	0.000116	3	0.000983	0.000139	4	6.732877	-3.007446	-3.835647	0.828201	2	36	38.70967742	2	8.25	0.000386	1
Low Abundance	gi|8279524	0.000146	5.559E-05	3	0.00118	0.000596	4	4.089041	-3.224026	-3.835647	0.611621	2	37	39.78494624	2.333333333	5.25	0.03943	1
Low Abundance	gi|6321837	0.000146	0.00016	2	0.000597	0.000348	4	8.082192	-2.928118	-3.835647	0.907529	2	38	40.86021505	2	6.25	0.096012	0
Low Abundance	gi|6322815	0.000139	6.576E-07	2	0.000806	0.000145	4	5.798561	-3.093665	-3.856985	0.76332	2	35	37.6344086	2	6.5	0.002714	1
Low Abundance	gi|6324804	0.000136	5.518E-05	4	0.002035	0.000701	4	14.96324	-2.691436	-3.866461	1.175026	2	34	36.55913978	3.25	8	0.012052	1
Low Abundance	gi|6320861	0.000131	0	1	0.000645	0.00017	3	4.923664	-3.19044	-3.882729	0.692288	2	33	35.48387097	2	2.333333		

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6322581	0.00013	7.319E-05	3	0.001802	0.000592	4	0.807692	-3.978811	-3.886057	-0.092754	2	31	33.33333333	3.333333333	9.25	0.010164	1
Low Abundance	gi|6319424	0.00013	5.777E-05	3	0.000105	2.77E-05	3	13.86154	-2.744245	-3.886057	1.141811	2	32	34.40860215	1	3	0.546202	0
Low Abundance	gi|6321594	0.000126	7.388E-05	2	0.002142	0.000406	4	17	-2.669181	-3.899629	1.230449	2	30	32.25806452	2	10.25	0.001456	1
Low Abundance	gi|6323967	0.000125	0	1	0.001091	0.000184	3	8.728	-2.962175	-3.90309	0.940915	2	29	31.1827957	2	5		
Low Abundance	gi|1038376	0.00012	6.64E-05	3	0.000618	0.000224	4	5.15	-3.209012	-3.920819	0.711807	2	28	30.10752688	3	6.75	0.016256	1
Low Abundance	gi|6320432	0.000119	5.143E-05	3	0.001831	0.000693	4	15.38655	-2.737312	-3.924453	1.187141	2	27	29.03225806	2.333333333	4.25	0.015522	1
Low Abundance	gi|6320560	0.000117	4.226E-05	2	0.002215	0.000423	4	18.93162	-2.654626	-3.931814	1.277188	2	26	27.95698925	2	5.75	0.001911	1
Low Abundance	gi|6320839	0.000115	0	1	0.00115	0.000602	4	10	-2.939302	-3.939302	1	2	25	26.88172043	2	4.5		
Low Abundance	gi|6323768	0.000108	0.0001282	3	0.001796	0.000419	4	17.38889	-2.726304	-3.966576	1.240272	2	23	24.7311828	1.666666667	11	0.002167	1
Low Abundance	gi|6321619	0.000108	9.652E-06	2	0.001878	0.000934	4	16.62963	-2.745694	-3.966576	1.220883	2	24	25.80645161	2	5.5	0.032216	1
Low Abundance	gi|6319597	0.000107	4.781E-05	2	0.001013	0.000402	4	9.46729	-2.994391	-3.970616	0.976226	2	21	22.58064516	3	9	0.018961	1
Low Abundance	gi|6324321	0.000107	0	1	0.001171	0.00038	4	10.94393	-2.931443	-3.970616	1.039173	2	22	23.65591398	2	4.75		
Low Abundance	gi|6325025	0.000105	4.233E-05	4	0.001567	0.000486	4	10	-2.978811	-3.978811	1	2	19	20.43010753	5.75	30	0.008918	1
Low Abundance	gi|6321203	0.000105	9.663E-05	2	0.00105	0.000527	4	14.92381	-2.804931	-3.978811	1.17388	2	20	21.50537634	1.5	8.75	0.033492	1
Low Abundance	gi|6320789	0.000097	0	1	0.001155	0.000362	4	11.90722	-2.937418	-4.013228	1.07581	2	18	19.35483871	2	5.5		
Low Abundance	gi|6324601	0.000095	5.708E-05	4	0.001474	0.000286	4	15.51579	-2.831503	-4.022276	1.190774	2	17	18.27956989	2.5	9	0.001814	1
Low Abundance	gi|6319552	0.000089	0	1	0.00022	0	1	2.47191	-3.657577	-4.05061	0.393033	2	16	17.20430108	2	2		
Low Abundance	gi|6321236	0.000086	4.019E-05	3	0.001808	0.000747	4	21.02326	-2.742802	-4.065502	1.3227	2	15	16.12903226	2.666666667	8	0.018944	1
Low Abundance	gi|6320548	0.00008	0	1	0.000745	0.000347	4	9.3125	-3.127844	-4.09691	0.969066	2	14	15.05376344	3	5.5		
Low Abundance	gi|6321498	0.000079	3.164E-05	3	0.001102	0.000323	4	13.94937	-2.957818	-4.102373	1.144555	2	13	13.97849462	4	17	0.007502	1
Low Abundance	gi|6323509	0.000076	0	1	0.001042	0.000157	4	13.71053	-2.982132	-4.119186	1.137054	2	12	12.90322581	3	6.5		
Low Abundance	gi|1431856	0.000059	0	1	0.001903	0.000822	4	32.25424	-2.720561	-4.229148	1.508587	2	11	11.82795699	2	6.75		
Low Abundance	gi|6319695	0.000052	1.578E-05	2	0.000511	0.000148	4	9.826923	-3.291579	-4.283997	0.992418	2	10	10.75268817	3	9	0.007763	1
Low Abundance	gi|6324709	0.000051	0	1	0.001073	0.000104	3	21.03922	-2.9694	-4.29243	1.32303	2	9	9.677419355	2	4.333333		
Low Abundance	gi|6321376	0.00005	1.998E-05	2	0.000333	5.09E-05	4	6.66	-3.477556	-4.30103	0.823474	2	8	8.602150538	2.5	6.25	0.000625	1
Low Abundance	gi|6321429	0.000048	0	1	0.001012	0.000451	4	21.08333	-2.994819	-4.318759	1.323939	2	6	6.451612903	2	10.25		
Low Abundance	gi|6321859	0.000048	0	1	0.002136	0.000764	4	44.5	-2.670399	-4.318759	1.64836	2	7	7.52688172	2	8.25		
Low Abundance	gi|6320019	0.000033	0	1	0.001806	0.000714	4	54.72727	-2.743282	-4.481486	1.738204	2	4	4.301075269	2	5		
Low Abundance	gi|6320137	0.000033	0	1	0.001216	0.000516	4	36.84848	-2.915066	-4.481486	1.56642	2	5	5.376344086	2	5.75		
Low Abundance	gi|6320071	0.000032	0	1	0.001682	0.000632	4	52.5625	-2.774174	-4.49485	1.720676	2	3	3.225806452	2	4.5		
Low Abundance	gi|6319809	0.000028	0	1	0.001078	0.00032	4	38.5	-2.967381	-4.552842	1.585461	2	2	2.150537634	2	5.75		
Low Abundance	gi|6323335	0.000018	0	1	0.000971	0.000321	4	53.94444	-3.012781	-4.744727	1.731947	2	1	1.075268817	2	8.5		

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Proteins in Group)
94	17.45%	2.6139	2.5531915	1.196922768	13.8878	3.744681	0.702318	0.000278	0.0014774				2.905141844	1.704963284	7.011524823	5.009334	48	70.59%

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	DE300 Peptides AVG
DE300-only	gi|6325097	0	0	0	0.000711	0.000175	4	8.25
DE300-only	gi|3736267	0	0	0	0.001216	0.000934	4	4.5
DE300-only	gi|9755335	0	0	0	0.00076	0.000257	4	9.25
DE300-only	gi|6321412	0	0	0	0.001197	0.000537	4	8.75
DE300-only	gi|6323056	0	0	0	0.001102	0.00058	4	7.25
DE300-only	gi|6320242	0	0	0	0.000676	0.000339	4	4.75
DE300-only	gi|6320764	0	0	0	0.000946	0.000416	4	5.25
DE300-only	gi|6319326	0	0	0	0.001242	0.000887	4	4.75
DE300-only	gi|1431849	0	0	0	0.000845	0.000378	4	6
DE300-only	gi|6319564	0	0	0	0.002221	0.000376	4	5
DE300-only	gi|6325151	0	0	0	0.000816	7.52E-05	4	5.75
DE300-only	gi|6323873	0	0	0	0.000918	0.000359	4	6.25
DE300-only	gi|6323179	0	0	0	0.001799	0.000846	4	3.25
DE300-only	gi|6322331	0	0	0	0.000566	0.000217	4	16.25
DE300-only	gi|6322531	0	0	0	0.001372	0.000583	4	5
DE300-only	gi|6323332	0	0	0	0.002058	0.000575	4	4.5
DE300-only	gi|6323570	0	0	0	0.000964	0.000535	4	6
DE300-only	gi|6324580	0	0	0	0.001118	0.000199	4	5
DE300-only	gi|6322639	0	0	0	0.000534	0.000286	4	7.75
DE300-only	gi|6324109	0	0	0	0.000602	0.000227	4	3.5
DE300-only	gi|6320935	0	0	0	0.000391	0.000129	4	2.75
DE300-only	gi|6321332	0	0	0	0.001339	0.000568	4	3
DE300-only	gi|6324371	0	0	0	0.000971	0.000499	4	4
DE300-only	gi|6323530	0	0	0	0.001647	0.000757	4	3.5
DE300-only	gi|6320030	0	0	0	0.000215	0.000104	4	6
DE300-only	gi|6322569	0	0	0	0.000163	8.75E-05	4	3.25
DE300-only	gi|6324378	0	0	0	0.00089	0.000604	4	4.25
DE300-only	gi|6325439	0	0	0	0.000338	0.000144	4	3.75
DE300-only	gi|6320788	0	0	0	0.000785	0.000446	4	4
DE300-only	gi|6319931	0	0	0	0.000743	0.000364	4	5.75
DE300-only	gi|6320896	0	0	0	0.000718	0.000307	4	3.25
DE300-only	gi|6324088	0	0	0	0.000949	0.000615	4	5.5
DE300-only	gi|6319602	0	0	0	0.000919	0.000617	4	4.75
DE300-only	gi|6320332	0	0	0	0.000307	0.000112	4	8.75
DE300-only	gi|6323246	0	0	0	0.000981	0.000485	4	3.25
DE300-only	gi|6321430	0	0	0	0.00022	9.22E-05	4	2.75
DE300-only	gi|6320576	0	0	0	0.001276	0.000463	4	4
DE300-only	gi|6324911	0	0	0	0.00027	4.34E-05	4	5
DE300-only	gi|6322896	0	0	0	0.000956	0.000371	4	2.25
DE300-only	gi|6319568	0	0	0	0.000661	0.000331	4	3
DE300-only	gi|6323739	0	0	0	0.000722	0.000229	4	4.5
DE300-only	gi|6324783	0	0	0	0.000703	0.000247	4	3
DE300-only	gi|6320061	0	0	0	0.000235	0.000169	4	4.75
DE300-only	gi|6324950	0	0	0	0.000396	0.000221	4	4
DE300-only	gi|6321574	0	0	0	0.000807	0.000291	4	2.25
DE300-only	gi|6322097	0	0	0	0.00071	0.000252	4	3.25
DE300-only	gi|3736264	0	0	0	0.000487	0.000168	4	3
DE300-only	gi|6324328	0	0	0	0.000582	0.000339	4	3.25
DE300-only	gi|6321398	0	0	0	0.000525	0.000153	4	3
DE300-only	gi|6319793	0	0	0	0.000378	0.000229	4	3.75
DE300-only	gi|6321290	0	0	0	0.000529	0.000159	4	3.25
DE300-only	gi|6323182	0	0	0	0.000369	0.000229	4	4.5
DE300-only	gi|6319725	0	0	0	0.000435	0.000211	4	2.75
DE300-only	gi|6320930	0	0	0	0.000289	0.000199	4	2.25
DE300-only	gi|6323331	0	0	0	0.000457	0.00019	4	3
DE300-only	gi|6320607	0	0	0	0.00095	0.000657	4	3.25
DE300-only	gi|6324758	0	0	0	0.000457	0.000196	4	2.5
DE300-only	gi|6323932	0	0	0	0.000547	0.000191	4	2.5
DE300-only	gi|6323882	0	0	0	0.002051	0.000767	3	5.666667
DE300-only	gi|6324225	0	0	0	0.001143	0.000211	3	5.666667
DE300-only	gi|6322765	0	0	0	0.001223	0.000882	3	5
DE300-only	gi|6320662	0	0	0	0.002147	0.00067	3	5
DE300-only	gi|3736262	0	0	0	0.000614	0.000157	3	4
DE300-only	gi|6323089	0	0	0	0.000842	0.000658	3	5.333333
DE300-only	gi|6319370	0	0	0	0.000305	9.92E-05	3	2
DE300-only	gi|6325421	0	0	0	0.000422	6.04E-05	3	3
DE300-only	gi|6324682	0	0	0	0.000466	0.000208	3	3
DE300-only	gi|1431850	0	0	0	0.001105	6.87E-05	3	7.333333
DE300-only	gi|6323746	0	0	0	0.000733	0.000568	3	3
DE300-only	gi|6319351	0	0	0	0.000497	0.000243	3	2.333333
DE300-only	gi|6323562	0	0	0	0.002113	0.0004	3	3.666667
DE300-only	gi|6323891	0	0	0	0.000572	0.000415	3	3.333333
DE300-only	gi|6324702	0	0	0	0.000352	0.000179	3	2.666667
DE300-only	gi|2033676	0	0	0	0.000112	5.94E-05	3	2
DE300-only	gi|6320079	0	0	0	0.000978	0.000634	3	4
DE300-only	gi|6320527	0	0	0	0.00047	0.000117	3	2.333333
DE300-only	gi|6324899	0	0	0	0.000917	0.000262	3	5.333333

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE300-only	gi|6320175	0	0	0	0.000439	0.000333	3									2		
DE300-only	gi|6323974	0	0	0	0.001109	0.000711	3									2.333333		
DE300-only	gi|6321427	0	0	0	0.000888	0.000394	3									3.666667		
DE300-only	gi|6321898	0	0	0	0.000984	0.00034	3									2.333333		
DE300-only	gi|6319413	0	0	0	0.000553	0.000179	3									3		
DE300-only	gi|6320941	0	0	0	0.000894	0.000347	3									2.333333		
DE300-only	gi|6321401	0	0	0	0.000718	0.000113	3									2		
DE300-only	gi|6323681	0	0	0	0.001354	0.000396	3									3		
DE300-only	gi|6319430	0	0	0	0.000919	0.000475	3									2.666667		
DE300-only	gi|6320983	0	0	0	0.000323	7.94E-05	3									3.333333		
DE300-only	gi|6320235	0	0	0	0.000707	0.000149	3									2.666667		
DE300-only	gi|6321896	0	0	0	0.000596	0.00027	3									2.666667		
DE300-only	gi|6324716	0	0	0	0.000681	0.000418	3									2.333333		
DE300-only	gi|6324761	0	0	0	0.000497	0.000346	3									3		
DE300-only	gi|6322633	0	0	0	0.000512	0.000151	3									2.333333		
DE300-only	gi|6322049	0	0	0	0.000347	0.000347	3									3.333333		
DE300-only	gi|6324318	0	0	0	0.001663	0.001134	3									4.333333		
DE300-only	gi|6322667	0	0	0	0.000427	0.000389	3									2		
DE300-only	gi|6324535	0	0	0	0.001021	0.000773	3									2.333333		
DE300-only	gi|6321816	0	0	0	0.000111	5.76E-05	3									2.333333		
DE300-only	gi|6320724	0	0	0	0.00055	0.000275	3									2.666667		
DE300-only	gi|6324696	0	0	0	0.001491	0.0006	3									2		
DE300-only	gi|6324283	0	0	0	0.000157	4.57E-05	3									2.333333		
DE300-only	gi|6321854	0	0	0	0.00064	0.000191	3									3.333333		
DE300-only	gi|6325103	0	0	0	0.000496	0.000103	3									2		
DE300-only	gi|6323955	0	0	0	0.000487	0.000305	3									2.333333		
DE300-only	gi|6324508	0	0	0	0.000466	0.000154	3									2.666667		
DE300-only	gi|6323864	0	0	0	0.000255	8.67E-05	3									2.333333		
DE300-only	gi|6322155	0	0	0	0.000568	0.000165	3									2.333333		
DE300-only	gi|6579194	0	0	0	0.000093	3.94E-05	3									2		
DE300-only	gi|6320510	0	0	0	0.000872	7.42E-05	3									3		
DE300-only	gi|6324074	0	0	0	0.0014	0.000489	3									3		
DE300-only	gi|6323826	0	0	0	0.000602	0.000316	3									3		
DE300-only	gi|6323639	0	0	0	0.000369	0.000247	3									2.333333		
DE300-only	gi|3736260	0	0	0	0.001151	0.000297	2									2.5		
DE300-only	gi|6322707	0	0	0	0.000477	1.05E-05	2									2.5		
DE300-only	gi|6319698	0	0	0	0.000353	0.000196	2									2.5		
DE300-only	gi|6324594	0	0	0	0.001402	0.000416	2									2.5		
DE300-only	gi|6324982	0	0	0	0.000975	0.000708	2									2.5		
DE300-only	gi|6320006	0	0	0	0.000313	0.000386	2									4		
DE300-only	gi|6321814	0	0	0	0.000977	0.000451	2									4		
DE300-only	gi|6319509	0	0	0	0.000745	6.18E-05	2									2.5		
DE300-only	gi|6320798	0	0	0	0.000958	0.00035	2									3.5		
DE300-only	gi|6320078	0	0	0	0.002013	0.000317	2									2.5		
DE300-only	gi|6324993	0	0	0	0.00035	0.000123	2									3		
DE300-only	gi|6320066	0	0	0	0.00058	7.85E-05	2									2.5		
DE300-only	gi|2780871	0	0	0	0.000499	6.52E-05	2									3.5		
DE300-only	gi|6322770	0	0	0	0.000281	2.65E-05	2									2		
DE300-only	gi|6323958	0	0	0	0.000348	9.96E-05	2									2		
DE300-only	gi|6323669	0	0	0	0.000471	0.000185	2									3		
DE300-only	gi|6320372	0	0	0	0.000327	3.15E-05	2									2		
DE300-only	gi|6323547	0	0	0	0.001047	2.71E-05	2									4		
DE300-only	gi|6320899	0	0	0	0.001849	0.001328	2									3		
DE300-only	gi|6320279	0	0	0	0.000148	0.000128	2									2		
DE300-only	gi|6320249	0	0	0	0.000513	3.62E-05	2									3		
DE300-only	gi|6321829	0	0	0	0.001789	0.000776	2									2		
DE300-only	gi|6321606	0	0	0	0.000737	0.000575	2									2		
DE300-only	gi|6322116	0	0	0	0.000592	0.000449	2									4		
DE300-only	gi|6324725	0	0	0	0.0001	6.37E-06	2									2.5		
DE300-only	gi|6323752	0	0	0	0.000299	2.48E-05	2									3		
DE300-only	gi|6319685	0	0	0	0.000082	3.43E-05	2									2.5		
DE300-only	gi|6322127	0	0	0	0.001439	0.000412	2									2.5		
DE300-only	gi|6322845	0	0	0	0.000496	0.000142	2									2		
DE300-only	gi|6321807	0	0	0	0.000133	8.15E-06	2									2		
DE300-only	gi|6321796	0	0	0	0.000748	0.000345	2									2.5		
DE300-only	gi|6320917	0	0	0	0.000287	0.000267	2									2.5		
DE300-only	gi|6321217	0	0	0	0.000456	0.00014	2									2.5		
DE300-only	gi|6321776	0	0	0	0.000812	0.000441	2									3.5		
DE300-only	gi|6324474	0	0	0	0.000128	0.00011	2									2.5		
DE300-only	gi|6322174	0	0	0	0.000293	0.000228	2									2.5		
DE300-only	gi|6322746	0	0	0	0.000282	0.000187	2									2.5		
DE300-only	gi|6320440	0	0	0	0.000264	4.66E-05	2									2		
DE300-only	gi|1431857	0	0	0	0.000627	0.000489	2									2		
DE300-only	gi|6324475	0	0	0	0.000213	4.54E-05	2									2.5		
DE300-only	gi|1038379	0	0	0	0.001035	0.000387	2									2.5		
DE300-only	gi|1038375	0	0	0	0.000503	0.000194	2									2.5		
DE300-only	gi|6319527	0	0	0	0.000355	0.000197	2									2.5		
DE300-only	gi|6325220	0	0	0	0.001652	0.000485	2									3		
DE300-only	gi|6322261	0	0	0	0.000186	5.31E-05	2									2		
DE300-only	gi|6321806	0	0	0	0.000291	1.97E-05	2									2.5		
DE300-only	gi|6324363	0	0	0	0.000757	9.87E-05	2									3.5		
DE300-only	gi|6323460	0	0	0	0.000121	5.94E-05	2									2.5		
DE300-only	gi|6323278	0	0	0	0.000158	6.49E-05	2									2		
DE300-only	gi|6319558	0	0	0	0.000161	4.18E-06	2									2.5		
DE300-only	gi|6320893	0	0	0	0.000212	1.53E-05	2									2		
DE300-only	gi|6325375	0	0	0	0.000353	0.000234	2									2		
DE300-only	gi|6322634	0	0	0	0.000086	8.06E-06	2									3		
DE300-only	gi|6324727	0	0	0	0.000111	1.09E-05	2									3		
DE300-only	gi|6319591	0	0	0	0.00007	2.05E-05	2									2.5		
DE300-only	gi|6324524	0	0	0	0.000379	7.51E-05	2									2.5		
DE300-only	gi|6322638	0	0	0	0.000355	0.000277	2									2.5		
DE300-only	gi|6319926	0	0	0	0.000202	3.12E-05	2									2		
DE300-only	gi|6320777	0	0	0	0.000332	0.000208	2									3		
DE300-only	gi|6320393	0	0	0	0.00019	0.000136	2									2		
DE300-only	gi|6320240	0	0	0	0.000474	0.000376	2									2		
DE300-only	gi|6321692	0	0	0	0.000756	9.08E-05	2									2.5		
DE300-only	gi|6323717	0	0	0	0.000334	7.46E-05	2									2		
DE300-only	gi|6321632	0	0	0	0.000189	2.09E-06	2									2		
DE300-only	gi|6321865	0	0	0	0.000154	1.45E-05	2									2		
DE300-only	gi|9755326	0	0	0	0.002294	0.000304	2									2		
DE300-only	gi|6325418	0	0	0	0.000108	3.16E-05	2									2.5		
DE300-only	gi|6324857	0	0	0	0.000454	1E-05	2									2		
DE300-only	gi|6324859	0	0	0	0.001137	0.000562	2									2.5		
DE300-only	gi|6325146	0	0	0	0.000436	0.000289	2									2		
DE300-only	gi|6324552	0	0	0	0.000104	2.31E-06	2									2		
DE300-only	gi|6321826	0	0	0	0.000227	5.85E-05	2									3		
DE300-only	gi|6321456	0	0	0	0.000205	0.000135	2									2.5		
DE300-only	gi|6323299	0	0	0	0.000312	0.00013	2									2.5		
DE300-only	gi|6324258	0	0	0	0.00022	0	1									2		
DE300-only	gi|6321718	0	0	0	0.000811	0	1									4		
DE300-only	gi|6322426	0	0	0	0.000226	0	1									3		
DE300-only	gi|6324669	0	0	0	0.000274	0	1									2		
DE300-only	gi|6321004	0	0	0	0.000456	0	1									3		
DE300-only	gi|4274231	0	0	0	0.001059	0	1									2		
DE300-only	gi|6325337	0	0	0	0.000281	0	1									4		
DE300-only	gi|8279525	0	0	0	0.00031	0	1									2		
DE300-only	gi|1431848	0	0	0	0.000225	0	1									2		
DE300-only	gi|1431857	0	0	0	0.000483	0	1									2		
DE300-only	gi|1431852	0	0	0	0.000264	0	1									3		
DE300-only	gi|6319321	0	0	0	0.000248	0	1									2		
DE300-only	gi|6322459	0	0	0	0.000837	0	1									4		
DE300-only	gi|6322244	0	0	0	0.000791	0	1									2		
DE300-only	gi|6324515	0	0	0	0.000217	0	1									5		
DE300-only	gi|6323383	0	0	0	0.000265	0	1									2		
DE300-only	gi|6320849	0	0	0	0.000649	0	1									2		
DE300-only	gi|6322525	0	0	0	0.000401	0	1									3		

Locus	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF
gi|6320175	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323974	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321427	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321898	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319413	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320941	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321401	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323681	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319430	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320983	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320235	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321896	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324716	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324761	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322633	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322049	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324318	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322667	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324535	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321816	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320724	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324696	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324283	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321854	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325103	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323955	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324508	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323864	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322155	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6579194	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320510	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324074	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323826	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323639	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|3736260	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322707	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319698	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324594	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324982	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320006	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321814	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319509	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320798	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320078	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324993	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320066	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|2780871	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322770	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323958	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320372	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323547	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320899	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320279	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320249	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321829	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321606	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322116	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324725	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323752	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319685	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322127	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322845	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321807	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321796	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320917	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321217	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321776	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324474	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322174	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322746	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320440	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324475	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1038379	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1038375	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319527	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325220	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322261	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321806	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324363	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323460	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323278	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319558	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320893	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325375	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322634	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324727	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319591	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324524	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322638	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319926	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320777	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320393	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320240	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321692	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323717	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321632	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321865	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|9755326	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325418	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324859	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325146	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324552	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321826	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321456	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323299	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324258	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321718	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322426	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324669	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321004	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|4274231	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6325337	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|8279525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431848	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|1431852	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319321	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322459	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322244	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6324515	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6323383	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6320849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6322525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Locus	DE300-1_P	DE300-1_uP	DE300-1_S	DE300-1_SC	DE300-1_NSAF	DE300-2_P	DE300-2_uP	DE300-2_S	DE300-2_SC	DE300-2_NSAF	DE300-3_P	DE300-3_uP	DE300-3_S	DE300-3_SC	DE300-3_NSAF	DE300-4_P	DE300-4_uP	DE300-4_S	DE300-4_SC	DE300-4_NSAF
gi|6320175	X	X	X	X	X	2	2	6	7.67	0.000818	2	2	3	7.67	0.0003	2	2	3	6.39	0.000197
gi|6323974	X	X	X	X	X	2	2	2	11.11	0.000456	2	2	6	11.11	0.001004	3	3	17	14.53	0.001867
gi|6321427	2	2	4	10.32	0.000561	X	X	X	X	X	3	3	5	14.68	0.000777	6	6	13	31.35	0.001326
gi|6321898	2	2	8	14.04	0.000827	X	X	X	X	X	2	2	12	13.16	0.001374	3	3	10	19.59	0.000751
gi|6319413	3	3	5	11.58	0.000418	3	3	6	11.58	0.000756	X	X	X	X	X	3	3	8	10.64	0.000486
gi|6320941	3	3	7	21.46	0.001207	2	2	2	13.66	0.00052	2	2	5	15.61	0.000955	X	X	X	X	X
gi|6321401	2	2	5	17.13	0.000818	1	1	3	9.26	0.00074	X	X	X	X	X	3	3	5	25.46	0.000595
gi|6323681	2	2	10	10.04	0.00142	3	3	8	16.06	0.001713	X	X	X	X	X	4	4	9	23.29	0.000929
gi|6319430	2	2	10	15.77	0.001467	X	X	X	X	X	2	2	4	12.45	0.00065	4	4	6	21.99	0.00064
gi|6320983	3	3	5	7.54	0.000392	2	2	2	5.54	0.000236	X	X	X	X	X	5	5	6	17.52	0.000342
gi|6320235	3	3	3	24.24	0.000536	2	2	3	19.7	0.000808	X	X	X	X	X	3	3	6	24.75	0.000779
gi|6321896	2	2	3	8.56	0.000324	X	X	X	X	X	2	2	5	10.09	0.000599	4	4	11	11.93	0.000864
gi|6324716	X	X	X	X	X	3	3	7	12.16	0.001134	2	2	5	8.81	0.000595	2	2	4	9.42	0.000312
gi|6324761	3	3	11	10.98	0.00089	3	3	3	10.98	0.000366	X	X	X	X	X	3	3	4	9.84	0.000235
gi|6322633	X	X	X	X	X	2	2	2	6.69	0.00034	2	2	5	16.24	0.000623	3	3	7	27.39	0.000573
gi|6322049	3	3	3	8.92	0.000201	X	X	X	X	X	5	5	10	12.71	0.000743	2	2	2	3.61	9.75E-05
gi|6324318	4	4	13	29.05	0.001907	6	6	12	37.34	0.002654	X	X	X	X	X	3	3	4	16.6	0.000426
gi|6322667	2	2	2	6.56	0.000166	2	2	7	7.03	0.000874	X	X	X	X	X	2	2	4	6.09	0.000241
gi|6324535	X	X	X	X	X	3	3	9	17.72	0.001889	2	2	5	13.39	0.000771	2	2	4	13.39	0.000405
gi|6321816	3	3	5	4.53	0.000178	X	X	X	X	X	2	2	2	3.32	7.89E-05	2	2	3	2.82	7.76E-05
gi|6320724	X	X	X	X	X	2	2	7	4.8	0.000746	2	2	3	4.8	0.000235	4	4	13	10	0.000668
gi|6324696	2	2	7	19.05	0.001964	2	2	4	26.19	0.001692	X	X	X	X	X	2	2	4	26.19	0.000816
gi|6324283	2	2	2	4.62	0.000105	X	X	X	X	X	2	2	3	4.47	0.000175	3	3	5	5.81	0.000191
gi|6321854	2	2	5	7.12	0.000466	2	2	6	6.86	0.000844	X	X	X	X	X	6	6	9	23.22	0.00061
gi|6325103	X	X	X	X	X	2	2	4	7.9	0.000527	2	2	6	8.4	0.00058	2	2	6	8.15	0.000381
gi|6323955	2	2	7	5.45	0.000465	3	3	8	7.14	0.000802	X	X	X	X	X	2	2	4	5.45	0.000193
gi|6324508	3	3	3	16.53	0.000297	3	3	4	14.01	0.000597	X	X	X	X	X	2	2	7	10.36	0.000504
gi|6323864	2	2	3	6.32	0.000239	X	X	X	X	X	2	2	2	7	0.000177	3	3	6	8.8	0.000348
gi|6322155	2	2	6	9.41	0.000739	2	2	3	8.71	0.000557	3	3	3	13.24	0.000409	X	X	X	X	X
gi|6579194	2	2	2	3.6	8.21E-05	X	X	X	X	X	2	2	3	3.6	0.000136	2	2	2	3.37	5.97E-05
gi|6320510	X	X	X	X	X	3	3	4	21.33	0.000948	2	2	5	13.33	0.00087	4	4	7	28	0.000799
gi|6324074	3	3	7	24.18	0.001617	3	3	5	24.18	0.001742	X	X	X	X	X	3	3	5	23.53	0.00084
gi|6323826	4	4	10	22.33	0.000822	2	2	6	11.16	0.000744	X	X	X	X	X	3	3	4	16.28	0.000239
gi|6323639	2	2	2	8.59	0.000217	3	3	4	12.88	0.000654	X	X	X	X	X	2	2	3	7.98	0.000236
gi|3736260	X	X	X	X	X	2	2	3	20.59	0.000941	X	X	X	X	X	3	3	9	20.59	0.00136
gi|6322707	2	2	3	15.98	0.000484	X	X	X	X	X	X	X	X	X	X	3	3	4	22.83	0.000469
gi|6319698	X	X	X	X	X	X	X	X	X	X	2	2	2	9.56	0.000214	3	3	7	13.11	0.000491
gi|6324594	X	X	X	X	X	X	X	X	X	X	2	2	3	33.96	0.001108	3	3	7	44.34	0.001697
gi|6324982	X	X	X	X	X	3	3	9	8.92	0.001476	X	X	X	X	X	2	2	6	8.92	0.000474
gi|6320006	X	X	X	X	X	6	6	14	7.7	0.000586	X	X	X	X	X	2	2	2	2.83	4.04E-05
gi|6321814	X	X	X	X	X	X	X	X	X	X	3	3	6	14.85	0.000658	5	5	18	21.29	0.001296
gi|6319509	X	X	X	X	X	2	2	3	11.84	0.000701	X	X	X	X	X	3	3	7	19.74	0.000789
gi|6320798	3	3	8	11.81	0.000711	4	4	9	16.58	0.001205	X	X	X	X	X	X	X	X	X	X
gi|6320078	2	2	10	20.89	0.002237	X	X	X	X	X	X	X	X	X	X	3	3	11	20.89	0.001789
gi|6324993	X	X	X	X	X	3	3	4	8.4	0.000437	X	X	X	X	X	3	3	5	5.33	0.000263
gi|6320066	2	2	3	18.81	0.000525	X	X	X	X	X	X	X	X	X	X	3	3	5	23.76	0.000636
gi|2780871	3	3	7	11.01	0.000545	X	X	X	X	X	X	X	X	X	X	4	4	8	13.66	0.000453
gi|6322770	X	X	X	X	X	X	X	X	X	X	2	2	3	8.67	0.0003	2	2	4	8.42	0.000262
gi|6323958	2	2	4	7.06	0.000277	2	2	4	7.84	0.000418	X	X	X	X	X	X	X	X	X	X
gi|6323669	X	X	X	X	X	2	2	3	7.02	0.00034	X	X	X	X	X	4	4	11	13.19	0.000601
gi|6320372	2	2	5	5.93	0.000349	X	X	X	X	X	X	X	X	X	X	2	2	6	6.32	0.000305
gi|6323547	X	X	X	X	X	3	3	5	12.8	0.001066	X	X	X	X	X	5	5	10	22.4	0.001028
gi|6320899	X	X	X	X	X	X	X	X	X	X	2	2	3	23.26	0.00091	4	4	14	37.21	0.002789
gi|6320279	X	X	X	X	X	2	2	4	2.68	0.000238	X	X	X	X	X	2	2	2	2.57	5.74E-05
gi|6320249	3	3	5	13.41	0.000539	3	3	3	13.41	0.000488	X	X	X	X	X	X	X	X	X	X
gi|6321829	2	2	4	21.93	0.00124	2	2	5	21.93	0.002338	X	X	X	X	X	X	X	X	X	X
gi|6321606	X	X	X	X	X	2	2	5	13.73	0.001144	X	X	X	X	X	2	2	3	13.73	0.000331
gi|6322116	X	X	X	X	X	4	4	8	12.58	0.000909	X	X	X	X	X	4	4	5	10.66	0.000274
gi|6324725	X	X	X	X	X	X	X	X	X	X	2	2	3	3.59	9.6E-05	3	3	5	3.43	0.000105
gi|6323752	X	X	X	X	X	2	2	3	5.8	0.000281	X	X	X	X	X	4	4	7	10.54	0.000316
gi|6319685	X	X	X	X	X	2	2	2	1.47	5.81E-05	3	3	5	2.34	0.000107	X	X	X	X	X
gi|6322127	3	3	5	32.47	0.001148	2	2	5	25.97	0.001731	X	X	X	X	X	X	X	X	X	X
gi|6322845	2	2	3	13.06	0.000396	2	2	3	9.33	0.000597	X	X	X	X	X	X	X	X	X	X
gi|6321807	2	2	2	4.87	0.000128	X	X	X	X	X	X	X	X	X	X	2	2	3	6.14	0.000139
gi|6321796	X	X	X	X	X	X	X	X	X	X	2	2	3	12.02	0.000504	3	3	9	15.88	0.000992
gi|6320917	3	3	7	8.27	0.000476	X	X	X	X	X	X	X	X	X	X	2	2	2	4.81	9.88E-05
gi|6321217	X	X	X	X	X	3	3	3	16.32	0.000555	X	X	X	X	X	2	2	4	11.46	0.000357
gi|6321776	X	X	X	X	X	3	3	3	10.31	0.0005	X	X	X	X	X	4	4	14	16.88	0.001124
gi|6324474	X	X	X	X	X	3	3	4	3.86	0.000206	X	X	X	X	X	2	2	2	2.03	4.96E-05
gi|6322174	X	X	X	X	X	3	3	5	8.35	0.000454	X	X	X	X	X	2	2	3	5.45	0.000131
gi|6322746	X	X	X	X	X	3	3	4	7	0.000415	X	X	X	X	X	2	2	3	6.23	0.00015
gi|6320440	X	X	X	X	X	2	2	3	5.77	0.000231	X	X	X	X	X	2	2	8	5.19	0.000297
gi|1431857	X	X	X	X	X	2	2	5	11.31	0.000973	X	X	X	X	X	2	2	3	10.95	0.000281
gi|6324475	3	3	3	10.65	0.000245	X	X	X	X	X	2	2	2	8.33	0.000181	X	X	X	X	X
gi|1038379	3	3	5	28.15	0.001309	X	X	X	X	X	X	X	X	X	X	2	2	4	22.22	0.000761
gi|1038375	X	X	X	X	X	X	X	X	X	X	2	2	3	9.97	0.000366	3	3	8	18.07	0.00064
gi|6319527	3	3	5	15.36	0.000494	X	X	X	X	X	X	X	X	X	X	2	2	3	10.06	0.000215
gi|6325220	X	X	X	X	X	X	X	X	X	X	3	3	8	35.67	0.001995	3	3	8	24.84	0.001309
gi|6322261	2	2	5	5.45	0.000224	X	X	X	X	X	2	2	3	3.93	0.000149	X	X	X	X	X
gi|6321806	2	2	4	5.62	0.000305	X	X	X	X	X	X	X	X	X	X	3	3	5	7.78	0.000277
gi|6324363	X	X	X	X	X	X	X	X	X	X	3	3	6	9.65	0.000687	4	4	11	15.2	0.000826
gi|6323460	3	3	3	5.22	0.000163	X	X	X	X	X	X	X	X	X	X	2	2	2	3.69	7.89E-05
gi|6323278	X	X	X	X	X	2	2	4	2.11	0.000204	2	2	3	2.39	0.000112	X	X	X	X	X
gi|6319558	X	X	X	X	X	2	2	3	2.97	0.000164	X	X	X	X	X	3	3	6	3.69	0.000158
gi|6320893	2	2	3	4.55	0.000201	X	X	X	X	X	2	2	3	5.69	0.000223	X	X	X	X	X
gi|6325375	X	X	X	X	X	2	2	4	7.06	0.000519	X	X	X	X	X	2	2	3	9	0.000188
gi|6322634	X	X	X	X	X	X	X	X	X	X	3	3	3	3.65	9.13E-05	3	3	4	3.81	7.99E-05
gi|6324727	X	X	X	X	X	X	X	X	X	X	3	3	4	3.18	0.000104	3	3	7	2.58	0.000119
gi|6319591	X	X	X	X	X	X	X	X	X	X	3	3	3	3.23	8.44E-05	2	2	3	1.58	5.54E-05
gi|6324524	3	3	6	11.61	0.000432	2	2	3	6.92	0.000326	X	X	X	X	X	X	X	X	X	X
gi|6322638	X	X	X	X	X	3	3	5	8.88	0.000551	X	X	X	X	X	2	2	3	5.17	0.000159
gi|6319926	X	X	X	X	X	2	2	3	3.37	0.000224	X	X	X	X	X	2	2	5	3.79	0.00018
gi|6320777	X	X	X	X	X	3	3	5	7.36	0.000479	X	X	X	X	X	3	3	4	6.82	0.000185
gi|6320393	X	X	X	X	X	X	X	X	X	X	2	2	4	7.14	0.000287	2	2	2	3.85	9.41E-05
gi|6320240	X	X	X	X	X	X	X	X	X	X	2	2	7	7.84	0.000741	2	2	3	8.38	0.000208
gi|6321692	X	X	X	X	X	2	2	4	9.23	0.00082	X	X	X	X	X	3	3	7	13.46	0.000692
gi|6323717	2	2	2	12.02	0.000386	X	X	X	X	X	X	X	X	X	X	2	2	2	13.11	0.000281
gi|6321632	X	X	X	X	X	X	X	X	X	X	2	2	2	9.02	0.000191	2	2	3	9.02	0.000188
gi|6321865	X	X	X	X	X	X	X	X	X	X	2	2	3	4.62	0.000164	2	2	4	4.2	0.000144
gi|9755326	2	2	5	29.41	0.002079	2	2	4	29.41	0.002509	X	X	X	X	X	X	X	X	X	X
gi|6325418	X	X	X	X	X	X	X	X	X	X	2	2	3	3.22	0.00013	3	3	3	4.21	8.55E-05
gi|6324857	2	2	3	11.3	0.000461	X	X	X	X	X	X	X	X	X	X	2	2	4	13.04	0.000447
gi|6324859	X	X	X	X	X	3	3	4	25.18	0.001534	X	X	X	X	X	2	2	4	20.86	0.000739
gi|6325146	X	X	X	X	X	2	2	4	7.51	0.00064	X	X	X	X	X	2	2	3	8.71	0.000231
gi|6324552	2	2	3	3.5	0.000106	X	X	X	X	X	X	X	X	X	X	2	2	4	3.5	0.000103
gi|6321826	X	X	X	X	X	2	2	2	3.83	0.000185	X	X	X	X	X	4	4	6	8.52	0.000268
gi|6321456	3	3	4	9.55	0.0003	X	X	X	X	X	X	X	X	X	X	2	2	2	7.22	0.000109
gi|6323299	3	3	4	13.43	0.000404	X	X	X	X	X	X	X	X	X	X	2	2	3	8	0.00022
gi|6324258	2	2	3	6.02	0.00022	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321718	X	X	X	X	X	X	X	X	X	X	4	4	8	17.1	0.000811	X	X	X	X	X
gi|6322426	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	5.57	0.000226
gi|6324669	2	2	2	10.08	0.000274	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6321004	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	9.47	0.000456
gi|4274231	X	X	X	X	X	2	2	3	17.88	0.001059	X	X	X	X	X	X	X	X	X	X
gi|6325337	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	5	14.19	0.000281
gi|8279525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	16.06	0.00031
gi|1431848	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.81	0.000225
gi|1431857	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	13.16	0.000483
gi|1431852	3	3	4	9.16	0.000264	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
gi|6319321	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	4.67	0.000248
gi|6322459	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	28.37	0.000837
gi|6322244	X	X	X	X	X	X	X	X	X	X	2	2	4	14.14	0.000791	X	X	X	X	X
gi|6324515	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	6	8.44	0.000217
gi|6323383	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	9.97	0.000265
gi|6320849	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	12.63	0.000649
gi|6322525	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	12.03	0.000401

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE300-only	gi|6320009	0	0	0	0.000568	0	1									2		
DE300-only	gi|6320809	0	0	0	0.000816	0	1									2		
DE300-only	gi|6322237	0	0	0	0.000718	0	1									2		
DE300-only	gi|6322828	0	0	0	0.000252	0	1									2		
DE300-only	gi|6320718	0	0	0	0.002639	0	1									1		
DE300-only	gi|6322754	0	0	0	0.001115	0	1									3		
DE300-only	gi|6323871	0	0	0	0.000098	0	1									2		
DE300-only	gi|6325319	0	0	0	0.00065	0	1									3		
DE300-only	gi|6324511	0	0	0	0.000215	0	1									2		
DE300-only	gi|6319711	0	0	0	0.000134	0	1									2		
DE300-only	gi|6320276	0	0	0	0.002018	0	1									3		
DE300-only	gi|6324938	0	0	0	0.000714	0	1									2		
DE300-only	gi|6319721	0	0	0	0.00111	0	1									2		
DE300-only	gi|6321940	0	0	0	0.000344	0	1									2		
DE300-only	gi|6323511	0	0	0	0.000115	0	1									2		
DE300-only	gi|6323288	0	0	0	0.00022	0	1									2		
DE300-only	gi|6322452	0	0	0	0.000188	0	1									2		
DE300-only	gi|6319577	0	0	0	0.000675	0	1									3		
DE300-only	gi|6323975	0	0	0	0.000294	0	1									2		
DE300-only	gi|6320980	0	0	0	0.00034	0	1									2		
DE300-only	gi|6320881	0	0	0	0.000579	0	1									2		
DE300-only	g|1431853	0	0	0	0.000214	0	1									2		
DE300-only	gi|6324343	0	0	0	0.000072	0	1									2		
DE300-only	gi|6325386	0	0	0	0.000611	0	1									2		
DE300-only	gi|6322393	0	0	0	0.000535	0	1									2		
DE300-only	gi|6322919	0	0	0	0.000356	0	1									2		
DE300-only	gi|6320334	0	0	0	0.000249	0	1									2		
DE300-only	gi|6320914	0	0	0	0.00036	0	1									3		
DE300-only	gi|6322529	0	0	0	0.001353	0	1									3		
DE300-only	gi|6319849	0	0	0	0.001079	0	1									2		
DE300-only	gi|6323917	0	0	0	0.000074	0	1									2		
DE300-only	gi|6324429	0	0	0	0.000456	0	1									2		
DE300-only	gi|6322053	0	0	0	0.001987	0	1									2		
DE300-only	gi|6321842	0	0	0	0.000694	0	1									2		
DE300-only	gi|6321839	0	0	0	0.000436	0	1									2		
DE300-only	gi|6321301	0	0	0	0.000159	0	1									3		
DE300-only	gi|6325253	0	0	0	0.000459	0	1									2		
DE300-only	gi|6322288	0	0	0	0.000869	0	1									2		
DE300-only	gi|6320720	0	0	0	0.000359	0	1									2		
DE300-only	gi|6321644	0	0	0	0.000266	0	1									2		
DE300-only	gi|6323725	0	0	0	0.000423	0	1									3		
DE300-only	gi|6324421	0	0	0	0.000225	0	1									2		
DE300-only	gi|6324188	0	0	0	0.000296	0	1									2		
DE300-only	gi|6323201	0	0	0	0.000471	0	1									2		
DE300-only	gi|6321517	0	0	0	0.000963	0	1									2		
DE300-only	gi|6323452	0	0	0	0.000645	0	1									3		
DE300-only	gi|6681849	0	0	0	0.000727	0	1									1		
DE300-only	gi|6322156	0	0	0	0.00034	0	1									2		
DE300-only	gi|6322636	0	0	0	0.000149	0	1									2		
DE300-only	gi|6320418	0	0	0	0.000191	0	1									2		
DE300-only	gi|6325140	0	0	0	0.001111	0	1									3		
DE300-only	gi|6322168	0	0	0	0.000492	0	1									2		
DE300-only	gi|6319553	0	0	0	0.000073	0	1									2		
DE300-only	gi|6321628	0	0	0	0.000139	0	1									2		
DE300-only	gi|6323420	0	0	0	0.001894	0	1									1		
DE300-only	g|3736267	0	0	0	0.000265	0	1									2		
DE300-only	gi|6319530	0	0	0	0.000319	0	1									2		
DE300-only	gi|6321650	0	0	0	0.000329	0	1									2		
DE300-only	gi|6321704	0	0	0	0.000213	0	1									2		
DE300-only	gi|6320640	0	0	0	0.000258	0	1									2		
DE300-only	gi|6324433	0	0	0	0.000751	0	1									2		
DE300-only	gi|6323719	0	0	0	0.00081	0	1									2		
DE300-only	gi|6321793	0	0	0	0.001263	0	1									2		
DE300-only	gi|6319470	0	0	0	0.001779	0	1									3		
DE300-only	gi|6319530	0	0	0	0.000728	0	1									2		
DE300-only	gi|6323374	0	0	0	0.000027	0	1									2		
DE300-only	gi|6323402	0	0	0	0.000289	0	1									2		
DE300-only	gi|6325445	0	0	0	0.001326	0	1									3		
DE300-only	gi|6319500	0	0	0	0.000338	0	1									2		
DE300-only	gi|6322029	0	0	0	0.000097	0	1									2		
DE300-only	gi|6319569	0	0	0	0.00055	0	1									2		
DE300-only	gi|6322585	0	0	0	0.000126	0	1									2		
DE300-only	gi|6323147	0	0	0	0.000226	0	1									2		
DE300-only	gi|6319508	0	0	0	0.000221	0	1									2		
DE300-only	gi|6320033	0	0	0	0.000533	0	1									3		
DE300-only	gi|6324543	0	0	0	0.000159	0	1									2		
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**		
279	**52.34%**				**17.7631**	**2.268817**	**1.136128**		**0.0006367**						**2.980286738**	**1.538511**		

Group	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE300-0-1_P	DE300-0-1_uP	DE300-0-1_S	DE300-0-1_SC	DE300-0-1_NSAF	DE300-0-2_P	DE300-0-2_uP	DE300-0-2_S	DE300-0-2_SC	DE300-0-2_NSAF	DE300-0-3_P	DE300-0-3_uP	DE300-0-3_S	DE300-0-3_SC	DE300-0-3_NSAF	DE300-0-4_P	DE300-0-4_uP	DE300-0-4_S	DE300-0-4_SC	DE300-0-4_NSAF
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.6	0.000568
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	26.98	0.000816
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.08	0.000718	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	13.73	0.000252
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	5	21.78	0.002639	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	25.1	0.001115	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.59	9.81E-05
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	26.58	0.00065
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.44	0.000215	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.55	0.000134
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	15	21.99	0.002018
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	8.33	0.000714
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	7	14.81	0.00111
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.88	0.000344	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.09	0.000115
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	12.77	0.00022	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.11	0.000188	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	11.38	0.000675	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	12.03	0.000294
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	8.97	0.00034	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	16.85	0.000579	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.81	0.000214	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	0.99	7.16E-05	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.6	0.000611	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.36	0.000535	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	8.86	0.000356
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.45	0.000249	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	3.49	0.00036	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	17.77	0.001353	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	14.57	0.001079	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	3.13	7.43E-05	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	15.38	0.000456
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	17.39	0.001987	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	21.62	0.000694
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	11.52	0.000436	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	4.5	0.000159	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	10.26	0.000459	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	23.77	0.000869	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	12.59	0.000359
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	11.72	0.000266
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	13.49	0.000423
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	9.06	0.000225
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.07	0.000296
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	9	0.000471	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	9.04	0.000963	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	15.93	0.000645	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	1	3	7.55	0.000727
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	9.13	0.00034	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.48	0.000149	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.55	0.000191	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	16.67	0.001111	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	9.12	0.000492	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.25	7.33E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.9	0.000139	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	3	17.86	0.001894	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	9.68	0.000265	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	4.79	0.000319	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.56	0.000329	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	4.26	0.000213	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.7	0.000258	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	12.21	0.000751	X	X	X	X	X	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	17.93	0.00081	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	32.26	0.001263	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	29.55	0.001779	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	13.95	0.000728	X	X	X	X	X
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	1.76	2.74E-05
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.3	0.000289
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	26.45	0.001326
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	7.63	0.000338
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.64	9.66E-05
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	10	7.28	0.00055
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.15	0.000126
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	14.54	0.000226
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.18	0.000222
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	11.66	0.000533
DE300-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.4	0.000159

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE300 NSAF AVG	DE300 NSAF STD	DE300 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE300	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE300 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
noDE-only	gi|6325407	0.004077	0.0018869	4	0	0	0								1			
noDE-only	gi|1431855	0.002198	0.0009394	2	0	0	0								1			
noDE-only	gi|6323619	0.000447	0	1	0	0	0								1			
noDE-only	gi|6320142	0.002178	0	1	0	0	0								1			
noDE-only	gi|6320205	0.000208	0	1	0	0	0								2			
noDE-only	gi|6320860	0.000294	0	1	0	0	0								1			
Number of Proteins in Group	**Number of Proteins in Group (% of Total)**	**Sum of noDE NSAF AVG x 100**	**noDE Detected AVG**	**noDE Detected STD**	**Sum of DE NSAF AVG x 100**	**DE Detected AVG**	**DE Detected STD**	**noDE NSAF AVG**	**DE NSAF AVG**				**noDE Pep AVG**	**noDE Pep STD**	**DE Pep AVG**	**DE Pep STD**		
6	**1.12%**	**0.9402**	**1.6666667**	**1.211060142**				**0.001567**					**1.166666667**	**0.4082829**				

Group	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE300-0-1_P	DE300-0-1_uP	DE300-0-1_S	DE300-0-1_SC	DE300-0-1_NSAF	DE300-0-2_P	DE300-0-2_uP	DE300-0-2_S	DE300-0-2_SC	DE300-0-2_NSAF	DE300-0-3_P	DE300-0-3_uP	DE300-0-3_S	DE300-0-3_SC	DE300-0-3_NSAF	DE300-0-4_P	DE300-0-4_uP	DE300-0-4_S	DE300-0-4_SC	DE300-0-4_NSAF
noDE-only	1	1	55	5.78	0.003711	1	1	39	5.78	0.001569	1	1	97	5.78	0.005261	1	1	101	5.78	0.005768	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	13	13.56	0.001534	1	1	18	13.56	0.002862	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	12	6.95	0.000447	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	X	X	X	X	X	1	1	13	17.86	0.002178	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	2	2	6	15.92	0.000208	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	29	1.46	0.000294	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Supporting Table 2E: Proteins detected in noDE and/or DE600 replicates

Proteins detected in both DE conditions were sorted into two groups of high and low abundances based on their averaged NSAF values measured when DE was turned off (noDE NSAF AVG).
Averages ("AVG") and standard deviations ("STD") were calculated for NSAF values and Peptide counts across the 4 replicates of a DE condition.
t-test p-values were calculated using the TTEST function in MSExcel (NSAF t-test p-Value).

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600
High Abundance	gi|6321631	0.089245	0.0307299	4	0.035601	0.013379	4	0.398913	-1.448538
High Abundance	gi|6322468	0.056902	0.0110847	4	0.030521	0.011811	4	0.536378	-1.515401
High Abundance	gi|6321968	0.054496	0.0104952	4	0.021787	0.00847	4	0.399791	-1.661803
High Abundance	gi|1038378	0.040924	0.0037701	4	0.022812	0.003537	4	0.557424	-1.641837
High Abundance	gi|6319279	0.039967	0.0080495	4	0.016602	0.004016	4	0.415393	-1.77984
High Abundance	gi|6322697	0.037728	0.004085	4	0.010883	0.002518	4	0.288459	-1.963251
High Abundance	gi|6323073	0.035041	0.0052874	4	0.008866	0.003955	4	0.253018	-2.052272
High Abundance	gi|6322790	0.030639	0.0056721	4	0.011796	0.008444	4	0.385	-1.928265
High Abundance	gi|6321693	0.029306	0.0078327	4	0.010389	0.0039	4	0.354501	-1.983426
High Abundance	gi|6322409	0.028438	0.0093006	4	0.017868	0.012124	4	0.628314	-1.747924
High Abundance	gi|6324486	0.020489	0.0049482	4	0.006773	0.001514	4	0.330568	-2.169219
High Abundance	gi|6320255	0.016329	0.005011	4	0.003418	0.001229	4	0.209321	-2.466228
High Abundance	gi|6321464	0.016263	0.0104511	4	0.004347	0.001636	2	0.267294	-2.36181
High Abundance	gi|9755341	0.015824	0.0025789	4	0.006608	0.003968	4	0.417594	-2.17993
High Abundance	gi|6320359	0.013516	0.0015829	4	0.005089	0.002055	4	0.376517	-2.293368
High Abundance	gi|6323138	0.013418	0.0035944	4	0.007958	0.001608	4	0.593084	-2.099196
High Abundance	gi|6323196	0.013086	0.0040826	4	0.009202	0.001659	3	0.703194	-2.036118
High Abundance	gi|6323004	0.012217	0.0029473	4	0.009918	0.00263	4	0.81182	-2.003576
High Abundance	gi|6319314	0.011825	0.0031741	4	0.009358	0.00243	4	0.791374	-2.028817
High Abundance	gi|6322978	0.009927	0.0035095	4	0.011282	0.003292	4	1.136496	-1.947614
High Abundance	gi|6323613	0.009356	0.0019107	4	0.009014	0.004684	4	0.963446	-2.045082
High Abundance	gi|6320269	0.00911	0.0027517	4	0.002268	0.001056	4	0.248957	-2.644357
High Abundance	gi|6321408	0.008197	0.0018995	4	0.010493	0.004881	3	1.280102	-1.9791
High Abundance	gi|6319673	0.00789	0.0006584	4	0.003604	0.000784	4	0.456781	-2.443215
High Abundance	gi|6320148	0.00789	0.001499	4	0.00468	0.002968	4	0.593156	-2.329754
High Abundance	gi|6324027	0.007695	0.0023053	4	0.010315	0.004732	4	1.340481	-1.986531
High Abundance	gi|6320963	0.007322	0.0023735	4	0.004488	0.003175	2	0.612947	-2.347947
High Abundance	gi|6324670	0.006571	0.0018952	4	0.004479	0.001552	4	0.681631	-2.348819
High Abundance	gi|6323615	0.006483	0.0019291	4	0.00433	0.002097	4	0.667901	-2.363512
High Abundance	gi|6322271	0.006476	0.0026614	4	0.005247	0.002841	4	0.810222	-2.280089
High Abundance	gi|6319505	0.006391	0.0015172	4	0.002798	0.001461	4	0.437803	-2.553152
High Abundance	gi|6320215	0.006169	0.0015034	4	0.002806	0.00157	4	0.454855	-2.551912
High Abundance	gi|6320128	0.006127	0.0029448	4	0.00324	0.001804	3	0.528807	-2.489455
High Abundance	gi|6323294	0.006126	0.0027463	4	0.007531	0.002686	3	1.22935	-2.123147
High Abundance	gi|6321025	0.00602	0.0021373	4	0.005186	0.000784	4	0.861462	-2.285167
High Abundance	gi|6320590	0.005993	0.002091	4	0.006024	0.002769	4	1.005173	-2.220115
High Abundance	gi|6322583	0.005947	0.002258	4	0.005266	0.004031	4	0.885488	-2.278519
High Abundance	gi|6322794	0.005885	0.0011539	4	0.00443	0.001433	3	0.752761	-2.353596
High Abundance	gi|6320655	0.005876	0.001226	4	0.008648	0.007097	4	1.471749	-2.063084
High Abundance	gi|6320304	0.005749	0.0021378	4	0.004505	0.000577	4	0.783615	-2.346305
High Abundance	gi|6321184	0.005739	0.0024514	4	0.00403	0.000642	4	0.702213	-2.394695
High Abundance	gi|6320949	0.005297	0.0012303	4	0.001815	0.000486	4	0.342647	-2.741123
High Abundance	gi|6324120	0.005255	0.0010446	4	0.007096	0.001158	4	1.350333	-2.148986
High Abundance	gi|6319972	0.005174	0.0010909	4	0.00713	0.001477	4	1.378044	-2.14691
High Abundance	gi|6319483	0.004895	0.0014228	4	0.004604	0.002148	4	0.940552	-2.336865
High Abundance	gi|6321524	0.004766	0.0017336	4	0.00204	0.000317	4	0.428032	-2.69037
High Abundance	gi|6324534	0.00454	0.0011418	4	0.010719	0.003658	4	2.361013	-1.969846
High Abundance	gi|6323077	0.004456	0.0007734	4	0.001895	0.001081	3	0.425269	-2.722391
High Abundance	gi|6323072	0.004322	0.0016035	4	0.008287	0.001212	4	1.917399	-2.081603
High Abundance	gi|6319559	0.004142	0.000987	4	0.00657	0.00272	4	1.58619	-2.182435
High Abundance	gi|6322984	0.004123	0.0007924	4	0.002937	0.001358	4	0.712345	-2.532096
High Abundance	gi|6321754	0.004062	0.0007343	4	0.002167	0.001408	4	0.533481	-2.664141
High Abundance	gi|8655890	0.004039	0.0022002	4	0.003604	0.001438	4	0.964595	-2.409381
High Abundance	gi|6324151	0.004039	0.0008696	4	0.003896	0.000996	4	0.8923	-2.443215
High Abundance	gi|6323104	0.003953	0.0014655	3	0.002385	0	1	0.603339	-2.622512
High Abundance	gi|6323090	0.003925	0.0006235	4	0.005919	0.001611	4	1.508025	-2.227752
High Abundance	gi|6320228	0.003915	0.0009042	4	0.002102	0.001123	3	0.536909	-2.677367
High Abundance	gi|1038379	0.003833	0.0015058	4	0.004792	0.002747	4	1.250196	-2.319483
High Abundance	gi|6325196	0.003811	0.0012089	4	0.003901	0.001297	4	1.023616	-2.408824
High Abundance	gi|6323763	0.003676	0.0008584	4	0.004746	0.00088	4	1.291077	-2.323672
High Abundance	gi|6319396	0.003464	0.0013192	4	0.003404	0.001754	4	0.982679	-2.46801
High Abundance	gi|6320950	0.00335	0.0012392	4	0.002437	0.000699	4	0.727463	-2.613144
High Abundance	gi|6323163	0.003242	0.0022117	4	0.002842	0.001117	4	0.876619	-2.546376
High Abundance	gi|6323371	0.003123	0.0010263	4	0.002643	0.000798	3	0.846302	-2.577903
High Abundance	gi|6321977	0.003107	0.0005829	4	0.002082	0.001037	4	0.6701	-2.681519
High Abundance	gi|6319315	0.003028	0.0005642	4	0.004982	0.001537	4	1.64531	-2.302596
High Abundance	gi|6323057	0.003025	0.0004902	4	0.001615	0	1	0.533884	-2.791827
High Abundance	gi|6321315	0.00302	0.0018134	4	0.00248	0.00049	3	0.821192	-2.605548
High Abundance	gi|6320679	0.003006	0.0017893	4	0.005953	0.004929	4	1.980373	-2.225264
High Abundance	gi|1431847	0.003005	0.0009009	4	0.004149	0.001475	4	1.380699	-2.382057
High Abundance	gi|6322605	0.002896	0.0011085	4	0.003318	0.000731	4	1.145718	-2.479124
High Abundance	gi|6321772	0.002821	0.00075	4	0.004096	0.002725	4	1.451967	-2.38764
High Abundance	gi|6322120	0.002803	0.0005083	4	0.005616	0.000428	3	2.003568	-2.250573
High Abundance	gi|6324445	0.002779	0.0007174	4	0.003892	0.001141	4	1.400504	-2.409827
High Abundance	gi|6322564	0.002737	0.0007168	4	0.005844	0.003645	4	2.135185	-2.23329
High Abundance	gi|6322847	0.002661	0.0009261	3	0.006775	0.000128	2	2.546035	-2.169091
High Abundance	gi|6323387	0.002605	0.0007836	4	0.007279	0.001005	4	2.794242	-2.137928
High Abundance	gi|6321249	0.002598	0.0005352	4	0.010822	0	1	4.165512	-1.965692
High Abundance	gi|6320978	0.002598	0.0005352	4	0.010822	0	1	4.165512	-1.965692
High Abundance	gi|6321786	0.002568	0.0008615	3	0.005392	0.003246	3	2.099688	-2.26825
High Abundance	gi|6323474	0.002537	0.000832	4	0.00129	0.000817	4	0.508475	-2.88941
High Abundance	gi|6323386	0.002527	0.0013219	4	0.004948	0.000751	4	1.958053	-2.30557
High Abundance	gi|6323577	0.00252	0.0008462	4	0.000957	0.000312	3	0.379762	-3.019088
High Abundance	gi|6325126	0.002511	0.0009648	4	0.002578	0.001241	3	1.026683	-2.588717
High Abundance	gi|3736268	0.002496	0.0006565	4	0.005013	0.002445	3	2.008413	-2.299902
High Abundance	gi|6320065	0.002434	0.0013313	4	0.007959	0.001938	2	3.269926	-2.099141
High Abundance	gi|6321335	0.002424	0.0003522	4	0.004566	0.001213	3	1.883663	-2.340464
High Abundance	gi|6322668	0.002273	0.0004578	4	0.002149	0	1	0.945447	-2.667764
High Abundance	gi|6321362	0.00223	0.0006323	4	0.003854	0.002061	4	1.728251	-2.414088
High Abundance	gi|6322138	0.002207	0.000866	4	0.005968	0.001989	4	2.704123	-2.224171
High Abundance	gi|6322284	0.002206	0.0004999	4	0.002149	0	1	0.974161	-2.667764
High Abundance	gi|6325058	0.002175	0.0006199	4	0.003631	0.001691	4	1.669425	-2.439974
High Abundance	gi|6321648	0.002154	0.0003065	4	0.005801	0.004488	4	2.693129	-2.236497
High Abundance	gi|6323840	0.002039	0.0005044	4	0.002796	0.001264	4	1.37126	-2.553463
High Abundance	gi|6319666	0.001922	0.0005228	4	0.002449	0.001552	2	1.274194	-2.611011
High Abundance	gi|6321291	0.0019	0.0009582	4	0.006641	0.001377	4	3.495263	-2.177767
High Abundance	gi|6319965	0.001871	0	1	0.002463	0	1	1.316408	-2.608536
High Abundance	gi|6325016	0.001829	0.000394	4	0.002908	0.001107	4	1.58994	-2.536406
High Abundance	gi|6325176	0.001797	0.0003761	4	0.001644	0.000433	2	0.914858	-2.784098
High Abundance	gi|6324452	0.001776	0.0007938	4	0.00279	0.000827	4	1.570946	-2.554396
High Abundance	gi|6320905	0.001754	0.0007026	4	0.001526	0.000795	4	0.870011	-2.816445
High Abundance	gi|6321407	0.001753	0.0001109	3	0.001278	0	1	0.729036	-2.893469
High Abundance	gi|6321587	0.001753	0.0001109	3	0.001917	0	1	1.093554	-2.717378
High Abundance	gi|6324756	0.001742	0.0002751	2	0.003659	0	1	2.100459	-2.436638
High Abundance	gi|6324262	0.001621	0.0007381	4	0.003283	0.001445	4	2.025293	-2.483729
High Abundance	gi|6320882	0.001527	0.0003252	4	0.003719	0.000333	4	2.435494	-2.429574
High Abundance	gi|6323288	0.001526	0.000417	4	0.004584	0.001162	4	3.003932	-2.338755

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE600 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
High Abundance	gi|6324637	0.001484	0.0008663	4	0.001847	0.000448	4	1.244609	-2.733533	-2.828566	0.095033	1	25	18.93939394	7.25	4.25	0.493681	0
High Abundance	gi|6321679	0.001482	0.0007832	4	0.004657	0.001414	4	3.142375	-2.331894	-2.829152	0.497258	1	24	18.18181818	9.25	17.75	0.012621	1
High Abundance	gi|6320781	0.001401	0.0003751	4	0.003299	0.001572	3	2.354747	-2.481618	-2.853562	0.371944	1	23	17.42424242	4	2.666667	0.166914	0
High Abundance	gi|6319814	0.00138	0	1	0.008105	0	1	5.873188	-2.091247	-2.860121	0.768874	2	101	100	1	2		
High Abundance	gi|1431847	0.001378	0.0004714	3	0.002313	0.000377	4	1.67852	-2.635824	-2.860751	0.224926	1	22	16.66666667	2.333333333	2.75	0.050561	0
High Abundance	gi|6325300	0.001286	0.0003953	3	0.005617	0	1	4.367807	-2.250496	-2.890759	0.640263	2	100	99.00990099	3	1		
High Abundance	gi|6325006	0.001251	0.0009425	3	0.004946	0.001149	4	3.953637	-2.305746	-2.902743	0.596997	2	99	98.01980198	2.666666667	1.5	0.005793	1
High Abundance	gi|6324945	0.00122	0.0009316	4	0.00324	0.001289	4	2.655738	-2.489455	-2.91364	0.424185	1	21	15.90909091	3	3.25	0.047895	1
High Abundance	gi|6324260	0.001209	0.0006283	4	0.002529	0.000988	4	2.091811	-2.597051	-2.917574	0.320523	1	20	15.15151515	2.75	2.25	0.072979	0
High Abundance	gi|6319307	0.001205	0.0006478	4	0.002787	0.001156	4	2.312863	-2.554863	-2.919013	0.36415	1	19	14.39393939	3.75	5.25	0.065623	0
High Abundance	gi|6320121	0.001197	0.0005492	4	0.002843	0.000911	3	2.375104	-2.546223	-2.921906	0.375683	1	18	13.63636364	4.5	2.666667	0.067115	0
High Abundance	gi|6323567	0.001187	0.0006256	3	0.00225	0.001594	2	1.895535	-2.647817	-2.925549	0.277732	1	17	12.87878788	2.333333333	3	0.512161	0
High Abundance	gi|6324533	0.001167	0.0004606	3	0.006016	0.00196	4	5.155099	-2.220692	-2.932929	0.712237	2	98	97.02970297	2.666666667	2.75	0.012779	1
High Abundance	gi|1431855	0.001152	0.0002631	4	0.001213	0.000376	4	1.052951	-2.916139	-2.938548	0.022408	1	16	12.12121212	4.25	1	0.798414	0
High Abundance	gi|6322325	0.00111	0.0002411	2	0.008389	0.003241	3	7.557658	-2.07629	-2.954677	0.878387	2	97	96.03960396	3.5	2.666667	0.059057	0
High Abundance	gi|6324463	0.001107	0.0004562	4	0.003403	0.001018	3	3.074074	-2.468138	-2.955852	0.487714	1	15	11.36363636	3.5	3.666667	0.044892	1
High Abundance	gi|6323087	0.00108	0.0002282	4	0.002414	0.000742	4	2.235185	-2.617263	-2.966576	0.349314	1	14	10.60606061	7.75	5.75	0.031655	1
High Abundance	gi|6319585	0.001056	0.0004812	3	0.005756	0.002033	3	5.450758	-2.239879	-2.976336	0.736457	2	96	95.04950495	1.666666667	3.666667	0.050446	0
High Abundance	gi|6324808	0.00104	0.0005113	3	0.002415	0	1	2.322115	-2.617083	-2.982967	0.365884	1	13	9.848484848	3.333333333	1		
High Abundance	gi|6319378	0.001033	0.0001728	2	0.001182	0	1	1.14424	-2.927383	-2.9859	0.058517	1	12	9.090909091	1.5	2		
High Abundance	gi|6319806	0.001028	0.0007237	4	0.003308	0.001569	4	3.217899	-2.480434	-2.988007	0.507572	1	11	8.333333333	4.25	8.25	0.054582	0
High Abundance	gi|6322599	0.001004	0.0005152	4	0.003228	0.00056	4	3.215139	-2.491066	-2.998266	0.5072	1	10	7.575757576	4	4.75	0.001133	1
High Abundance	gi|6323481	0.000987	0.0006673	4	0.002532	0.001992	2	2.56535	-2.596536	-3.005683	0.409147	1	9	6.818181818	2.5	3	0.464584	0
High Abundance	gi|6325114	0.000969	0.0003805	3	0.007285	0.001714	3	7.51806	-2.13757	-3.013676	0.876106	2	95	94.05940594	3.666666667	2	0.019649	1
High Abundance	gi|6322910	0.000964	0.0004746	4	0.007365	0.002817	4	7.640041	-2.132827	-3.015923	0.883096	2	94	93.06930693	2.75	2.25	0.018408	1
High Abundance	gi|6324707	0.00096	0.0002577	4	0.004349	0.001446	4	4.530208	-2.361611	-3.017729	0.656118	2	93	92.07920792	14.5	15.25	0.016708	1
High Abundance	gi|6324298	0.000959	0	1	0.004165	0.002271	2	4.343066	-2.380385	-3.018181	0.637796	2	92	91.08910891	2	2		
High Abundance	gi|6320226	0.000944	0.0005776	4	0.002016	0.000846	4	2.135593	-2.695509	-3.025028	0.329519	1	8	6.060606061	7	4.75	0.08751	0
High Abundance	gi|6322505	0.000944	0.0002374	4	0.003811	0.001184	4	4.037076	-2.418961	-3.025028	0.606067	2	91	90.0990099	11	11.5	0.014846	1
High Abundance	gi|6324923	0.00094	0.0002014	4	0.001458	0.000387	4	1.551064	-2.836242	-3.026872	0.19063	1	7	5.303030303	1.5	1.75	0.069037	0
High Abundance	gi|6325331	0.000911	0.0005313	4	0.001518	0.000743	4	1.666301	-2.818728	-3.040482	0.221753	1	6	4.545454545	5.75	4.25	0.237009	0

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG	noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Proteins with p-Value < 0.05 (% of Proteins in Group)
138	**28.45%**	**95.979**	**3.7971014**	**0.581458276**	**76.6284**	**3.413043**	**0.994351**	**0.006955**	**0.0055528**	**6.678743961**	**5.62392236**	**4.791062802**	**3.834553**	**43**	**34.96%**

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE600 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6323729	0.000886	0.0002884	4	0.00088	0.00025	2	0.993228	-3.055517	-3.052566	-0.002951	1	5	3.787878788	1	2	0.980734	0
Low Abundance	gi|6321987	0.000884	0.0004026	3	0.003747	0.000575	3	4.238688	-2.426316	-3.053548	0.627231	2	90	89.10891089	1.666666667	4	0.003186	1
Low Abundance	gi|6323848	0.000853	5.087E-05	2	0.004946	0.001149	4	5.798359	-2.305746	-3.069051	0.763305	2	89	88.11881188	3.5	1.5	0.005575	1
Low Abundance	gi|6323324	0.00085	0.0005116	4	0.004066	0.001892	3	4.783529	-2.390833	-3.070581	0.679748	2	88	87.12871287	2.75	3.333333	0.091482	0
Low Abundance	gi|6323391	0.000799	0	1	0.001109	0.00036	3	1.387985	-2.955068	-3.097453	0.142385	1	4	3.03030303	2	3.333333		
Low Abundance	gi|6324233	0.000787	0.00044	4	0.005802	0.001136	4	7.3723	-2.236422	-3.104025	0.867603	2	87	86.13861386	3.75	4.75	0.001353	1
Low Abundance	gi|6321973	0.000785	0.0002581	4	0.004652	0.001237	4	5.926115	-2.33236	-3.10513	0.77277	2	86	85.14851485	5.25	6	0.006852	1
Low Abundance	gi|6322058	0.000758	0.0005851	4	0.001103	0.000624	2	1.455145	-2.957424	-3.120331	0.162906	1	3	2.272727273	2	2	0.58245	0
Low Abundance	gi|6321563	0.000731	0.0002768	4	0.001456	0.000424	4	1.991792	-2.836839	-3.136083	0.299244	1	2	1.515151515	4.5	5.5	0.034031	1
Low Abundance	gi|6322002	0.000706	0.0002692	4	0.001433	0.000575	4	2.029745	-2.843754	-3.151195	0.307441	1	1	0.757575758	4	3.25	0.080092	0
Low Abundance	gi|6323861	0.000695	0.0001588	4	0.002628	0.001102	4	3.781295	-2.580375	-3.158015	0.577641	2	85	84.15841584	8	10.25	0.037807	1
Low Abundance	gi|6325036	0.000678	0.0005354	4	0.002325	0.000829	3	3.429204	-2.633577	-3.16877	0.535193	2	84	83.16831683	3	4	0.052219	0
Low Abundance	gi|6322565	0.000592	0.0003229	4	0.003243	0.000631	4	5.478041	-2.489053	-3.227678	0.738625	2	83	82.17821782	3.75	5.75	0.001089	1
Low Abundance	gi|6324907	0.000581	0.0001725	3	0.003136	0.001233	4	5.39759	-2.503624	-3.235824	0.7322	2	82	81.18811881	2.666666667	3.25	0.02394	1
Low Abundance	gi|6323464	0.000559	0.0003827	4	0.003255	0.000849	4	5.822898	-2.487449	-3.252588	0.765139	2	81	80.1980198	5.25	7.5	0.00389	1
Low Abundance	gi|6323208	0.000546	0.0002841	3	0.0026	0.000647	2	4.761905	-2.585027	-3.262807	0.677781	2	80	79.20792079	2	2.5	0.107652	0
Low Abundance	gi|6325178	0.000537	0.0002627	4	0.001441	0	1	2.683426	-2.841336	-3.270026	0.42869	2	78	77.22772277	3.25	1		
Low Abundance	gi|6319668	0.000537	0.0002627	4	0.001441	0	1	2.683426	-2.841336	-3.270026	0.42869	2	79	78.21782178	3.25	1		
Low Abundance	gi|6320846	0.000525	0	1	0.003469	0.001179	2	6.607619	-2.459796	-3.279841	0.820045	2	77	76.23762376	2	2		
Low Abundance	gi|6325229	0.000513	0.0001867	2	0.003868	0.001082	4	7.539961	-2.412514	-3.289883	0.877369	2	76	75.24752475	1.5	6	0.00675	1
Low Abundance	gi|6322608	0.00049	0.0001071	4	0.002081	0.001089	4	4.246939	-2.681728	-3.309804	0.628076	2	75	74.25742574	2.75	3.5	0.060718	0
Low Abundance	gi|6322912	0.000485	7.247E-05	4	0.003638	0.000956	4	7.501031	-2.439137	-3.314258	0.875121	2	74	73.26732673	4.5	7	0.006889	1
Low Abundance	gi|6319603	0.000456	0.0003563	3	0.002882	0.00134	4	6.320175	-2.540306	-3.341035	0.800729	2	72	71.28712871	5.666666667	7.75	0.031277	1
Low Abundance	gi|6321522	0.000456	0.0002485	3	0.002412	0.00218	3	5.289474	-2.617623	-3.341035	0.723412	2	73	72.27722772	2	2.333333	0.259469	0
Low Abundance	gi|6323585	0.000454	0.0001934	4	0.001898	0.000659	4	4.180617	-2.721704	-3.342944	0.62124	2	71	70.2970297	4.25	5.25	0.017893	1
Low Abundance	gi|6323619	0.000447	0	1	0.002114	0	1	4.729306	-2.674895	-3.349692	0.674797	2	70	69.30693069	1	2		
Low Abundance	gi|6325167	0.000444	0.0003366	4	0.003184	0.003195	4	7.171171	-2.497027	-3.352617	0.85559	2	69	68.31683168	2.75	2.75	0.184615	0
Low Abundance	gi|6325403	0.00044	7.871E-05	4	0.002072	0.000927	4	4.709091	-2.68361	-3.356547	0.672937	2	68	67.32673267	4.75	6	0.038359	1
Low Abundance	gi|6319901	0.000432	0.0001175	4	0.002176	0.000701	4	5.037037	-2.662341	-3.364516	0.702175	2	67	66.33663366	5	5.25	0.014248	1
Low Abundance	gi|6322783	0.000431	3.004E-05	2	0.002478	0.000757	2	5.74942	-2.605899	-3.365523	0.759624	2	66	65.34653465	2	2	0.162362	0
Low Abundance	gi|6323470	0.000426	7.068E-05	2	0.001692	0.000958	3	3.971831	-2.7716	-3.37059	0.598991	2	65	64.35643564	2.5	3	0.148314	0
Low Abundance	gi|6319726	0.000424	0.0002274	3	0.001666	0.000993	4	3.929245	-2.778325	-3.372634	0.594309	2	64	63.36633663	2.666666667	3	0.083962	0
Low Abundance	gi|6323554	0.000418	0	1	0.000738	0.000323	3	1.76555	-3.131944	-3.378824	0.24688	2	63	62.37623762	1	2.666667		
Low Abundance	gi|6324951	0.000404	0.0002468	4	0.006899	0.001235	4	17.07673	-2.161214	-3.393619	1.232405	2	62	61.38613861	5	11.25	0.001383	1
Low Abundance	gi|6320362	0.000395	0.0001931	4	0.003304	0.001136	4	8.364557	-2.48096	-3.403403	0.922443	2	61	60.3960396	3.75	4	0.013075	1
Low Abundance	gi|6325326	0.000385	8.272E-05	3	0.001571	0.000989	4	4.080519	-2.803824	-3.414539	0.610715	2	60	59.40594059	2.333333333	2.5	0.095422	0
Low Abundance	gi|6320936	0.000379	8.388E-05	4	0.003368	0.000801	4	8.886544	-2.472628	-3.421361	0.948733	2	59	58.41584158	6.5	11.75	0.004703	1
Low Abundance	gi|6321013	0.000356	3.694E-05	4	0.002367	0.001101	4	6.648876	-2.625802	-3.44855	0.822748	2	58	57.42574257	4.75	6.75	0.035299	1
Low Abundance	gi|6322666	0.000324	0.0001428	4	0.001547	0.000402	4	4.774691	-2.81051	-3.489455	0.678945	2	57	56.43564356	12.5	15.5	0.005581	1
Low Abundance	gi|6322732	0.00032	0	1	0.004624	0	1	14.45	-2.334982	-3.49485	1.159868	2	56	55.44554455	2	3		
Low Abundance	gi|6325290	0.00031	6.308E-05	3	0.000886	0.000429	3	2.858065	-3.052566	-3.508638	0.456072	2	55	54.45544554	1	3.333333	0.143235	0
Low Abundance	gi|6320016	0.000304	0.0002023	4	0.001682	0.000819	4	5.532895	-2.774174	-3.517126	0.742952	2	53	52.47524752	6	9.75	0.039666	1
Low Abundance	gi|6320710	0.000304	0	1	0.001055	0.00065	3	3.470395	-2.976748	-3.517126	0.540379	2	54	53.46534653	1	2.666667		
Low Abundance	gi|6319625	0.000275	7.403E-05	2	0.001439	0.000251	3	5.232727	-2.841939	-3.560667	0.718728	2	52	51.48514851	2.5	2.333333	0.00912	1
Low Abundance	gi|1431857	0.000271	0.000214	4	0.003455	0.000578	4	12.74908	-2.461552	-3.567031	1.105479	2	51	50.4950495	2	7.25	0.000636	1
Low Abundance	gi|6322434	0.00026	0.0002101	4	0.001936	0.000526	4	7.446154	-2.713095	-3.585027	0.871932	2	49	48.51485149	2	4.25	0.0043	1
Low Abundance	gi|6325166	0.00026	2.008E-05	2	0.000853	0.000527	3	3.280769	-3.069051	-3.585027	0.515976	2	50	49.5049505	1	2.333333	0.190466	0
Low Abundance	gi|6321721	0.000256	0.0001613	3	0.001626	0.000437	4	6.351563	-2.788879	-3.59176	0.802881	2	48	47.52475248	2.666666667	2.75	0.004511	1
Low Abundance	gi|6321673	0.000252	3.779E-05	3	0.000993	0	1	3.940476	-3.003051	-3.598599	0.595549	2	47	46.53465347	3.333333333	3		
Low Abundance	gi|6323209	0.000235	0.0001001	2	0.002329	0.000877	4	9.910638	-2.632831	-3.628932	0.996102	2	46	45.54455446	1.5	3	0.016154	1
Low Abundance	gi|6322476	0.00022	0	1	0.001297	0.000386	4	5.895455	-2.88706	-3.657577	0.770517	2	45	44.55445545	1	4.25		
Low Abundance	gi|6325292	0.000216	0.0001511	3	0.001653	0.000972	3	7.652778	-2.781727	-3.665546	0.883819	2	44	43.56435644	2.666666667	2.666667	0.121242	0
Low Abundance	gi|6319395	0.000199	8.669E-05	4	0.002542	0.001011	4	12.77387	-2.594824	-3.701147	1.106322	2	43	42.57425743	5.75	14.25	0.018472	1
Low Abundance	gi|6322012	0.000188	0.0001907	2	0.002003	0.0005	4	10.65426	-2.698319	-3.725842	1.027523	2	42	41.58415842	3.5	4	0.003113	1
Low Abundance	gi|6322722	0.000164	0	1	0.000715	0.000323	3	4.359756	-3.145694	-3.785156	0.639462	2	41	40.59405941	2	2.666667		
Low Abundance	gi|6322294	0.000153	2.118E-05	2	0.002015	0.000651	4	13.16993	-2.695725	-3.815309	1.119584	2	40	39.6039604	2.5	2.75	0.010497	1
Low Abundance	gi|6321643	0.000147	7.262E-05	2	0.001418	0.000425	4	9.646259	-2.848324	-3.832683	0.984359	2	38	37.62376238	4	5.75	0.00757	1
Low Abundance	gi|6324250	0.000147	5.914E-05	2	0.002094	0.001323	2	14.2449	-2.679023	-3.832683	1.153659	2	39	38.61386139	2	2.5	0.284628	0
Low Abundance	gi|6320077	0.000146	0.000116	3	0.001455	0.000842	4	9.965753	-2.837137	-3.835647	0.99851	2	35	34.65346535	2	6	0.051096	0
Low Abundance	gi|8279524	0.000146	5.559E-05	3	0.001743	0.00055	4	5.705479	-3.079355	-3.835647	0.756292	2	36	35.64356436	2.333333333	4.25	0.009589	1
Low Abundance	gi|6321837	0.000146	0.00016	2	0.000833	0.000297	4	11.93836	-2.758703	-3.835647	1.076945	2	37	36.63366337	2	4	0.02396	1
Low Abundance	gi|6322815	0.000139	6.576E-07	2	0.001097	0.000218	4	7.892086	-2.959793	-3.856985	0.897192	2	34	33.66336634	2	3.75	0.003101	1
Low Abundance	gi|6324804	0.000136	5.518E-05	4	0.002129	0.000721	4	15.65441	-2.671824	-3.866461	1.194637	2	33	32.67326733	3.25	4.5	0.011409	1
Low Abundance	gi|6322581	0.00013	7.319E-05	3	0.001851	0.001064	4	2.838462	-3.432974	-3.886057	0.453083	2	31	30.69306931	3.333333333	6.5	0.047503	1
Low Abundance	gi|6319424	0.00013	5.777E-05	3	0.000369	0.00014	3	14.23846	-2.732594	-3.886057	1.153463	2	32	31.68316832	1	4	0.082703	0
Low Abundance	gi|6321594	0.000126	7.388E-05	2	0.001712	0.000961	4	13.5873	-2.766496	-3.899629	1.133133	2	30	29.7029703	2	4.75	0.044918	1
Low Abundance	gi|6323967	0.000125	0	1	0.001352	0.00065	4	10.816	-2.869023	-3.90309	1.034067	2	29	28.71287129	2	2.75		
Low Abundance	gi|1038376	0.00012	6.64E-05	3	0.001131	0.000631	4	9.425	-2.946537	-3.920819	0.974281	2	28	27.72277228	3	4	0.048078	1
Low Abundance	gi|6320432	0.000119	5.143E-05	3	0.001893	0.001178	3	15.90756	-2.722849	-3.924453	1.201604	2	27	26.73267327	2.333333333	2.666667	0.12054	0
Low Abundance	gi|6320560	0.000117	4.226E-05	2	0.002399	0.001501	3	20.50427	-2.61997	-3.931814	1.311844	2	26	25.74257426	2	3.666667	0.118871	0
Low Abundance	gi|6320839	0.000115	0	1	0.001067	0.00055	3	9.278261	-2.971836	-3.939302	0.967467	2	25	24.75247525	2	3		
Low Abundance	gi|6323768	0.000108	0.0001282	3	0.001694	0.00087	4	15.90741	-2.764977	-3.966576	1.201599	2	23	22.77227723	1.666666667	5.75	0.033739	1
Low Abundance	gi|6321619	0.000108	9.652E-06	2	0.001718	0.000495	3	15.68519	-2.771087	-3.966576	1.19549	2	24	23.76237624	2	3.333333	0.030056	1
Low Abundance	gi|6319597	0.000107	4.781E-05	2	0.001723	0.00044	4	16.1028	-2.763715	-3.970616	1.206901	2	21	20.79207921	3	6.5	0.004631	1
Low Abundance	gi|6324321	0.000107	0	1	0.002438	0.00015	4	22.78505	-2.612966	-3.970616	1.35765	2	22	21.78217822	2	3.75		
Low Abundance	gi|6325025	0.000105	4.233E-05	4	0.001967	0.000589	4	8.457143	-3.051587	-3.978811	0.927224	2	19	18.81188119	5.75	19.75	0.007816	1
Low Abundance	gi|6321203	0.000105	9.663E-05	2	0.000888	0.000483	4	18.73333	-2.706196	-3.978811	1.272615	2	20	19.8019802	1.5	5.25	0.043818	1
Low Abundance	gi|6320789	0.000097	0	1	0.001276	0.000515	3	13.15464	-2.894149	-4.013228	1.119079	2	18	17.82178218	2	3		

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE600 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
Low Abundance	gi|6324601	0.000095	5.708E-05	4	0.002015	0.000543	4	21.21053	-2.695725	-4.022276	1.326551	2	17	16.83168317	2.5	5.75	0.005514	1
Low Abundance	gi|6319552	0.000089	0	1	0.000704	0	1	7.910112	-3.152427	-4.05061	0.898183	2	16	15.84158416	2	2		
Low Abundance	gi|6321236	0.000086	4.019E-05	3	0.002266	0.000753	4	26.34884	-2.64474	-4.065502	1.420761	2	15	14.85148515	2.666666667	4.5	0.010076	1
Low Abundance	gi|6320548	0.00008	0	1	0.000792	0.000108	4	9.9	-3.101275	-4.09691	0.995635	2	14	13.86138614	3	3		
Low Abundance	gi|6321498	0.000079	3.164E-05	3	0.001066	0.000149	4	13.49367	-2.972243	-4.102373	1.13013	2	13	12.87128713	4	7.5	0.000575	1
Low Abundance	gi|6323509	0.000076	0	1	0.001543	0.000623	4	20.30263	-2.811634	-4.119186	1.307552	2	12	11.88118812	3	4.25		
Low Abundance	gi|1431856	0.000059	0	1	0.002973	0.000695	4	50.38983	-2.526805	-4.229148	1.702343	2	11	10.89108911	2	6.5		
Low Abundance	gi|6319695	0.000052	1.578E-05	2	0.000943	0.000333	4	18.13462	-3.025488	-4.283997	1.258508	2	10	9.900990099	3	6.25	0.012619	1
Low Abundance	gi|6324709	0.000051	0	1	0.001141	0.000515	4	41.98039	-2.669383	-4.29243	1.623046	2	9	8.910891089	2	3.25		
Low Abundance	gi|6321376	0.00005	1.998E-05	2	0.000647	0.000241	3	12.94	-3.189096	-4.30103	1.111934	2	8	7.920792079	2.5	4	0.048944	1
Low Abundance	gi|6321429	0.000048	0	1	0.001295	0.000473	4	26.97917	-2.88773	-4.318759	1.431029	2	6	5.940594059	2	6.5		
Low Abundance	gi|6321859	0.000048	0	1	0.002962	0.000935	3	61.5	-2.529884	-4.318759	1.788875	2	7	6.930693069	2	5		
Low Abundance	gi|6320019	0.000033	0	1	0.001866	0.000395	4	56.54545	-2.729088	-4.481486	1.752398	2	4	3.96039604	2	4		
Low Abundance	gi|6320137	0.000033	0	1	0.00264	0.000667	4	80	-2.578396	-4.481486	1.90309	2	5	4.95049505	2	5.25		
Low Abundance	gi|6320071	0.000032	0	1	0.001896	0.000873	4	59.25	-2.722162	-4.494485	1.772688	2	3	2.97029703	2	4.5		
Low Abundance	gi|6319809	0.000028	0	1	0.001985	0.000286	4	70.89286	-2.702239	-4.552842	1.850602	2	2	1.98019802	2	4.5		
Low Abundance	gi|6323335	0.000018	0	1	0.000949	0.000138	4	52.72222	-3.022734	-4.744727	1.721994	2	1	0.99009901	2	4.25		
Number of Proteins in Group		Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG			noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD	Number of Proteins with p-Value < 0.05	Protein s with p-Value < 0.05 (% of Protein s in Group)
95		19.59%	2.9718	2.6105263	1.187655807	19.871	3.463158	0.872884	0.000313	0.0020917			2.915789474	1.696692946	4.714035088	3.003634	47	69.12%

Group	noDE 1_P	noDE 1_uP	noDE 1_S	noDE 1_SC	noDE 1_NSAF	noDE 2_P	noDE 2_uP	noDE 2_S	noDE 2_SC	noDE 2_NSAF	noDE 3_P	noDE 3_uP	noDE 3_S	noDE 3_SC	noDE 3_NSAF	noDE 4_P	noDE 4_uP	noDE 4_S	noDE 4_SC	noDE 4_NSAF	DE600 0-1_P	DE600 0-1_uP	DE600 0-1_S	DE600 0-1_SC	DE600 0-1_NSAF	DE600 0-2_P	DE600 0-2_uP	DE600 0-2_S	DE600 0-2_SC	DE600 0-2_NSAF	DE600 0-3_P	DE600 0-3_uP	DE600 0-3_S	DE600 0-3_SC	DE600 0-3_NSAF	DE600 0-4_P	DE600 0-4_uP	DE600 0-4_S	DE600 0-4_SC	DE600 0-4_NSAF
Low Abundance	1	2	2	3.9	3.96E-05	3	3	7	7.81	8.27E-05	3	3	11	7.81	0.000175	2	2	5	4.41	8.39E-05	8	8	19	15.79	0.002778	4	4	12	10.02	0.002018	6	6	14	14.26	0.001566	5	5	13	11.21	0.001696
Low Abundance	X	X	X	X	X	X	X	2	6	5.56	8.93E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Low Abundance	2	2	3	5.2	7E-05	2	2	4	5.4	5.57E-05	4	4	7	11.2	0.000131	X	X	X	X	X	4	4	15	11	0.002584	2	2	6	6.4	0.001189	6	6	18	15.2	0.002372	6	6	19	15.8	0.00292
Low Abundance	X	X	X	X	X	3	3	7	5.44	8.03E-05	X	X	X	X	X	X	X	X	X	X	3	3	6	5.6	0.000851	2	2	5	4.61	0.000816	4	4	8	6.92	0.000868	3	3	5	4.78	0.000633
Low Abundance	X	X	X	X	X	4	4	9	4.79	4.61E-05	3	3	12	2.8	8.29E-05	5	5	15	5.38	0.000109	7	7	14	7.51	0.000888	6	6	17	6.85	0.00124	7	7	23	8.03	0.001116	10	10	18	12.15	0.001018
Low Abundance	X	X	X	X	X	X	X	X	X	X	3	3	4	7.74	7.64E-05	X	X	X	X	X	5	5	14	13.85	0.002456	4	4	7	9.16	0.001412	5	5	9	13.44	0.001208	3	3	7	8.76	0.001095
Low Abundance	X	X	X	X	X	X	X	X	X	X	2	2	3	5.61	5.85E-05	X	X	X	X	X	6	6	16	17.05	0.002865	7	7	19	22.25	0.003913	6	6	21	19.13	0.002877	7	7	14	16.63	0.002236
Low Abundance	4	4	7	3.98	4.13E-05	2	2	8	2.03	6.36E-05	X	X	X	X	X	X	X	X	X	X	8	8	19	8.81	0.001387	5	5	12	6.1	0.001007	7	7	13	7.37	0.000726	5	5	10	6.02	0.000651
Low Abundance	X	X	X	X	X	2	2	2	7.32	5.09E-05	X	X	X	X	X	X	X	X	X	X	3	3	9	13.01	0.002101	4	4	10	17.89	0.002685	3	3	13	14.63	0.002321	3	3	7	13.01	0.001458
Low Abundance	X	X	X	X	X	2	2	8	2.04	6.37E-05	X	X	X	X	X	X	X	X	X	X	4	4	7	4.92	0.000512	4	4	11	4.67	0.000925	4	4	9	4.24	0.000503	X	X	X	X	X
Low Abundance	X	X	X	X	X	2	2	4	3.72	4.82E-05	X	X	X	X	X	X	X	X	X	X	7	7	17	13.35	0.001879	4	4	7	8.09	0.00089	7	7	11	12.2	0.00093	8	8	15	14.76	0.001479
Low Abundance	X	X	X	X	X	2	2	2	8.53	4.85E-05	X	X	X	X	X	X	X	X	X	X	5	5	13	15.76	0.002893	3	3	8	9.82	0.002048	7	7	23	20.41	0.003916	X	X	X	X	X
Low Abundance	2	2	2	6.07	3.25E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	13.32	0.001409	3	3	5	11.92	0.001157	3	3	19	8.64	0.002925	6	6	11	21.03	0.001975
Low Abundance	2	2	2	5.61	3.25E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	11	13.79	0.002213	5	5	15	16.36	0.003472	7	7	13	23.13	0.002001	4	4	16	15.19	0.002872
Low Abundance	2	2	2	5.91	3.16E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	8	15.23	0.001566	3	3	5	11.59	0.001126	5	5	21	12.95	0.003145	5	5	10	17.05	0.001746
Low Abundance	2	2	2	4.6	2.79E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	11	16.2	0.001895	5	5	14	11	0.001981	5	5	18	16.8	0.002372	6	6	11	19	0.00169
Low Abundance	2	2	2	3.34	1.79E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	8	6.68	0.000886	4	4	8	7.07	0.001019	6	6	13	9.64	0.001101	3	3	8	4.88	0.00079

Group	noDE 1_P	noDE 1_uP	noDE 1_S	noDE 1_SC	noDE 1_NSAF	noDE 2_P	noDE 2_uP	noDE 2_S	noDE 2_SC	noDE 2_NSAF	noDE 3_P	noDE 3_uP	noDE 3_S	noDE 3_SC	noDE 3_NSAF	noDE 4_P	noDE 4_uP	noDE 4_S	noDE 4_SC	noDE 4_NSAF	DE600 0-1_P	DE600 0-1_uP	DE600 0-1_S	DE600 0-1_SC	DE600 0-1_NSAF	DE600 0-2_P	DE600 0-2_uP	DE600 0-2_S	DE600 0-2_SC	DE600 0-2_NSAF	DE600 0-3_P	DE600 0-3_uP	DE600 0-3_S	DE600 0-3_SC	DE600 0-3_NSAF	DE600 0-4_P	DE600 0-4_uP	DE600 0-4_S	DE600 0-4_SC	DE600 0-4_NSAF
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	7	7	16	11.47	0.001264	6	6	20	8.81	0.001818	7	7	22	8.72	0.00133	8	8	13	12.39	0.000916
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	8.61	0.00103	2	2	4	6.22	0.000948	3	3	11	9.09	0.001734	2	2	6	5.5	0.001103
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	7	7	12	11.44	0.001105	3	3	13	4.49	0.001377	8	8	31	13.58	0.002185	6	6	18	9.95	0.001479
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	4.95	0.000609	2	2	2	2.97	0.000729	5	5	15	9.62	0.001398	5	5	6	11.74	0.000543
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.92	0.000437	6	6	10	14.04	0.001676	4	4	6	10.49	0.000669	5	5	6	11.17	0.00078
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	7.45	0.000729	2	2	8	5.92	0.001341	3	3	10	7.45	0.001115	2	2	3	4.23	0.00039
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	6.45	0.001042	2	2	3	4.23	0.000599	3	3	6	7.46	0.000797	4	4	12	10.48	0.001859
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	19.28	0.00197	4	4	6	15.03	0.001942	5	5	7	20.26	0.001507	2	2	4	8.82	0.001004
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	8	9.94	0.00137	4	4	8	7.95	0.001576	4	4	5	9.15	0.000655	2	2	3	4.57	0.000458
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	13	15.89	0.00434	4	4	10	21.71	0.00384	5	5	18	27.91	0.004597	3	3	13	18.6	0.003871
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.9	0.000373	4	4	4	8.23	0.000572	5	5	8	9.24	0.000761	3	3	13	5.34	0.001441
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	13.32	0.001409	3	3	5	11.92	0.001157	3	3	19	8.64	0.002925	6	6	11	21.03	0.001975
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	17.58	0.002524	4	4	8	23.81	0.002903	4	4	6	18.32	0.001448	3	3	5	20.15	0.001407
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	14	14	34	9.49	0.001323	15	15	30	9.89	0.001342	22	22	53	13.87	0.001577	19	19	36	12.65	0.001249
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	12.36	0.001935	2	2	3	12.36	0.001113	5	5	12	26.59	0.002961	6	6	14	28.46	0.004029
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	6	9.53	0.000835	3	3	7	7.27	0.00112	6	6	12	16.16	0.001277	6	6	10	15.02	0.001241
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	11	24.85	0.002836	5	5	10	21.86	0.002966	3	3	9	14.07	0.001775	5	5	7	18.86	0.00161
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	8	8.3	0.000673	4	4	10	6.15	0.000967	4	4	5	5.27	0.000322	4	4	6	6.15	0.00045
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	6.47	0.001591	2	2	5	6.47	0.001144	5	5	13	15.7	0.001978	3	3	10	9.47	0.001774
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.13	0.00051	3	3	10	8.88	0.001954	2	2	6	5.52	0.00078	3	3	7	9.27	0.001061
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	12.3	0.002303	4	4	12	25.67	0.006357	5	5	14	36.36	0.004933	3	3	8	19.25	0.003287
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	8.37	0.001406	3	3	6	7.35	0.001213	4	4	11	10.2	0.001479	4	4	7	9.39	0.001098
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	3.87	0.000289	3	3	4	6.39	0.00066	2	2	3	4.2	0.000332	3	3	4	5.88	0.000517
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	12	3.78	0.000482	7	7	20	5.13	0.000924	10	10	17	6.85	0.000522	6	6	13	4.94	0.000466
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	5.37	0.000308	3	3	3	4.38	0.000266	5	5	9	7.16	0.00053	3	3	3	4.65	0.000206
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	6.05	0.001159	3	3	6	8.3	0.001333	3	3	7	8.52	0.001034	3	3	6	8.3	0.001034
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	5.6	0.000561	3	3	5	4.3	0.000645	4	4	7	7.16	0.000601	3	3	5	5.47	0.0005
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	5.14	0.00079	2	2	3	4.04	0.000545	3	3	3	7.71	0.000363	4	4	5	8.44	0.000705
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	9.79	0.001099	4	4	10	11.91	0.002108	2	2	4	4.89	0.000561	3	3	7	9.79	0.001144
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.73	0.000582	4	4	8	10.14	0.001339	5	5	11	13.01	0.001224	3	3	5	6.42	0.000649
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.19	0.000536	3	3	7	7.05	0.001439	3	3	4	10.79	0.000547	4	4	5	11.2	0.001435
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	11	15.23	0.001899	4	4	8	13.63	0.001588	4	4	10	13.83	0.00132	2	2	5	7.01	0.00077
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	9.9	0.000682	3	3	10	9.5	0.001962	4	4	6	13.27	0.000783	2	2	3	6.93	0.000456
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	9	21.46	0.003539	2	2	8	15.98	0.003619	2	2	10	15.98	0.003009	3	3	9	21.46	0.003158
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	12.84	0.001412	4	4	6	15.85	0.001624	4	4	13	17.21	0.00234	2	2	6	10.93	0.00126
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	6	4.22	0.000325	2	2	5	1.64	0.000312	7	7	16	6.23	0.000664	4	4	9	3.9	0.000435
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	12.64	0.002839	2	2	3	18.13	0.001633	3	3	7	24.73	0.002534	2	2	5	18.13	0.002111
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	14.56	0.001625	3	3	6	13.75	0.001602	4	4	13	13.75	0.002309	2	2	7	11.19	0.00145
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	8	2.11	0.000393	3	3	10	1.14	0.000564	4	4	12	1.99	0.000451	3	3	7	1.14	0.000306
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	10	5.74	0.000899	4	4	6	5.32	0.00062	5	5	8	6.78	0.00055	4	4	11	5.53	0.000882
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	14.76	0.000636	3	3	4	19.56	0.001462	2	2	7	8.86	0.001702	2	2	4	10.7	0.001134
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	9	14.96	0.000204	4	4	9	13.39	0.00234	7	7	17	26.77	0.00294	3	3	9	13.39	0.000807
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	9.21	0.000922	4	4	9	13.28	0.001909	2	2	4	5.78	0.000564	2	2	3	6.85	0.000494
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	11	18.67	0.002423	4	4	10	15.6	0.002534	2	2	3	7.16	0.000506	2	2	2	7.67	0.000393
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	9	8.01	0.000609	3	3	7	4.01	0.000545	3	3	4	4.32	0.000207	2	2	4	2.99	0.000241
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	8.91	0.001335	2	2	2	10.47	0.000768	2	2	3	10.85	0.000766	2	2	5	10.85	0.001489
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	4.55	0.000379	2	2	5	4.11	0.000726	5	5	10	10.56	0.000966	3	3	4	6.16	0.000451
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	4.69	0.000384	4	4	6	5.92	0.000663	5	5	8	6.81	0.000588	3	3	4	3.91	0.000343
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	22.08	0.001678	3	3	6	32.47	0.002213	2	2	5	14.29	0.002139	2	2	5	14.29	0.002994
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.83	0.000277	2	2	3	4.83	0.000479	3	3	6	5.8	0.000637	2	2	4	4.67	0.000495
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	8.15	0.000877	4	4	6	10.39	0.001211	2	2	3	7.54	0.000403	3	3	4	9.98	0.000626
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	15.08	0.001325	2	2	7	7.38	0.002134	3	3	8	13.23	0.001622	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	9	24.18	0.003177	5	5	10	29.1	0.00406	4	4	7	24.18	0.00188	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	8	21.24	0.003049	X	X	X	X	X	5	5	12	25.66	0.003499	4	4	8	20.8	0.00272
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	8.94	0.00057	X	X	X	X	X	3	3	7	7.95	0.000764	3	3	6	7.28	0.000763
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	12.35	0.002331	2	2	3	17.06	0.001163	2	2	4	12.35	0.001808
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	10	14.75	0.00174	5	5	12	13.54	0.002401	3	3	7	9.7	0.000932	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.42	0.000636	2	2	3	6.42	0.000636	2	2	9	9.85	0.00127	4	4	16	12.21	0.002632
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	8.06	0.002477	2	2	4	8.06	0.000732	2	2	4	8.06	0.000732	2	2	5	8.61	0.001067
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	6	6	8	9.04	0.000863	2	2	3	9.04	0.000863	2	2	3	3.05	0.000215	3	3	3	5.66	0.000251
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	8.58	0.001214	2	2	4	4.38	0.000462	2	2	4	4.38	0.000462	2	2	4	4.38	0.000269
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	9.62	0.002208	2	2	4	10.26	0.00127	X	X	X	X	X	2	2	3	5.77	0.000739
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	8	6.67	0.00112	X	X	X	X	X	6	6	12	16.75	0.001286	4	4	7	11.71	0.000875
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.93	0.000602	X	X	X	X	X	2	2	3	6.99	0.000461	3	3	6	10.49	0.001075
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	9	14.53	0.00381	3	3	5	17.52	0.001408	2	2	5	10.68	0.001642
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	5	5	8	4.27	0.000457	2	2	8	1.73	0.000304	4	4	8	3.69	0.000355
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	9.13	0.001367	3

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE600 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE600-1_P	DE600-1_uP	DE600-1_S	DE600-1_SC	DE600-1_NSAF	DE600-2_P	DE600-2_uP	DE600-2_S	DE600-2_SC	DE600-2_NSAF	DE600-3_P	DE600-3_uP	DE600-3_S	DE600-3_SC	DE600-3_NSAF	DE600-4_P	DE600-4_uP	DE600-4_S	DE600-4_SC	DE600-4_NSAF
DE600-only	gi|6320896	0	0	0	0.001242	0.000294	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	9.09	0.00145	X	X	X	X	X	X	X	X	X	X	3	3	4	9.09	0.001035
DE600-only	gi|6323746	0	0	0	0.00128	0.000241	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	13.13	0.00145	X	X	X	X	X	3	3	5	13.13	0.001109	X	X	X	X	X
DE600-only	gi|6324982	0	0	0	0.000803	1.13E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	10.15	0.000795	X	X	X	X	X	2	2	4	7.69	0.000811	X	X	X	X	X
DE600-only	gi|6323891	0	0	0	0.001153	0.000434	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	7.86	0.000846	4	4	6	14	0.00146	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322097	0	0	0	0.001036	0.000293	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	15.09	0.001243	2	2	4	6.74	0.000828
DE600-only	gi|3736264	0	0	0	0.000982	0.000946	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	7	6.43	0.001651	2	2	2	7.62	0.000314	X	X	X	X	X
DE600-only	gi|6319793	0	0	0	0.000455	0.00012	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	6.04	0.00037	3	3	5	5.62	0.00054
DE600-only	gi|6323681	0	0	0	0.003624	0.00219	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	10.04	0.002075	2	2	13	10.04	0.005172	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320983	0	0	0	0.000337	6.34E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.65	0.000382	X	X	X	X	X	2	2	2	6.21	0.000292	X	X	X	X	X
DE600-only	gi|6319725	0	0	0	0.000425	0.00016	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.8	0.000312	2	2	3	3.99	0.000538	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320930	0	0	0	0.000528	9.94E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.42	0.000598	X	X	X	X	X	2	2	4	5.21	0.000458	X	X	X	X	X
DE600-only	gi|6323669	0	0	0	0.000853	0.000413	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	7.02	0.000561	3	3	7	10	0.001144
DE600-only	gi|6323547	0	0	0	0.000953	0.000602	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	12.8	0.001378	X	X	X	X	X	2	2	2	12.8	0.000527	X	X	X	X	X
DE600-only	gi|6321896	0	0	0	0.000807	0.000572	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	4	15.29	0.001212	2	2	2	7.34	0.000403	X	X	X	X	X
DE600-only	gi|6324716	0	0	0	0.000724	0.000457	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	7.6	0.001047	X	X	X	X	X	2	2	2	10.64	0.000401	X	X	X	X	X
DE600-only	gi|6320249	0	0	0	0.001387	0.000637	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	16.46	0.001838	X	X	X	X	X	X	X	X	X	X	2	2	4	11.59	0.000937
DE600-only	gi|6322049	0	0	0	0.000558	9.54E-05	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	6.45	0.00049	X	X	X	X	X	3	3	5	8.35	0.000625	X	X	X	X	X
DE600-only	gi|6324318	0	0	0	0.00219	0.000391	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	12.86	0.002466	3	3	7	14.11	0.001914	X	X	X	X	X
DE600-only	gi|6321816	0	0	0	0.000227	0.000102	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	2.62	0.000299	X	X	X	X	X	2	2	2	2.72	0.000155
DE600-only	gi|6320724	0	0	0	0.000556	0.0003	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.8	0.000344	X	X	X	X	X	X	X	X	X	X	2	2	5	4.8	0.000768
DE600-only	gi|6321776	0	0	0	0.000475	8.94E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.75	0.000538	X	X	X	X	X	2	2	2	11.56	0.000412	X	X	X	X	X
DE600-only	gi|6324474	0	0	0	0.000302	0.000248	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	2.41	0.000478	2	2	2	2.51	0.000127	X	X	X	X	X
DE600-only	gi|6322174	0	0	0	0.000486	5.27E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	5.45	0.000449	2	2	4	5.11	0.000524
DE600-only	gi|6322746	0	0	0	0.000278	3.01E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	5.64	0.000256	2	2	2	8.37	0.000299
DE600-only	gi|6324475	0	0	0	0.000522	0.000235	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.18	0.000688	X	X	X	X	X	2	2	2	8.1	0.000356
DE600-only	gi|6324515	0	0	0	0.000525	0.000285	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	6	6.61	0.000727	X	X	X	X	X	X	X	X	X	X	2	2	3	5.06	0.000324
DE600-only	gi|6319527	0	0	0	0.000691	0.000197	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	9.78	0.00083	2	2	3	10.06	0.000552	X	X	X	X	X
DE600-only	gi|6322828	0	0	0	0.00149	0.000281	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	13.73	0.001689	X	X	X	X	X	2	2	4	13.73	0.001292	X	X	X	X	X
DE600-only	gi|6325375	0	0	0	0.001388	0.000112	2									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	10.46	0.001467	X	X	X	X	X	X	X	X	X	X	3	3	7	14.11	0.001309
DE600-only	gi|6322634	0	0	0	0.000192	5.47E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	2.95	0.000231	2	2	3	2.49	0.000154	X	X	X	X	X
DE600-only	gi|6320056	0	0	0	0.000316	5.96E-05	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	3	0.000359	X	X	X	X	X	3	3	5	4.58	0.000274	X	X	X	X	X
DE600-only	gi|6324511	0	0	0	0.000665	0.000189	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.05	0.000799	3	3	4	11.09	0.000531	X	X	X	X	X
DE600-only	gi|6319926	0	0	0	0.000459	0.000137	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.93	0.000362	3	3	4	7.43	0.000556	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6321940	0	0	0	0.000583	0.000223	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.88	0.000741	2	2	2	9.03	0.000426	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6323286	0	0	0	0.001403	0.000292	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	12.77	0.00161	X	X	X	X	X	X	X	X	X	X	2	2	5	12.77	0.001197
DE600-only	gi|6324343	0	0	0	0.000111	3.15E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	1.3	0.000133	2	2	3	1.07	8.85E-05	X	X	X	X	X
DE600-only	gi|6322919	0	0	0	0.000868	6.32E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	8.86	0.000823	2	2	5	8.31	0.000913	X	X	X	X	X
DE600-only	gi|6325418	0	0	0	0.000219	3.54E-07	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.1	0.00022	2	2	3	4.32	0.000219	X	X	X	X	X
DE600-only	gi|6325017	0	0	0	0.00152	0.000286	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	14.5	0.001722	X	X	X	X	X	2	2	4	14.5	0.001318	X	X	X	X	X
DE600-only	gi|6325253	0	0	0	0.000628	6.81E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.92	0.00058	2	2	3	10.26	0.000676
DE600-only	gi|6322420	0	0	0	0.000285	0.000107	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.86	0.000209	2	2	3	4.86	0.000361	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320181	0	0	0	0.000946	9.19E-05	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	9.21	0.000881	X	X	X	X	X	2	2	6	9.21	0.001011	X	X	X	X	X
DE600-only	gi|6325360	0	0	0	0.000977	8.28E-05	2									2.5			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	9.41	0.001035	3	3	4	15.68	0.000918	X	X	X	X	X
DE600-only	gi|6322507	0	0	0	0.00112	0.0002	2									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	11.46	0.001262	X	X	X	X	X	2	2	2	11.46	0.000979
DE600-only	gi|6324594	0	0	0	0.005607	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	38.68	0.005607	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324899	0	0	0	0.001322	0	1									4			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	13.38	0.001322	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324993	0	0	0	0.00054	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	8.4	0.00054	X	X	X	X	X
DE600-only	gi|6320941	0	0	0	0.001874	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	14.15	0.001874
DE600-only	gi|6323182	0	0	0	0.000289	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	2.93	0.000289	X	X	X	X	X
DE600-only	gi|6320066	0	0	0	0.001141	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	18.81	0.001141
DE600-only	gi|6321718	0	0	0	0.001283	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	5.7	0.001283	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6319430	0	0	0	0.000822	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	9.54	0.000822	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6319646	0	0	0	0.00019	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2.89	0.00019	X	X	X	X	X
DE600-only	gi|6323958	0	0	0	0.000675	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.51	0.000675	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320899	0	0	0	0.001022	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	13.95	0.001022	X	X	X	X	X
DE600-only	gi|6320235	0	0	0	0.00261	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	16.67	0.00261	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324669	0	0	0	0.001277	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	17.05	0.001277	X	X	X	X	X
DE600-only	gi|6321829	0	0	0	0.005214	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	21.05	0.005214	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324761	0	0	0	0.000603	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.18	0.000603	X	X	X	X	X
DE600-only	gi|6322116	0	0	0	0.000491	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.04	0.000491
DE600-only	gi|6322667	0	0	0	0.001412	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	9.84	0.001412	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324758	0	0	0	0.000752	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.59	0.000752	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322845	0	0	0	0.000983	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.19	0.000983	X	X	X	X	X
DE600-only	gi|6321796	0	0	0	0.000566	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	12.02	0.000566	X	X	X	X	X
DE600-only	gi|6324273	0	0	0	0.001086	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.31	0.001086
DE600-only	gi|1431848	0	0	0	0.000433	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	4.16	0.000433	X	X	X	X	X
DE600-only	gi|6321217	0	0	0	0.002408	0	1									4			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	7	23.61	0.002408	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324283	0	0	0	0.000443	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.51	0.000443	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|1431852	0	0	0	0.000616	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	9.16	0.000616	X	X	X	X	X
DE600-only	gi|1431857	0	0	0	0.001808	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	10.58	0.001808	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6323955	0	0	0	0.000486	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	3.57	0.000486	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324508	0	0	0	0.001206	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	16.25	0.001206	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6323864	0	0	0	0.001118	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	5	9.93	0.001118	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322244	0	0	0	0.000998	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	15.66	0.000998	X	X	X	X	X
DE600-only	gi|6323383	0	0	0	0.00148	0	1									4			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	4	5	21.31	0.00148	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322525	0	0	0	0.000883	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	4	7.57	0.000883	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324195	0	0	0	0.001603	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	7	13.83	0.001603	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320809	0	0	0	0.001569	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	20.63	0.001569	X	X	X	X	X
DE600-only	gi|6323237	0	0	0	0.001293	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	8.75	0.001293
DE600-only	gi|6323460	0	0	0	0.000397	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	5.53	0.000397	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6323278	0	0	0	0.000285	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	2.39	0.000285	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6319558	0	0	0	0.000203	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	2.87	0.000203	X	X	X	X	X
DE600-only	gi|6320893	0	0	0	0.000875	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	4.55	0.000875
DE600-only	gi|6320510	0	0	0	0.001757	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	16.89	0.001757	X	X	X	X	X
DE600-only	gi|6323871	0	0	0	0.000754	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	7.44	0.000754	X	X	X	X	X
DE600-only	gi|6325319	0	0	0	0.000973	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	16.46	0.000973
DE600-only	gi|6324938	0	0	0	0.000598	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.33	0.000598	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6319721	0	0	0	0.00122	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	18.52	0.00122	X	X	X	X	X
DE600-only	gi|6321411	0	0	0	0.000238	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	4.08	0.000238	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6321457	0	0	0	0.00219	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	22.03	0.00219	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320777	0	0	0	0.000237	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.64	0.000237	X	X	X	X	X
DE600-only	gi|6320393	0	0	0	0.000315	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	6.04	0.000315	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320240	0	0	0	0.000534	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.84	0.000534	X	X	X	X	X
DE600-only	gi|6320980	0	0	0	0.000493	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	8.97	0.000493
DE600-only	gi|6320881	0	0	0	0.002808	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	15.22	0.002808	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|1431853	0	0	0	0.000518	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	7.01	0.000518	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322393	0	0	0	0.001028	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	13.04	0.001028
DE600-only	gi|6321865	0	0	0	0.000724	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	4.34	0.000724	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|9755326	0	0	0	0.003101	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	29.41	0.003101	X	X	X	X	X
DE600-only	gi|6323826	0	0	0	0.001382	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	6	11.63	0.001382	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320914	0	0	0	0.000388	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	3.38	0.000388	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324206	0	0	0	0.000132	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2.71	0.000132	X	X	X	X	X
DE600-only	gi|6321301	0	0	0	0.000346	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	3.26	0.000346
DE600-only	gi|6324552	0	0	0	0.000344	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	3.5	0.000344	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6321826	0	0	0	0.000689	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	5.22	0.000689	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|1462717	0	0	0	0.000149	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	1.99	0.000149	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6321601	0	0	0	0.000415	0	1									3			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	3	6	5.36	0.000415	X	X	X	X	X
DE600-only	gi|6321818	0	0	0	0.000674	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	11.56	0.000674	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6319899	0	0	0	0.00089	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	15.77	0.00089	X	X	X	X	X
DE600-only	gi|6321995	0	0	0	0.000868	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.05	0.000868	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6323045	0	0	0	0.000587	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	9.2	0.000587	X	X	X	X	X
DE600-only	gi|6324839	0	0	0	0.003624	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	23.58	0.003624
DE600-only	gi|6322156	0	0	0	0.000828	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	6.49	0.000828	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322636	0	0	0	0.000602	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	5	4.9	0.000602	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320418	0	0	0	0.000471	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.47	0.000471	X	X	X	X	X
DE600-only	gi|6325140	0	0	0	0.0008	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	11.81	0.0008
DE600-only	gi|6322168	0	0	0	0.001083	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.01	0.001083	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324731	0	0	0	0.00066	0	1									1			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	2	3.45	0.00066	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|1160064	0	0	0	0.000417	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	7.02	0.000417	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320598	0	0	0	0.000542	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	4.25	0.000542	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6320152	0	0	0	0.001253	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.64	0.001253	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324798	0	0	0	0.00118	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	10.96	0.00118	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|1431853	0	0	0	0.000279	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	2.68	0.000279	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324156	0	0	0	0.000941	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	11.2	0.000941	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6322485	0	0	0	0.001946	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	4	16.95	0.001946	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	gi|6324521	0	0	0	0.000652	0	1									2			X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	8.08	0.000652	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Group	Locus	noDE NSAF AVG	noDE NSAF STD	noDE Detected # Out of 4	DE600 NSAF AVG	DE600 NSAF STD	DE600 Detected # Out of 4	NSAF AVG Ratio	Log NSAF AVG DE600	Log NSAF AVG noDE	Log NSAF AVG Ratio	PAM cluster #	Protein rank in cluster	Number of Proteins in clusters (% of Total)	noDE Peptides AVG	DE600 Peptides AVG	NSAF t-test p-Value	t-test p-Value < 0.05?
DE600-only	gi|6321599	0	0	0	0.000624	0	1									2		
DE600-only	gi|6320863	0	0	0	0.000654	0	1									2		
DE600-only	gi|6320478	0	0	0	0.000723	0	1									2		
DE600-only	gi|6321753	0	0	0	0.001348	0	1									2		
DE600-only	gi|6320869	0	0	0	0.001333	0	1									2		
DE600-only	gi|6322321	0	0	0	0.001793	0	1									2		
DE600-only	gi|6324595	0	0	0	0.001395	0	1									2		
DE600-only	gi|6324856	0	0	0	0.000691	0	1									2		
DE600-only	gi|6321646	0	0	0	0.000757	0	1									2		
DE600-only	gi|6324208	0	0	0	0.000534	0	1									2		
DE600-only	gi|1431843	0	0	0	0.000269	0	1									2		
DE600-only	gi|6325172	0	0	0	0.00012	0	1									3		
DE600-only	gi|6323273	0	0	0	0.000511	0	1									2		
Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD		
231	47.63%				24.8572	2.199134	1.195717		0.0010761						2.641774892	1.302037		

Group	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE600-0-1_P	DE600-0-1_uP	DE600-0-1_S	DE600-0-1_SC	DE600-0-1_NSAF	DE600-0-2_P	DE600-0-2_uP	DE600-0-2_S	DE600-0-2_SC	DE600-0-2_NSAF	DE600-0-3_P	DE600-0-3_uP	DE600-0-3_S	DE600-0-3_SC	DE600-0-3_NSAF	DE600-0-4_P	DE600-0-4_uP	DE600-0-4_S	DE600-0-4_SC	DE600-0-4_NSAF
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		2	2	3	8.94	0.000624	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		2	2	4	6.64	0.000654	X	X	X	X	X	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			2	2	2	6.57	0.000723	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			2	2	4	10.2	0.001348	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			2	2	3	17.04	0.001333	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			2	2	4	14.03	0.001793	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X			2	2	3	13.62	0.001395	X	X	X	X	X	X	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				2	2	3	13.64	0.000691	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				2	2	3	14.56	0.000757	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				2	2	5	5.19	0.000534	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				2	2	3	4.09	0.000269	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				3	3	4	2.69	0.00012	X	X	X
DE600-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X				2	2	3	7.75	0.000511	X	X	X

Group	noDE-1_P	noDE-1_uP	noDE-1_S	noDE-1_SC	noDE-1_NSAF	noDE-2_P	noDE-2_uP	noDE-2_S	noDE-2_SC	noDE-2_NSAF	noDE-3_P	noDE-3_uP	noDE-3_S	noDE-3_SC	noDE-3_NSAF	noDE-4_P	noDE-4_uP	noDE-4_S	noDE-4_SC	noDE-4_NSAF	DE600-0-1_P	DE600-0-1_uP	DE600-0-1_S	DE600-0-1_SC	DE600-0-1_NSAF	DE600-0-2_P	DE600-0-2_uP	DE600-0-2_S	DE600-0-2_SC	DE600-0-2_NSAF	DE600-0-3_P	DE600-0-3_uP	DE600-0-3_S	DE600-0-3_SC	DE600-0-3_NSAF	DE600-0-4_P	DE600-0-4_uP	DE600-0-4_S	DE600-0-4_SC	DE600-0-4_NSAF
noDE-only	3	3	22	25.2	0.002022	2	2	31	18.9	0.001699	4	4	31	25.2	0.00229	2	2	26	17.32	0.002023	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	3	3	25	25.2	0.002298	3	3	33	26.77	0.001809	4	4	31	25.2	0.00229	2	2	26	17.32	0.002023	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	37	11.46	0.002751	1	1	41	11.46	0.001818	1	1	28	11.46	0.001673	1	1	27	11.46	0.001699	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	22	7.59	0.001771	2	2	12	13.79	0.000576	3	3	18	21.38	0.001165	3	3	53	21.38	0.003611	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	28	15.09	0.003084	1	1	24	15.09	0.001576	1	1	33	15.09	0.002921	1	1	34	15.09	0.003169	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	55	5.78	0.003711	1	1	39	5.78	0.001569	1	1	97	5.78	0.005261	1	1	101	5.78	0.005768	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	35	20.75	0.002299	1	1	83	20.75	0.007347	1	1	115	20.75	0.010718	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	19	19.23	0.001696	1	1	16	19.23	0.001925	1	1	11	19.23	0.001393	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	26	13.16	0.002662	1	1	14	13.16	0.000855	X	X	X	X	X	1	1	11	13.16	0.000953	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	2	2	17	24.76	0.00189	3	3	41	38.1	0.002718	2	2	30	30.48	0.002681	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	21	1.62	0.000158	1	1	25	1.62	0.000253	1	1	10	1.62	0.000107	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	19	13.79	0.00152	X	X	X	X	X	1	1	3	25.29	0.000341	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	13	13.56	0.001534	1	1	18	13.56	0.002862	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	1	1	55	12.04	0.005945	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	13	3.33	0.000251	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	3	11.45	0.000226	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	X	X	X	X	X	2	2	4	13.29	0.000131	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	8	7.27	0.000359	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	X	X	X	X	X	1	1	13	17.86	0.002178	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	2	2	6	15.92	0.000208	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
noDE-only	X	X	X	X	X	1	1	29	1.46	0.000294	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X

Number of Proteins in Group	Number of Proteins in Group (% of Total)	Sum of noDE NSAF AVG x 100	noDE Detected AVG	noDE Detected STD	Sum of DE NSAF AVG x 100	DE Detected AVG	DE Detected STD	noDE NSAF AVG	DE NSAF AVG				noDE Pep AVG	noDE Pep STD	DE Pep AVG	DE Pep STD
21	4.33%	3.9916	2.4285714	1.287300609				0.001901					1.492063492	0.682573135		