

Supporting Information for:

An Automated Matrix-Assisted Laser Desorption/Ionization Quadrupole Fourier Transform Ion Cyclotron Resonance Mass Spectrometer for ‘Bottom up’ Proteomics

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Yeast data									Mascot scores	
Protein name	Abbrev	Query	% MeCN	Precursor mass (exp)	Error	ppm error	Peptide sequence	Variable modification	Top score	Second
Ribosomal protein L26B	Rpl26bp	11	15.4%	943.501	0.004	4.2	DDEVLVVR		30.1	8.2
Zinc-cluster protein involved in activating gluconeogenic genes; related to Gal4p	Cat8p	15	23.7%	949.4674	0.006	6.3	NNLSFNNK		12	None
Ribosomal protein S7B	Rps7bp	60	19.2%	983.557	0.002	2.0	HVIFLAER		35.4	8
Ribosomal protein L2A	Rpl2ap	91	16.0%	1022.558	0.003	2.9	VVFRDPYK		3.3	None
Ribosomal protein S9B	Rps9bp	98	20.7%	1031.577	0.001	1.0	LFEGNALIR		0.5	None
40S ribosomal protein S12	Rps12p	107	24.8%	1040.531	0.002	1.9	QLGEWAGLGK	Pyro-glu (N-term Q)	16.5	None
Ribosomal protein S14A	Rps14ap	150	13.9%	1091.539	0.003	2.7	DNSQVFGVAR		18.4	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	161	15.8%	1107.629	0	0.0	VVDLVEHVAK		13	None
Ribosomal protein L21A	Rpl21ap	168	16.7%	1119.514	0.001	0.9	CRQEFLER	Pyro-cmC (N-term camc)	32.4	3
Ribosomal protein S11B	Rps11bp	173	28.3%	1131.576	0.001	0.9	CPFTGLVSIR	Pyro-cmC (N-term camc)	22.4	None

Adenylate kinase	Adk1p	178	26.1%	1135.569	0.003	2.6	NGFILDGFPR	Deamidation (NQ)	8.8	None
40S ribosomal gene product S6B	Rps6bp	188	12.9%	1160.513	0.003	2.6	TFEIDDEHR		13.7	None
Translation elongation factor 2 (EF-2)	Eft2p	191	14.0%	1163.531	0.003	2.6	EGPIFGGEEMR		32	0.8
Malate synthase 2	Dal7p	197	10.8%	1171.587	-0.004	-3.4	WDYIFSTIK		13.3	None
Member of 70 kDa heat shock protein family	Ssa2p	203	20.2%	1182.641	0.001	0.8	FELSGIPPAPR		7.8	None
Arginosuccinate synthetase	Arg1p	204	14.4%	1184.547	0.001	0.8	DSFVTPNYSR		4.4	None
Ribosomal protein S4B	Rps4bp	206	32.3%	1185.713	0.001	0.8	ESLPLIVFLR		13.3	None
NADP-linked glutamate dehydrogenase	Gdh3p	208	25.4%	1187.599	0.002	1.7	EIGYLFGAYR		0.6	None
3-phosphoglycerate kinase	Pgk1p	209	24.9%	1188.639	0	0.0	ELPGVAFLSEK		11.1	None
Ribosomal protein L13A	Rpl13ap	213	8.5%	1193.535	0.004	3.4	AVQDNGESAFR	Deamidation (NQ)	5.8	2.9
Cyclophilin peptidyl-prolyl cis-trans isomerase	Cph1p	214	18.2%	1194.559	0.002	1.7	GFGYAGSPFHR		0.3	None
Zuo1p	Zuo1p	223	16.8%	1204.527	0.001	0.8	NHTWSEFER		3.4	None
Constitutively expressed heat shock protein	Hsc82p	225	22.9%	1208.62	0.001	0.8	RAPFDLFESK		20.2	12.3
Ribosomal protein L10	Rpl10	229	13.3%	1219.661	0.004	3.3	GAWGKPHGLAAR		1.1	None
Ribosomal protein S11B	Rps11bp	231	16.2%	1221.661	-0.001	-0.8	NVPHVSPAFR		31.9	None
Ribosomal protein L7A/B	Rpl17ap	233	17.3%	1225.619	-0.001	-0.8	LSNPSSGGWGVPR		30.7	None
Pyruvate kinase	Cdc19p	234	18.6%	1226.664	0.002	1.6	TNNPETLVALR		3.9	None
3-phosphoglycerate kinase	Pgk1p	242	27.6%	1231.647	0.002	1.6	ELPGVAFLSEK	Carbamyl (N-term)	0.9	None
60S ribosomal protein P0	Rpp0p	250	16.4%	1241.63	0.001	0.8	LREYLEEYK		35	None
Vacuolar ATPase V1 domain subunit B (60 kDa)	Vma2p	253	11.8%	1243.668	0.001	0.8	AVEQGFNVKPR		4.1	0.7
Ribosomal protein L10	Rpl10	255	29.7%	1245.709	0.001	0.8	VDIGQIIFSVR		4.4	None
Ribosomal protein L7A/B	Rpl17ap	256	31.6%	1246.617	0.004	3.2	QANNFLWPFK	Pyro-glu (N-term Q)	15.4	None
Ribosomal protein L7A/B	Rpl17ap	258	32.3%	1247.599	0.002	1.6	QANNFLWPFK	Deamidation (NQ), Pyro-	15.1	None

								glu (N-term Q)		
Ribosomal protein S25A	Rps25ap	261	10.6%	1250.664	0.002	1.6	AQHAVILDQEK		1	None
Ribosomal protein L20A	Rpl20ap	263	12.2%	1251.685	0.003	2.4	RLPTESVPEPK		58.4	10.3
Ribosomal protein S13	Rps13p	264	25.3%	1252.752	0.002	1.6	GLTPSQIGVLLR		7	None
Ribosomal protein S5	Rps5p	271	20.7%	1263.646	0	0.0	DASLVDYVQVR		6.8	None
Translation elongation factor EF-1 gamma	Tef4p	276	21.4%	1265.642	0.002	1.6	STFVLDDWKR		6.2	None
60S ribosomal protein P0	Rpp0p	279	26.9%	1266.614	0.001	0.8	GFLSDLPDFEK		10.5	None
Phosphoglycerate mutase	Gpm1p	281	15.0%	1267.641	0	0.0	HLEGISDADIAK		47	None
Aspartyl-tRNA synthetase, mitochondrial	Msd1p	284	18.8%	1268.628	-0.001	-0.8	EKLAYPEYEK		4.5	None
Member of 70 kDa heat shock protein family	Ssa2p	289	21.7%	1273.683	0.001	0.8	LVNHFIQEFK		6.1	0.7
60S ribosomal protein P0	Rpp0p	298	21.9%	1282.665	-0.002	-1.6	AGAVAPEDIWVR		14.9	None
Ribosomal protein S17B	Rps17bp	307	21.2%	1295.757	0.001	0.8	LPLSVINVSAQR		4.6	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	309	11.3%	1296.623	0.002	1.5	TVDGPSHKDWR		12.4	None
Member of 70 kDa heat shock protein family	Ssa2p	312	25.2%	1298.596	-0.001	-0.8	FEELCADLFR		10.8	None
NADPH dehydrogenase (old yellow enzyme), isoform 2	Oye2p	313	20.7%	1299.588	0	0.0	DWAVEYYAQR		10.9	None
Ribosomal protein S8A/B	Rps8ap	315	21.9%	1300.712	-0.002	-1.5	AAIVQIDATPFR		5.9	None
Translation elongation factor EF-1 beta	Efb1p	316	18.4%	1301.606	0.002	1.5	AFQSAYPEFSR		20.7	None
Alcohol dehydrogenase	Adh1p	317	26.3%	1311.669	-0.002	-1.5	SIGGEVFIDFTK		10.4	None
Translation initiation factor eIF-5A	Hyp2p	318	26.4%	1311.758	0.003	2.3	VHLVAIDFTGK		0.4	None
Asparagine synthetase	Asn2p	320	11.4%	1319.519	-0.001	-0.8	ADWGCAEDPSGR		4.8	None
Translation elongation factor EF-1 alpha	Tef2p	321	26.6%	1325.746	0.001	0.8	EHALLAFTLGVR		27.3	None
Ribosomal protein L13A	Rpl13ap	324	15.1%	1332.641	-0.001	-0.8	NQEIFDANVQR		28.9	None
Alcohol dehydrogenase	Adh1p	326	21.1%	1337.574	0	0.0	CCSDVFNQVVK	Pyro-cmC (N-term camc)	12.9	None

Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	329	11.3%	1339.626	-0.001	-0.7	TVDGPSHKDWR	Carbamyl (N-term)	26.5	None
60S ribosomal protein L11B	Rpl11b	330	20.0%	1340.661	0	0.0	TTKEDTVSWFK		9.5	None
Pyruvate kinase	Cdc19p	331	18.1%	1341.693	0	0.0	KGDTYVSIQGFK		30	None
Constitutively expressed heat shock protein	Hsc82p	335	20.9%	1347.656	-0.001	-0.7	HFSVEGQLEFR		21.3	None
Ribosomal protein S1A	Rps1ap	336	24.2%	1350.741	0	0.0	DIFPLQNIHVR		18.7	None
Ribosomal protein L16B	Rpl16bp	338	24.7%	1352.672	0	0.0	AEALNISGEFFR		27.4	None
Transketolase 1	Tkl1p	340	25.1%	1355.65	-0.001	-0.7	FFGFTPEGVAER		17.2	None
Ribosomal protein L10	Rpl10	344	11.1%	1363.664	0.002	1.5	EAGEVKDDGAFVK		24.1	5
Enolase	Eno2p	347	23.2%	1372.628	-0.005	-3.6	IGLDCASSEFFK		17.1	None
Pyruvate decarboxylase	Pdc1p	349	15.4%	1374.636	-0.002	-1.5	NPVILADACCSR		10.5	None
Pyruvate kinase	Cdc19p	351	22.3%	1377.688	0.002	1.5	NGVHMFASFIR	Deamidation (NQ)	12.1	None
Ribosomal protein S29B	Rps29bp	352	17.6%	1378.65	-0.003	-2.2	AHENVWFShPR		23.2	None
Ribosomal protein S13	Rps13p	354	23.6%	1380.846	0.001	0.7	KGLTPSQIGVLLR		41.4	None
Ribosomal protein S8A/B	Rps8ap	356	14.4%	1395.663	0	0.0	IESSVESQFSAGR		30	None
Ribosomal protein L16A	Rpl16ap	359	24.5%	1410.678	0	0.0	AEELNISGEFFR		42.1	None
Ribosomal protein S14A	Rsp14ap	361	10.8%	1414.695	0.001	0.7	IEDVTPVPSDSTR		15.9	None
Ribosomal protein P2B	Rpp2bp	365	15.2%	1429.705	0	0.0	AVVESVGAEVDEAR		23.6	4
O-acetylhomoserine-O-acetylserine sulfhydrylase	Met17p	366	16.7%	1432.696	0.001	0.7	FQNPTSNVLEER		9.7	None
Vitamin B12-(cobalamin)-independent isozyme of methionine synthase	Met6p	367	26.1%	1434.657	0	0.0	SAYYTWAAEAER		21.5	None
Ribosomal protein S3	Rps3p	369	15.3%	1436.678	0	0.0	ELAEEGYSGVEVR		16.9	None
G-beta like protein	Asc1p	370	14.4%	1437.685	-0.004	-2.8	LWDVATGETYQR		38.4	2.5
O-acetylhomoserine-O-acetylserine sulfhydrylase	Met17p	372	15.2%	1438.624	-0.001	-0.7	FVEGDNPEEFKEK		19	0.8
3-phosphoglycerate kinase	Pgk1p	374	25.4%	1438.811	-0.003	-2.1	ASAPGSVILLENLR		18.7	None
Ribosomal protein S16B	Rps16bp	375	14.4%	1442.761	-0.002	-1.4	VTGGGHVSQVYAIR		23.9	7.3
Ribosomal protein L4A	Rpl4ap	376	8.3%	1443.652	0.003	2.1	AGHQTSAESWGTGR		22.9	None
3-phosphoglycerate kinase	Pgk1p	377	15.7%	1443.695	0.002	1.4	AHSSMVGFDLPQR		17.1	None

EF-3 (translational elongation factor 3)	Yef3p	379	17.2%	1444.778	-0.001	-0.7	EALASGQFRPLTR		4.7	None
Alcohol dehydrogenase	Adh1p	380	23.4%	1446.797	0	0.0	VVGLSTLPEIYEK		3.5	None
40S ribosomal protein S24A	Rps24ap	383	18.8%	1450.807	0.003	2.1	KQFVVDVLHPNR		12.9	None
Heat shock protein of HSP70 family, cytoplasmic	Ssa1p	389	21.6%	1470.698	-0.001	-0.7	TTPSFVAFTDTER		10.9	0.4
Cystathione beta-synthase	Cys4p	391	31.4%	1471.732	0.001	0.7	QLEDLNLFDNLR	Pyro-glu (N-term Q)	25.2	1.6
Heat shock protein of HSP70 family, homolog of SSB1	Ssb2p	396	21.8%	1477.754	-0.003	-2.0	VTPSFVAFTPQER		18.9	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	400	8.9%	1480.781	0.004	2.7	LNKETTYDEIKK		16	3.3
Saccharopine reductase	Lys9p	401	22.1%	1481.676	-0.003	-2.0	FGIEWADGTTETR		5	1.1
Ribosomal protein L24B	Rpl24bp	402	20.1%	1481.856	-0.001	-0.7	AQRPITGASLDLIK		16.8	4.3
Ribosomal protein L27B	Rpl27bp	407	19.4%	1489.779	0	0.0	SHPFGHALVAGIER		33.3	4
Enolase	Eno2p	409	22.3%	1496.8	0.001	0.7	NVPLYQHLADLSK		27.9	9.1
Phosphofructokinase alpha subunit	Pfk1p	412	33.0%	1505.825	0.001	0.7	LDGLIILGGFEGFR		2.9	0.4
Constitutively expressed heat shock protein	Hsc82p	414	21.3%	1512.784	0.006	4.0	GVVDSIDLPLNLSR		35.7	24.4
Triosephosphate isomerase	Tpi1p	417	14.3%	1515.839	-0.002	-1.3	KPQVTVGAQNAYLK		41.1	None
Pyruvate kinase	Cdc19p	419	17.9%	1517.662	-0.001	-0.7	EPVSDWTDDVEAR		17.4	None
Poly(A) binding protein, cytoplasmic and nuclear	Pab1p	422	22.5%	1523.705	0.001	0.7	GFGFVHFEEEGAAK		26.3	None
EF-3 (translational elongation factor 3)	Yef3p	424	25.9%	1524.856	0.001	0.7	LVEDPQVIAPFLGK		7.3	None
Member of 70 kDa heat shock protein family	Ssa2p	426	25.2%	1525.736	0.001	0.7	ARFEELCADLFR		35	4
Ribosomal protein S8A/B	Rps8ap	435	23.8%	1546.721	0.001	0.6	QWFEAHYGQTLGK	Pyro-glu (N-term Q)	23	None
Member of 70 kDa heat shock protein family	Ssa2p	438	16.7%	1552.752	0	0.0	LVTDYFNGKEPNR	Deamidation (NQ)	11.9	None
Enolase	Eno2p	440	15.3%	1556.735	-0.002	-1.3	AVYAGENFHHGDKL		27.7	None
Enolase	Eno2p	441	15.7%	1557.722	0.001	0.6	AVTAGENFHHGDKL	Deamidation (NQ)	18.4	None
Thioredoxin-peroxidase	Tsa1p	447	24.3%	1561.797	-0.002	-1.3	DYGVLIIEEGVALR		64.8	3.1

Constitutively expressed heat shock protein	Hsc82p	450	23.6%	1564.742	0.001	0.6	SISNDWEDPLYVK		11.2	None
Ribosomal protein S7A	Rps7ap	452	28.3%	1571.884	0.003	1.9	ILEDLVFPTEIVGK		14.1	None
Enolase	Eno2p	455	26.4%	1577.791	-0.003	-1.9	AVDDFLLSLDGTANK		10.6	None
Pyruvate decarboxylase	Pdc1p	464	17.4%	1590.788	-0.001	-0.6	VATTGEWDKTQDK		2	None
Ribosomal protein L27B	Rpl27bp	467	14.2%	1593.765	0.002	1.3	SVVSTETFEQPSQR		4.6	None
Pyruvate decarboxylase	Pdc1p	468	17.3%	1595.853	-0.003	-1.9	YGGVYVGTLSKPEVK		11	None
Triosephosphate isomerase	Tpi1p	476	17.3%	1613.734	-0.002	-1.2	SYFHEDDKFIADK		56.2	13.4
Enolase	Eno2p	480	42.4%	1620.8	0.001	0.6	AVDDFLLSLDGTANK	Carbamyl (N-term)	21.6	None
Ribosomal protein S8A/B	Rps8ap	481	21.1%	1624.773	0	0.0	IETGNFSWASEGISK		14.1	None
Translation elongation factor 2 (EF-2)	Eft2p	483	18.6%	1626.702	0.004	2.5	IMADDYGWDVTDAR		2.3	None
Cofilin, actin binding and severing protein	Cof1p	489	28.6%	1634.851	0.005	3.1	IVFFTWSPTAPVR		16.4	None
Ribosomal protein S16B	Rps16bp	490	26.4%	1636.904	0.001	0.6	VNGSPITLVEPEILR	Deamidation (NQ)	14.5	None
Ribosomal protein L10	Rpl10	491	24.2%	1637.818	-0.002	-1.2	WGFTNLDREPEYLK		5.3	None
Tropomyosin I	Rpm1p	494	16.6%	1643.788	-0.002	-1.2	VAALEEQRREEWER		12.1	None
Hsp70 protein	Pdr13p	495	31.3%	1643.856	0	0.0	VFAQFSSFVDSVIK		1.1	0.7
Vacuolar ATPase V1 domain subunit A (69 kDa)	Tfp1p	497	25.7%	1645.779	0.001	0.6	FYDSNYPEFPVLR		27.8	None
Alpha subunit of fatty acid synthase	Fas2p	498	33.0%	1648.868	0.001	0.6	QIAPAELEGLLDLER	Pyro-glu (N-term Q)	9.9	None
Cystathione gamma-lyase	Cys3p	500	17.5%	1651.747	-0.001	-0.6	QSSPANPIGTYEYSR	Pyro-glu (N-term Q)	2.2	None
Alcohol dehydrogenase	Adh1p	503	25.3%	1660.843	0.001	0.6	VLGIDGGEGKEELFR	Carbamyl (N-term)	25.1	None
Uridinephosphoglucose pyrophosphorylase	Ugp1p	505	35.8%	1663.791	0.003	1.8	FENELDSFFTLFR		5.9	None
Ribosomal protein S8A/B	Rps8ap	507	16.9%	1666.882	0.003	1.8	IAGVVYHPSNNELVR		19.5	None
Carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase	Ura2p	511	36.4%	1670.854	-0.002	-1.2	DTEFLFDVFIQAVK		3.2	0.2

Member of 70 kDa heat shock protein family	Ssa2p	514	12.2%	1674.722	-0.001	-0.6	ATAGDTHLGGEDFDN		29	None
Cyclophilin peptidyl-prolyl cis-trans isomerase	Cph1p	516	23.4%	1674.864	0.002	1.2	HVVFGEVVDGYDIVK		48.8	3.7
Ribosomal protein S25A	Rps25ap	521	13.6%	1684.854	0.001	0.6	AQHAVILDQEKYDR		2.5	None
Ykl056cp	Ykl056cp	522	14.6%	1686.848	0.002	1.2	LQETNPPEEVPKFEK		13.4	None
Aspartic beta semi-aldehyde dehydrogenase	Hom2p	525	27.4%	1690.957	0.001	0.6	FILLLANHPHFELK		0.3	None
Putative S-adenosyl-L-homocystein hydrolase	Sah1p	526	22.8%	1691.842	0.001	0.6	VQSEYLGIPPEEGPFK		24.3	None
3-phosphoglycerate kinase	Pgk1p	534	27.3%	1718.869	0.002	1.2	TIVWNGPPGVFEFEK		8.4	None
3-phosphoglycerate kinase	Pgk1p	535	27.4%	1719.853	0.002	1.2	TIVWNGPPGVFEFEK	Deamidation (NQ)	9.2	None
Glyceraldehyde-3-phosphate dehydrogenase 1	Tdh1p	543	23.0%	1735.777	-0.007	-4.0	LISWYDNEYGY SAR		43.7	3.7
Glucose-6-phosphate isomerase	Pgi1p	544	39.7%	1737.992	0.004	2.3	NLVNDEIIAALIELAK		1.2	None
Phosphofructokinase alpha subunit	Pfk1p	553	30.7%	1747.964	0.002	1.1	NKLDGLIILGGFEGFR		8.7	None
Pyruvate kinase	Cdc19p	554	25.4%	1747.97	-0.002	-1.1	GDLGIEIPAPEVLAVQ		27.6	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	560	22.1%	1752.763	0	0.0	LVSWYDNEYGYSTR	Deamidation (NQ)	12.6	None
3-phosphoglycerate kinase	Pgk1p	561	20.4%	1753.922	0.001	0.6	ISHVSTGGGASLELLE		28	None
Translation elongation factor 2 (EF-2)	Eft2p	563	9.7%	1758.854	0	0.0	WTNKDTDAEGKPLER		16.1	None
Pyruvate kinase	Cdc19p	567	22.2%	1760.859	0.001	0.6	IENQQGVNNFDEILK	Deamidation (NQ)	6.9	None
60S ribosomal protein P0	Rpp0p	569	25.7%	1763.911	0.002	1.1	GNVGFVFTNEPLTEIK		6.1	None
ATP-dependent RNA helicase of DEAD box family	Ded1p	570	12.3%	1764.807	0	0.0	TGPSPQPESQGSFYQ		1.8	None
Ribosomal protein L10	Rpl10	571	22.4%	1765.912	-0.003	-1.7	KWGFTNLDRPEYLK		4.8	None
3-phosphoglycerate kinase	Pgk1p	572	28.0%	1767.005	0.001	0.6	ALENPTRPFLAILGGA		6.9	None
Enolase	Eno2p	575	15.6%	1769.81	-0.001	-0.6	DGKYDLDFKNPESDK		36.8	0.5
Triosephosphate isomerase	Tpi1p	576	16.4%	1769.836	-0.001	-0.6	RSYFHEDDKFIADK		30.2	2.5

Ribosomal protein S21B	Rps21bp	577	29.8%	1771.914	0	0.0	AIPGEYITYALSGYVR		19.7	None
Pyruvate decarboxylase	Pdc1p	580	26.9%	1776.947	-0.001	-0.6	LIDLTKQFPAFVTPMGK		12.1	None
Glyceraldehyde-3-phosphate dehydrogenase 1	Tdh1p	582	30.3%	1778.79	0	0.0	LISWYDNEYGY SAR	Carbamyl (N-term)	6.6	3
Translation initiation factor eIF4A	Tif2p	586	23.3%	1783.852	-0.001	-0.6	GVFGYGFEEPSAIQQ		11.7	None
GTP-binding protein	Gsp1p	587	28.9%	1783.908	0.004	2.2	SNYNFEKPFLWLAR		21.1	None
Actin	Act1p	588	22.6%	1789.887	0.002	1.1	SYELPDGQVITIGNER		0.9	None
Pyruvate kinase	Cdc19p	589	27.0%	1790.984	0.006	3.4	GDLGIEIPAEVLAVQ	Carbamyl (N-term)	35.8	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	593	28.5%	1794.784	-0.001	-0.6	LVSWYDNEYGYSTR	Carbamyl (N-term)	67	None
Alpha subunit of fatty acid synthase	Fas2p	594	38.6%	1794.853	-0.003	-1.7	QDVEALIEFIYDTEK	Pyro-glu (N-term Q)	36.1	None
Aldolase	Fba1p	595	21.1%	1794.908	-0.007	-3.9	SPIILQTSNGGAAYFA	Deamidation (NQ)	1.7	None
HSP70 family member, highly homologous to Ssa1p and Sse2p	Sse1p	597	28.3%	1796.827	0.001	0.6	DFDLAITEHFADEFK		16.7	11
Ribosomal protein L9A	Rpl9ap	604	24.4%	1804.954	0.003	1.7	YVYAHFPINVNIVEK		31.8	None
Large ribosomal subunit protein L30	Rpl30p	608	19.5%	1815.87	-0.009	-5.0	VYYFQGGNNELGTAV		3.9	None
Enolase	Eno2p	613	17.1%	1839.92	0.005	2.7	SIVPSGASTGVHEALE		25.2	None
6-phosphogluconate dehydrogenase	Gnd1p	618	26.2%	1849.922	0.001	0.5	AYREEPDLENLLFNK		20	None
Enolase	Eno2p	620	23.4%	1853.984	-0.001	-0.5	TAGIQIVADDLTVTNP		25.4	None
EF-3 (translational elongation factor 3)	Yef3p	624	34.7%	1859.004	0	0.0	IVVEYIAAIGADLIDER		4.4	None
Aldolase	Fba1p	625	24.7%	1861.954	-0.003	-1.6	TGVIVGEDVHNLFTYA		21.2	None
Uridinephosphoglucose pyrophosphorylase	Ugp1p	627	34.7%	1862.922	0.002	1.1	AKFENELDSFFTLFR		1.8	1.7
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	630	11.7%	1881.923	0.001	0.5	YAGEVSHDDKHIIVDG		48.4	None
Hexokinase I	Hxk1p	634	26.2%	1884.926	0	0.0	DTLPLGFTFSYPASQN		13	None

							K			
Asparaginyl-tRNA synthetase	Ded81p	636	28.5%	1890.845	0.003	1.6	EGIDTDAYYWFIDQR		2.2	None
Aldolase	Fba1p	637	22.9%	1900.891	-0.008	-4.2	VNLDTDCQYAYLTGIR		17.8	None
Threonine synthase	Thr4p	638	32.7%	1900.973	0.001	0.5	FVPSGNFGDILAGYF AK		2.8	None
Ribosomal protein S19A/B	Rps19bp	640	31.8%	1927.944	0.001	0.5	DVAAQDFINAYASFLQ R		69	None
Ribosomal protein L19A	Rpl19ap	641	20.1%	1928.929	0.006	3.1	VWLDPNETSEIAQAN SR		9.3	None
Ribosomal protein S8A/B	Rps8ap	642	36.2%	1929.881	-0.001	-0.5	CDGYILEGEELAFYLR	Pyro-cmC (N-term camc)	74.1	None
Tryptophan synthetase	Trp5p	647	34.3%	1947.049	0.003	1.5	LELLSHIADSFVYVVS R		38.5	5.2
Alkyl hydroperoxide reductase	Ahp1p	648	17.9%	1947.851	-0.001	-0.5	FQYIAISQSDADSESC K		18.9	None
Ribosomal protein S19A/B	Rps19bp	652	35.3%	1970.945	-0.004	-2.0	DVAAQDFINAYASFLQ R	Carbamyl (N-term)	28.7	None
Translation elongation factor 2 (EF-2)	Eft2p	656	18.2%	1976.917	0.002	1.0	AEQLYEGPADDANCIA IK		4.6	None
Ribosomal protein L7A/B	Rpl17ap	657	18.3%	1978.962	-0.003	-1.5	HFIQGGSFGNREEFIN K		2.1	None
Ribosomal protein S3	Rps3p	658	35.1%	1989.982	-0.002	-1.0	LVADGVFYAELNEFFT R		48.3	None
Ribosomal protein L7A/B	Rpl17ap	659	24.6%	1991.006	0.002	1.0	LIEPYVAYGYPSYSTIR		45.3	None
Pyruvate decarboxylase	Pdc1p	664	19.6%	1996.898	-0.005	-2.5	WAGNANELNAAAYAAD GYAR		55.8	None
Pyruvate decarboxylase	Pdc1p	666	20.0%	1997.887	0	0.0	WAGNANELNAAAYAAD GYAR	Deamidation (NQ)	30.9	18.7
Ribosomal protein L14A/B	Rpl14bp	672	37.0%	2033.164	-0.003	-1.5	QAINLGQVVLTPLTFA LPR	Pyro-glu (N-term Q)	64.6	None
Aldolase	Fba1p	674	21.1%	2034.027	-0.009	-4.4	SIAPAYGIPVVLHSDH CAK		3.8	None
Glyceraldehyde-3-phosphate dehydrogenase 1	Tdh1p	683	22.7%	2058.054	0.001	0.5	IATYQERDPANLPWG SLK		4.2	1.1

Ribosomal protein L5	Rpl5p	688	30.6%	2091.977	-0.002	-1.0	FPGWDFETEEIDPELLR		21.6	None
Aldolase	Fba1p	693	12.6%	2099.026	-0.01	-4.8	DYIMSPVGNPEGPEKPNKK		4.7	None
Vitamin B12-(cobalamin)-independent isozyme of methionine synthase	Met6p	694	30.7%	2107.139	0.004	1.9	VFNLPLFPTTTIGSFPQTK		8.2	None
Member of conserved eukaryotic 14-3-3 gene family	Bmh2p	698	33.1%	2126.967	0.014	6.6	QAFDDAIAELDTLSEESYK	Pyro-glu (N-term Q)	53.7	None
Triosephosphate isomerase	Tpi1p	700	36.4%	2132.114	-0.005	-2.3	FALGQGVGVILCIGETLEEK		32.9	None
Phosphoglycerate mutase	Gpm1p	701	29.0%	2142.119	-0.002	-0.9	YVDPNVLPETESLALVIDR		9.3	None
Glyceraldehyde-3-phosphate dehydrogenase 3	Tdh3p	710	27.1%	2169.022	0.005	2.3	FVKLVSWYDNEYGYSTR	Carbamyl (N-term)	6.2	None
Ribosomal protein S10B	Rps10bp	711	23.3%	2170.112	0.006	2.8	EYLNLP EHVPGTYIQER		36.7	0.4
Phosphoglycerate mutase	Gpm1p	712	31.8%	2185.127	0	0.0	YVDPNVLPETESLALVIDR	Carbamyl (N-term)	8.4	None
Isopropylmalate isomerase	Leu1p	715	19.8%	2190.1	0.018	8.2	HLVHEVTSPQAFEGLENAGR		63.1	None
Ubiquitin activating enzyme, similar to Uba2p	Uba1p	723	35.5%	2252.147	-0.005	-2.2	NGFVNLALPFFGFSEPIASPK	Deamidation (NQ)	2	None
Pyruvate kinase	Cdc19p	727	32.2%	2265.186	0.008	3.5	IIVYVDDGVL SFQVLEVVDK		19.1	1.2
Pyruvate decarboxylase	Pdc1p	728	29.8%	2269.174	-0.004	-1.8	WGLKPYLFVLNNDGYTIEK		39.9	3
Pyruvate decarboxylase	Pdc1p	730	34.4%	2272.165	-0.009	-4.0	QVNVNTVFGLPGDFNLSLLDK	Pyro-glu (N-term Q)	20.8	None
Ribosomal protein L21A	Rpl21ap	733	29.1%	2274.18	0.002	0.9	IVSTEGNV PQT LAPVPYETFI		22.9	None
Pyruvate decarboxylase	Pdc1p	736	31.9%	2289.203	0.003	1.3	QVNVNTVFGLPGDFNLSLLDK		15.3	None
Glucokinase	Glk1p	737	27.9%	2315.182	0.002	0.9	LGFTFSYPVDQTSLSNGTLIR		3.4	None
3-phosphoglycerate kinase	Pgk1p	739	19.1%	2326.106	0.015	6.4	TVTDKEGIPAGWQGL		18	None

							DNGPESR			
3-phosphoglycerate kinase	Pgk1p	740	19.6%	2327.117	0.014	6.0	TVTDKEGIPAGWQGL DNGPESR	Deamidation (NQ)	4.6	None
Saccharopine dehydrogenase	Lys1p	742	30.0%	2327.189	0.009	3.9	EASEFFSHDLLPSLEL LPQR		17.3	None
Ribonucleotide reductase	Rnr4p	744	35.7%	2337.16	-0.004	-1.7	SIHTYIEFVADGLLQGF GNEK		12.4	2.6
Zuo1p	Zuo1p	746	28.6%	2350.063	0.009	3.8	KGTDYDFYEAOWPVF EAEAR		13.5	None
Ribosomal protein L7A/B	Rpl17ap	754	38.8%	2379.279	-0.005	-2.1	YGILSIDDLIHEIITVGP HFK		35.7	None
Saccharopine reductase	Lys9p	757	24.8%	2386.081	0.002	0.8	SFLSYCGGLPAPEDS DNPLGYK		12.7	None
Pyruvate decarboxylase	Pdc1p	758	28.6%	2387.191	0	0.0	AQYNEIQGWDHLSLL PTFGAK		12.7	None
3-phosphoglycerate kinase	Pgk1p	759	37.3%	2390.242	0.005	2.1	GVEVVLPVDFIADAFS ADANTK		4.7	None
Hexokinase I	Hxk1p	761	14.5%	2392.18	0.014	5.9	TKYDVAVDEQSPRPG QQAFEK		10.8	None
Phosphofructokinase alpha subunit	Pfk1p	762	31.4%	2402.139	0.003	1.2	TFIHFGCDVFVAVYEGY EGLLR		37.9	None
Translation elongation factor EF-1 alpha	Tef2p	766	20.2%	2429.338	0.014	5.8	VETGVIPKGMVVTAFAP AGVTTEVK		16.9	None
Translation elongation factor EF-1 gamma	Tef4p	770	26.6%	2435.071	0.012	4.9	GQDFAPAFDVAPDWE SYEYTK		6.2	None
Cytoplasmic member of the HSP70 family	Ssb1p	776	20.3%	2462.129	0.012	4.9	TFTTCADNQTTVQFP VYQGER		23.4	None
60S ribosomal protein P0	Rpp0p	778	34.6%	2472.258	0.004	1.6	DLLAVAIAASYHYPEIE DLVDR		4	3.5
Alcohol dehydrogenase	Adh1p	779	23.3%	2474.169	0.01	4.0	YSGVCHTDLHAWHG DWPLPVK		10.1	None
Pyruvate kinase	Cdc19p	780	21.9%	2480.287	0.011	4.4	GVNLPGTDVDLPALS EKDKEDLR		34.9	None
Pyruvate decarboxylase	Pdc1p	785	31.0%	2530.388	0.009	3.6	LKQVNVNTVFGLPGD EFNLSLLDK		0.6	0.2

G-beta like protein	Asc1p	790	30.5%	2558.266	-0.003	-1.2	VFSLDPQYLVDDL RPE FAGYSK		13.5	None
Pyruvate kinase	Cdc19p	791	29.6%	2568.214	-0.003	-1.2	GVFPFVFEKEPVSDW TDDVEAR		48.6	None
Translation elongation factor 2 (EF-2)	Eft2p	793	33.9%	2572.358	0.016	6.2	VTDGALVVDTIEGVC VQTETVLR		7.1	None
Member of 70 kDa heat shock protein family	Ssa2p	796	29.8%	2584.256	0.012	4.6	SEVFSTYADNQPGVLI QVFEGER		11.7	None
111 total proteins from 226 identified peptides										
From Mascot results, only 31 incorrectly assigned										
Only 44 hits had second best score										