Supporting Information

A Proteome fractionation strategy using continuous free-flow electrophoresis coupled off-line to rapid reversed-phase high-performance liquid chromatography

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Supplementary Table 1. LIM 1215 cytosolic peptides identified from selected wells from 2D FFE-IEF/RP-HPLC by ESI-MS/MS.

Preliminary analysis has identified in excess of 254 peptides (77 individual proteins) using the 2D FFE-IEF/RP-HPLC method, encompassing intracellular proteins that vary over a Mr range 11-119K. The length of tryptic peptides analysed ranged from 6–36 residues and the theoretical peptide pI values varied from 3.66 to 12.00. For this preliminary study, only 0.8% of each selected FFE fraction was subjected to MS analysis.

Supplementary Table 1. LIM 1215 cytosolic peptides identified from selected wells from 2D FFE-IEF/RP-HPLC by ESI-MS/MS

ID #	ID	FFE Well	Score [a]	Protein M_r [b]	Protien Calc pI [b]	% Seq. cov.	# Unique peptides	Protein subcellular location [c]	Peptide amino acid sequences [d]	Peptide theoretical pI	FFE pool pH	Δ pI/pH	Peptide theoretical mass [M+H]+ (mi) [e]	Peptide experimental [M+H]+ (mi) [g]	Δ mass	Δ ppm
001	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens [h]															
		19	De novo	41736	5.29	5%	1	Cytoplasmic	Ac-DDDIAALVVDNGSGMCK + Oxidation (M) [f]	3.66	3.31	0.35	1838.78	1839.06	-0.28	153
002	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
		21	De novo	41736	5.29	5%	1	Cytoplasmic	Ac-DDDIAALVVDNGSGMCK + Oxidation (M) [f]	3.66	3.41	0.25	1838.78	1838.98	-0.20	109
003	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
		21	De novo	41793	5.31	5%	2	Cytoplasmic	Ac-EEEIAALVIDNGSGMCK + Oxidation (M) [f]	3.83	3.41	0.42	1894.84	1895.06	-0.22	115
									Ac-EEEIAALVIDNGSGMCK [f]	3.83	3.41	0.42	1878.85	1879.16	-0.31	167
004	P12277 KCRB_HUMAN (CKB..)Creatine kinase, B chain (EC 2.7.3.2) (B-CK).- Homo sapiens															
		24	96	42907	5.34	6%	1	Cytoplasmic	TDLNPDNLQGGDDLDPNYVLSSR	3.66	3.70	-0.04	2518.17	2518.38	-0.21	83
005	P00338 LDHA_HUMAN (LDHA)L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH musc- Homo sapiens															
		24	91	36824	8.46	4%	1	Cytoplasmic	DLADELALVDVIEDK	3.66	3.70	-0.04	1657.85	1657.75	0.10	62
006	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
		24	De novo	41793	5.31	5%	1	Cytoplasmic	Ac-EEEIAALVIDNGSGMCK + Oxidation (M) [f]	3.83	3.70	0.13	1894.84	1895.20	-0.36	189
007	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens															
		24	63	27902	4.73	4%	1	Cytoplasmic	DICNDVLSLLEK [f]	3.84	3.70	0.14	1419.70	1419.52	0.18	130
008	P02593 CALM_HUMAN Calmodulin. - Homo sapiens															
		24	De novo	16706	4.09	9%	1	Cytoplasm	Ac-ADQLTEEQIAEFK	4.00	3.70	0.30	1563.75	1563.76	-0.01	4
009	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens															
	P09104 ENOG_HUMAN (ENO2)Gamma enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)- Homo sapiens															
	P13929 ENOB_HUMAN (ENO3)Beta enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) - Homo sapiens															
		25	115	47356	6.99	5%	1	Cytoplasmic	SGETEDTFIADLVVGLCTGQIK [f]	3.77	3.80	-0.03	2354.14	2354.46	-0.32	134
010	P12277 KCRB_HUMAN (CKB..)Creatine kinase, B chain (EC 2.7.3.2) (B-CK).- Homo sapiens															
		25	62	42907	5.34	6%	1	Cytoplasmic	TDLNPDNLQGGDDLDPNYVLSSR	3.66	3.80	-0.14	2518.17	2518.62	-0.45	179
011	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens															
		25	63	27902	4.73	4%	1	Cytoplasmic	DICNDVLSLLEK [f]	3.84	3.80	0.04	1419.70	1419.86	-0.16	110
012	P00338 LDHA_HUMAN (LDHA)L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH musc- Homo sapiens															
		25	38	36824	8.46	6%	1	Cytoplasmic	DDVFLSVPCILGQNGISDLVK [f]	3.77	3.80	-0.03	2290.16	2290.36	-0.20	86
013	P02593 CALM_HUMAN Calmodulin. - Homo sapiens															
		25	De novo	16706	4.09	9%	1	Cytoplasm	Ac-ADQLTEEQIAEFK	4.00	3.80	0.20	1563.75	1563.54	0.21	137
014	P05092 PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A.- Homo sapiens.															
		25	Sequest / 1.3809	17881	7.82	6%	1	Cytoplasmic	ITIADCGQLE [f]	3.80	3.80	0.00	1120.52	1120.43	0.09	80
015	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens															
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens															
		28	180	58349	7.95	6%	2	Cytosol	AEGSDVANAVLDGADCIMLSGETAK [f]	3.66	4.21	-0.55	2495.13	2495.14	-0.01	5
									CCSGAIIVLTK [f]	4.21	4.21	0.00	1223.60	1223.68	-0.08	64
016	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens															
		28	139	83429	4.97	3%	2	Cytoplasmic	NPDDITQEEYGEFYK	3.84	4.21	-0.37	1847.80	1847.90	-0.10	55
									EGLELPEDEEEK	3.77	4.21	-0.44	1416.64	1416.58	0.06	41
017	P00338 LDHA_HUMAN (LDHA)L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH musc- Homo sapiens															
		28	114	36824	8.46	10%	2	Cytoplasmic	DLADELALVDVIEDK	3.66	4.21	-0.55	1657.85	1657.92	-0.07	40
									DDVFLSVPCILGQNGISDLVK [f]	3.77	4.21	-0.44	2290.16	2290.40	-0.24	103

018	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens														
	P09104 ENOG_HUMAN (ENO2)Gamma enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)- Homo sapiens														
	P13929 ENOB_HUMAN (ENO3)Beta enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) - Homo sapiens														
	28	101	47356	6.99	5%	1	Cytoplasmic	SGETEDTFIADLVVGLCTGQIK [f]	3.77	4.21	-0.44	2354.14	2354.38	-0.24	100
019	P23528 COF1_HUMAN (CFL1..)Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18).- Homo sapiens														
	28	104	18723	8.22	12%	1	Intranuclear & cytoplasmic	EILVGDVGQTVDDPYATFVK	3.84	4.21	-0.37	2166.10	2166.32	-0.22	103
020	P12277 KCRB_HUMAN (CKB..)Creatine kinase, B chain (EC 2.7.3.2) (B-CK).- Homo sapiens														
	28	104	42907	5.34	8%	2	Cytoplasmic	DLFDPIIEDR	3.84	4.21	-0.37	1232.62	1232.34	0.28	224
								TDLNPDNLQGGDDLDPNYVLSSR	3.66	4.21	-0.55	2518.17	2518.30	-0.13	52
021	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens														
	28	81	27902	4.73	4%	1	Cytoplasmic	DICNDVLSLLEK [f]	3.84	4.21	-0.37	1419.70	1419.54	0.16	116
022	P00938 TPIS_HUMAN (TPI1..)Triosephosphate isomerase (EC 5.3.1.1) (TIM).- Homo sapiens														
	28	74	26812	6.51	8%	1	Glycosome	VPADTEVVCAPPTAYIDFAR f	3.84	4.21	-0.37	2193.05	2193.30	-0.25	112
023	P09525 ANX4_HUMAN (ANXA4..)Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chrom- Homo sapiens														
	28	54	35961	5.85	3%	1	?	VLLVLCGGDD [f]	3.67	4.21	-0.54	1061.52	1061.27	0.25	234
024	P05092 PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A.- Homo sapiens.														
	28	38	17881	7.82	6%	1	Cytoplasmic	ITIADCGQLE [f]	3.80	4.21	-0.41	1120.52	1120.49	0.03	26
025	P06366 RS14_HUMAN 40S ribosomal protein S14 (PRO2640).- Homo sapiens														
	28	32	16273	10.07	9%	1	Cytosolic small ribosomal subunit	IEDVTPIPSDSTR	4.03	4.21	-0.18	1429.72	1429.58	0.14	96
026	P00441 SODC_HUMAN Superoxide dismutase [Cu-Zn].- Homo sapiens														
	28	Sequest / 1.7258	15805	5.70	7%	1	Cytoplasmic	LACGVIGIAQ [f]	3.80	4.21	-0.41	1002.53	1002.38	0.15	149
027	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens														
	30	172	47356	6.99	9%	2	Cytoplasmic	DATNVGDEGGFAPNILENK	3.91	4.58	-0.67	1960.93	1961.16	-0.23	120
								SGETEDTFIADLVVGLCTGQIK [†]	3.77	4.58	-0.81	2354.14	2354.46	-0.32	134
028	P07900 HS9A_HUMAN (HSPCA..)Heat shock protein HSP 90-alpha (HSP 86).- Homo sapiens														
	30	135	84896	4.94	3%	2	Cytoplasmic	NPDDITNEEYGEFYK	3.84	4.58	-0.74	1833.78	1834.18	-0.40	217
								EGLELPEDEEEK	3.77	4.58	-0.81	1416.64	1416.88	-0.24	171
029	P00354 G3P1_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, muscle (EC 1.2.1.12) - Homo sapiens														
	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens)														
	30	89	36027	6.60	5%	1	Cytoplasmic	IISNASCTTNCLAPLAK [†]	4.21	4.58	-0.37	1835.89	1835.92	-0.03	17
030	P23528 COF1_HUMAN (CFL1..)Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18).- Homo sapiens														
	30	89	18723	8.22	12%	1	Intranuclear & cytoplasmic	EILVGDVGQTVDDPYATFVK	3.84	4.58	-0.74	2166.10	2166.08	0.02	8
031	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens														
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	30	69	58349	7.95	2%	1	Cytosol	CCSGAIIVLTK [†]	4.21	4.58	-0.37	1223.60	1223.58	0.02	18
032	P00938 TPIS_HUMAN (TPI1..)Triosephosphate isomerase (EC 5.3.1.1) (TIM).- Homo sapiens														
	30	68	26812	6.51	8%	1	Glycosome	VPADTEVVCAPPTAYIDFAR [†]	3.84	4.58	-0.74	2193.05	2193.06	-0.01	3
033	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens														
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens														
	30	Sequest / 2.1621	41736	5.29	2%	1	Cytoplasmic	DLTDYLMK	4.21	4.58	-0.37	998.49	998.60	-0.11	113
034	P00441 SODC_HUMAN Superoxide dismutase [Cu-Zn].- Homo sapiens														
	30	Sequest / 1.7276	15805	5.70	7%	1	Cytoplasmic	LACGVIGIAQ [†]	3.80	4.58	-0.78	1002.53	1002.43	0.10	99
035	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens														
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens														
	32	305	50152	4.94	14%	4	Microtubule	TIGGGDDSFNTFFSETGAGK	4.03	4.88	-0.85	2007.89	2008.04	-0.15	73

									AVFVDLEPTVIDEVR	3.91	4.88	-0.97	1701.91	1701.73	0.18	104
									EIIDLVLDR	4.03	4.88	-0.85	1085.62	1085.54	0.08	74
									FDGALNVDLTEFQTNLVPYPR	4.03	4.88	-0.85	2409.21	2408.88	0.33	137
036	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens															
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens															
		32	212	58349	7.95	10%	3	Cytosol	LAPITSDPTEATAVGAVEASFK	4.14	4.88	-0.74	2175.12	2175.32	-0.20	93
									CCSGAIIVLTK [f]	4.21	4.88	-0.67	1223.60	1223.48	0.12	99
									GIFPVLCKDPVQEAWAEDVDLR [f]	3.96	4.88	-0.92	2558.26	2558.40	-0.14	55
037	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens															
		32	181	36073	8.58	11%	2	Cytoplasmic	WGDAGAEYVVESTGVFTTMEK	4.00	4.88	-0.88	2277.04	2277.40	-0.36	159
									IISNASCTTNCLAPLAK [†]	4.21	4.88	-0.67	1835.89	1836.00	-0.11	61
038	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens															
		32	149	83429	4.97	3%	2	Cytoplasmic	ELISNASDALDK	4.03	4.88	-0.85	1275.64	1275.74	-0.10	76
									NPDDITQEEYGEFYK	3.84	4.88	-1.04	1847.80	1847.84	-0.04	23
039	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
		32	141	41736	5.29	8%	2	Cytoplasmic	DLTDYLMK	4.21	4.88	-0.67	998.49	998.44	0.05	47
									LCYVALDFEQEMATAASSSSLEK [f]	3.83	4.88	-1.05	2551.16	2551.64	-0.48	189
040	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens															
		32	121	47356	6.99	6%	2	Cytoplasmic	SCNCLLLK [f]	4.21	4.88	-0.67	1009.47	1009.52	-0.05	50
									SGETEDTFIADLVVGLCTGQIK [f]	3.77	4.88	-1.11	2354.14	2354.54	-0.40	168
041	P11021 GR78_HUMAN (HSPA5..)78 kDa glucose-regulated protein precursor (GRP 78) (Immunog- Homo sapiens															
		32	116	72404	5.07	3%	1	Endoplasmic reticulum lumen	LYGSAGPPPTGEEDTAEKDEL	3.77	4.88	-1.11	2175.99	2176.02	-0.03	12
042	P40227 TCPZ_HUMAN T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta)- Homo sapiens															
		32	95	58024	6.24	5%	1	Cytoplasmic	VATAQDDITGDGTTSNVLIIGELLK	3.84	4.88	-1.04	2544.34	2544.46	-0.12	47
043	P13641 SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1.- Homo sapiens															
		32	91	13282	11.56	17%	1	Nuclear	YFILPDSLPLDTLLVDVEPK	3.84	4.88	-1.04	2287.25	2287.68	-0.43	189
044	P23528 COF1_HUMAN (CFL1..)Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18).- Homo sapiens															
		32	61	18723	8.22	12%	1	Intranuclear & cytoplasmic	EILVGDVGQTVDDPYATFVK	3.84	4.88	-1.04	2166.10	2166.30	-0.20	94
045	P22392 NDKB_HUMAN (NME2..)Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kin- Homo sapiens															
		32	58	17298	8.52	6%	1	Nuclear & cytoplasmic	GDFCIQVGR [f]	4.21	4.88	-0.67	1052.48	1052.60	-0.12	111
046	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens															
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens															
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens															
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens															
		32	57	50063	4.81	2%	1	Microtubule	TAVCDIPPR [f]	4.21	4.88	-0.67	1029.50	1029.46	0.04	43
047	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens															
		32	49	53510	5.52	3%	1	Intermediate filament	LEGLTDEINFLR	4.14	4.88	-0.74	1419.75	1419.48	0.27	189
048	P07864 LDHC_HUMAN (LDHC)L-lactate dehydrogenase C chain (EC 1.1.1.27) (LDH-C) (LDH test- Homo sapiens															
	P00338 LDHA_HUMAN (LDHA)L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH musc- Homo sapiens															
	P07195 LDHB_HUMAN L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)- Homo sapiens															
		32	45	38166	7.06	4%	1	Cytoplasmic	VIGSGCNLDSAR [f]	4.21	4.88	-0.67	1249.58	1249.58	0.00	4
049	X01677 glyceraldehyde-3-phosphate dehydrogenase - Homo sapiens															
		34	344	36205	8.26	17%	4	Cytoplasmic	WGDAGAEYVVESTGVFTTMEK	4.00	5.14	-1.14	2277.04	2276.78	0.26	114
									IISNASCTTNCLAPLAK [†]	4.21	5.14	-0.93	1835.89	1836.24	-0.35	192

									VIPELDGK	4.37	5.14	-0.77	870.49	870.38	0.11	131
									VPTANVSVVDLTCR [†]	4.21	5.14	-0.93	1531.78	1532.04	-0.26	170
050	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens															
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens															
		34	340	58349	7.95	15%	5	Cytosol	LDIDSPPITAR	4.21	5.14	-0.93	1197.65	1197.72	-0.07	60
									FGVEQDVDMVFASFIR	4.03	5.14	-1.11	1859.90	1860.36	-0.46	247
									GDLGIEIPAEK	4.14	5.14	-1.00	1141.61	1141.62	-0.01	8
									LAPITSDPTEATAVGAVEASFK	4.14	5.14	-1.00	2175.12	2174.90	0.22	100
									GIFPVLCKDPVQEAWAEDVDLR [f]	3.96	5.14	-1.18	2558.26	2558.56	-0.30	117
051	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens															
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens															
		34	245	50152	4.94	9%	3	Microtubule	TIGGGDDSFNTFFSETGAGK	4.03	5.14	-1.11	2007.89	2008.16	-0.27	133
									AVFVDLEPTVIDEVR	3.91	5.14	-1.23	1701.91	1701.86	0.05	27
									EIIDLVLDR	4.03	5.14	-1.11	1085.62	1085.36	0.26	240
052	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens															
		34	220	83429	4.97	7%	3	Cytoplasmic	ELISNASDALDK	4.03	5.14	-1.11	1275.64	1275.64	0.00	3
									GVVDSEDLPLNISR	4.03	5.14	-1.11	1513.79	1513.88	-0.09	62
									DLVVLLFETALLSSGFSLEDPQTHSNR	4.31	5.14	-0.83	2988.53	2988.98	-0.45	150
053	P05092 PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A.- Homo sapiens.															
		34	197	17881	7.82	31%	4	Cytoplasmic	VNPTVFFDIAVDGEPLGR	4.03	5.14	-1.11	1946.00	1946.06	-0.06	30
									IIPGFMCQGGDFTR [†]	4.21	5.14	-0.93	1599.73	1599.78	-0.05	31
									FEDENFILK	4.14	5.14	-1.00	1154.57	1154.70	-0.13	110
									KITIADCGQLE [†]	4.32	5.14	-0.82	1248.61	1248.70	-0.09	68
054	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
		34	131	41736	5.29	8%	2	Cytoplasmic	DLTDYLMK	4.21	5.14	-0.93	998.49	998.41	0.08	77
									EKLCYVALDFEQEMATAASSSSLEK [f]	4.08	5.14	-1.06	2808.30	2808.76	-0.46	165
055	P13639 EF2_HUMAN (EEF2..)Elongation factor 2 (EF-2).- Homo sapiens															
		34	128	96132	6.42	6%	3	Cytoplasmic	DGAGFLINLIDSPGHVDFSSEVTAALR	4.22	5.14	-0.92	2801.41	2801.88	-0.47	167
									TFCQLILDPIFK [f]	4.21	5.14	-0.93	1495.79	1495.68	0.11	72
									EGIPALDNFLDKL	4.03	5.14	-1.11	1444.77	1444.62	0.15	103
056	P00441 SODC_HUMAN Superoxide dismutase [Cu-Zn].- Homo sapiens															
		34	112	15805	5.70	23%	1	Cytoplasmic	HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR [f]	4.14	5.14	-1.00	3721.80	3722.59	-0.79	213
057	P10599 THIO_HUMAN (TXN..)Thioredoxin.- Homo sapiens															
		34	82	11606	4.82	13%	1	Cytoplasmic	TAFQEALDAAGDK	4.03	5.14	-1.11	1336.64	1336.58	0.06	44
058	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens															
		34	66	53510	5.52	3%	1	Intermediate filament	LEGLTDEINFLR	4.14	5.14	-1.00	1419.75	1419.70	0.05	34
059	P13641 SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1.- Homo sapiens															
		34	63	13282	11.56	17%	1	Nuclear	YFILPDSLPLDTLLVDVEPK	3.84	5.14	-1.30	2287.25	2287.86	-0.61	268
060	P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens															
		34	58	27873	4.68	9%	1	Cytoplasmic	EKVETELQGVCDTVLGLLDSHLIK [f]	4.29	5.14	-0.85	2697.40	2697.73	-0.33	122
061	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens															
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens															
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens															
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens															

	34	57	50063	4.81	2%	1	Microtubule	TAVCDIPPR [f]	4.21	5.14	-0.93	1029.50	1029.40	0.10	101
062	P22234 PUR6_HUMAN Multifunctional protein ADE2.- Homo sapiens														
	34	De novo	47079	6.94	2%	1	?	Ac-ATAEVLNIGK	6.05	5.14	0.91	1057.59	1057.38	0.21	198
063	P78371 TCPB_HUMAN (CCT2..)T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta).- Homo sapiens														
	34	53	57488	6.01	4%	1	Cytoplasmic	MLPTIIADNAGYDSADLVAQLR	3.93	5.14	-1.21	2347.20	2346.68	0.52	220
064	P00938 TPIS_HUMAN (TPI1..)Triosephosphate isomerase (EC 5.3.1.1) (TIM).- Homo sapiens														
	34	52	26812	6.51	12%	1	Glycosome	ELASQPDVDGFLVGGASLKPEFVDIINAK	4.11	5.14	-1.03	3029.58	3030.22	-0.64	210
065	P07864 LDHC_HUMAN (LDHC)L-lactate dehydrogenase C chain (EC 1.1.1.27) (LDH-C) (LDH test- Homo sapiens P00338 LDHA_HUMAN (LDHA)L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH musc- Homo sapiens P07195 LDHB_HUMAN L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)- Homo sapiens														
	34	48	38166	7.06	4%	1	Cytoplasmic	VIGSGCNLDSAR [f]	4.21	5.14	-0.93	1249.58	1249.56	0.02	20
066	P25232 RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3).- Homo sapiens														
	34	De novo	17719	10.99	5%	1	Cytoplasmic	Ac-SLVIPEK	5.72	5.14	0.58	827.49	827.40	0.09	106
067	P29316 RL2B_HUMAN (RPL23A)60S ribosomal protein L23a.- Homo sapiens														
	34	47	17695	10.44	8%	1	Cytosolic large ribosomal subunit	LAPDYDALDVANK	3.93	5.14	-1.21	1404.70	1404.68	0.02	15
068	P23528 COF1_HUMAN (CFL1..)Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18).- Homo sapiens														
	34	43	18723	8.22	17%	1	Intranuclear & cytoplasmic	NIILEEGKEILVGDVGQTVDDPYATFVK	4.02	5.14	-1.12	3062.59	3062.92	-0.33	107
069	P00558 PGK1_HUMAN Phosphoglycerate kinase 1 (Primer recognition protein 2) (PRP 2)- Homo sapiens														
	34	37	44597	8.30	3%	1	?	VLPGVDALSNI	3.80	5.14	-1.34	1097.62	1097.45	0.17	155
070	Q01469 FABE_HUMAN Fatty acid-binding protein, epidermal (E-FABP)- Homo sapiens														
	34	De novo	15164	6.60	7%	1	Cytoplasmic	Ac-ATVQQLEGR	6.05	5.14	0.91	1043.55	1043.58	-0.03	30
071	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	36	273	58349	7.95	10%	4	Cytosol	GDYPLEAVR	4.37	5.38	-1.01	1019.52	1019.64	-0.12	121
								LDIDSPPITAR	4.21	5.38	-1.17	1197.65	1197.66	-0.01	10
								IYVDDGLISLQVK	4.21	5.38	-1.17	1462.82	1462.86	-0.04	30
								LAPITSDPTEATAVGAVEASFK	4.14	5.38	-1.24	2175.12	2174.82	0.30	137
072	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens														
	36	175	53510	5.52	7%	3	Intermediate filament	LSELEAALQR	4.53	5.38	-0.85	1129.62	1129.68	-0.06	52
								LVSESSDVLPK	4.37	5.38	-1.01	1173.64	1173.46	0.18	151
								ASLEAAIADAEQR	4.14	5.38	-1.24	1344.68	1344.48	0.20	146
073	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens														
	36	156	47356	6.99	9%	4	Cytoplasmic	EGLELLK	4.53	5.38	-0.85	801.47	801.51	-0.04	47
								YISPDQLADLYK	4.21	5.38	-1.17	1425.73	1425.70	0.03	19
								FTASAGIQVVGDDLTVTNPK	4.21	5.38	-1.17	2033.06	2033.12	-0.06	32
074	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	36	112	83429	4.97	7%	3	Cytoplasmic	IDIIPNPQER	4.37	5.38	-1.01	1194.65	1194.84	-0.19	160
								YESLTDPSKLDSGK	4.56	5.38	-0.82	1539.75	1539.49	0.26	172
								DLVVLLFETALLSSGFSLEDPQTHSNR	4.31	5.38	-1.07	2988.53	2988.96	-0.43	143
075	P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens														
	36	65	27873	4.68	9%	1	Cytoplasmic	EKVETELQGVCDTVLGLLDSHLIK [f]	4.29	5.38	-1.09	2697.40	2697.73	-0.33	122
076	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens														
	36	63	50063	4.81	2%	1	Microtubule	TAVCDIPPR	5.50	5.38	0.12	1029.50	1029.48	0.02	23
077	P14174 MIF_HUMAN (MIF..)Macrophage migration inhibitory factor (MIF) (Phenylpyruvate t- Homo sapiens														

	36	57	12511	8.24	7%	1	Extracellular space	LLCGLLAER [†]	4.37	5.38	-1.01	1045.57	1045.62	-0.05	46
078	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	36	75	35922	8.58	4%	1	Cytoplasmic	VPTANVSVVDLTCR [†]	4.21	5.38	-1.17	1531.78	1531.92	-0.14	92
079	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens														
	36	77	41736	5.29	4%	1	Cytoplasmic	SYELPDGQVITIGNER	4.14	5.38	-1.24	1790.89	1791.14	-0.25	138
080	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	38	213	41736	5.29	17%	4	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	5.56	-0.81	1954.07	1954.40	-0.34	171
								QEYDESGPSIVHR	4.65	5.56	-0.91	1516.70	1516.42	0.28	187
								YPIE(me-H)GIVTNWDDMEK	4.31	5.56	-1.25	1960.91	1960.88	0.03	16
								SYELPDGQVITIGNER	4.14	5.56	-1.42	1790.89	1791.06	-0.17	94
081	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens														
	38	179	47356	6.99	9%	3	Cytoplasmic	EGLELLK	4.53	5.56	-1.03	801.47	801.38	0.09	115
								VVIGMDVAASEFFR	4.37	5.56	-1.19	1540.78	1540.74	0.04	28
								FTASAGIQVVGDDLTVTNPK	4.21	5.56	-1.35	2033.06	2033.34	-0.28	140
082	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens														
	38	165	53510	5.52	6%	3	Intermediate filament	LQAEIEGLK	4.53	5.56	-1.03	1000.57	1000.54	0.03	28
								LSELEAALQR	4.53	5.56	-1.03	1129.62	1129.78	-0.16	140
								LVSESSDVLPK	4.37	5.56	-1.19	1173.64	1173.64	0.00	3
083	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens Q13509 TBB4_HUMAN (TUBB4)Tubulin beta-4 chain (Tubulin beta-III).- Homo sapiens														
	38	101	50263	4.79	4%	1	Microtubule	GHYTEGAELVDSVLDVVR	4.31	5.56	-1.25	1958.98	1959.20	-0.22	111
084	P22314 UBA1_HUMAN (UBE1)Ubiquitin-activating enzyme E1 (A1S9 protein).- Homo sapiens														
	38	97	118876	5.49	2%	1	Cytoplasmic	IIPAIATTTAAVVGLVCLELYK [f]	4.37	5.56	-1.19	2317.31	2317.60	-0.29	125
085	P23821 RS7_HUMAN 40S ribosomal protein S7 (S8).- Homo sapiens														
	38	92	22127	10.09	11%	1	Cytosolic small ribosomal subunit	TLTAVHDAILEDLVFPSEIVGK	4.31	5.56	-1.25	2367.28	2366.90	0.38	161
086	O00299 CLI1_HUMAN (CLIC1..)Chloride intracellular channel protein 1 (Nuclear chloride i- Homo sapiens														
	38	87	26923	5.09	8%	1	Nuclear membrane (small amount in cytoplasm)	LAALNPESNTAGLDIFAK	4.37	5.56	-1.19	1844.98	1844.52	0.46	247
087	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	38	78	83429	4.97	3%	1	Cytoplasmic	DLVVLLFETALLSSGFSLEDPQTHSNR	4.31	5.56	-1.25	2988.53	2989.20	-0.67	224
088	P07195 LDHB_HUMAN (LDHB)L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH hear- Homo sapiens														
	38	75	36507	5.72	5%	1	Cytoplasmic	LIAPVAEEEATVPNNK	4.25	5.56	-1.31	1694.90	1694.76	0.14	81
089	P04075 ALFA_HUMAN (ALDOA..)Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type - Homo sapiens														
	38	70	39289	8.39	8%	1	Glycosome	TVPPAVTGITFLSGGQSEEEASINLNAINK	4.25	5.56	-1.31	3057.57	3057.22	0.35	116
090	P05092 PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A.- Homo sapiens.														
	38	69	17881	7.82	9%	1	Cytoplasmic	SIYGEKFEDENFILK	4.41	5.56	-1.15	1831.91	1831.96	-0.05	26
091	P07741 APT_HUMAN (APRT)Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).- Homo sapiens														
	38	63	19477	5.79	11%	1	Cytoplasmic	GFLFGPSLAQELGLGCVLIR [f]	4.37	5.56	-1.19	2148.15	2148.30	-0.15	69
092	O00764 PDXK_HUMAN (PDXK..)Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase).- Homo sapiens														
	38	61	35102	5.75	7%	1	Cytoplasmic	VVPLADIITPNQFEAELLSGR	4.14	5.56	-1.42	2282.24	2282.36	-0.12	53
093	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														

	38	59	36073	8.58	5%	1	Cytoplasmic	LVINGNPITIFQERDPSK	6.07	5.56	0.51	2041.11	2041.28	-0.17	84
094	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens														
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	38	73	58349	7.95	9%	1	Cytosol	TATESFASDPILYRPVAVALDTK	4.56	5.56	-1.00	2465.29	2464.74	0.55	224
								LAPITSDPTEATAVGAVEASFK	4.14	5.56	-1.42	2175.12	2175.52	-0.40	185
095	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	38	42	50457	9.10	8%	1	Cytoplasmic	DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK [f]	4.46	5.56	-1.10	3979.09	3979.20	-0.11	29
096	Q06830 PDX1_HUMAN Peroxiredoxin 1 (Thioredoxin peroxidase 2)- Homo sapiens														
	38	Sequest / 2.3900	22052	5.66	4%	3	Cytoplasmic	GLFIIDDK	4.21	5.56	-1.35	920.51	920.51	0.00	1
097	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens														
	40	123	53510	5.52	6%	3	Intermediate filament	LQAEIEGLK	4.53	5.73	-1.20	1000.57	1000.56	0.01	8
								LSELEAALQR	4.53	5.73	-1.20	1129.62	1129.48	0.14	125
								LVSESSDVLPK	4.37	5.73	-1.36	1173.64	1173.72	-0.08	71
098	P00938 TPIS_HUMAN (TPI1..)Triosephosphate isomerase (EC 5.3.1.1) (TIM).- Homo sapiens														
	40	98	26812	6.51	7%	1	Glycosome	VAHALAEGLGVIACIGEK [f]	4.65	5.73	-1.08	1808.96	1809.36	-0.40	222
099	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	40	81	83429	4.97	3%	1	Cytoplasmic	DLVVLLFETALLSSGFSLEDPQTHSNR	4.31	5.73	-1.42	2988.53	2989.10	-0.57	190
100	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	40	76	36073	8.58	5%	1	Cytoplasmic	LVINGNPITIFQERDPSK	6.07	5.73	0.34	2041.11	2041.40	-0.29	143
101	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens														
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	40	43	58349	7.95	4%	1	Cytosol	LAPITSDPTEATAVGAVEASFK	4.14	5.73	-1.59	2175.12	2174.62	0.50	229
102	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens														
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	40	65	41736	5.29	5%	1	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	5.73	-0.98	1954.07	1954.48	-0.41	212
103	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens														
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens														
	40	39	50152	4.94	2%	1	Microtubule	DVNAAIATIK	5.84	5.73	0.11	1015.58	1015.47	0.11	107
104	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens														
	41	126	47356	6.99	8%	2	Cytoplasmic	AAVPSGASTGIYEALELR	4.53	5.77	-1.24	1804.94	1805.34	-0.40	219
								FTASAGIQVVGDDLTVTNPK	4.21	5.77	-1.56	2033.06	2033.16	-0.10	51
105	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens														
	41	123	53510	5.52	4%	2	Intermediate filament	LSELEAALQR	4.53	5.77	-1.24	1129.62	1129.56	0.06	55
								LQAEIEGLK	4.53	5.77	-1.24	1000.57	1000.56	0.01	8
106	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens														
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	41	98	41736	5.29	8%	2	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	5.77	-1.02	1954.07	1954.30	-0.23	120
								QEYDESGPSIVHR	4.65	5.77	-1.12	1516.70	1516.63	0.07	48
107	P00938 TPIS_HUMAN (TPI1..)Triosephosphate isomerase (EC 5.3.1.1) (TIM).- Homo sapiens														
	41	96	26812	6.51	7%	1	Glycosome	VAHALAEGLGVIACIGEK [f]	4.65	5.77	-1.12	1808.96	1809.00	-0.04	23
108	P22314 UBA1_HUMAN (UBE1)Ubiquitin-activating enzyme E1 (A1S9 protein).- Homo sapiens														
	41	75	118876	5.49	2%	1	Cytoplasmic	IIPAIATTTAAVVGLVCLELYK [f]	4.37	5.77	-1.40	2317.31	2317.40	-0.09	39
109	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens														
	P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	41	72	58349	7.95	6%	2	Cytosol	NTGIICTIGPASR f	5.84	5.77	0.07	1360.69	1360.66	0.03	22
								TATESFASDPILYRPVAVALDTK	4.56	5.77	-1.21	2465.29	2465.42	-0.13	52

110	P05783 K1CR_HUMAN (KRT18..)Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 1- Homo sapiens															
	41	53	47897	5.34	6%	2	Intermediate filament	IVLQIDNAR	5.84	5.77	0.07	1041.61	1041.54	0.07	63
								LQLETEIEALKEELLFMK + Oxidation (M)	4.32	5.77	-1.45	2193.17	2193.30	-0.13	58
111	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens															
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens															
	41	32	50152	4.94	2%	1	Microtubule	DVNAAIATIK	5.84	5.77	0.07	1015.58	1015.46	0.12	117
112	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens															
	43	88	83429	4.97	3%	1	Cytoplasmic	DLVVLLFETALLSSGFSLEDPQTHSNR	4.31	5.90	-1.59	2988.53	2989.10	-0.57	190
113	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
	43	62	41736	5.29	4%	1	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	5.90	-1.15	1954.07	1954.48	-0.41	212
114	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens															
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens															
	43	48	50152	4.94	2%	1	Microtubule	DVNAAIATIK	5.84	5.90	-0.06	1015.58	1015.57	0.01	9
115	P05787 K2C8_HUMAN (KRT8..)Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).- Homo sapiens															
	43	44	53510	5.52	2%	1	Intermediate filament	LSELEAALQR	4.53	5.90	-1.37	1129.62	1129.52	0.10	90
116	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens															
	43	37	47356	6.99	6%	1	Cytoplasmic	HIADLAGNSEVILPVPAFNVINGGSHAGNK	5.99	5.90	0.09	3011.57	3012.12	-0.55	183
117	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens															
	43	41	36073	8.58	5%	1	Cytoplasmic	LVINGNPITIFQERDPSK	6.07	5.90	0.17	2041.11	2040.76	0.35	171
118	P17008 RS16_HUMAN 40S ribosomal protein S16.- Homo sapiens															
	43	26	16314	10.21	7%	1	Cytosolic small ribosomal subunit	LLEPVLLLGK	6.00	5.90	0.10	1094.72	1094.61	0.11	99
119	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
	46	119	41736	5.29	11%	3	Cytoplasmic	EITALAPSTMK	6.10	6.11	-0.01	1161.62	1161.58	0.04	33
								VAPEEHPVLLTEAPLNPK	4.75	6.11	-1.36	1954.07	1954.38	-0.32	161
								QEYDESGPSIVHR	4.65	6.11	-1.46	1516.70	1516.48	0.22	147
120	P32119 PDX2_HUMAN (PRDX2..)Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Th- Homo sapiens															
	46	90	22052	5.66	14%	2	Cytoplasmic	KEGGLGPLNIPLLADVTR	6.07	6.11	-0.04	1863.07	1862.84	0.23	124
								QITVNDLPVGR	5.84	6.11	-0.27	1211.67	1211.68	-0.01	4
121	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens															
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens															
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens															
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens															
	Q13509 TBB4_HUMAN (TUBB4)Tubulin beta-4 chain (Tubulin beta-III).- Homo sapiens															
	Q99867 TBBQ_HUMAN (TUBB4Q..)Tubulin beta-4q chain.- Homo sapiens															
	46	51	50063	4.81	2%	1	Microtubule	FPGQLNADLR	5.84	6.11	-0.27	1130.60	1130.78	-0.18	163
122	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens															
	46	51	50457	9.10	5%	1	Cytoplasmic	VETGVLKPGMVVTFAPVNVTTEVK	6.11	6.11	0.00	2515.38	2515.10	0.28	113
123	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens															
	46	46	47356	6.99	6%	1	Cytoplasmic	HIADLAGNSEVILPVPAFNVINGGSHAGNK	5.99	6.11	-0.12	3011.57	3011.26	0.31	103
124	P05209 TBA1_HUMAN Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens															
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens															
	46	40	50152	4.94	2%	1	Microtubule	DVNAAIATIK	5.84	6.11	-0.27	1015.58	1015.50	0.08	78
125	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens															
	48	89	50457	9.10	6%	2	Cytoplasmic	LPLQDVYK	5.83	6.22	-0.39	975.55	975.56	-0.01	9

									VETGVLKPGMVVTFAPVNVTTEVK	6.11	6.22	-0.11	2515.38	2515.92	-0.54	213
126	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
		48	70	41736	5.29	7%	2	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	6.22	-1.47	1954.07	1954.36	-0.29	151
									GYSFTTTAER	6.00	6.22	-0.22	1132.53	1132.62	-0.09	82
127	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens															
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens															
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens															
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens															
	Q13509 TBB4_HUMAN (TUBB4)Tubulin beta-4 chain (Tubulin beta-III).- Homo sapiens															
	Q99867 TBBQ_HUMAN (TUBB4Q..)Tubulin beta-4q chain.- Homo sapiens															
		48	49	50063	4.81	2%	1	Microtubule	FPGQLNADLR	5.84	6.22	-0.38	1130.60	1130.70	-0.10	92
128	P07737 PRO1_HUMAN Profilin I.- Homo sapiens															
		48	44	14923	8.47	12%	1	Cytoskeleton	TFVNITPAEVGVLVGK	5.66	6.22	-0.56	1643.94	1644.11	-0.17	105
129	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens															
		48	42	36073	8.58	7%	1	Cytoplasmic	VIHDNFGIVEGLMTTVHAITATQK + Oxidation (M)	5.99	6.22	-0.23	2611.36	2610.84	0.52	197
130	P32119 PDX2_HUMAN (PRDX2..)Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Th- Homo sapiens															
		50	145	22052	5.66	18%	3	Cytoplasmic	GLFIIDGK	5.84	6.37	-0.53	862.50	862.51	-0.01	7
									QITVNDLPVGR	5.84	6.37	-0.53	1211.67	1211.44	0.23	194
									KEGGLGPLNIPLLADVTR	6.07	6.37	-0.30	1863.07	1863.34	-0.27	145
131	P05209 TBA1_HUMAN (TUBA1)Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens															
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens															
	Q13748 TBA2_HUMAN Tubulin alpha-2 chain (Alpha-tubulin 2).- Homo sapiens															
		50	122	50816	4.94	5%	2	Microtubule	DVNAAIATIK	5.84	6.37	-0.53	1015.58	1015.52	0.06	58
									IHFPLATYAPVISAEK	6.75	6.37	0.38	1756.96	1757.16	-0.20	112
132	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens															
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens															
	P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens															
	P03996 ACTA_HUMAN (ACTA2..)Actin, aortic smooth muscle (Alpha-actin 2).- Homo sapiens															
	P04270 ACTC_HUMAN (ACTC..)Actin, alpha cardiac.- Homo sapiens															
	P12718 ACTH_HUMAN (ACTG2..)Actin, gamma-enteric smooth muscle (Alpha-actin 3).- Homo sapiens															
		50	109	41736	5.29	7%	2	Cytoplasmic	EITALAPSTMK	6.10	6.37	-0.27	1161.62	1161.47	0.15	128
									VAPEEHPVLLTEAPLNPK	4.75	6.37	-1.62	1954.07	1954.54	-0.47	243
133	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens															
		50	78	36073	8.58	7%	1	Cytoplasmic	VIHDNFGIVEGLMTTVHAITATQK + Oxidation (M)	5.99	6.37	-0.38	2611.36	2610.78	0.58	220
134	P07737 PRO1_HUMAN Profilin I.- Homo sapiens															
		50	56	14923	8.47	11%	1	Cytoplasmic	TFVNITPAEVGVLVGK	5.66	6.37	-0.71	1643.94	1644.14	-0.20	123
135	P06733 ENOA_HUMAN (ENO1..)Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyas- Homo sapiens															
		50	53	47356	6.99	6%	1	Cytoplasmic	HIADLAGNSEVILPVPAFNVINGGSHAGNK	5.99	6.37	-0.38	3011.57	3012.31	-0.74	246
136	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens															
		50	50	50457	9.10	5%	1	Cytoplasmic	VETGVLKPGMVVTFAPVNVTTEVK	6.11	6.37	-0.26	2515.38	2515.92	-0.54	213
137	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens															
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens															
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens															
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens															
	Q13509 TBB4_HUMAN (TUBB4)Tubulin beta-4 chain (Tubulin beta-III).- Homo sapiens															

	Q99867 TBBQ_HUMAN (TUBB4Q..)Tubulin beta-4q chain.- Homo sapiens															
	50	58	50063	4.81	2%	1	Microtubule	FPGQLNADLR	5.84	6.37	-0.53	1130.60	1130.82	-0.22	198
138	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens														
	50	Sequest / 1.8740	27745	4.73	5%	1	Cytoplasmic	FLIPNASQAESK	6.00	6.37	-0.37	1304.69	1304.74	-0.06	42
139	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	52	107	50457	9.10	7%	2	Cytoplasmic	LPLQDVYK	5.83	6.50	-0.67	975.55	975.58	-0.03	29
								VETGVLKPGMVVTFAPVNVTTEVK	6.11	6.50	-0.39	2515.38	2515.90	-0.52	205
140	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	52	78	36073	8.58	7%	1	Cytoplasmic	VIHDNFGIVEGLMTTVHAITATQK + Oxidation (M)	5.99	6.50	-0.51	2611.36	2611.50	-0.14	55
141	P04350 TBBX_HUMAN (TUBB5)Tubulin beta-5 chain (Tubulin 5 beta).- Homo sapiens														
	P05217 TBB2_HUMAN (TUBB2)Tubulin beta-2 chain.- Homo sapiens														
	P05218 TBB5_HUMAN (TUBB5)Tubulin beta-5 chain.- Homo sapiens														
	P07437 TBB1_HUMAN (TUBB1)Tubulin beta-1 chain.- Homo sapiens														
	Q13509 TBB4_HUMAN (TUBB4)Tubulin beta-4 chain (Tubulin beta-III).- Homo sapiens														
	Q99867 TBBQ_HUMAN (TUBB4Q..)Tubulin beta-4q chain.- Homo sapiens														
	52	56	50063	4.81	2%	1	Microtubule	FPGQLNADLR	5.84	6.50	-0.66	1130.60	1130.72	-0.12	110
142	P07737 PRO1_HUMAN Profilin I.- Homo sapiens														
	52	52	14923	8.47	12%	1	Cytoplasmic	TFVNITPAEVGVLVGK	5.66	6.50	-0.84	1643.94	1643.99	-0.05	32
143	P05209 TBA1_HUMAN (TUBA1)Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens														
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens														
	52	34	50152	4.94	2%	1	Microtubule	DVNAAIATIK	5.84	6.50	-0.66	1015.58	1015.42	0.16	156
144	P05783 KICR_HUMAN Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18).- Homo sapiens														
	52	29	47927	5.34	2%	1	Intermediate filament	IVLQIDNAR	5.84	6.50	-0.66	1041.61	1041.66	-0.05	52
145	P05209 TBA1_HUMAN (TUBA1)Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens														
	Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens														
	Q13748 TBA2_HUMAN Tubulin alpha-2 chain (Alpha-tubulin 2).- Homo sapiens														
	55	162	50816	4.94	9%	3	Microtubule	DVNAAIATIK	5.84	6.73	-0.89	1015.58	1015.53	0.05	48
								IHFPLATYAPVISAEK	6.75	6.73	0.02	1756.96	1757.20	-0.24	134
								VGINYQPPTVVPGGDLAK	5.80	6.73	-0.93	1824.99	1825.22	-0.23	128
146	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens														
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	55	122	41736	5.29	13%	3	Cytoplasmic	VAPEEHPVLLTEAPLNPK	4.75	6.73	-1.98	1954.07	1954.46	-0.39	202
								KDLYANTVLSGGTTMYPGIADR	5.96	6.73	-0.77	2343.17	2342.98	0.19	79
								EITALAPSTMK	6.10	6.73	-0.63	1161.62	1161.56	0.06	51
147	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	55	79	50457	9.10	7%	2	Cytoplasmic	VETGVLKPGMVVTFAPVNVTTEVK	6.11	6.73	-0.62	2515.38	2515.42	-0.04	14
								LPLQDVYK	5.83	6.73	-0.90	975.55	975.58	-0.03	29
148	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	55	60	36073	8.58	7%	1	Cytoplasmic	VIHDNFGIVEGLMTTVHAITATQK + Oxidation (M)	5.99	6.73	-0.74	2611.36	2611.69	-0.33	128
149	Q04917 143F_HUMAN (YWHAH..)14-3-3 protein eta (Protein AS1).- Homo sapiens														
	P27348 143T_HUMAN (YWHAQ)14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-ce- Homo sapiens														
	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens														
	P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens														
	P35214 143G_HUMAN (YWHAG)14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (K- Homo sapiens														
	P42655 143E_HUMAN (YWHAE)14-3-3 protein epsilon (Mitochondrial import stimulation facto- Homo sapiens														
	P31946 143B_HUMAN (YWHAB)14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-- Homo sapiens														

	55	30	28244	4.76	3%	1	?	NLLSVAYK	8.59	6.73	1.86	907.53	907.52	0.01	6
150	P05209 TBA1_HUMAN (TUBA1)Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens P05215 TBA4_HUMAN Tubulin alpha-4 chain (Alpha-tubulin 4).- Homo sapiens Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens Q13748 TBA2_HUMAN Tubulin alpha-2 chain (Alpha-tubulin 2).- Homo sapiens														
	57	72	50816	4.94	3%	1	Microtubule	IHFPLATYAPVISAEK	6.75	7.00	-0.25	1756.96	1757.24	-0.28	157
151	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	57	49	50457	9.10	5%	1	Cytoplasmic	VETGVLKPGMVVTFAPVNVTTEVK	6.11	7.00	-0.89	2515.38	2515.94	-0.56	221
152	Q04917 143F_HUMAN (YWHAH..)14-3-3 protein eta (Protein AS1).- Homo sapiens P27348 143T_HUMAN (YWHAQ)14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-ce- Homo sapiens P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens P35214 143G_HUMAN (YWHAG)14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (K- Homo sapiens P42655 143E_HUMAN (YWHAE)14-3-3 protein epsilon (Mitochondrial import stimulation facto- Homo sapiens P31946 143B_HUMAN (YWHAB)14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-- Homo sapiens														
	57	32	28244	4.76	3%	1	?	NLLSVAYK	8.59	7.00	1.59	907.53	907.37	0.16	171
153	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	59	60	36073	8.58	5%	1	Cytoplasmic	LVINGNPITIFQERDPSK	6.07	7.15	-1.08	2041.11	2040.92	0.19	92
154	P05209 TBA1_HUMAN (TUBA1)Tubulin alpha-1 chain (Alpha-tubulin 1).- Homo sapiens P05215 TBA4_HUMAN Tubulin alpha-4 chain (Alpha-tubulin 4).- Homo sapiens Q9BQE3 TBA6_HUMAN Tubulin alpha-6 chain (Alpha-tubulin 6).- Homo sapiens Q13748 TBA2_HUMAN Tubulin alpha-2 chain (Alpha-tubulin 2).- Homo sapiens														
	59	56	50816	4.94	3%	1	Microtubule	IHFPLATYAPVISAEK	6.75	7.15	-0.40	1756.96	1757.14	-0.18	100
155	P09211 GTP_HUMAN (GSTP1..)Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GS- Homo sapiens														
	59	51	23442	5.44	9%	1	?	ALPGQLKPFETLLSQNQGGK	8.64	7.15	1.49	2126.16	2126.64	-0.48	225
156	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	59	47	50457	9.10	5%	1	Cytoplasmic	VETGVLKPGMVVTFAPVNVTTEVK	6.11	7.15	-1.04	2515.38	2515.96	-0.58	229
157	Q04917 143F_HUMAN (YWHAH..)14-3-3 protein eta (Protein AS1).- Homo sapiens P27348 143T_HUMAN (YWHAQ)14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-ce- Homo sapiens P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens P35214 143G_HUMAN (YWHAG)14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (K- Homo sapiens P42655 143E_HUMAN (YWHAE)14-3-3 protein epsilon (Mitochondrial import stimulation facto- Homo sapiens P31946 143B_HUMAN (YWHAB)14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-- Homo sapiens														
	59	41	28244	4.76	3%	1	?	NLLSVAYK	8.59	7.15	1.44	907.53	907.44	0.09	94
158	P02261 H2AC_HUMAN (HIST1H2AJ..)Histone H2A.c/d/i/n/p (H2A.1) (H2A/c) (H2A/d) (H2A/i) (H- Homo sapiens P20670 H2AO_HUMAN (HIST2H2AA..)Histone H2A.o (H2A/o) (H2A.2) (H2a-615).- Homo sapiens P20671 H2AG_HUMAN (HIST1H2AD..)Histone H2A.g (H2A/g) (H2A.3).- Homo sapiens P04908 H2AM_HUMAN (HIST1H2AB..)Histone H2A.m (H2A/m).- Homo sapiens P28001 H2AA_HUMAN (HIST1H2AE..)Histone H2A.a (H2A/a) (H2A.2).- Homo sapiens Q93077 H2AL_HUMAN (HIST1H2AC..)Histone H2A.l (H2A/l).- Homo sapiens Q99878 H2AE_HUMAN (HIST1H2AK..)Histone H2A.e (H2A/e).- Homo sapiens														
	64	76	13952	10.90	14%	1	Nuclear	VTIAQGGVLPNIQAVLLPK	8.72	7.56	1.16	1931.17	1931.32	-0.15	78
159	P09211 GTP_HUMAN (GSTP1..)Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GS- Homo sapiens														
	64	76	23442	5.44	9%	1	?	ALPGQLKPFETLLSQNQGGK	8.64	7.56	1.08	2126.16	2126.58	-0.42	197
160	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens Q05639 EF12_HUMAN Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1).- Homo sapiens														

	64	54	50457	9.10	2%	1	Cytoplasmic	IGGIGTVPVGR	9.75	7.56	2.19	1025.61	1025.70	-0.09	87
161	Q04917 143F_HUMAN (YWHAH..)14-3-3 protein eta (Protein AS1).- Homo sapiens														
	P27348 143T_HUMAN (YWHAQ)14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-ce- Homo sapiens														
	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens														
	P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens														
	P35214 143G_HUMAN (YWHAG)14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (K- Homo sapiens														
	P42655 143E_HUMAN (YWHAE)14-3-3 protein epsilon (Mitochondrial import stimulation facto- Homo sapiens														
	P31946 143B_HUMAN (YWHAB)14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-- Homo sapiens														
	64	46	29174	4.63	3%	1	Cytoplasmic	NLLSVAYK	8.59	7.56	1.03	907.53	907.39	0.14	149
162	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	64	48	36073	8.58	4%	1	Cytoplasmic	GALQNIIPASTGAAK	8.75	7.56	1.19	1411.79	1411.66	0.13	93
163	P07195 LDHB_HUMAN L-lactate dehydrogenase B chain.- Homo sapiens														
	64	45	36507	5.72	5%	2	Cytoplasmic	IVVVTAGVR	9.75	7.56	2.19	913.58	913.55	0.03	37
								FIIPQIVK	8.75	7.56	1.19	957.61	957.63	-0.02	17
164	P07737 PRO1_HUMAN Profilin I.- Homo sapiens														
	64	27	14923	8.47	6%	1	Cytoplasmic	TLVLLMGK	8.41	7.56	0.85	874.54	874.51	0.03	38
165	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	Q05639 EF12_HUMAN Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1).- Homo sapiens														
	68	58	50457	9.10	2%	1	Cytoplasmic	IGGIGTVPVGR	9.75	7.88	1.87	1025.61	1025.48	0.13	128
166	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens														
	P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens														
	P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens														
	P03996 ACTA_HUMAN (ACTA2..)Actin, aortic smooth muscle (Alpha-actin 2).- Homo sapiens														
	P04270 ACTC_HUMAN (ACTC..)Actin, alpha cardiac.- Homo sapiens														
	P12718 ACTH_HUMAN (ACTG2..)Actin, gamma-enteric smooth muscle (Alpha-actin 3).- Homo sapiens														
	68	68	41736	5.29	4%	3	Cytoplasmic	AVFPSIVGR	9.79	7.88	1.91	945.55	945.62	-0.07	72
								GILTLK	8.75	7.88	0.87	644.43	644.43	0.00	7
167	P09211 GTP_HUMAN (GSTP1..)Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GS- Homo sapiens														
	68	68	23442	5.44	9%	1	?	ALPGQLKPFETLLSQNQGGK	8.64	7.88	0.76	2126.16	2126.64	-0.48	225
168	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	68	54	36073	8.58	4%	1	Cytoplasmic	GALQNIIPASTGAAK	8.75	7.88	0.87	1411.79	1411.82	-0.03	21
169	P07195 LDHB_HUMAN L-lactate dehydrogenase B chain.- Homo sapiens														
	68	48	36507	5.72	5%	2	Cytoplasmic	IVVVTAGVR	9.75	7.88	1.87	913.58	913.56	0.02	26
								FIIPQIVK	8.75	7.88	0.87	957.61	957.58	0.03	35
170	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	68	29	83429	4.97	1%	1	Cytoplasmic	ALLFIPR	9.79	7.88	1.91	829.53	829.55	-0.02	24
171	Q04917 143F_HUMAN (YWHAH..)14-3-3 protein eta (Protein AS1).- Homo sapiens														
	P27348 143T_HUMAN (YWHAQ)14-3-3 protein tau (14-3-3 protein theta) (14-3-3 protein T-ce- Homo sapiens														
	P29312 143Z_HUMAN (YWHAZ)14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-- Homo sapiens														
	P31947 143S_HUMAN (SFN..)14-3-3 protein sigma (Stratifin) (Epithelial cell marker prote- Homo sapiens														
	P35214 143G_HUMAN (YWHAG)14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (K- Homo sapiens														
	P42655 143E_HUMAN (YWHAE)14-3-3 protein epsilon (Mitochondrial import stimulation facto- Homo sapiens														
	P31946 143B_HUMAN (YWHAB)14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-- Homo sapiens														
	68	35	29174	4.63	3%	1	Cytoplasmic	NLLSVAYK	8.59	7.88	0.71	907.53	907.42	0.11	116
172	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens														
	Q05639 EF12_HUMAN Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1).- Homo sapiens														

	73	54	50457	9.10	2%	1	Cytoplasmic	IGGIGTVPVGR	9.75	8.27	1.48	1025.61	1025.58	0.03	30
173	P09211 GTP_HUMAN (GSTP1..)Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GS- Homo sapiens														
	73	60	23442	5.44	9%	1	?	ALPGQLKPFETLLSQNQGGK	8.64	8.27	0.37	2126.16	2126.42	-0.26	122
174	P04406 G3P2_HUMAN (GAPD)Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (- Homo sapiens														
	73	55	36073	8.58	4%	1	Cytoplasmic	GALQNIIPASTGAAK	8.75	8.27	0.48	1411.79	1411.74	0.05	36
175	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens P03996 ACTA_HUMAN (ACTA2..)Actin, aortic smooth muscle (Alpha-actin 2).- Homo sapiens P04270 ACTC_HUMAN (ACTC..)Actin, alpha cardiac.- Homo sapiens P12718 ACTH_HUMAN (ACTG2..)Actin, gamma-enteric smooth muscle (Alpha-actin 3).- Homo sapiens														
	73	45	41736	5.29	2%	1	Cytoplasmic	AVFPSIVGR	9.79	8.27	1.52	945.55	945.62	-0.07	72
176	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	73	38	83429	4.97	1%	1	Cytoplasmic	ALLFIPR	9.79	8.27	1.52	829.53	829.50	0.03	36
177	P07195 LDHB_HUMAN L-lactate dehydrogenase B chain.- Homo sapiens														
	73	Sequest / 1.8592	36507	5.72	2%	1	Cytoplasmic	FIIPQIVK	8.75	8.27	0.48	957.61	957.49	0.12	129
178	P39019 RS19_HUMAN 40S ribosomal protein S19.- Homo sapiens														
	73	Sequest / 1.7168	15929	10.31	5%	1	Cytosolic small ribosomal subunit	ALAAFLK	8.80	8.27	0.53	733.46	733.39	0.07	97
179	P04720 EF11_HUMAN (EEF1A1..)Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact- Homo sapiens Q05639 EF12_HUMAN Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1).- Homo sapiens														
	77	55	50457	9.10	2%	1	Cytoplasmic	IGGIGTVPVGR	9.75	8.63	1.12	1025.61	1025.64	-0.03	28
180	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens P03996 ACTA_HUMAN (ACTA2..)Actin, aortic smooth muscle (Alpha-actin 2).- Homo sapiens P04270 ACTC_HUMAN (ACTC..)Actin, alpha cardiac.- Homo sapiens P12718 ACTH_HUMAN (ACTG2..)Actin, gamma-enteric smooth muscle (Alpha-actin 3).- Homo sapiens														
	77	58	41736	5.29	4%	3	Cytoplasmic	AVFPSIVGR	9.79	8.63	1.16	945.55	945.62	-0.07	72
								GILTLK	8.75	8.63	0.12	644.43	644.43	0.00	7
								AVFPSIVGRPR	12.00	8.63	3.37	1198.71	1198.96	-0.25	212
181	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	77	42	58349	7.95	1%	1	Cytosol	APIIAVTR	9.79	8.63	1.16	840.53	840.60	-0.07	82
182	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens														
	77	26	83429	4.97	1%	1	Cytoplasmic	ALLFIPR	9.79	8.63	1.16	829.53	829.52	0.01	12
183	P02570 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin).- Homo sapiens P02571 ACTG_HUMAN Actin, cytoplasmic 2 (Gamma-actin).- Homo sapiens P02568 ACTS_HUMAN Actin, alpha skeletal muscle (Alpha-actin 1).- Homo sapiens P03996 ACTA_HUMAN (ACTA2..)Actin, aortic smooth muscle (Alpha-actin 2).- Homo sapiens P04270 ACTC_HUMAN (ACTC..)Actin, alpha cardiac.- Homo sapiens P12718 ACTH_HUMAN (ACTG2..)Actin, gamma-enteric smooth muscle (Alpha-actin 3).- Homo sapiens														
	82	65	41736	5.29	4%	2	Cytoplasmic	AVFPSIVGRPR	12.00	9.08	2.92	1198.71	1198.70	0.01	5
								GILTLK	8.75	9.08	-0.33	644.43	644.35	0.08	131
184	P14618 KPY1_HUMAN (PKM2..)Pyruvate kinase, M1 isozyme (EC 2.7.1.40) (Pyruvate kinase mu- Homo sapiens P14786 KPY2_HUMAN (PKM2..)Pyruvate kinase, M2 isozyme (EC 2.7.1.40).- Homo sapiens														
	82	37	58349	7.95	1%	1	Cytosol	APIIAVTR	9.79	9.08	0.71	840.53	840.48	0.05	60

185	P08238 HS9B_HUMAN (HSPCB..)Heat shock protein HSP 90-beta (HSP 84) (HSP 90).- Homo sapiens																
		82	Sequest / 2.0522	83429	4.97	1%	1	Cytoplasmic	ALLFIPR	9.79	9.08	0.71	829.53	829.47	0.06	72
										Average pI error ±		0.86		Average ppm error ±		103

(a) Mascot score unless identified by other means. The cross correlation score has been listed for Sequest identifications. De novo refers to manual interpretation of the MS/MS data.

(b) Based on the sequence in the database entry.

(c) Where possible, this information was extracted from the protein annotation.

(d) Amino acid sequence in one-letter notation. All cysteines are modified by carboxymethylation (+58Da). Ac = N-terminal acetylation (+42Da). Me = Methylation (+14Da). Oxidation (M) indicates methionine sulphoxide (+16Da).

(e) Theoretical values obtained from Protein Prospector. Clauser K. R., Baker P. R. and Burlingame A. L., Role of accurate mass measurement (+/- 10 ppm) in protein identification strategies employing MS or MS/MS and database searching. Anal. Chem.,1999, 71, pp 2871-2882

(f) The pK value for carboxymethylated cysteine of 4.00 taken from the pK value of aspartic acid was used for all calculations of peptides containing cysteine

(g) Experimental values were obtained using only the 2+ parent ion where possible.

(h) Multiple protein entries are listed where the peptide sequence coverage did not allow for the discrimination of protein isoforms

(i) Methylated-histidine is shown as (me-H). Yao X, Grade S, Wriggers W, Rubenstein PA. His(73), often methylated, is an important structural determinant for actin. A mutagenic analysis of HIS(73) of yeast actin. J Biol Chem. 1999, 274 pp 37443-37449.