

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
193	Q02788	(CA26_MOUSE) Collagen alpha 2(VI) chain precursor	Mouse	10/15	42	13%	6.1	6.0	93803	109743
194	Q02788	(CA26_MOUSE) Collagen alpha 2(VI) chain precursor	Mouse	9/15	56	11%	6.2	6.0	93803	109743
195	Q02788	(CA26_MOUSE) Collagen alpha 2(VI) chain precursor	Mouse	8/18	46	11%	6.2	6.0	93803	109743
196	Q02788	(CA26_MOUSE) Collagen alpha 2(VI) chain precursor	Mouse	11/20	34	12%	6.3	6.0	93803	109743
260	Q99MD9	(Q99MD9) Testis-specific histone binding protein NASP	Mouse	15/17	41	28%	4.0	4.4	92145	84059
339	Q64727	(VINC_MOUSE) Vinculin (Metavinculin)	Mouse	21/30	34	24%	6.1	5.8	89424	116513
369	Q6P5G9	(Q6P5G9) Hypothetical protein	Mouse	6/7	19	10%	4.8	4.9	88487	89185
393	Q61316	(HS74_MOUSE) Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2)	Mouse	19/20	43	28%	5.2	5.2	87064	94073
412	Q61316	(HS74_MOUSE) Heat shock 70-related protein APG-2	Mouse	19/21	49	28%	5.2	5.2	87064	94073
436	P20918	(PLMN_MOUSE) Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin]	Mouse	9/9	29	15%	6.7	6.2	86712	90723
442	P08113	(ENPL_MOUSE) Endoplasmin precursor (Endoplasmic reticulum protein 99) (94 kDa glucose-regulated protein) (GRP94) (ERP99) (Polymorphic tumor rejection antigen 1)(Tumor rejection antigen gp96)	Mouse	11/13	34	14%	4.7	4.7	85873	92418
507	P08113	(ENPL_MOUSE) Endoplasmin precursor (Endoplasmic reticulum protein 99) (94 kDa glucose-regulated protein) (GRP94) (ERP99) (Polymorphic tumor rejection antigen 1)(Tumor rejection antigen gp96)	Mouse	17/18	53	24%	4.7	4.7	83202	92418

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527	Q9WU78-02-00-00 (PDC61_MOUSE)	Splice isoform 3; Variant Displayed; Conflict Displayed; from Q9WU78 Programmed cell death 6 interacting protein (ALG-2 interacting protein X) (ALG-2 interacting protein 1)(E2F1-inducible protein)(Eig2)	Mouse	10/13	60	16%	6.6	6.2	83405	97269
539	P48722-00-00-00 (HS74L_MOUSE)	Splice isoform 1; Variant Displayed; Conflict Displayed; from P48722 Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-related protein APG-1)	Mouse	14/15	43	23%	5.6	5.5	83405	95178
551	P48722-00-00-00 (HS74L_MOUSE)	Splice isoform 1; Variant Displayed; Conflict Displayed; from P48722 Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-related protein APG-1)	Mouse	21/27	56	32%	5.7	5.5	82731	94322
563	P58252 (EF2_MOUSE)	Elongation factor 2 (EF-2)	Mouse	12/16	22	17%	7.4	6.4	82731	95122
569	P58252 (EF2_MOUSE)	Elongation factor 2 (EF-2)	Mouse	7/9	39	11%	7.2	6.4	82531	95122
602	Q01853 (TERA_MOUSE)	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	Mouse	10/18	65	17%	5.2	5.1	80093	89252
603	Q01853 (TERA_MOUSE)	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	Mouse	6/13	51	9%	5.3	5.1	79963	89252
611	P17156 (HS72_MOUSE)	Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	6/8	59	12%	5.6	5.6	80941	69698
643	Q64139 (Q64139)	CBP-140 (Fragment)	Mouse	6/11	56	13%	4.5	4.7	78933	72265
653	P07901 (HS90A_MOUSE)	Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	10/16	57	14%	5.2	4.9	79640	85003
675	P13020 (GELS_MOUSE)	Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin)	Mouse	6/12	28	12%	6.1	5.8	78614	86287

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686	P07901	(HS9A_MOUSE) Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	9/10	56	13%	5.2	4.9	77790	84604
709	P48722-00-00-00	(HS74L_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from P48722 Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-rela	Mouse	13/24	45	22%	5.5	5.5	76540	95178
710	P48722-01-00-00	(HS74L_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from P48722 Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-rela	Mouse	6/8	17	9%	5.5	5.7	76913	92935
742	P07901	(HS90A_MOUSE) Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	7/10	37	10%	5.2	4.9	76107	85003
750	P07901	(HS9A_MOUSE) Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	16/22	36	22%	5.1	4.9	76169	84604
755	gj 18079339	Aconitase 2, mitochondrial [Mus musculus]	Mouse	9/12	44	17%	8.1	8.1	75248	86151
757	P13020	(GELS_MOUSE) Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin)	Mouse	5/5	48	10%	6.0	5.8	75799	85888
783	gj 18079339	Aconitase 2, mitochondrial	Mouse	8/11	15	15%	7.9	8.1	75187	86151
786	gj 18079339	Aconitase 2, mitochondrial	Mouse	7/7	34	12%	7.8	8.1	75248	86151
791	Q99PF5	(FUBP2_RAT) Far upstream element binding protein 2 (FUSE binding protein 2) (KH type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting protein 1) (MAR	Rat	10/10	33	19%	7.2	6.4	74702	74466
792	Q91VR5	(Q91VR5) DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Mouse	5/9	46	11%	7.5	6.8	74762	83474

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795	Q8CAQ8-01-00-00 (IMMT_MOUSE)	Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8CAQ8 Mitochondrial inner membrane protein (Mitofilin)	Mouse	17/23	31	30%	6.2	6.2	74159	82878
802	Q61496 (DDX4_MOUSE)	DEAD-box protein 4 (VASA homolog) (Mvh)	Mouse	17/25	18	32%	5.9	5.8	74039	76423
803	Q61496 (DDX4_MOUSE)	DEAD-box protein 4 (VASA homolog) (Mvh)	Mouse	12/14	39	23%	5.9	5.8	73739	77278
807	P07901 (HS9A_MOUSE)	Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	12/16	54	17%	5.1	4.9	74219	84604
823	Q92111 (TRFE_MOUSE)	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin)	Mouse	16/19	34	28%	6.8	6.9	73441	76674
830	Q92111 (TRFE_MOUSE)	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin)	Mouse	19/23	54	29%	7.0	6.9	72731	76674
835	Q92111 (TRFE_MOUSE)	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin)	Mouse	18/19	17	24%	6.9	6.9	73144	76674
844	Q92111 (TRFE_MOUSE)	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin)	Mouse	14/17	56	22%	7.2	6.9	72554	76674
852	P26040 (EZRI_MOUSE)	Ezrin (p81) (Cytovillin) (Villin 2)	Mouse	5/8	39	9%	6.2	5.8	72731	69233
876	Q91VD9 (NUAM_MOUSE)	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-75Kd) (CI-75Kd)	Mouse	8/11	49	18%	5.4	5.5	71910	80724
885	P48722-00-00-00 (HS4L_MOUSE)	Splice isoform 1; Variant Displayed; Conflict Displayed; from P48722 Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat shock 70-related protein APG-1)	Mouse	8/13	43	11%	5.9	5.5	71736	94322

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887	Q8CAQ8-02-00-00 (IMMT_MOUSE)	Splice isoform 3; Variant Displayed; Conflict Displayed; from Q8CAQ8 Mitochondrial inner membrane protein (Mitofilin)	Mouse	12/16	26	24%	6.7	6.8	71446	78679
891 ^b	Q61316 (HS74_MOUSE)	Heat shock 70-related protein APG-2	Mouse	12/14	25	18%	4.9	5.2	71214	94073
921	Q91VD9 (NUAM_MOUSE)	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-75Kd) (CI-75Kd)	Mouse	9/12	51	19%	5.3	5.5	70013	80724
962	O88487 (DYI2_MOUSE)	Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)	Mouse	5/9	55	14%	5.3	5.2	68776	68352
965	Q8K2D4 (Q8K2D4)	Thimet oligopeptidase 1	Mouse	9/10	57	16%	5.9	5.7	68943	78775
1005	P20029 (GR78_MOUSE)	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	11/14	25	23%	5.1	5.1	66206	72377
1012	Q9CZD3 (SYG_MOUSE)	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS)	Mouse	7/15	67	13%	6.1	6.2	67342	82624
1018	P20029 (GR78_MOUSE)	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	17/17	31	34%	5.1	5.1	66367	72377
1040	P29341 (PAB1_MOUSE)	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1)	Mouse	5/6	51	10%	7.6	9.5	66853	70598
1052 ^b	gi 51708124	PREDICTED: similar to GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase) [Mus musculus]	Mouse	11/14	23	18%	6.8	8.4	66206	91506
1120	Q91WJ8-00-00-00 (FUB1_MOUSE)	Splice isoform 1; Variant Displayed; Conflict Displayed; from Q91WJ8 Far upstream element binding protein 1 (FUSE binding protein 1) (FBP)	Mouse	6/8	32	12%	7.5	7.7	64773	68497

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1125	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	16/19	34	33%	5.7	5.8	63166	68648
1131	Q9CQN1	(TRAL_MOUSE) Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (Tumor necrosis factor type 1 receptor associated protein) (TRAP-1) (TNFR--associated protein 1)	Mouse	7/11	35	14%	6.1	6.3	64668	80159
1134	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	8/10	53	13%	5.5	5.6	62606	69698
1135	Q64521	(GPD_M_MOUSE) Glycerol-3-phosphate dehydrogenase, mitochondrial precursor (EC 1.1.99.5) (GPD-M) (GPDH-M)	Mouse	16/20	28	26%	6.2	6.2	64302	80848
1139	P63017	(HS7C_MOUSE) Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	Mouse	9/14	45	18%	5.4	5.4	63269	70827
1144	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	10/15	58	19%	5.6	5.8	63269	68648
1150	P63017	(HSP7C_MOUSE) Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	Mouse	7/13	55	17%	5.3	5.4	63835	71055
1178	Q99K10	(Q99K10) Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)	Mouse	9/10	19	13%	7.0	8.1	63577	86151
1195	Q8C633	(Q8C633) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4922502J23	Mouse	8/10	40	37%	3.6	4.1	62809	42390
1221	P16627	(HS7L_MOUSE) Heat shock 70 kDa protein 1L (Heat shock 70 kDa protein 1-like) (Heat shock 70 kDa-like protein 1) (Spermatid-specific heat shock protein 70)	Mouse	14/16	40	26%	6.1	5.9	62252	70593
1269 ^b	Q62318-00-00-00	(TF1B_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from Q62318 Transcription intermediary factor 1-beta (TIF1-beta) (Tripartite motif protein 28)(KRAB-A interacting protein)(KRIP-1)	Mouse	6/12	20	10%	4.8	5.5	61405	90558

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1314 ^b	O35135	(O35135) Outer dense fiber protein	Mouse	6/7	39	11%	6.3	6.3	59759	71404
1328	O8R081	(ROL_MOUSE) Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	Mouse	10/18	46	23%	7.6	6.7	58875	60085
1362	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	9/12	49	19%	5.6	5.8	58618	68648
1368	O08553	(DPY2_MOUSE) Dihydropyrimidinase related protein-2 (DRP-2) (ULIP 2 protein)	Mouse	10/14	47	25%	6.5	6.0	58157	62132
1381	Q60864	(STI1_MOUSE) Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (mSTI1)	Mouse	10/11	40	26%	6.9	6.4	57801	63170
1382 ^b	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	9/10	29	17%	5.2	5.1	57953	72377
1389	Q60864	(STIP1_MOUSE) Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (mSTI1)	Mouse	10/15	56	23%	6.7	6.4	57903	63170
1395 ^c	P17156	(HSP72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	6/8	40	11%	4.4	5.6	57046	69983
1400	Q9CWJ9	(PUR9_MOUSE) Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformyl	Mouse	8/10	32	19%	6.9	6.3	57196	64117
1401	P14211	(CRTC_MOUSE) Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60)	Mouse	10/14	32	29%	4.1	4.3	56252	47965
1414	P06801	(MAOX_MOUSE) NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1)	Mouse	8/14	63	20%	7.5	7.2	56449	63958
1455	P61979-02-00-00	(HNRPK_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from P61979 Heterogeneous nuclear ribonucleoprotein K	Mouse	5/9	51	14%	5.3	5.7	56055	48708
1456	P61979	(P61979) Heterogeneous nuclear ribonucleoprotein K	Mouse	7/13	47	17%	5.4	5.4	56203	51230

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1460	O35098	(DPY4_MOUSE) Dihydropyrimidinase related protein-4 (DRP-4) (Collapsin response mediator protein 3) (CRMP-3) (UNC33-like phosphoprotein 4) (ULIP4 protein)	Mouse	4/6	32	11%	7.4	6.5	56449	62493
1467	P61979-02-00-00	(ROK_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from P61979 Heterogeneous nuclear ribonucleoprotein K	Mouse	12/18	58	25%	5.5	5.7	55859	48480
1473	P61979-02-00-00	(ROK_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from P61979 Heterogeneous nuclear ribonucleoprotein K	Mouse	6/11	33	16%	5.4	5.7	56153	48480
1474	Q9JHU9	(Q9JHU9) Myo-inositol 1-phosphate synthase A1	Mouse	9/14	64	17%	6.5	6.0	55908	61520
1477	Q8VC30	(Q8VC30) CDNA sequence BC021917	Mouse	8/9	21	22%	6.9	6.4	55908	59938
1492	Q9JHU9	(Q9JHU9) Myo-inositol 1-phosphate synthase A1	Mouse	7/13	54	19%	6.3	6.0	55614	61520
1499	Q9JHU9	(Q9JHU9) Myo-inositol 1-phosphate synthase A1	Mouse	5/8	56	11%	5.9	6.0	55517	61520
1505 ^b	Q01853	(TERA_MOUSE) Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	Mouse	15/22	42	23%	6.0	5.1	55517	89252
1516	P80317	(TCPZ_MOUSE) T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1)	Mouse	6/6	21	13%	5.2	6.7	55226	57837
1539	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	8/13	58	15%	7.3	5.6	54936	69698
1546	P52480	(KPYM_MOUSE) Pyruvate kinase, isozyme M2	Mouse	9/15	53	24%	5.5	7.4	54696	57719
1554 ^b	O62188	(DPY3_MOUSE) Dihydropyrimidinase related protein-3 (DRP-3) (Unc-33-like phosphoprotein) (ULIP protein)	Mouse	9/13	44	21%	8.0	6.0	53934	61897

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1557	Q9R0S3	(MM17_MOUSE) Matrix metalloproteinase-17 precursor (EC 3.4.24.-) (MMP-17) (Membrane-type matrix metalloproteinase 4) (MT-MMP 4) (Membrane-type-4 matrix metalloproteinase)(MT4-MMP)	Mouse	4/6	50	7%	6.3	5.9	54124	64279
1560 ^b	P80316	(TCPE_MOUSE) T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)	Mouse	10/15	34	22%	6.4	5.7	54124	59586
1567	P24549	(AL1A1_MOUSE) Retinal dehydrogenase 1 (EC 1.2.1.36) (RALDH1) (RALDH 1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic) (ALHDII)	Mouse	5/11	22	12%	5.9	7.9	53183	54929
1569	Q8C166	(CNE1_MOUSE) Copine I	Mouse	4/9	64	7%	8.3	5.4	54076	58849
1586	P11983	(TCP2_MOUSE) T-complex protein 1, alpha subunit B (TCP-1-alpha) (CCT-alpha) (Tailless complex polypeptide 1B) (TCP-1-B)	Mouse	10/15	34	12%	5.4	5.8	53934	60867
1589	P80316	(TCPE_MOUSE) T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)	Mouse	7/11	20	18%	6.1	5.7	53043	59586
1594 ^b	P80316	(TCPE_MOUSE) T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon)	Mouse	11/22	41	24%	5.8	5.7	53370	59586
1603	P63038	(CH60_MOUSE) 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1)(HSP-65)	Mouse	11/12	39	26%	5.5	5.9	52351	60917
1620	P63038	(CH60_MOUSE) 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1)(HSP-65)	Mouse	7/9	89	19%	5.4	5.9	52904	60917
1624	P42932	(TCPQ_MOUSE) T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta)	Mouse	8/10	52	17%	5.6	5.4	52534	59386

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1639 ^b	gi 51767886	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta) [Mus musculus]	Mouse	15/19	32	26%	7.6	8.7	52442	72640
1653	P80313	(TCPH_MOUSE) T-complex protein 1, eta subunit (TCP-1-eta) (CCT-eta)	Mouse	6/11	29	15%	8.3	8.0	51486	60127
1657	Q8BTS4	(NUP54_MOUSE) Nucleoporin p54 (54 kDa nucleoporin)	Mouse	11/13	20	24%	7.0	6.5	51985	55812
1659	P05214	(TBA3_MOUSE) Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) (Alpha-tubulin isotype M-alpha-3/7)	Mouse	7/13	72	23%	5.2	5.0	51803	49928
1661	Q00612	(G6P1_MOUSE) Glucose-6-phosphate 1-dehydrogenase X (EC 1.1.1.49) (G6PD)	Mouse	6/9	46	15%	6.5	6.1	51803	59094
1664	P05213	(TBA2_MOUSE) Tubulin alpha-2 chain (Alpha-tubulin 2)	Mouse	12/15	38	41%	5.2	4.9	51803	50120
1666	P27773	(PDA3_MOUSE) Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57)	Mouse	13/23	54	30%	6.0	6.0	51081	56586
1671	P27773	(PDA3_MOUSE) Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57)	Mouse	8/11	29	17%	6.1	6.0	51712	56586
1672	P80315	(TCPD_MOUSE) T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) (A45)	Mouse	8/10	61	18%	8.6	8.2	51576	58543
1691	P27773	(PDA3_MOUSE) Protein disulfide isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57)	Mouse	11/15	54	25%	5.9	6.0	50903	56586
1715	O08749	(DLDH_MOUSE) Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase)	Mouse	8/8	46	20%	7.6	8.0	50503	54748
1727	Q8K0E8	(Q8K0E8) Fibrinogen, B beta polypeptide	Mouse	10/14	26	29%	6.2	6.7	50503	55402
1730	Q8R086	(SUOX_MOUSE) Sulfite oxidase, mitochondrial precursor	Mouse	5/5	74	12%	5.8	5.7	50680	54413

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
1737	O08749	(DLDH_MOUSE) Dihydropyridine dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydropyridine dehydrogenase)	Mouse	7/9	19	21%	7.1	8.0	49974	54178
1775	P09103	(PDI_MOUSE) Protein disulfide isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase beta subunit) (Cellular thyroid hormone binding protein) (p55) (Erp59)	Mouse	11/12	40	25%	4.6	4.8	49668	57108
1777	Q61753	(SERA_MOUSE) D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (3-PGDH) (A10)	Mouse	8/11	48	17%	6.5	6.1	49538	56418
1778	P61979-02-00-00	(ROK_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from P61979 Heterogeneous nuclear ribonucleoprotein K	Mouse	6/11	36	14%	5.5	5.7	49843	48480
1786	Q99KP6-00-00-00	(PR19_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from Q99KP6 PRP19/PSO4 homolog (Nuclear matrix protein 200) (Nuclear matrix protein SNEV)	Mouse	7/13	63	22%	6.6	6.1	48934	55661
1803	P05213	(TBA2_MOUSE) Tubulin alpha-2 chain (Alpha-tubulin 2)	Mouse	12/18	33	45%	5.1	4.9	48379	50120
1804	P05214	(TBA3_MOUSE) Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7)	Mouse	9/10	46	30%	5.2	5.0	48295	49928
1812	P61979-02-00-00	(ROK_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from P61979 Heterogeneous nuclear ribonucleoprotein K	Mouse	6/10	28	18%	5.8	5.7	49278	48480
1815	Q62148	(DHA2_MOUSE) Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	Mouse	9/16	40	18%	5.6	5.8	49106	54691
1821	P07758	(A1T1_MOUSE) Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1) (Alpha-1 protease inhibitor 1) (Alpha-1-antiproteinase) (AAT)	Mouse	7/15	30	24%	4.5	5.4	48210	45974

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
1825	P30416	(FKB4_MOUSE) FK506-binding protein 4 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein)(52 kDa FK506 binding protein)(FKBP59)	Mouse	10/11	49	32%	5.7	5.5	48720	51409
1832	P24547-00-01-00	(IMD2_MOUSE) Splice isoform Displayed; Variant Displayed; Conflict Displayed; from P24547 Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP dehydrogenase 2)(IMPDH-II)(IMPD 2)	Mouse	6/9	10	13%	7.6	6.8	48252	55868
1838	Q00896	(A1AT3_MOUSE) Alpha-1-antitrypsin 1-3 precursor (Serine protease inhibitor 1-3) (Alpha-1 protease inhibitor 3)	Mouse	6/8	36	22%	4.6	5.3	47706	45996
1844	Q8JZK9	(Q8JZK9) Hmgcs1 protein (3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1)	Mouse	7/12	17	12%	5.9	5.7	48252	58160
1847	P80314	(TCPB_MOUSE) T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta)	Mouse	9/12	32	20%	6.4	6.0	47372	57310
1849	P21614	(VTDB_MOUSE) Vitamin D-binding protein precursor (DBP) (Group-specific component) (Gc-globulin) (VDB)	Mouse	10/14	27	30%	5.3	5.4	48126	53565
1853 ^b	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	11/17	42	24%	5.4	5.6	48126	69698
1856	Q8CIB4	(Q8CIB4) Aldehyde dehydrogenase family 6, subfamily A1	Mouse	12/17	51	29%	7.8	8.3	48041	58438
1857	Q00896	(A1T3_MOUSE) Alpha-1-antitrypsin 1-3 precursor (Serine protease inhibitor 1-3) (Alpha-1 protease inhibitor 3)	Mouse	5/12	49	20%	4.6	5.3	47041	45825
1862	Q9DBF1	(D7A1_MOUSE) Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)	Mouse	4/9	21	12%	6.4	6.0	47372	55935
1867 ^b	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	8/10	50	15%	5.5	5.8	47831	68648

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
1885	P24549	(DHA1_MOUSE) Aldehyde dehydrogenase 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)	Mouse	13/14	63	30%	8.4	7.9	46459	54302
1891	Q9DAH3	(Q9DAH3) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700010L19	Mouse	11/15	29	31%	6.0	5.8	47331	52571
1892	P68372	(TBBX_MOUSE) Tubulin beta-? Chain	Mouse	13/19	34	30%	5.0	4.8	46436	50255
1897 ^c	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	10/15	42	19%	5.6	5.1	46976	72377
1899	P24549	(DHA1_MOUSE) Aldehyde dehydrogenase 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)	Mouse	12/16	69	27%	8.1	7.9	46506	54302
1901	P62814	(VAB2_MOUSE) Vacuolar ATP synthase subunit B, brain isoform (EC 3.6.3.14) (V-ATPase B2 subunit) (Vacuolar proton pump B isoform 2) (Endomembrane proton pump 58 kDa subunit)	Mouse	9/17	60	21%	5.7	5.6	46976	56515
1902 ^d	Q03265	(ATPA_MOUSE) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	15/16	31	17%	8.5	9.2	46483	59716
1902 ^d	P24549	(DHA1_MOUSE) Aldehyde dehydrogenase 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)	Mouse		57	17%	8.5	7.9	46483	54302
1909	gj 56270548	Aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	Mouse	8/13	29	21%	6.9	6.6	46694	58087
1912	Q03265	(ATPA_MOUSE) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	7/11	45	16%	8.6	9.2	46366	59716
1930	P17563	(SBP1_MOUSE) Selenium-binding protein 1 (56 kDa selenium-binding protein) (SP56)	Mouse	17/24	64	43%	6.1	6.0	46529	52318

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
1931	P24549	(DHA1_MOUSE) Aldehyde dehydrogenase 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)	Mouse	7/11	51	21%	7.9	7.9	46459	54302
1938	P05214	(TBA3_MOUSE) Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7)	Mouse	5/7	64	16%	5.2	5.0	46576	49928
1963	Q61753	(SERA_MOUSE) D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (3-PGDH) (A10)	Mouse	8/13	14	22%	6.7	6.1	46087	56418
1970	Q63836	(SBP2_MOUSE) Selenium-binding protein 2 (56 kDa acetaminophen-binding protein) (AP56)	Mouse	12/20	70	25%	5.9	5.8	46203	52594
1971	P26443	(DHE3_MOUSE) Glutamate dehydrogenase, mitochondrial precursor (EC 1.4.1.3) (GDH)	Mouse	7/9	24	16%	7.5	8.1	46064	61298
1988 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	8/14	52	18%	5.4	5.8	45971	68648
1990	Q9D1A2	(CGL1_MOUSE) Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1) (CNDP dipeptidase 2)	Mouse	8/12	50	21%	5.5	5.4	45878	53190
1991	Q60972	(RBBP4_MOUSE) Chromatin assembly factor 1 subunit C (CAF-1 subunit C) (Chromatin assembly factor I p48 subunit) (CAF-I 48 kDa subunit) (CAF-Ip48) (Retinoblastoma binding protein p48)(Retinoblastoma-binding protein 4)(RBBP-4)	Mouse	7/14	37	20%	4.6	5.0	45855	51738
1996	Q8VCM7	(Q8VCM7) Fibrinogen, gamma polypeptide	Mouse	9/12	60	31%	5.3	5.5	45925	50044
2001	Q9Z2W0	(DNPEP_MOUSE) Aspartyl aminopeptidase (EC 3.4.11.21)	Mouse	4/4	25	12%	7.4	6.7	45832	52704
2009	P47738	(ALDH2_MOUSE) Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (AHD-M1) (ALDH1) (ALDH-E2)	Mouse	11/20	38	20%	7.7	7.5	45740	57015
2012	O35737	(ROH1_MOUSE) Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	Mouse	13/17	49	45%	6.0	5.9	45534	49037

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2020	P47738	(DHAM_MOUSE) Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (AHD-M1) (ALDHI) (ALDH-E2)	Mouse	8/12	34	21%	6.7	7.5	45146	56502
2029	P47738	(ALDH2_MOUSE) Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (AHD-M1) (ALDHI) (ALDH-E2)	Mouse	6/10	35	14%	8.1	7.5	45442	57015
2044	P47738	(DHAM_MOUSE) Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (AHD-M1) (ALDHI) (ALDH-E2)	Mouse	4/7	29	10%	7.2	7.5	45078	56502
2064	Q8VCM7	(Q8VCM7) Fibrinogen, gamma polypeptide	Mouse	10/12	58	29%	5.5	5.5	44829	50044
2067	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	19/20	57	37%	5.1	5.2	44335	56265
2075	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	13/17	54	36%	5.1	5.2	44581	56265
2082	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	10/14	44	31%	5.1	5.2	44492	56265
2086	P50431	(GLYC_MOUSE) Serine hydroxymethyltransferase, cytosolic (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT)	Mouse	8/11	62	16%	7.0	6.5	44649	53065
2090 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	9/10	62	19%	5.3	5.8	44626	68648
2093	Q99KJ8	(DCT2_MOUSE) Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide) (Dynamitin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein 23-48K) (GMP23-48K)	Mouse	9/12	31	38%	5.2	5.1	44492	43959
2095	Q60973	(RBB7_MOUSE) Histone acetyltransferase type B subunit 2 (Retinoblastoma binding protein p46) (Retinoblastoma-binding protein 7) (RBBP-7)	Mouse	5/10	14	20%	5.0	4.9	44514	47760
2101	Q922R8	(Q922R8) Txndc7 protein	Mouse	7/9	45	20%	5.2	5.0	44135	48469

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2115 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	10/13	17	18%	6.0	5.8	44268	68648
2117 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	7/11	33	15%	5.9	5.8	44313	70700
2125	Q9WTM5	(RUVB2_MOUSE) RuvB-like 2 (EC 3.6.1.-) (p47 protein)	Mouse	11/18	27	24%	5.6	5.5	43936	51252
2128	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	6/11	34	21%	5.3	5.3	43869	41766
2135	Q6P8X1	(Q6P8X1) Sorting nexin 6	Mouse	7/11	65	20%	6.0	5.7	43891	46891
2153 ^d	Q9DBC7	(KAP0_MOUSE) cAMP-dependent protein kinase type I-alpha regulatory subunit	Mouse	12/16	53	20%	5.3	5.3	43452	43312
2153 ^d	gij58476100	Hnrpf protein [Mus musculus]	Mouse		43	27%	5.3	5.3	43452	43943
2170	Q9JHX6	(Q9JHX6) Allantoicase (EC 3.5.3.4)	Mouse	5/7	35	18%	6.4	5.9	43539	46633
2174	P68373	(TBA6_MOUSE) Tubulin alpha-6 chain (Alpha-tubulin 6) (Alpha-tubulin isotype M-alpha-6)	Mouse	9/10	21	26%	6.2	5.0	43430	49877
2187	P05064	(ALDOA_MOUSE) Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase 1)	Mouse	7/10	23	29%	8.4	8.4	43299	39656
2197	Q9DBC7	(KAP0_MOUSE) cAMP-dependent protein kinase type I-alpha regulatory subunit	Mouse	9/12	41	26%	5.4	5.3	43212	43312
2200	P17182	(ENOA_MOUSE) Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	Mouse	10/15	42	32%	6.7	6.4	42909	46980
2203	Q9Z2X1	(Q9Z2X1) Heterogeneous nuclear ribonucleoprotein F	Mouse	11/14	56	33%	5.2	5.3	42974	46043
2219	P24549	(DHA1_MOUSE) Aldehyde dehydrogenase 1A1 (EC 1.2.1.3) (Aldehyde dehydrogenase, cytosolic) (ALDH class 1) (ALHDII) (ALDH-E1)	Mouse	9/12	24	25%	8.1	7.9	42930	54302

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2223	P54775	(PRS6_MOUSE) 26S protease regulatory subunit 6B (MIP224) (MB67 interacting protein) (TAT-binding protein-7) (TBP-7) (CIP21)	Mouse	12/16	58	28%	5.2	5.2	42650	47366
2224	Q9Z2X1	(Q9Z2X1) Heterogeneous nuclear ribonucleoprotein F	Mouse	7/12	31	27%	5.2	5.3	42822	46043
2225	P54869	(HMCM_MOUSE) Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Fragment)	Mouse	10/15	38	23%	7.7	8.0	42736	53752
2227	P54869	(HMCM_MOUSE) Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Fragment)	Mouse	7/9	45	18%	8.0	8.0	42565	54265
2231	P17182	(ENOA_MOUSE) Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	Mouse	11/19	43	35%	7.3	6.4	42801	46980
2236	Q61598-01-00-00	(GDIC_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q61598 Rab GDP dissociation inhibitor beta-2 (Rab GDI beta-2) (GDI-3)	Mouse	9/15	53	30%	6.1	6.5	42608	47084
2241	P17182	(ENOA_MOUSE) Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	Mouse	9/20	25	27%	7.4	6.4	42586	46980
2249	Q9Z2N8	(AL6A_MOUSE) Actin-like protein 6A (53 kDa BRG1-associated factor A) (Actin-related protein Baf53a)	Mouse	9/13	49	19%	5.4	5.4	42565	47931
2269	P17182	(ENOA_MOUSE) Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	Mouse	7/14	51	25%	6.5	6.4	42372	46980
2275	P46471	(PRS7_MOUSE) 26S protease regulatory subunit 7 (MSS1 protein)	Mouse	24/30	51	52%	5.9	5.7	42033	48486
2276	P68373	(TBA6_MOUSE) Tubulin alpha-6 chain (Alpha-tubulin 6) (Alpha-tubulin isotype M-alpha-6)	Mouse	11/12	29	26%	6.3	5.0	42181	49877

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2283	Q8VEH6	(Q8VEH6) Dopamine-responsive protein	Mouse	7/10	48	23%	4.9	4.8	42181	44201
2285	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	5/10	36	15%	5.4	5.3	42075	41766
2295	Q9QY83	(AL7B_MOUSE) Actin-like protein 7B (Actin-like-7-beta) (Actin-like 7B) (T-actin 1) (Testis-specific actin 1)	Mouse	6/13	46	22%	5.4	5.5	42033	46486
2297	Q9ERW2	(Q9ERW2) PTB-associated splicing factor (Fragment)	Mouse	7/11	62	18%	7.2	7.4	42117	43924
2299	Q9CZ13	(UCR1_MOUSE) Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2)	Mouse	10/12	55	31%	5.5	5.8	41822	53420
2306 ^b	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	9/12	31	15%	6.5	5.8	41738	70700
2308	Q9CXT8	(MPPB_MOUSE) Mitochondrial processing peptidase beta subunit, mitochondrial precursor (EC 3.4.24.64) (Beta-MPP) (P-52)	Mouse	8/9	40	26%	6.0	6.6	41843	55378
2324	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	6/11	47	18%	5.3	5.3	41591	42108
2328	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	5/8	42	21%	5.3	5.3	41507	41710
2329	Q9DAJ2	(TEK1_MOUSE) Tektin-1	Mouse	7/8	50	16%	5.6	5.5	41654	48953
2340	Q9JII5-01-00-00	(DZP1_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q9JII5 DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1)	Mouse	7/16	47	27%	9.4	8.7	41341	43287
2343	Q9D1O6	(TXN4_MOUSE) Thioredoxin domain containing protein 4 precursor (Endoplasmic reticulum protein ERp44)	Mouse	8/12	30	26%	5.2	5.1	41424	47222

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2346	Q61578	(ADRO_MOUSE) NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin--NADP(+) reductase)	Mouse	10/13	24	24%	8.3	8.9	41361	54168
2350	P35487	(ODPAT_MOUSE) Pyruvate dehydrogenase E1 component alpha subunit, testis-specific form, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A type II)	Mouse	8/10	51	15%	8.2	8.8	41341	44183
2356	Q9JII5-01-00-00	(DZP1_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q9JII5 DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1)	Mouse	6/12	46	20%	9.7	8.7	41237	43287
2369	P63038	(CH60_MOUSE) 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1)(HSP-65)	Mouse	8/10	60	19%	6.1	5.9	41257	60917
2374	P62196	(PRS8_MOUSE) 26S protease regulatory subunit 8 (Proteasome subunit p45) (p45/SUG) (Proteasome 26S subunit ATPase 5) (mSUG1)	Mouse	14/18	33	35%	7.7	7.1	40927	45597
2377	Q91W90	(TXN5_MOUSE) Thioredoxin domain containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46)	Mouse	5/7	41	18%	5.2	5.5	40968	46386
2381	Q6P919	(Q6P919) Tufm protein	Mouse	8/10	28	23%	6.8	7.7	40947	47763
2390	Q9D1Q6	(TXN4_MOUSE) Thioredoxin domain containing protein 4 precursor (Endoplasmic reticulum protein ERp44)	Mouse	11/13	31	33%	5.2	5.1	40968	47222
2398	P16460	(ASSY_MOUSE) Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate ligase)	Mouse	8/8	63	21%	8.9	8.4	40783	46555
2411	O35490	(BHMT_MOUSE) Betaine--homocysteine S-methyltransferase (EC 2.1.1.5)	Mouse	10/14	73	41%	8.6	8.0	40721	44992

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2412 ^b	Q9Z1D1	(IF34_MOUSE) Eukaryotic translation initiation factor 3 subunit 4 (eIF-3 delta) (eIF3 p44) (eIF-3 RNA-binding subunit) (eIF3 p42) (Eif3p42) (eIF3g)	Mouse	6/11	23	21%	5.5	5.7	40660	35616
2413	P61164	(ACTZ_MOUSE) Alpha-centractin (Centractin)(Centrosome-associated homolog)(Actin-RPV)(ARP1)	Mouse	7/11	16	23%	6.7	6.2	40619	42587
2423	P29758	(OAT_MOUSE) Ornithine aminotransferase, mitochondrial precursor (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase)	Mouse	9/13	55	17%	6.0	6.2	40619	48324
2451	O88844	(IDHC_MOUSE) Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)	Mouse	17/24	68	42%	7.4	6.5	39830	46630
2462	Q9Z105	(Q9Z105) Protein phosphatase-1 regulatory subunit 7	Mouse	11/11	56	34%	5.0	4.9	40293	41380
2469	Q9CZ44-00-00-00	(NF1C_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from Q9CZ44 NSFL1 cofactor p47 (p97 cofactor)	Mouse	6/10	59	24%	5.1	5.0	40172	40685
2475	P09041	(PGK2_MOUSE) Phosphoglycerate kinase, testis specific (EC 2.7.2.3)	Mouse	12/15	60	44%	6.7	6.4	39930	44723
2483	P09041	(PGK2_MOUSE) Phosphoglycerate kinase, testis specific (EC 2.7.2.3)	Mouse	8/9	59	27%	7.0	6.4	40010	44723
2485	Q9CZ44-00-00-00	(NF1C_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from Q9CZ44 NSFL1 cofactor p47 (p97 cofactor)	Mouse	8/9	48	33%	5.2	5.0	40111	40685
2491	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	7/7	17	20%	5.1	5.2	40051	56265
2492 ^b	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	8/8	54	16%	5.5	5.8	39970	68648

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2495	P15105	(GLNA_MOUSE) Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS) Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS)	Mouse	8/12	54	27%	7.1	6.5	39610	42118
2504	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	9/16	43	30%	5.3	5.3	39036	41766
2511	P50247	(SAHH_MOUSE) Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) (Liver copper binding protein) (CUBP)	Mouse	6/10	26	16%	6.6	6.1	39650	47526
2522	P42209	(SEP1_MOUSE) Septin 1 (Differentiation protein 6) (Diff6 protein) Septin 1 (Differentiation protein 6) (Diff6 protein)	Mouse	5/8	68	14%	5.5	5.7	39650	41868
2526	Q8JZR8	(Q8JZR8) Acetyl-Coenzyme A acyltransferase 2 (Mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Mouse	7/7	45	28%	9.1	8.3	39530	42288
2534	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	7/12	28	21%	5.2	5.3	39431	41766
2535	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	10/17	50	31%	5.2	5.3	39272	41710
2536	gjl220637	Zinc finger protein [Mus musculus]	Mouse	5/9	62	22%	8.9	9.0	39490	39639
2553	Q9Z2I9	(SCB1_MOUSE) Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.5) (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP-specific succinyl-CoA synthetase beta subunit)	Mouse	10/15	53	25%	5.5	6.6	38997	50424
2559	Q921F2	(TDBP_MOUSE) TAR DNA-binding protein-43 (TDP-43)	Mouse	7/8	36	17%	6.6	6.3	39154	44519
2562	P55302	(AMRP_MOUSE) Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1)	Mouse	7/13	36	21%	7.3	7.4	39056	42189
2568	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	5/7	62	15%	5.1	5.3	39075	42052

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2576	P09411	(PGK1_MOUSE) Phosphoglycerate kinase 1 (EC 2.7.2.3)	Mouse	7/12	10	27%	8.5	7.5	38997	44377
2584 ^b	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	10/11	37	19%	4.6	5.1	38957	72377
2587	P55302	(AMRP_MOUSE) Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1)	Mouse	6/9	42	20%	7.5	7.4	38879	42189
2591	Q924M7	(Q924M7) Phosphomannose isomerase (Mpi1 protein)	Mouse	8/14	35	24%	5.7	5.6	38626	47229
2612	P62334	(PRSX_MOUSE) 26S protease regulatory subunit S10B (Proteasome subunit p42) (Proteasome 26S subunit ATPase 6)	Mouse	10/14	36	31%	7.8	7.1	38181	44145
2614	P42208	(SEP2_MOUSE) Septin 2 (NEDD5 protein)	Mouse	6/9	35	22%	6.4	6.1	38509	41499
2624	P29758	(OAT_MOUSE) Ornithine aminotransferase, mitochondrial precursor (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase)	Mouse	6/9	26	15%	6.7	6.2	38529	48324
2633	O08749	(DLDH_MOUSE) Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase)	Mouse	6/7	45	17%	6.0	8.0	38451	54748
2645 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	11/18	45	21%	6.6	5.8	38297	68648
2647	Q9Z2I8	(SCB2_MOUSE) Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit)	Mouse	8/15	50	25%	5.4	5.8	38143	44028
2648 ^b	P08109	(HS7C_MOUSE) Heat shock cognate 71 kDa protein	Mouse	10/16	58	17%	5.6	5.4	38104	70827

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2655 ^c	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	7/9	38	17%	5.1	5.2	38066	56265
2656 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	11/16	37	19%	5.3	5.8	37894	68648
2681	Q922R8	(Q922R8) Txndc7 protein	Mouse	6/8	38	17%	6.6	5.0	37685	48469
2688	P14206	RSSA_MOUSE) 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)	Mouse	6/11	28	21%	4.7	4.7	37477	32567
2699	Q61990-02-00-00	(PCB2_MOUSE) Splice isoform 3; Variant Displayed; Conflict Displayed; from Q61990 Poly(rC)-binding protein 2 (Alpha-CP2) (Putative Putative heterogeneous nuclear ribonucleoprotein X) (hnRNP X) (CTBP) (CBP)	Mouse	10/13	33	46%	6.7	6.6	37515	37177
2702	Q8BK64	(AHA1_MOUSE) Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1)	Mouse	8/15	58	25%	5.5	5.4	37308	38093
2712	Q922Y1	(U33K_MOUSE) UBA/UBX 33.3 kDa protein	Mouse	5/11	34	24%	5.3	5.2	37458	33552
2714	P61963	(AN1H_MOUSE) WD-repeat protein An11 homolog	Mouse	4/7	33	15%	5.3	5.3	37439	38901
2717 ^b	O35135	(O35135) Outer dense fiber protein	Mouse	7/10	59	16%	5.8	6.3	37364	71404
2722	Q99KV1	(DJBB_MOUSE) DnaJ homolog subfamily B member 11 precursor	Mouse	9/15	31	31%	6.5	5.9	37009	40530
2744	Q9JK48-00-00-00	(SHLB1_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from Q9JK48 SH3 domain GRB2-like protein B1 (EC 2.3.1.-) (Endophilin B1)	Mouse	6/8	30	16%	5.7	5.8	36953	41115
2745	P56480	(ATPB_MOUSE) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	7/9	38	17%	5.1	5.2	37027	56265
2750	Q91WM2	(CECR5_MOUSE) Cat eye syndrome critical region protein 5 homolog precursor	Mouse	7/10	58	19%	6.9	7.8	36841	46562

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2752	O88544	(CSN4_MOUSE) COP9 signalosome complex subunit 4 (Signalosome subunit 4) (SGN4) (JAB1-containing signalosome subunit 4)	Mouse	10/14	36	38%	5.6	5.6	36804	46541
2753 ^c	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	8/8	9	14%	6.1	5.1	36953	72377
2770	Q9Z0S1	(BNT1_MOUSE) 3'(2'),5'-bisphosphate nucleotidase 1 (EC 3.1.3.7) (Bisphosphate 3'-nucleotidase 1) (PAP-inositol-1,4-phosphatase) (PIP)	Mouse	6/14	48	27%	5.8	5.5	36656	33517
2771	gjl15029834	Serpib1a protein [Mus musculus]	Mouse	8/10	33	23%	6.1	5.9	36620	42719
2778 ^c	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	9/15	32	17%	5.3	5.8	36564	68648
2783 ^c	Q01853	(TERA_MOUSE) Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	Mouse	8/13	44	12%	5.8	5.1	36583	89936
2787	Q9CQM9	(TXL2_MOUSE) Thioredoxin-like protein 2 (PKC-interacting cousin of thioredoxin) (PKC-theta-interacting protein) (PKCq-interacting protein)	Mouse	8/16	52	31%	5.5	5.4	36362	37754
2794	P60335	(PCBP1_MOUSE) Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1)	Mouse	12/18	63	48%	7.3	6.7	36162	37987
2798	Q64442	(DHSO_MOUSE) Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase) (Fragment)	Mouse	8/11	56	26%	7.0	6.6	36253	40066
2803 ^b	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	11/15	42	16%	5.0	5.6	36235	69698
2804	Q07417	(ACADS_MOUSE) Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor (EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydrogenase)	Mouse	6/7	26	23%	6.9	9.0	36326	45203

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2809	Q8VIG3	(TSA2_MOUSE) Testis-specific gene A2 (Male meiotic metaphase chromosome-associated acidic protein) (Meichroacidin)	Mouse	8/9	46	23%	4.2	4.5	36162	34161
2810	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	7/8	44	26%	5.2	5.3	36344	41710
2838	Q9CR16	(PPID_MOUSE) 40 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin-40) (CYP-40)	Mouse	10/14	39	29%	7.9	7.1	35710	40985
2840	P05064	(ALFA_MOUSE) Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase 1)	Mouse	9/12	73	34%	8.5	8.4	35782	39200
2845	Q8VIG3	(TSGA2_MOUSE) Testis-specific gene A2 protein (Male meiotic metaphase chromosome-associated acidic protein) (Meichroacidin)	Mouse	11/14	40	32%	3.6	4.5	35746	34218
2861	P05064	(ALFA_MOUSE) Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase 1)	Mouse	11/17	25	36%	8.7	8.4	35566	39200
2875	Q9CRC1	(Q9CRC1) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933425L11	Mouse	6/19	7	28%	7.8	7.1	35352	39802
2890 ^c	P17156	(HSP72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	14/17	64	23%	8.6	5.6	35139	69983
2891 ^b	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	7/8	36	12%	4.6	5.1	35157	72377
2892 ^b	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	11/12	31	16%	4.7	5.1	35192	72377
2893	Q9R1T2	(SAE1_MOUSE) Ubiquitin-like 1 activating enzyme E1A (SUMO-1 activating enzyme subunit 1)	Mouse	9/15	19	30%	5.3	5.2	35051	39052

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2901	Q6NZD0	(Q6NZD0) Heat shock protein 8	Mouse	6/6	33	12%	6.8	5.3	35033	71056
2906	O35855	(BCAM_MOUSE) Branched-chain-amino-acid aminotransferase, mitochondrial precursor (EC 2.6.1.42) (BCAT(m))	Mouse	6/13	27	17%	8.3	8.6	34875	44669
2910	Q9CX34	(SUGT_MOUSE) Suppressor of G2 allele of SKP1 homolog	Mouse	7/9	50	25%	5.5	5.3	34963	38420
2911	Q9CX34	(SUGT_MOUSE) Suppressor of G2 allele of SKP1 homolog	Mouse	9/13	36	29%	5.3	5.3	34910	38420
2919 ^c	P63017	(HSP7C_MOUSE) Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	Mouse	9/10	59	16%	8.2	5.4	34753	71055
2925 ^b	P09041	(PGK2_MOUSE) Phosphoglycerate kinase, testis specific (EC 2.7.2.3)	Mouse	7/9	61	24%	5.3	6.4	34683	44723
2933 ^c	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	6/10	26	11%	5.1	5.6	34665	69983
2939	Q9QXD6	(F16P_MOUSE) Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)	Mouse	11/15	53	36%	6.4	6.2	34335	37157
2944 ^b	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	7/9	48	12%	4.9	5.6	34457	69698
2946	Q9Z1Z2	(STRA_MOUSE) Serine-threonine kinase receptor-associated protein (UNR-interacting protein)	Mouse	6/15	29	25%	5.1	5.0	34370	38774
2949	gjl18250284	Isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	Mouse	7/9	45	18%	5.7	6.3	34318	40069
2953	Q8BG05-01-00-00	(ROA3_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8BG05 Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Mouse	5/7	52	23%	7.5	8.5	34094	37291
2956 ^c	P54869	(HMCM_MOUSE) Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Fragement)	Mouse	8/12	78	20%	6.2	8.0	34112	53752

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
2957	P47199	(QOR_MOUSE) Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-crystallin)	Mouse	8/11	19	32%	8.4	8.2	33923	35246
2969 ^c	P52480	(KPYM_MOUSE) Pyruvate kinase, isozyme M2 (EC 2.7.1.40)	Mouse	7/12	50	18%	6.3	7.4	34077	57719
2973 ^c	Q01853	(TERA_MOUSE) Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit (Valosin-containing protein) (VCP)	Mouse	9/14	34	16%	6.0	5.1	34009	89936
2975	Q9J116	(AKA1_MOUSE) Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo-keto reductase family 1 member A1)	Mouse	8/11	31	29%	7.7	6.9	33855	36661
2980	Q93092	(TAL1_MOUSE) Transaldolase (EC 2.2.1.2)	Mouse	7/15	46	24%	7.2	6.6	33821	37363
2990	O8CG76	(ARK72_MOUSE) Aflatoxin B1 aldehyde reductase member 2 (EC 1.-.-.-)	Mouse	7/9	36	26%	7.0	8.4	33702	41028
2991	P68372	(TBBX_MOUSE) Tubulin beta-? chain	Mouse	11/15	58	23%	5.8	4.8	33719	50255
2994	Q9J116	(AKA1_MOUSE) Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo-keto reductase family 1 member A1)	Mouse	6/9	55	19%	7.8	6.9	33821	36661
3000	O35864-00-00-00	(CSN5_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from O35864 COP9 signalosome complex subunit 5 (EC 3.4.-.-) (Signalosome subunit 5) (SGN5)(Jun activation domain-binding protein 1)(Kip1 C-terminus interacting protein 2)	Mouse	7/9	29	25%	6.3	6.1	33634	37525
3011	Q9QZD9	(IF32_MOUSE) Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1)	Mouse	7/11	58	27%	5.6	5.4	33348	36837
3020	P54923	(ADPRH_MOUSE) ADP-ribosylarginine hydrolase (EC 3.2.2.19) (ADP-ribose-L-arginine cleaving enzyme)	Mouse	6/9	27	20%	5.5	5.5	33130	40328

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3028	Q8BG05-01-00-00 (ROA3_MOUSE)	Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8BG05 Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Mouse	6/8	40	26%	9.0	8.5	33214	37063
3033	Q8BG05-01-00-00 (ROA3_MOUSE)	Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8BG05 Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Mouse	9/12	18	28%	8.8	8.5	33247	37063
3037	Q8CDS2	(Q8CDS2) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930447E08	Mouse	7/13	39	31%	4.7	4.9	33130	31745
3042	Q9QZ08	(NAGK_MOUSE) N-acetylglucosamine kinase (EC 2.7.1.59) (GlcNAc kinase)	Mouse	7/12	53	24%	5.4	5.4	33031	37587
3055	Q9CWS0	(DDH1_MOUSE) NG,NG-dimethylarginine dimethylaminohydrolase 1 (EC 3.5.3.18) (Dimethylargininase 1) (Dimethylarginine dimethylaminohydrolase 1) (DDAHI) (DDAH-1)	Mouse	7/12	33	36%	5.7	5.6	32832	31230
3057 ^b	P09405	(NUCL_MOUSE) Nucleolin (Protein C23)	Mouse	6/8	21	11%	6.8	4.7	32848	76603
3075	P45377	(ALD2_MOUSE) Aldose reductase-related protein 2 (EC 1.1.1.21) (AR) (Aldehyde reductase) (Fibroblast growth factor regulated protein) (FR-1 protein)	Mouse	6/9	53	25%	6.2	6.0	32389	35967
3078	P47753	(CAZ1_MOUSE) F-actin capping protein alpha-1 subunit (CapZ alpha-1)	Mouse	9/11	26	40%	5.4	5.3	32405	32919
3083	Q8BG05-01-00-00 (ROA3_MOUSE)	Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8BG05 Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Mouse	9/14	19	29%	9.3	8.5	32226	37063
3084	Q8BG05-01-00-00 (ROA3_MOUSE)	Splice isoform 2; Variant Displayed; Conflict Displayed; from Q8BG05 Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Mouse	8/12	19	28%	9.7	8.5	32210	37063
3099 ^c	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	5/6	63	6%	5.0	5.6	32259	69698

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3122	P10518	(HEM2_MOUSE) Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (Porphobilinogen synthase) (ALADH)	Mouse	8/14	43	24%	6.6	6.3	32032	36000
3124	P47753	(CAZ1_MOUSE) F-actin capping protein alpha-1 subunit (CapZ alpha-1)	Mouse	7/11	22	37%	5.4	5.3	32016	32919
3127	P16125	(LDHB_MOUSE) L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H)	Mouse	10/15	32	35%	5.8	5.7	31756	36418
3130	P45376	(ALDR_MOUSE) Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase)	Mouse	4/7	18	17%	7.0	6.8	31885	35921
3133 ^b	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	6/7	23	7%	5.1	5.6	31742	69698
3134	Q9D1M0	(SC13_MOUSE) SEC13-related protein (SEC13-like protein 1)	Mouse	6/10	42	23%	5.2	5.2	31827	35925
3135	P45376	(ALDR_MOUSE) Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase)	Mouse	7/9	40	26%	7.4	6.8	31514	35921
3158 ^b	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	11/13	21	18%	5.6	5.8	31570	68648
3160	P16858	(G3P_MOUSE) Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)	Mouse	4/9	14	18%	8.6	8.5	31443	35941
3165	Q8CDS2	(Q8CDS2) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930447E08	Mouse	6/11	38	28%	5.2	4.9	31429	31745
3170 ^c	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	12/13	10	23%	5.8	5.1	31471	72377
3178	P16858	(G3P_MOUSE) Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)	Mouse	7/12	25	26%	9.0	8.5	31315	35656
3190	P08249	(MDHM_MOUSE) Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	Mouse	8/14	56	27%	9.5	8.8	31273	35574

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3199	P21300	(ALD1_MOUSE) Aldose reductase-related protein 1 (EC 1.1.1.21) (AR) (Aldehyde reductase) (VAS deferens androgen-dependent protein) (MVDP) (Aldo-keto reductase family 1 member B7)	Mouse	4/4	58	20%	7.6	6.9	31049	35835
3209	Q9D7G0	(PRPS1_MOUSE) Ribose-phosphate pyrophosphokinase I (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase I) (PRS-I)	Mouse	4/4	43	12%	7.0	6.6	31021	35208
3211	P47757-00-00-00	(CAPB_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from P47757 F-actin capping protein beta subunit (CapZ beta)	Mouse	8/12	68	27%	6.2	5.5	31007	31195
3212	gij15079395	RIKEN cDNA 4931406C07 [Mus musculus]	Mouse	6/10	43	18%	6.2	5.9	30951	35430
3214 ^c	P68372	(TBBX_MOUSE) Tubulin beta-? Chain	Mouse	7/14	35	18%	5.5	4.8	30784	50255
3223	P07356	(ANX2_MOUSE) Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobindin 8) (P36) (Protein I) (Placental anticoagulant protein IV) (PAP-IV)	Mouse	10/14	37	24%	8.0	7.5	30826	38806
3225	P47754	(CAZ2_MOUSE) F-actin capping protein alpha-2 subunit (CapZ alpha-2)	Mouse	8/15	50	41%	5.7	5.6	30770	32816
3226 ^d	P52196	(THTR_MOUSE) Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese)	Mouse	13/14	20	30%	8.4	7.8	30826	33542
3226 ^{ed}	P24549	(AL1A1_MOUSE) Retinal dehydrogenase 1 (EC 1.2.1.36) (RALDH1) (RALDH 1) (Aldehyde dehydrogenase family 1 member A1) (Aldehyde dehydrogenase, cytosolic) (ALHDII)	Mouse		18	15%	8.4	7.9	30826	54929
3227	P68372	(TBBX_MOUSE) Tubulin beta-? chain	Mouse	12/12	45	17%	5.5	4.79	30812	50255
3227	O35639	(ANXA3_MOUSE) Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedlin)	Mouse		38	23%	5.5	5.3	30812	36389

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3229 ^b	P07901	(HS9A_MOUSE) Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)	Mouse	5/6	66	9%	5.2	4.9	30756	84604
3232 ^d	g 31543902	Thioredoxin-like 1 [Mus musculus]	Mouse	15/18	43	41%	5.1	4.8	30577	32616
3232 ^d	P57776-00-00-00	(EF1D_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from P57776 Elongation factor 1-delta (EF-1-delta)	Mouse		43	27%	5.1	4.9	30577	31257
3233	Q8K0V8	(Q8K0V8) RIKEN cDNA B430104H02 (Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430104H02 product:weakly similar to 2-HYDROXYHEPTA-2,4-DIENE-1,7-DIOATE ISOMERASE)	Mouse	7/9	38	38%	6.9	8.4	30715	35053
3235	Q91YR9	(Q91YR9) Leukotriene B4 12-hydroxydehydrogenase	Mouse	7/7	22	21%	8.7	8.1	30632	35856
3242	P14152	(MDHC_MOUSE) Malate dehydrogenase, cytoplasmic (EC 1.1.1.37)	Mouse	5/10	43	22%	6.3	6.2	30412	36494
3244	O35639	(ANX3_MOUSE) Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedin)	Mouse	14/17	45	35%	5.6	5.3	30563	36217
3249	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	9/12	54	37%	9.2	8.7	30549	35971
3256 ^b	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	8/10	28	13%	5.0	5.6	30371	69698
3258	P57776-00-00-00	(EF1D_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from P57776 Elongation factor 1-delta (EF-1-delta)	Mouse	7/10	48	27%	4.9	4.9	30467	31143
3262	Q9WUP7-01-00-00	(UCL5_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q9WUP7 Ubiquitin carboxyl-terminal hydrolase isozyme L5 (EC 3.4.19.12) (UCH-L5) (Ubiquitin thiolesterase L5)(Ubiquitin C-terminal hydrolase UCH37)	Mouse	8/13	26	24%	5.3	5.3	30275	37749

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3265	gij22203753	Inorganic pyrophosphatase 2 [Mus musculus]	Mouse	7/10	45	28%	6.1	6.5	30316	38090
3267	O8CHP8	(Q8CHP8) RIKEN cDNA 1700012G19	Mouse	10/12	53	29%	5.2	5.2	30044	34975
3271	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	8/12	54	34%	8.6	8.7	30126	35971
3272	Q9D051	(ODPB_MOUSE) Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B)	Mouse	12/16	12	38%	5.5	6.4	29990	39254
3277	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	16/21	28	46%	9.2	8.7	30031	35971
3281	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	14/20	53	48%	9.6	8.7	29923	35971
3290	O8CHP8	(Q8CHP8) RIKEN cDNA 1700012G19	Mouse	5/7	52	23%	5.1	5.2	30004	34519
3293	Q9D819	(IPYR_MOUSE) Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase)	Mouse	11/14	28	43%	5.4	5.4	29896	32646
3296	P13707	(GPDA_MOUSE) Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic (EC 1.1.1.8) (GPD-C) (GPDH-C)	Mouse	6/13	39	19%	7.3	6.8	29882	37417
3299	Q80Y75	(TSR6_MOUSE) Testis spermatocyte apoptosis-related gene 6 protein (Testis and spermatogenesis cell related protein 6)	Mouse	6/11	53	21%	8.0	7.0	29923	36132
3313	gij12856949	Unnamed protein product [Mus musculus]	Mouse	6/9	29	29%	4.8	4.9	29668	28825
3328 ^c	P68372	(TBBX_MOUSE) Tubulin beta-? chain	Mouse	4/15	64	14%	5.3	4.8	29455	50255

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3330	Q9DB25	(ALG5_MOUSE) Dolichyl-phosphate beta-glucosyltransferase (EC 2.4.1.117) (DoIP-glucosyltransferase)	Mouse	5/8	39	20%	7.0	8.8	29322	37166
3337	P57776-01-00-00	(EF1D_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from P57776 Elongation factor 1-delta (EF-1-delta)	Mouse	6/7	11	23%	5.0	4.8	29362	28580
3342	P00342	(LDHC_MOUSE) L-lactate dehydrogenase C chain (EC 1.1.1.27) (LDH-C) (LDH testis subunit) (LDH-X)	Mouse	6/7	42	13%	8.5	8.4	29138	35758
3380	P17751	(TPIS_MOUSE) Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)	Mouse	5/5	22	27%	5.5	7.1	28760	26565
3383	P00342	(LDHC_MOUSE) L-lactate dehydrogenase C chain (EC 1.1.1.27) (LDH-C) (LDH testis subunit) (LDH-X)	Mouse	12/18	56	35%	8.8	8.4	28786	35758
3407	P68372	(TBBX_MOUSE) Tubulin beta-? chain	Mouse	11/17	51	17%	5.1	4.8	28489	50255
3409	Q9DB05	(SNAA_MOUSE) Alpha-soluble NSF attachment protein (SNAP-alpha) (N-ethylmaleimide-sensitive factor attachment protein, alpha)	Mouse	14/14	22	57%	5.3	5.3	28476	33624
3420	Q8CG74	(Q8CG74) Albumin (Fragment)	Mouse	8/14	65	18%	5.7	5.5	28208	24237
3442	Q60930	(POR2_MOUSE) Voltage-dependent anion-selective channel protein 2 (VDAC-2) (mVDAC2) (mVDAC6) (Outer mitochondrial membrane protein porin 2)	Mouse	5/7	44	23%	7.8	7.4	27580	31713
3452	Q61425	(HCDH_MOUSE) Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase)	Mouse	4/8	47	13%	8.8	8.8	27717	34442
3457	Q9D8Y0	(EFD2_MOUSE) EF-hand domain-containing protein 2 (Swiprosin 1)	Mouse	7/10	32	22%	5.1	5.0	27617	26775

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3464	gij14715044	Cytoskeleton-associated protein 1 [Mus musculus]	Mouse	6/6	56	24%	5.2	5.1	27654	27654
3466	O35459	(ECH1_MOUSE) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)	Mouse	7/12	31	23%	6.5	7.6	27580	36095
3481	O8CHP8	(Q8CHP8) RIKEN cDNA 1700012G19	Mouse	5/7	52	23%	5.3	5.2	27320	34519
3482	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	8/12	55	25%	9.7	8.7	27246	35971
3483	Q60932-01-00-00	(POR1_MOUSE) Splice isoform Mt-VDAC1; Variant Displayed; Conflict Displayed; from Q60932 Voltage-dependent anion-selective channel protein 1 (VDAC-1) (mVDAC1)	Mouse	8/14	30	49%	9.5	8.6	27320	30737
3485	O88569	(ROA2_MOUSE) Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	Mouse	8/13	56	29%	9.3	8.7	27332	35971
3486 ^b	P17156	(HSP72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	7/12	61	11%	4.7	5.6	27197	69983
3499 ^c	P20029	(GR78_MOUSE) 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP)	Mouse	9/11	56	17%	8.1	5.1	27063	72377
3508	P21107-01-00-00	(TPM3_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from P21107 Tropomyosin alpha 3 chain (Tropomyosin 3) (Tropomyosin gamma)	Mouse	7/14	24	22%	4.8	4.8	26929	29003
3519	P21107-01-00-00	(TPM3_MOUSE) Splice isoform 2; Variant Displayed; Conflict Displayed; from P21107 Tropomyosin alpha 3 chain (Tropomyosin 3) (Tropomyosin gamma)	Mouse	9/11	57	27%	4.6	4.8	26627	29003
3525	Q99L13	(DH3I_MOUSE) 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) (HIBADH)	Mouse	8/12	14	29%	6.4	8.4	26556	35417

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3528	Q9R1P4	(PSA1_MOUSE) Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain)	Mouse	7/7	20	41%	6.5	6.0	26484	29813
3532	P47757-00-00-00	(CAPB_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from P47757 F-actin capping protein beta subunit (CapZ beta)	Mouse	4/11	59	14%	5.7	5.5	26436	31195
3577	P62259	(143E_MOUSE) 14-3-3 protein epsilon (14-3-3E)	Mouse	6/10	44	27%	4.4	4.6	25546	29155
3586	Q9Z1Q5	(CLI1_MOUSE) Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (p64 CLCP)	Mouse	4/10	67	25%	5.2	5.1	25535	27207
3592 ^c	Q03265	(ATPA_MOUSE) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	8/13	29	20%	8.8	9.2	25581	59716
3606	Q9CR00	(PSD9_MOUSE) 26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	Mouse	6/10	27	29%	6.3	6.0	25295	24876
3636	P70195	(PSB7_MOUSE) Proteasome subunit beta type 7 precursor (EC 3.4.25.1) (Proteasome subunit Z) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z)	Mouse	6/8	59	15%	6.3	8.1	24740	29872
3640	Q9D5U2	(Q9D5U2) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921521F21	Mouse	8/9	54	32%	7.0	7.5	24759	34153
3650	P24142	(PHB_MOUSE) Prohibitin (B-cell receptor associated protein 32) (BAP 32)	Mouse	8/11	43	37%	5.6	5.6	24615	29859
3651	P67778	(PHB_MOUSE) Prohibitin (B-cell receptor associated protein 32) (BAP 32)	Mouse	7/9	55	31%	5.5	5.6	24539	29802
3663	Q9CXW3	(CYBP_MOUSE) Calcyclin-binding protein (CacyBP) (Siah-interacting protein)	Mouse	5/9	51	39%	8.0	7.6	24387	26608

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3675	Q99KB8	(GLO2_MOUSE) Hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase II) (Glx II)	Mouse	6/10	61	33%	7.2	6.5	24274	28883
3687 ^c	P63017	(HS7C_MOUSE) Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	Mouse	6/7	24	12%	8.4	5.4	24143	70827
3689	P57759	(ER29_MOUSE) Endoplasmic reticulum protein ERp29 precursor	Mouse	10/12	70	38%	5.9	5.9	24078	28805
3691 ^c	P17156	(HS72_MOUSE) Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)	Mouse	11/12	35	17%	9.0	5.6	24115	69698
3693	Q9DBJ1	(PMG1_MOUSE) Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1)	Mouse	14/16	61	52%	7.3	6.8	23947	28797
3721	Q9CQE8	(CN166_MOUSE) Protein C14orf166 homolog	Mouse	5/14	64	27%	9.3	6.4	23781	28249
3727	Q9CQ60	(6PGL_MOUSE) 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)	Mouse	7/10	26	37%	5.5	5.6	23744	27465
3736	Q9CQA3	(DHSB_MOUSE) Succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor (EC 1.3.5.1) (Ip) (Iron-sulfur subunit of complex II)	Mouse	7/12	65	26%	9.2	9.0	23716	31793
3737	Q9DCW4	(ETFB_MOUSE) Electron transfer flavoprotein beta-subunit (Beta-ETF)	Mouse	7/12	55	37%	8.8	8.6	23698	27521
3748	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	6/6	36	14%	6.9	5.8	23524	68648
3750	O35723	(DJB3_MOUSE) DnaJ homolog subfamily B member 3 (DnaJ protein homolog 3) (Heat shock J3 protein) (HSJ-3) (MSJ-1)	Mouse	6/8	49	21%	6.4	5.9	23533	26662
3752	Q9R0P9	(UCHL1_MOUSE) Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5) (PGP 9.5)	Mouse	9/11	53	33%	5.2	5.1	23388	25165
3753	Q99LX7	(Q99LX7) Echs1 protein (Fragment)	Mouse	5/9	14	20%	8.4	8.8	23451	31636

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3760	O35969	(GAMT_MOUSE) Guanidinoacetate N-methyltransferase (EC 2.1.1.2)	Mouse	6/10	53	44%	5.5	5.4	23288	26319
3761 ^b	P07724	(ALBU_MOUSE) Serum albumin precursor	Mouse	9/10	47	17%	6.6	5.8	23370	70700
3771	Q9Z2M7	(PMM2_MOUSE) Phosphomannomutase 2 (EC 5.4.2.8) (PMM 2)	Mouse	6/12	48	30%	6.1	6.0	23288	27981
3773	Q9QUM9	(PSA6_MOUSE) Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain)	Mouse	9/14	33	29%	6.7	6.3	23180	27811
3775	Q9Z2U1	(PSA5_MOUSE) Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain)	Mouse	5/12	48	31%	4.5	4.7	23126	26565
3787	Q9JKB1	(UCL3_MOUSE) Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3.4.19.12) (UCH-L3) (Ubiquitin thiolesterase L3)	Mouse	10/17	56	46%	4.9	5.0	22894	26306
3790	Q8CG74	(Q8CG74) Albumin (Fragment)	Mouse	5/9	22	23%	6.1	5.5	23046	24237
3800	P10649	(GSTM1_MOUSE) Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST class-mu 1) (Glutathione S-transferase GT8.7) (pmGT10) (GST 1-1)	Mouse	14/21	65	64%	8.9	8.1	22612	25936
3802	O08807	(PDX4_MOUSE) Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase A0372) (Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme AOE372)	Mouse	8/12	28	27%	6.4	6.7	22823	31033
3807	O08807	(PDX4_MOUSE) Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase A0372) (Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme AOE372)	Mouse	6/6	56	27%	6.3	6.7	22726	31261
3808	P14602-00-00-00	(HSB1_MOUSE) Splice isoform A; Variant Displayed; Conflict Displayed; from P14602 Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Growth-related 25 kDa protein)(P25)(HSP25)	Mouse	5/10	72	29%	6.4	6.1	22718	23000

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3809 ^b	P63260	(ACTG_MOUSE) Actin, cytoplasmic 2 (Gamma-actin)	Mouse	4/5		10%	5.5	5.3	22788	41766
3815	O9R0P9	(UCL1_MOUSE) Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5) (PGP 9.5) (Mouse	5/10	58	28%	5.3	5.1	22542	25165
3816	P10649	(GSTM1_MOUSE) Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST class-mu 1) (Glutathione S-transferase GT8.7) (pmGT10) (GST 1-1)	Mouse	9/13	56	40%	8.3	8.1	22533	25936
3830	O08709-00-01-00	(PRDX6_MOUSE) Splice isoform Displayed; Variant strain C57BL/6J and strain FVB/N; Conflict Displayed; from O08709 Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cysperoxiredoxin)(1-Cys PRX Acidic calcium-independent phospholipase A2)(EC 3.1.1.-aiPLA2)(Non-selenium glutathione peroxidase)(EC .11.1.7)(NSGPx)	Mouse	8/12	60	37%	6.6	6.0	22507	24680
3836	P17751	(TPIS_MOUSE) Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)	Mouse	4/10	41	17%	7.8	7.1	22481	26565
3842	P15626	(GSTM2_MOUSE) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2) (Glutathione S-transferase pmGT2) (GST 5-5)	Mouse	11/22	54	46%	7.3	7.3	22109	25740
3844	O08709-00-00-00	(PDX6_MOUSE) Splice isoform Displayed; Variant Displayed; Conflict Displayed; from O08709 Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cysperoxiredoxin)(1-Cys PRX Acidic calcium-independent phospholipase A2)(EC 3.1.1.-aiPLA2)(Non-selenium glutathione peroxidase)(EC 1.11.1.7)(NSGPx)	Mouse	6/13	19	33%	6.0	5.7	22377	24724
3849	P15626	(GTM2_MOUSE) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2) (Glutathione S-transferase pmGT2) (GST 5-5)	Mouse	8/14	58	27%	8.2	7.3	22178	25569

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3851	Q99PT1	(GDIR_MOUSE) Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1)	Mouse	7/10	59	33%	5.2	5.1	22247	23393
3860	Q9R1P1	(PSB3_MOUSE) Proteasome subunit beta type 3 (EC 3.4.25.1) (Proteasome theta chain) (Proteasome chain 13) (Proteasome component C10-II)	Mouse	4/6	39	30%	6.4	6.2	22058	23235
3867	Q9D5J8	(Q9D5J8) Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930431E11	Mouse	6/9	60	21%	6.2	5.6	22007	27446
3874	P15626	(GTM2_MOUSE) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2) (Glutathione S-transferase pmGT2) (GST 5-5)	Mouse	9/22	49	41%	7.0	7.3	21913	25569
3879	P15626	(GTM2_MOUSE) Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2) (Glutathione S-transferase pmGT2) (GST 5-5)	Mouse	6/13	53	36%	7.9	7.3	21871	25569
3889	Q6P919	(Q6P919) Tufm protein	Mouse	11/12	42	33%	5.9	7.7	21820	47763
3901 ^c	O35737	(ROH1_MOUSE) Heterogeneous nuclear ribonucleoprotein H (hnRNP H) Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	Mouse	4/6	48	14%	6.8	5.9	21610	49322
3903	P49722	(PSA2_MOUSE) Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3)	Mouse	4/11	45	30%	7.4	8.4	21543	25892
3916	Q00623	(APA1_MOUSE) Apolipoprotein A-I precursor (Apo-AI) (ApoA-I)	Mouse	8/9	60	26%	5.5	5.6	21294	30569
3917	P20108	(PRDX3_MOUSE) Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Perioredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein) (PRX III)	Mouse	6/12	39	28%	6.2	7.2	21385	28337

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
3926	P99026	(PSB4_MOUSE) Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain)(Proteasome chain 3)	Mouse	5/12	43	27%	5.7	5.5	21261	29097
3944	Q9JHI5	(Q9JHI5) Isovaleryl dehydrogenase precursor (Isovaleryl coenzyme A dehydrogenase) (Isovaleryl CoA dehydrogenase)	Mouse	7/9	20	19%	6.6	8.5	21105	46695
3951	Q8CG74	(Q8CG74) Albumin (Fragment)	Mouse	6/11	58	11%	5.2	5.5	20877	24237
3957	P19157	(GTP1_MOUSE) Glutathione S-transferase P 1 (EC 2.5.1.18) (GST YF-YF) (GST-piB) (GST class-pi) (Gst P1) (Preadipocyte growth factor)	Mouse	6/12	55	44%	8.7	8.1	20748	23463
3959	P19157	(GSTP1_MOUSE) Glutathione S-transferase P 1 (EC 2.5.1.18) (GST YF-YF) (GST-piB) (GST class-pi) (Gst P1) (Preadipocyte growth factor)	Mouse	11/15	22	52%	9.1	8.1	20756	23634
3966	P19157	(GSTP1_MOUSE) Glutathione S-transferase P 1 (EC 2.5.1.18) (GST YF-YF) (GST-piB) (GST class-pi) (Gst P1) (Preadipocyte growth factor)	Mouse	4/8	27	31%	8.0	8.1	20700	23634
3992	Q9ERE7	(MED2_MOUSE) Mesoderm development candidate 2	Mouse	4/6	20	25%	6.0	6.1	20334	25305
3993	Q9CPU0	(LGUL_MOUSE) Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase)	Mouse	5/14	28	23%	5.2	5.3	20161	20665
3994	P09671	(SODM_MOUSE) Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)	Mouse	4/16	45	20%	8.1	8.8	20232	24816
4000	Q9R1P3	(PSB2_MOUSE) Proteasome subunit beta type 2 (EC 3.4.25.1) (Proteasome component C7-I) (Macropain subunit C7-I) (Multicatalytic endopeptidase complex subunit C7-I)	Mouse	4/4	55	19%	7.0	6.5	20161	23063

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
4005	Q9R0Y5	(KAD1_MOUSE) Adenylate kinase isoenzyme 1 (EC 2.7.4.3) (ATP-AMP transphosphorylase) (AK1) (Myokinase)	Mouse	7/14	60	47%	5.5	5.7	20068	21640
4008	P35700	(PRDX1_MOUSE) Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3) (Macrophage 23 kDa stress protein)	Mouse	7/10	59	33%	8.7	8.3	20083	22390
4018 ^c	Q03265	(ATPA_MOUSE) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14)	Mouse	7/10	38	18%	6.5	9.2	20013	59830
4019	Q9WUL7	(ARL3_MOUSE) ADP-ribosylation factor-like protein 3	Mouse	6/7	40	31%	7.9	6.7	19943	20645
4022	Q9DBP5	(KCY_MOUSE) UMP-CMP kinase (EC 2.7.4.14) (Cytidylate kinase) (Deoxycytidylate kinase) (Cytidine monophosphate kinase)	Mouse	7/12	27	40%	5.8	5.7	19905	22379
4029	Q9D892	(ITPA_MOUSE) Inosine triphosphate pyrophosphatase (EC 3.6.1.19) (ITPase) (Inosine triphosphatase)	Mouse	4/8	51	28%	5.5	5.6	19698	22225
4038	Q9DCX2	(ATPQ_MOUSE) ATP synthase D chain, mitochondrial (EC 3.6.3.14)	Mouse	6/9	45	40%	5.6	5.5	19545	18664
4062	P70296	(PEBP_MOUSE) Phosphatidylethanolamine-binding protein (PEBP) (HCNPPp) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)]	Mouse	5/8	36	40%	5.1	5.2	19052	20857
4086	Q62252	(SP17_MOUSE) Sperm surface protein Sp17 (Sperm autoantigenic protein 17)	Mouse	5/9	59	38%	4.8	4.8	18527	17285
4103	O88851-00-00-00	(RBB9_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from O88851 Retinoblastoma-binding protein 9 (RBBP-9) (B5T overexpressed gene protein) (Bog protein)	Mouse	4/9	47	30%	5.7	5.6	18165	20898
4111	P10649	(GSTM1_MOUSE) Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST class-mu 1) (Glutathione S-transferase GT8.7) (pmGT10) (GST 1-1)	Mouse	15/22	34	32%	7.4	8.1	17892	25936

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
4129	O88851-00-00-00	(RBB9_MOUSE) Splice isoform 1; Variant Displayed; Conflict Displayed; from O88851 Retinoblastoma-binding protein 9 (RBBP-9) (B5T overexpressed gene protein) (Bog protein)	Mouse	4/5	38	30%	5.8	5.6	17106	20898
4133	P09528	(FRIH_MOUSE) Ferritin heavy chain (Ferritin H subunit)	Mouse	4/5	42	15%	5.7	5.5	17000	20922
4181	Q9CQU0	(TL19_MOUSE) Thioredoxin-like protein p19 precursor (Endoplasmic reticulum protein ERp19)	Mouse	4/8	58	33%	5.3	5.1	15005	19036
4196	P18760	(COF1_MOUSE) Cofilin, non-muscle isoform (Cofilin-1)	Mouse	5/10	25	33%	8.7	8.3	14655	18645
4209	P54227	(STN1_MOUSE) Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Prosolin) (Metablastin) (Pr22 protein)(Leukemia-associated gene protein)	Mouse	5/10	34	31%	5.8	5.8	14435	17133
4218	O70492	(SNX3_MOUSE) Sorting nexin 3 (SDP3 protein)	Mouse	5/5	30	32%	8.8	8.7	14273	18803
4222	O01768	(NDKB_MOUSE) Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-M2) (P18)	Mouse	4/6	62	34%	7.8	7.0	14092	17352
4228	Q9R0P5	(DEST_MOUSE) Destrin (Actin-depolymerizing factor) (ADF) (Sid 23) Destrin (Actin-depolymerizing factor) (ADF) (Sid 23)	Mouse	4/9	22	36%	8.5	8.2	13951	18721
4235	P17742	(PPIA_MOUSE) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (SP18)	Mouse	4/8	27	21%	8.1	7.9	13800	18000
4241	O01768	(NDKB_MOUSE) Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-M2) (P18)	Mouse	4/5	55	28%	7.2	7.0	13832	17352
4244	P17742	(PPIA_MOUSE) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (SP18)	Mouse	6/10	21	44%	7.8	7.9	13741	17829

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
4251	P17742	(PPIA_MOUSE) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (SP18)	Mouse	6/14	41	52%	8.4	7.9	13478	17829
4259	P08228	(SODC_MOUSE) Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	Mouse	6/12	73	39%	6.4	6.0	13265	15802
4265	P62204	(CALM_MOUSE) Calmodulin (CaM)	Mouse	5/10	38	45%	3.7	4.1	13021	16696
4269	P15532	(NDKA_MOUSE) Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23)(NDPK-A)(nm23-M1)	Mouse	4/8	52	32%	7.1	6.8	12900	17197
4271	P99029	(PDX5_MOUSE) Peroxiredoxin 5, mitochondrial precursor (Prx-V) (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166)(Liver tissue 2D-page spot 2D-0014IV)	Mouse	7/8	23	34%	8.5	9.1	12895	21884
4282	P61089	(UBCN_MOUSE) Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19)(Ubiquitin-protein ligase N)(Ubiquitin carrier protein N)(Ubc13)(Bendless-like ubiquitin conjugating enzyme)	Mouse	4/7	23	42%	6.0	6.1	12662	17127
4284	P62869	(ELOB_MOUSE) Transcription elongation factor B polypeptide 2 (RNA polymerase II transcription factor SIII subunit B) (SIII p18) (Elongin B) (EloB) (Elongin 18 kDa subunit)	Mouse	4/12	58	61%	4.6	4.9	12564	13162
4288	Q9CPT4	(CS010_MOUSE) Protein C19orf10 homolog precursor (Stromal cell-derived growth factor SF20) (Interleukin-25) (IL-25)	Mouse	4/8	25	28%	6.5	6.3	12526	18085
4306	Q00915	(RET1_MOUSE) Retinol-binding protein I, cellular (Cellular retinol-binding protein) (CRBP) (mCRBPI)	Mouse	4/6	61	34%	5.3	5.1	11915	15705
4307	P62965	(RET3_MOUSE) Retinoic acid-binding protein I, cellular (CRABP-I)	Mouse	8/8	56	52%	5.5	5.3	11668	15451

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
4310	P70349	(HNT1_MOUSE) Histidine triad nucleotide-binding protein 1 (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1)(PKCI-1)	Mouse	4/10	34	65%	6.8	6.4	11524	13637
4314	gij40254574	Fatty acid binding protein 9, testis [Mus musculus]	Mouse	6/10	25	54%	8.3	7.6	11471	15008
4317	P11404	(FABH_MOUSE) Fatty acid-binding protein, heart (H-FABP) (Mammary-derived growth inhibitor) (MDGI)	Mouse	5/9	80	37%	5.6	6.2	11369	14679
4321	P16045	(LEG1_MOUSE) Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin)	Mouse	4/5	34	39%	5.2	5.3	11125	14725
4327	gij26389590	Unnamed protein product [Mus musculus]	Mouse	4/10	7	32%	8.9	8.5	10915	15096
4334	P11404	(FABH_MOUSE) Fatty acid-binding protein, heart (H-FABP) (Heart-type fatty acid-binding protein) (Mammary-derived growth inhibitor) (MDGI)	Mouse	4/9	40	33%	6.0	6.2	10607	14679
4340	O35215	(DOPD_MOUSE) D-dopachrome tautomerase (EC 5.3.3.-)	Mouse	4/10	79	41%	6.7	6.2	10403	13052
4344	P01942-00-04-00	(HBA_MOUSE) Splice isoform of P01942 Hemoglobin alpha chain	Mouse	4/6	56	38%	8.9	8.1	10307	15016
4352	P02088-00-00-00	(HBB1_MOUSE) Splice isoform of P02088 Hemoglobin beta-1 chain (B1) (Hemoglobin beta-major chain)	Mouse	7/12	58	52%	8.3	7.3	10295	15699
4353	P02088-00-01-00	(HBB1_MOUSE) Splice isoform of from P02088 Hemoglobin beta-1 chain (B1) (Hemoglobin beta-major chain)	Mouse	4/8	26	30%	9.2	7.3	10299	15664

Spot ID	Accession No.	Protein name	Taxonomy	Matched peptides/total peptides in digest ^a	RMS Error (ppm)	Sequence coverage	Experimental pI	Theoretical pI	Experimental MW	Theoretical MW
4360	Q61171	PRDX2_MOUSE) Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA)	Mouse	7/14	58	29%	5.1	5.2	19155	21936
4361	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	8/14	49	24%	5.3	5.3	39134	41710
4362	P68033	(ACTC_MOUSE) Actin, alpha cardiac (Alpha-cardiac actin)	Mouse	13/19	31	37%	5.3	5.2	39312	41992
4363	P60710	(ACTB_MOUSE) Actin, cytoplasmic 1 (Beta-actin)	Mouse	8/14	38	24%	5.5	5.3	32749	41710
4364 ^c	P99024	(TBB5_MOUSE) Tubulin beta-5 chain	Mouse	6/9	56	17%	5.5	4.8	30330	49639
4366	P68040	(GBLP_MOUSE) Guanine nucleotide-binding protein beta subunit 2-like 1 (Receptor of activated protein kinase C 1) (RACK1) (Receptor for activated C kinase) (p205)(12-3)	Mouse	9/12	48	38%	7.3	7.6	22498	35511
4367	P99024	(TBB5_MOUSE) Tubulin beta-5 chain	Mouse	7/20	28	21%	4.8	4.8	46788	50095
4368	Q9ERD7	(TBB3_MOUSE) Tubulin beta-3	Mouse	7/10	41	16%	5.1	4.8	46764	50842

^a Autolysis tryptic peptides and eventual keratin contaminants were not taken into account in the total number of peptides in digest.

^b C-terminal fragment.

^c N-terminal fragment.

^d Mixture.