

Supplementary materials

Table S1 The sequences of plasmid primers and siRNA

Plasmid/siRNA name	Primer/siRNA sequence
Flag-C-Hsp90 α	
F1	5'-GGACGACGATGACAAGTTTGAGGGGAAGACTTTAGTGTC-3'
F2	5'-CCGCTCGAGATGGATTACAAGGACGACGATGACAAG-3'
R	5'-CGCGGATCCTTAGTCTACTTCTCCATGCGTG-3'
Flag-N-Hsp90 α	
F1	5'-GGACGACGATGACAAG GACCAACCGATGGAGGAGGAG-3'
F2	5'-CCGCTCGAGATGGATTACAAGGACGACGATGACAAG-3'
R	5'-CGCGGATCCTCATTGAGCCTCATCATCGCTTA-3'
Flag-M-Hsp90 α	
F1	5'-GGACGACGATGACAAGAAGGAAGACAAAGAAGAAGAAAAAG-3'
F2	5'-CCGCTCGAGATG GATTACAAGGACGACGATGACAAG-3'
R	5'-CGCGGATCCTCACATATAGATCACTTCTAAGCC-3'
Flag-Hsp90 α	
F	5'-CCGCTCGAGATGGATTACAAGGATGACGACGATAAGATGCTGAGGAAACCCAGACC-3'
R	5'-CGCGGATCCTTAGTCTACTTCTCCATGCGTG-3'
Flag-Hsp90 α E47A	
F	5'-AAGAGATCTTCTGAGAGCGCTCATTCAAATTCATCA-3'
R	5'-TGATGAATTTGAAATGAGCGCTCTCAGAAAGATCTCTT-3'
Flag-Hsp90 α D93A	
F	5'-GAACTCTCACTATTGTGGCTACTGGAATTGGAATGAC-3'
R	5'-GTCATTCCAATTCAGTAGCCACAATAGTGAGAGTTC-3'
NC siRNA	
	Sense: 5'-UUCUCCGAACGUGUCACGUTT-3'; Antisense: 5'-ACGUGACACGUUCGGAGAATT-3'.
Hsp90 siRNA	
#1	Sense: 5'-CCCUUCUAAUUUGUCCACGTT-3'; Antisense: 5'-CGUGGGACAAUAGAAGGTT-3'.
#2	Sense: 5'-GGACAGUUGGAAUUCAGAGTT-3'; Antisense: 5'-CUCUGAAUCCAACUGUCCTT-3'.
PGK1 siRNA	
#1	Sense: 5'-GCUUCUGGGAACAAGGUUATT-3'; Antisense: 5'-UAACCUUGUCCAGAAGCTT-3'.
#2	Sense: 5'-CCUGGAAGGUAAAGUCCUUTT-3'; Antisense: 5'-AAGGACUUUACCUCCAGGTT-3'.

Table S1 Continued

Plasmid/siRNA name	Primer/siRNA sequence
HOP siRNA	
#1	Sense: 5'-GCUACUCCGAAGCUAUUAATT-3'; Antisense: 5'-UUAAUAGCUUCGGAGUAGCTT-3'.
#2	Sense: 5'-GCAAGACUGUCGACCUAAATT-3'; Antisense: 5'-UUUAGGUCGACAGUCUUGCTT-3'.
#3	Sense: 5'-GCCAGAGCCAAUGGAAGAATT-3'; Antisense: 5'-UUCUUCCAUUGGCUCUGGCTT-3'.
CDC37 siRNA	
#1	Sense: 5'-ACACAAGACCUUCGUGGAATT-3'; Antisense: 5'-UUCCACGAAGGUCUUGUGUTT-3'.
#2	Sense: 5'-CGGCAGUUCUUCACUAAGATT-3'; Antisense: 5'-UCUUGUGAAGAACUGCCGTT-3'.
GSK3 β siRNA	
#1	Sense: 5'-GCUGGAGUAUACACCAACUTT-3'; Antisense: 5'-AGUUGGUGUAUACUCCAGCTT-3'.
#2	Sense: 5'-GGACAAGAGAUUUAAAGAUUTT-3'; Antisense: 5'-AUUCUAAAUCUCUUGUCCTT-3'.

Table S2 Mass spectrometry analysis of proteins interacting with glycogen synthase kinase-3

Accession	Score	Mass	Matches	Sequences	emPAI	Name
sp P35579 MYH9_HUMAN	1.026	227,646	47	32	0.84	Myosin-9 OS = Homo sapiens OX = 9606 GN = MYH9 PE = 1 SV = 4
sp P60709 ACTB_HUMAN	344	42,052	18	10	2.11	Actin, cytoplasmic 1 OS = Homo sapiens OX = 9606 GN = ACTB PE = 1 SV = 1
tr A0A075B6Z2 A0A075B6Z2_HUMAN	248	2,220	27	1	1.81	T cell receptor alpha joining 56 (Fragment) OS = Homo sapiens OX = 9606 GN = TRAJ56 PE = 4 SV = 1
tr H0YH81 H0YH81_HUMAN	189	38,226	7	5	0.65	ATP synthase subunit beta (Fragment) OS = Homo sapiens OX = 9606 GN = ATP5F1B PE = 1 SV = 1
sp P06702 S10A9_HUMAN	159	13,291	7	2	1.49	Protein S100-A9 OS = Homo sapiens OX = 9606 GN = S100A9 PE = 1 SV = 1
sp Q02413 DSG1_HUMAN	139	114,702	7	7	0.22	Desmoglein-1 OS = Homo sapiens OX = 9606 GN = DSG1 PE = 1 SV = 2
sp P31944 CASPE_HUMAN	138	27,947	5	5	0.76	Caspase-14 OS = Homo sapiens OX = 9606 GN = CASP14 PE = 1 SV = 2
sp P81605 DCD_HUMAN	133	11,391	5	5	2.73	Dermcidin OS = Homo sapiens OX = 9606 GN = DCD PE = 1 SV = 2
tr A0A0C4DGB6 A0A0C4DGB6_HUMAN	121	71,177	4	4	0.2	Serum albumin OS = Homo sapiens OX = 9606 GN = ALB PE = 1 SV = 1
tr A0A087WVQ9 A0A087WVQ9_HUMAN	116	48,195	5	4	0.39	Elongation factor 1-alpha 1 OS = Homo sapiens OX = 9606 GN = EEF1A1 PE = 1 SV = 1
sp Q6UWP8 SBSN_HUMAN	114	60,562	6	4	0.3	Suprabasin OS = Homo sapiens OX = 9606 GN = SBSN PE = 1 SV = 2
sp P01040 CYTA_HUMAN	113	11,000	4	4	1.98	Cystatin-A OS = Homo sapiens OX = 9606 GN = CSTA PE = 1 SV = 1
sp P14923 PLAK_HUMAN	109	82,434	5	4	0.22	Junction plakoglobin OS = Homo sapiens OX = 9606 GN = JUP PE = 1 SV = 3
sp P00558 PGK1_HUMAN	99	44,985	5	3	0.43	Phosphoglycerate kinase 1 OS = Homo sapiens OX = 9606 GN = PGK1 PE = 1 SV = 3
sp P15924 DESP_HUMAN	96	334,021	6	4	0.05	Desmoplakin OS = Homo sapiens OX = 9606 GN = DSP PE = 1 SV = 3
tr F8VPE3 F8VPE3_HUMAN	95	14,598	3	2	0.87	Myosin light polypeptide 6 (Fragment) OS = Homo sapiens OX = 9606 GN = MYL6 PE = 1 SV = 1
sp P12273 PIP_HUMAN	94	16,847	3	3	0.73	Prolactin-inducible protein OS = Homo sapiens OX = 9606 GN = PIP PE = 1 SV = 1
sp Q9ULV4 COR1C_HUMAN	92	53,899	5	4	0.27	Coronin-1C OS = Homo sapiens OX = 9606 GN = CORO1C PE = 1 SV = 1
sp P29508 SPB3_HUMAN	91	44,594	7	5	0.43	Serpin B3 OS = Homo sapiens OX = 9606 GN = SERPINB3 PE = 1 SV = 2
sp P31151 S10A7_HUMAN	90	11,578	5	5	2.69	Protein S100-A7 OS = Homo sapiens OX = 9606 GN = S100A7 PE = 1 SV = 4
sp P68871 HBB_HUMAN	90	16,102	3	3	0.77	Hemoglobin subunit beta OS = Homo sapiens OX = 9606 GN = HBB PE = 1 SV = 2
sp P02489 CRYAA_HUMAN	86	20,011	3	1	0.17	Alpha-crystallin A chain OS = Homo sapiens OX = 9606 GN = CRYAA PE = 1 SV = 2
sp Q5D862 FILA2_HUMAN	86	249,296	4	4	0.05	Filaggrin-2 OS = Homo sapiens OX = 9606 GN = FLG2 PE = 1 SV = 1
sp Q71U36 TBA1A_HUMAN	82	50,788	4	3	0.21	Tubulin alpha-1A chain OS = Homo sapiens OX = 9606 GN = TUBA1A PE = 1 SV = 1
sp P01834 IGKC_HUMAN	78	11,929	2	1	0.66	Immunoglobulin kappa constant OS = Homo sapiens OX = 9606 GN = IGKC PE = 1 SV = 2

Table S2 Continued

Accession	Score	Mass	Matches	Sequences	emPAI	Name
sp P62805 H4_HUMAN	77	11,360	3	3	1.22	Histone H4 OS = Homo sapiens OX = 9606 GN = HIST1H4A PE = 1 SV = 2
sp P07900 HSP90A_HUMAN	77	85,006	1	1	0.04	Heat shock protein HSP 90-alpha OS = Homo sapiens OX = 9606 GN = HSP90AAA1 PE = 1 SV = 5
tr A0A0B4J259 A0A0B4J259_HUMAN	72	15,661	2	2	0.48	Lysozyme OS = Homo sapiens OX = 9606 GN = LYZ PE = 1 SV = 1
tr J3QRS3 J3QRS3_HUMAN	70	20,501	2	2	0.35	Myosin regulatory light chain 12A OS = Homo sapiens OX = 9606 GN = MYL12A PE = 1 SV = 1
tr Q5JP53 Q5JP53_HUMAN	66	48,135	3	3	0.22	Tubulin beta chain OS = Homo sapiens OX = 9606 GN = TUBB PE = 1 SV = 1
sp Q96P63 SPB12_HUMAN	66	46,646	3	3	0.23	Serp1n B12 OS = Homo sapiens OX = 9606 GN = SERPINB12 PE = 1 SV = 1
sp Q08554 DSC1_HUMAN	66	101,406	4	2	0.1	Desmocollin-1 OS = Homo sapiens OX = 9606 GN = DSC1 PE = 1 SV = 2
sp P05109 S10A8_HUMAN	65	10,885	4	3	2.01	Protein S100-A8 OS = Homo sapiens OX = 9606 GN = S100A8 PE = 1 SV = 1
sp Q86YZ3 HORN_HUMAN	62	283,140	5	4	0.06	Hornerin OS = Homo sapiens OX = 9606 GN = HRNR PE = 1 SV = 2
tr E7EUT5 E7EUT5_HUMAN	61	28,024	2	2	0.25	Glyceraldehyde-3-phosphate dehydrogenase OS = Homo sapiens OX = 9606 GN = GAPDH PE = 1 SV = 1
sp P06733 ENOA_HUMAN	60	47,481	2	2	0.14	Alpha-enolase OS = Homo sapiens OX = 9606 GN = ENO1 PE = 1 SV = 2
sp P07355 ANXA2_HUMAN	59	38,808	2	2	0.18	Annexin A2 OS = Homo sapiens OX = 9606 GN = ANXA2 PE = 1 SV = 2
sp Q13835 PKP1_HUMAN	58	84,119	1	1	0.04	Plakophilin-1 OS = Homo sapiens OX = 9606 GN = PKP1 PE = 1 SV = 2
sp P04040 CATA_HUMAN	56	59,947	2	2	0.11	Catalase OS = Homo sapiens OX = 9606 GN = CAT PE = 1 SV = 3
sp Q08188 TGM3_HUMAN	56	76,926	3	3	0.13	Protein-glutamine gamma-glutamyltransferase E OS = Homo sapiens OX = 9606 GN = TGM3 PE = 1 SV = 4
tr E9PKE3 E9PKE3_HUMAN	55	68,991	2	2	0.1	Heat shock cognate 71 kDa protein OS = Homo sapiens OX = 9606 GN = HSPA8 PE = 1 SV = 1
sp Q9NZT1 CALL5_HUMAN	54	15,883	4	3	1.17	Calmodulin-like protein 5 OS = Homo sapiens OX = 9606 GN = CALML5 PE = 1 SV = 2
sp P25705 ATPA_HUMAN	53	59,828	1	1	0.05	ATP synthase subunit alpha, mitochondrial OS = Homo sapiens OX = 9606 GN = ATP5F1A PE = 1 SV = 1
sp P69905 HBA_HUMAN	53	15,305	1	1	0.22	Hemoglobin subunit alpha OS = Homo sapiens OX = 9606 GN = HBA1 PE = 1 SV = 2
sp Q9HCY8 S10AE_HUMAN	52	11,826	1	1	0.29	Protein S100-A14 OS = Homo sapiens OX = 9606 GN = S100A14 PE = 1 SV = 1
sp Q09666 AHNK_HUMAN	49	629,213	1	1	0.01	Neuroblast differentiation-associated protein AHNK OS = Homo sapiens OX = 9606 GN = AHNK PE = 1 SV = 2
sp P10599 THIO_HUMAN	45	12,015	1	1	0.29	Thioredoxin OS = Homo sapiens OX = 9606 GN = TXN PE = 1 SV = 3
tr A0A1B0GU92 A0A1B0GU92_HUMAN	43	60,677	1	1	0.05	Uncharacterized protein OS = Homo sapiens OX = 9606 PE = 1 SV = 1

Table S2 Continued

Accession	Score	Mass	Matches	Sequences	emPAI	Name
tr B1AK87 B1AK87_HUMAN	41	29,562	1	1	0.11	Capping protein (actin filament) muscle Z-line, beta, isoform CRA_a OS = Homo sapiens OX = 9606 GN = CAPZB PE = 1 SV = 1
sp P20930 FLA_HUMAN	41	435,036	2	2	0.02	Flaggrin OS = Homo sapiens OX = 9606 GN = FLG PE = 1 SV = 3
tr A0A0U1RRH7 A0A0U1RRH7_HUMAN	39	18,541	1	1	0.18	Histone H2A OS = Homo sapiens OX = 9606 PE = 3 SV = 1
sp Q01469 FABP5_HUMAN	38	15,497	1	1	0.22	Fatty acid-binding protein, epidermal OS = Homo sapiens OX = 9606 GN = FABP5 PE = 1 SV = 3
sp P25311 ZA2G_HUMAN	37	34,465	2	2	0.2	Zinc-alpha-2-glycoprotein OS = Homo sapiens OX = 9606 GN = AZGP1 PE = 1 SV = 2
tr F5GYA2 F5GYA2_HUMAN	37	28,749	2	1	0.12	Uracil-DNA glycosylase OS = Homo sapiens OX = 9606 GN = UNG PE = 1 SV = 1
sp P47929 LEG7_HUMAN	37	15,123	1	1	0.23	Galectin-7 OS = Homo sapiens OX = 9606 GN = LGALS7 PE = 1 SV = 2
sp P31025 LCN1_HUMAN	36	19,409	1	1	0.17	Lipocalin-1 OS = Homo sapiens OX = 9606 GN = LCN1 PE = 1 SV = 1
tr H0YK49 H0YK49_HUMAN	35	24,259	2	1	0.29	Electron transfer flavoprotein subunit alpha, mitochondrial OS = Homo sapiens OX = 9606 GN = ETFA PE = 1 SV = 1
tr A0A1W2PQ63 A0A1W2PQ63_HUMAN	34	84,612	1	1	0.04	Pleckstrin homology-like domain family B member 2 (Fragment) OS = Homo sapiens OX = 9606 GN = PHLDB2 PE = 1 SV = 1
sp O75223 GGCT_HUMAN	32	21,222	2	2	0.34	Gamma-glutamylcyclotransferase OS = Homo sapiens OX = 9606 GN = GGCT PE = 1 SV = 1
tr A0A087X0D5 A0A087X0D5_HUMAN	33	36,873	1	1	0.09	Pro-cathepsin H OS = Homo sapiens OX = 9606 GN = CTSH PE = 1 SV = 1
sp P05089 ARGI1_HUMAN	32	34,884	3	2	0.2	Arginase-1 OS = Homo sapiens OX = 9606 GN = ARG1 PE = 1 SV = 2
sp Q6R2W3 SCND3_HUMAN	32	153,452	1	1	0.02	SCAN domain-containing protein 3 OS = Homo sapiens OX = 9606 GN = ZBED9 PE = 2 SV = 1
sp P06312 KV401_HUMAN	32	13,486	1	1	0.25	Immunoglobulin kappa variable 4-1 OS = Homo sapiens OX = 9606 GN = IGKV4-1 PE = 1 SV = 1
tr M0R1V7 M0R1V7_HUMAN	32	7,128	2	2	1.25	Ubiquitin-60S ribosomal protein L40 (Fragment) OS = Homo sapiens OX = 9606 GN = UBA52 PE = 1 SV = 1
sp O95969 SG1D2_HUMAN	31	10,260	1	1	0.34	Secretoglobulin family 1D member 2 OS = Homo sapiens OX = 9606 GN = SCGB1D2 PE = 2 SV = 1
sp Q81W75 SPA12_HUMAN	31	47,259	2	2	0.14	Serpin A12 OS = Homo sapiens OX = 9606 GN = SERPINA12 PE = 1 SV = 1
sp Q9NS67 GPR27_HUMAN	31	40,590	1	1	0.08	Probable G-protein coupled receptor 27 OS = Homo sapiens OX = 9606 GN = GPR27 PE = 2 SV = 1
sp Q9H2G2 SLK_HUMAN	31	143,234	1	1	0.02	STE20-like serine/threonine-protein kinase OS = Homo sapiens OX = 9606 GN = SLK PE = 1 SV = 1
sp P78524 ST5_HUMAN	31	127,603	1	1	0.03	Suppression of tumorigenicity 5 protein OS = Homo sapiens OX = 9606 GN = ST5 PE = 1 SV = 3

Table S2 Continued

Accession	Score	Mass	Matches	Sequences	emPAI	Name
sp O94906 PRPF6_HUMAN	30	107,656	1	1	0.03	Pre-mRNA-processing factor 6 OS = Homo sapiens OX = 9606 GN = PRPF6 PE = 1 SV = 1
sp P53597 SUCA_HUMAN	30	36,626	1	1	0.09	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS = Homo sapiens OX = 9606 GN = SUCLG1 PE = 1 SV = 4
tr E5RGS9 E5RGS9_HUMAN	30	6,260	1	1	0.58	Chromatin accessibility complex protein 1 OS = Homo sapiens OX = 9606 GN = CHRAC1 PE = 1 SV = 1
sp Q8N436 CPXM2_HUMAN	30	86,443	1	1	0.04	Inactive carboxypeptidase-like protein X2 OS = Homo sapiens OX = 9606 GN = CPXM2 PE = 2 SV = 3
tr F8WAJ0 F8WAJ0_HUMAN	29	84,148	1	1	0.04	RNA helicase OS = Homo sapiens OX = 9606 GN = DDX31 PE = 1 SV = 2
sp Q9BPV8 P2Y13_HUMAN	29	41,275	1	1	0.08	P2Y purinoceptor 13 OS = Homo sapiens OX = 9606 GN = P2RY13 PE = 2 SV = 3
tr K7EQQ1 K7EQQ1_HUMAN	28	18,732	1	1	0.18	Cleft lip and palate transmembrane protein 1 (Fragment) OS = Homo sapiens OX = 9606 GN = CLPTM1 PE = 1 SV = 1
tr E7EQB2 E7EQB2_HUMAN	28	78,459	3	3	0.13	Lactotransferrin (Fragment) OS = Homo sapiens OX = 9606 GN = LTF PE = 1 SV = 1
tr A0A0U1RQ15 A0A0U1RQ15_HUMAN	27	58,026	1	1	0.06	Sorbin and SH3 domain-containing protein 1 (Fragment) OS = Homo sapiens OX = 9606 GN = SORBS1 PE = 1 SV = 1
sp P11279 LAMP1_HUMAN	27	45,367	1	1	0.07	Lysosome-associated membrane glycoprotein 1 OS = Homo sapiens OX = 9606 GN = LAMP1 PE = 1 SV = 3
tr C9JM00 C9JM00_HUMAN	27	18,305	1	1	0.18	Serpin B7 (Fragment) OS = Homo sapiens OX = 9606 GN = SERPINB7 PE = 1 SV = 8
sp P14618 KPYM_HUMAN	27	58,470	1	1	0.06	Pyruvate kinase PKM OS = Homo sapiens OX = 9606 GN = PKM PE = 1 SV = 4
tr A0A087WX19 A0A087WX19_HUMAN	26	76,884	1	1	0.04	IQ domain-containing protein E OS = Homo sapiens OX = 9606 GN = IQCE PE = 1 SV = 1
tr R4GMN1 R4GMN1_HUMAN	26	56,043	1	1	0.06	Motile sperm domain-containing protein 2 OS = Homo sapiens OX = 9606 GN = MOSPD2 PE = 1 SV = 1
tr A0A286YES1 A0A286YES1_HUMAN	26	50,242	1	1	0.07	Immunoglobulin heavy constant gamma 3 (Fragment) OS = Homo sapiens OX = 9606 GN = IGHG3 PE = 1 SV = 1
sp Q9ULJ3 ZBT21_HUMAN	26	120,564	1	1	0.03	Zinc finger and BTB domain-containing protein 21 OS = Homo sapiens OX = 9606 GN = ZBTB21 PE = 1 SV = 2
sp O94776 MTA2_HUMAN	25	75,717	1	1	0.04	Metastasis-associated protein MTA2 OS = Homo sapiens OX = 9606 GN = MTA2 PE = 1 SV = 1
sp Q7ZZZ1 TICRR_HUMAN	25	212,721	1	1	0.02	Treslin OS = Homo sapiens OX = 9606 GN = TICRR PE = 1 SV = 2
sp P22528 SPR1B_HUMAN	25	10,337	1	1	0.34	Cornifin-B OS = Homo sapiens OX = 9606 GN = SPR1B PE = 1 SV = 2
sp Q5T750 XP32_HUMAN	25	28,557	1	1	0.12	Skin-specific protein 32 OS = Homo sapiens OX = 9606 GN = XP32 PE = 1 SV = 1
tr K7EL99 K7EL99_HUMAN	24	14,836	1	1	0.23	Tubulin-folding cofactor B (Fragment) OS = Homo sapiens OX = 9606 GN = TBCB PE = 1 SV = 2

Table S2 Continued

Accession	Score	Mass	Matches	Sequences	emPAI	Name
tr H7C4W4 H7C4W4_HUMAN	23	2,420	1	1	1.61	Follistatin-related protein 1 (Fragment) OS = Homo sapiens OX = 9606 GN = FSTL1 PE = 1 SV = 1
tr A0A0G2 QD0 A0A0G2 QD0_HUMAN	23	63,847	1	1	0.05	Lanosterol synthase (Fragment) OS = Homo sapiens OX = 9606 GN = LSS PE = 1 SV = 1
sp Q14807 KIF22_HUMAN	23	73,616	1	1	0.04	Kinesin-like protein KIF22 OS = Homo sapiens OX = 9606 GN = KIF22 PE = 1 SV = 5
sp Q9BX63 FANCL_HUMAN	23	142,785	2	1	0.02	Fanconi anemia group J protein OS = Homo sapiens OX = 9606 GN = BRIPI PE = 1 SV = 1
sp Q92556 ELMO1_HUMAN	23	84,517	1	1	0.04	Engulfment and cell motility protein 1 OS = Homo sapiens OX = 9606 GN = ELMO1 PE = 1 SV = 2
tr F5H070 F5H070_HUMAN	23	150,248	1	1	0.02	Lysine-specific demethylase 3A OS = Homo sapiens OX = 9606 GN = KDM3A PE = 1 SV = 2
sp O94988 FA13A_HUMAN	23	117,600	1	1	0.03	Protein FAM13A OS = Homo sapiens OX = 9606 GN = FAM13A PE = 1 SV = 2
tr H3BN02 H3BN02_HUMAN	23	129,653	1	1	0.03	Integrin alpha-X OS = Homo sapiens OX = 9606 GN = ITGAX PE = 1 SV = 1
tr HOYE71 HOYE71_HUMAN	23	10,673	1	1	0.32	Uncharacterized protein OBSCN-AS1 (Fragment) OS = Homo sapiens OX = 9606 GN = OBSCN-AS1 PE = 4 SV = 1
tr F5H6E2 F5H6E2_HUMAN	22	119,719	1	1	0.03	Unconventional myosin-1c OS = Homo sapiens OX = 9606 GN = MYO1C PE = 1 SV = 1
tr A0A0D9SENI1 A0A0D9SENI1_HUMAN	21	88,213	1	1	0.04	Prolyl endopeptidase FAP OS = Homo sapiens OX = 9606 GN = FAP PE = 1 SV = 1
sp Q8NB4 GOLM1_HUMAN	21	45,477	1	1	0.07	Golgi membrane protein 1 OS = Homo sapiens OX = 9606 GN = GOLM1 PE = 1 SV = 1
tr U3KPT7 U3KPT7_HUMAN	20	25,117	1	1	0.13	Synaptosomal-associated protein 47 (Fragment) OS = Homo sapiens OX = 9606 GN = SNAP47 PE = 1 SV = 1
sp Q9NV70 EXOC1_HUMAN	20	102,772	1	1	0.03	Exocyst complex component 1 OS = Homo sapiens OX = 9606 GN = EXOC1 PE = 1 SV = 4
sp Q6NWWY9 PR40B_HUMAN	19	99,638	1	1	0.03	Pre-mRNA-processing factor 40 homolog B OS = Homo sapiens OX = 9606 GN = PRPF40B PE = 1 SV = 1
sp Q9H2Y7 ZN106_HUMAN	19	210,693	1	1	0.02	Zinc finger protein 106 OS = Homo sapiens OX = 9606 GN = ZNF106 PE = 1 SV = 1
tr E5RIG8 E5RIG8_HUMAN	19	15,899	1	1	0.21	Pro-neuregulin-1, membrane-bound isoform (Fragment) OS = Homo sapiens OX = 9606 GN = NRG1 PE = 1 SV = 1
sp Q92540 SMG7_HUMAN	19	127,886	1	1	0.03	Protein SMG7 OS = Homo sapiens OX = 9606 GN = SMG7 PE = 1 SV = 2
tr E7ERF2 E7ERF2_HUMAN	19	47,394	1	1	0.07	T-complex protein 1 subunit alpha OS = Homo sapiens OX = 9606 GN = TCP1 PE = 1 SV = 1
tr A0A0G2 JMZ6 A0A0G2 JMZ6_HUMAN	18	99,019	1	1	0.03	Kinesin-like protein (Fragment) OS = Homo sapiens OX = 9606 GN = KIF5C PE = 1 SV = 1
tr MQZJ5 MQZJ5_HUMAN	17	25,892	1	1	0.13	Calcium-binding mitochondrial carrier protein ScaMC-3 (Fragment) OS = Homo sapiens OX = 9606 GN = SLC25A23 PE = 1 SV = 1

Table S2 Continued

Accession	Score	Mass	Matches	Sequences	emPAI	Name
tr H0Y798 H0Y798_HUMAN	16	9,189	1	1	0.38	Propionyl-CoA carboxylase alpha chain, mitochondrial (Fragment) OS = Homo sapiens OX = 9606 GN = PCCA PE = 1 SV = 1
tr H0YIP0 H0YIP0_HUMAN	16	24,350	1	1	0.14	Methionine--tRNA ligase, cytoplasmic (Fragment) OS = Homo sapiens OX = 9606 GN = MARS PE = 1 SV = 1
sp Q4VNC0 AT135_HUMAN	16	139,119	1	1	0.02	Probable cation-transporting ATPase 13A5 OS = Homo sapiens OX = 9606 GN = ATP13A5 PE = 2 SV = 1
sp Q6PIF6 MYO7B_HUMAN	16	243,612	1	1	0.01	Unconventional myosin-VIIIb OS = Homo sapiens OX = 9606 GN = MYO7B PE = 1 SV = 2
tr H0Y525 H0Y525_HUMAN	15	8,648	1	1	0.4	Ethylmalonyl-CoA decarboxylase (Fragment) OS = Homo sapiens OX = 9606 GN = ECHDC1 PE = 1 SV = 1
sp Q6E0U4 DMKN_HUMAN	15	47,282	1	1	0.07	Dermokine OS = Homo sapiens OX = 9606 GN = DMKN PE = 1 SV = 3