

Supplementary Table 2. 22DS group<Control group

Accession	Description	MW [kDa]	Area					
			#01 Control1	#02 Control2	#03 Control3	#04 22DS1_1	#05 22DS2_1	#06 22DS3_1
Q6PJT7	Zinc finger CCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 - [ZC3HE_HUMAN]	82.8	5.452E6	5.508E6	5.568E6	0.000E0	0.000E0	0.000E0
Q92600	Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1 - [RCD1_HUMAN]	33.6	1.335E7	1.288E7	1.228E7	0.000E0	0.000E0	0.000E0
Q9UEY8	Gamma-adducin OS=Homo sapiens GN=ADD3 PE=1 SV=1 - [ADDG_HUMAN]	79.1	1.362E7	1.466E7	1.356E7	0.000E0	0.000E0	0.000E0
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	45.4	3.515E7	3.495E7	3.225E7	0.000E0	0.000E0	0.000E0
Q9UBD5	Origin recognition complex subunit 3 OS=Homo sapiens GN=ORC3 PE=1 SV=1 - [ORC3_HUMAN]	82.2	1.217E7	1.365E7	1.288E7	0.000E0	0.000E0	0.000E0
Q12974	Protein tyrosine phosphatase type IVA 2 OS=Homo sapiens GN=PTP4A2 PE=1 SV=1 - [TP4A2_HUMAN]	19.1	9.014E6	8.991E6	9.991E6	0.000E0	0.000E0	0.000E0
P52756	RNA-binding protein 5 OS=Homo sapiens GN=RBM5 PE=1 SV=2 - [RBM5_HUMAN]	92.1	1.093E7	9.640E6	1.025E7	0.000E0	0.000E0	0.000E0
P56385	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2 - [ATP5I_HUMAN]	7.9	3.580E7	4.082E7	3.681E7	0.000E0	0.000E0	0.000E0
Q9Y2D4	Exocyst complex component 6B OS=Homo sapiens GN=EXOC6B PE=1 SV=3 - [EXC6B_HUMAN]	94.1	6.532E6	5.692E6	5.781E6	0.000E0	0.000E0	0.000E0
O95155	Ubiquitin conjugation factor E4 B OS=Homo sapiens GN=UBE4B PE=1 SV=1 - [UBE4B_HUMAN]	146.1	4.958E8	4.424E8	5.190E8	0.000E0	0.000E0	0.000E0
O75340	Programmed cell death protein 6 OS=Homo sapiens GN=PDCC6 PE=1 SV=1 - [PDCC6_HUMAN]	21.9	7.486E7	6.373E7	7.261E7	0.000E0	0.000E0	0.000E0
Q9H0R6	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial OS=Homo sapiens GN=QRSL1 PE=1 SV=2 - [GATA_HUMAN]	57.4	7.568E6	8.843E6	7.653E6	0.000E0	0.000E0	0.000E0
P29323	Ephrin type-B receptor 2 OS=Homo sapiens GN=EPHB2 PE=1 SV=5 - [EPHB2_HUMAN]	117.4	3.212E7	2.678E7	2.849E7	0.000E0	0.000E0	0.000E0
Q29RF7	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDSSA PE=1 SV=1 - [PDS5A_HUMAN]	150.7	2.769E7	3.352E7	3.045E7	0.000E0	0.000E0	0.000E0
P50336	Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1 - [PPOX_HUMAN]	50.7	1.766E7	1.456E7	1.661E7	0.000E0	0.000E0	0.000E0
Q9H7Z7	Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1 - [PTGES2_HUMAN]	41.9	2.632E7	2.476E7	2.133E7	0.000E0	0.000E0	0.000E0
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4 - [F1142_HUMAN]	55.4	8.833E6	1.074E7	1.079E7	0.000E0	0.000E0	0.000E0
Q9C0E8	Protein lunapark OS=Homo sapiens GN=LNP PE=1 SV=2 - [LNP_HUMAN]	47.7	2.006E7	2.154E7	1.727E7	0.000E0	0.000E0	0.000E0
P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=1 SV=4 - [RPAB3_HUMAN]	17.1	1.823E7	1.623E7	2.031E7	0.000E0	0.000E0	0.000E0
Q96TA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	84.1	1.001E7	1.257E7	1.167E7	0.000E0	0.000E0	0.000E0
P48728	Aminomethyltransferase, mitochondrial OS=Homo sapiens GN=AMT PE=1 SV=1 - [GCST_HUMAN]	43.9	7.981E6	7.047E6	6.308E6	0.000E0	0.000E0	0.000E0
Q9BRJ7	Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 - [SDOS_HUMAN]	23.3	5.064E6	6.432E6	5.619E6	0.000E0	0.000E0	0.000E0
Q5T160	Probable arginine-tRNA ligase, mitochondrial OS=Homo sapiens GN=RARS2 PE=1 SV=1 - [SYRM_HUMAN]	65.5	7.609E6	9.739E6	8.866E6	0.000E0	0.000E0	0.000E0
Q9BW72	HIG1 domain family member 2A, mitochondrial OS=Homo sapiens GN=HIGD2A PE=1 SV=1 - [HIG2A_HUMAN]	11.5	1.135E8	9.546E7	9.022E7	0.000E0	0.000E0	0.000E0
P98164	Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3 - [LRP2_HUMAN]	521.6	1.799E7	2.316E7	2.078E7	0.000E0	0.000E0	0.000E0
Q15349	Ribosomal protein S6 kinase alpha-2 OS=Homo sapiens GN=RPS6KA2 PE=1 SV=2 - [KS6A2_HUMAN]	83.2	5.038E6	4.064E6	5.179E6	0.000E0	0.000E0	0.000E0
Q8NHP6	Motile sperm domain-containing protein 2 OS=Homo sapiens GN=MOSPD2 PE=1 SV=1 - [MSPD2_HUMAN]	59.7	3.865E7	3.861E7	3.049E7	0.000E0	0.000E0	0.000E0
Q14839	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN]	217.9	5.524E7	4.577E7	4.284E7	0.000E0	0.000E0	0.000E0
Q96A26	Protein FAM162A OS=Homo sapiens GN=FAM162A PE=1 SV=2 - [F162A_HUMAN]	17.3	2.841E7	3.679E7	3.583E7	0.000E0	0.000E0	0.000E0
Q99459	Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 - [CDC5L_HUMAN]	92.2	4.728E7	6.104E7	4.958E7	0.000E0	0.000E0	0.000E0
Q9Y3D6	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2 - [FIS1_HUMAN]	16.9	4.273E7	3.271E7	3.530E7	0.000E0	0.000E0	0.000E0
Q9UPY8	Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 - [MARE3_HUMAN]	32.0	2.142E7	2.691E7	2.097E7	0.000E0	0.000E0	0.000E0
Q9HB90	Ras-related GTP-binding protein C OS=Homo sapiens GN=RRAGC PE=1 SV=1 - [RRAGC_HUMAN]	44.2	8.866E6	9.284E6	6.999E6	0.000E0	0.000E0	0.000E0
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 - [SMCA5_HUMAN]	121.8	4.919E7	4.387E7	3.644E7	0.000E0	0.000E0	0.000E0
Q9NX62	Inositol monophosphatase 3 OS=Homo sapiens GN=IMPAD1 PE=1 SV=1 - [IMPA3_HUMAN]	38.7	4.526E7	5.382E7	3.969E7	0.000E0	0.000E0	0.000E0
Q6P3R8	Serine/threonine-protein kinase Nek5 OS=Homo sapiens GN=NEK5 PE=2 SV=1 - [NEK5_HUMAN]	81.4	1.406E7	1.132E7	1.040E7	0.000E0	0.000E0	0.000E0
Q15120	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial OS=Homo sapiens GN=PKD3 PE=1 SV=1 - [PKD3_HUMAN]	46.9	4.129E6	3.611E6	4.964E6	0.000E0	0.000E0	0.000E0
O94829	Importin-13 OS=Homo sapiens GN=IPO13 PE=1 SV=3 - [IPO13_HUMAN]	108.1	2.464E6	2.438E6	1.821E6	0.000E0	0.000E0	0.000E0
Q9Y2W2	WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=1 SV=1 - [WBP11_HUMAN]	70.0	1.155E7	8.332E6	9.735E6	0.000E0	0.000E0	0.000E0
O95470	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3 - [SGPL1_HUMAN]	63.5	1.056E8	1.071E8	7.780E7	0.000E0	0.000E0	0.000E0
Q9BZE1	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2 - [RM37_HUMAN]	48.1	2.599E7	2.449E7	1.857E7	0.000E0	0.000E0	0.000E0
P30519	Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 - [HMOX2_HUMAN]	36.0	1.657E7	1.929E7	1.364E7	0.000E0	0.000E0	0.000E0
Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 - [MACD1_HUMAN]	35.5	1.091E7	1.133E7	8.114E6	0.000E0	0.000E0	0.000E0
O75427	Leucine-rich repeat and calponin homology domain-containing protein 4 OS=Homo sapiens GN=LRCH4 PE=1 SV=2 - [LRCH4_HUMAN]	73.4	9.946E6	1.053E7	7.436E6	0.000E0	0.000E0	0.000E0
Q9HC35	Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3 - [EMAL4_HUMAN]	108.8	1.997E7	2.848E7	2.639E7	0.000E0	0.000E0	0.000E0
Q9UMF0	Intercellular adhesion molecule 5 OS=Homo sapiens GN=ICAM5 PE=1 SV=3 - [ICAM5_HUMAN]	97.1	5.166E7	7.394E7	6.785E7	0.000E0	0.000E0	0.000E0
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 - [DIAP1_HUMAN]	141.3	7.769E7	1.038E8	7.667E7	0.000E0	0.000E0	0.000E0
O14497	AT-rich interactive domain-containing protein 1A OS=Homo sapiens GN=ARID1A PE=1 SV=3 - [AR1A_HUMAN]	241.9	5.132E7	6.042E7	7.331E7	0.000E0	0.000E0	0.000E0
Q96A06	Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens GN=PBXIP1 PE=1 SV=1 - [PBIP1_HUMAN]	80.6	2.501E7	3.523E7	2.776E7	0.000E0	0.000E0	0.000E0
Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1 - [SLK_HUMAN]	142.6	8.822E6	1.050E7	7.290E6	0.000E0	0.000E0	0.000E0
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1 - [P4K2A_HUMAN]	54.0	4.505E6	6.495E6	6.086E6	0.000E0	0.000E0	0.000E0
Q9H4A6	Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 - [GOLP3_HUMAN]	33.8	1.437E7	1.536E7	1.051E7	0.000E0	0.000E0	0.000E0
Q9HCU4	Cadherin EGF LAG seven-pass G-type receptor 2 OS=Homo sapiens GN=CELSR2 PE=1 SV=1 - [CELR2_HUMAN]	317.3	1.444E7	1.111E7	1.005E7	0.000E0	0.000E0	0.000E0
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]	67.4	4.323E6	2.951E6	4.143E6	0.000E0	0.000E0	0.000E0
Q92785	Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=1 SV=2 - [REQU_HUMAN]	44.1	9.381E6	1.000E7	6.737E6	0.000E0	0.000E0	0.000E0
P54619	5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1 - [AAKG1_HUMAN]	37.6	5.485E6	8.153E6	6.475E6	0.000E0	0.000E0	0.000E0
Q9BQB6	Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1 - [VKOR1_HUMAN]	18.2	3.039E7	2.844E7	2.027E7	0.000E0	0.000E0	0.000E0
Q8NFV4	Alpha/beta hydrolase domain-containing protein 11 OS=Homo sapiens GN=ABHD11 PE=2 SV=1 - [ABHDB_HUMAN]	34.7	1.136E7	1.199E7	1.632E7	0.000E0	0.000E0	0.000E0
Q92620	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens GN=DHX38 PE=1 SV=2 - [PRP16_HUMAN]	140.4	7.682E6	5.824E6	5.230E6	0.000E0	0.000E0	0.000E0
P50148	Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens GN=GNAQ PE=1 SV=4 - [GNAQ_HUMAN]	42.1	1.562E7	1.582E7	1.074E7	0.000E0	0.000E0	0.000E0
Q9Y3C0	WASH complex subunit CCDC53 OS=Homo sapiens GN=CCDC53 PE=1 SV=1 - [CCD53_HUMAN]	21.2	5.776E6	8.677E6	6.899E6	0.000E0	0.000E0	0.000E0
O95983	Methyl-CpG-binding domain protein 3 OS=Homo sapiens GN=MBD3 PE=1 SV=1 - [MBD3_HUMAN]	32.8	1.163E7	1.082E7	7.692E6	0.000E0	0.000E0	0.000E0
Q7Z7H8	39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 - [RM10_HUMAN]	29.3	2.561E7	2.070E7	1.688E7	0.000E0	0.000E0	0.000E0
Q9Y5Q9	General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1 - [TF3C3_HUMAN]	101.2	1.595E7	1.426E7	1.043E7	0.000E0	0.000E0	0.000E0
P48059	LIM and senescent cell antigen-like-containing domain protein 1 OS=Homo sapiens GN=LIMS1 PE=1 SV=4 - [LIMS1_HUMAN]	37.2	1.588E7	1.829E7	2.382E7	0.000E0	0.000E0	0.000E0
Q96AX1	Vacuolar protein sorting-associated protein 33A OS=Homo sapiens GN=VPS33A PE=1 SV=1 - [VP33A_HUMAN]	67.6	5.987E6	9.025E6	6.982E6	0.000E0	0.000E0	0.000E0
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 - [INF2_HUMAN]	135.5	5.672E6	7.113E6	4.662E6	0.000E0	0.000E0	0.000E0
P60604	Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 - [UB2G2_HUMAN]	18.6	2.400E7	1.972E7	1.562E7	0.000E0	0.000E0	0.000E0
O95837	Guanine nucleotide-binding protein subunit alpha-14 OS=Homo sapiens GN=GNA14 PE=1 SV=1 - [GNA14_HUMAN]	41.5	1.341E7	1.212E7	8.649E6	0.000E0	0.000E0	0.000E0
Q8N5Z0	Kynurenine/alpha-aminoacidate aminotransferase, mitochondrial OS=Homo sapiens GN=AADAT PE=1 SV=2 - [AADAT_HUMAN]	47.3	7.665E6	1.150E7	8.568E6	0.000E0	0.000E0	0.000E0
Q9NWX8	BRISCA and BRCA1-A complex member 1 OS=Homo sapiens GN=BABAM1 PE=1 SV=1 - [BABA1_HUMAN]	36.5	4.012E6	6.255E6	5.126E6	0.000E0	0.000E0	0.000E0
Q8IWS0	PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1 - [PHF6_HUMAN]	41.3	1.188E7	9.396E6	7.496E6	0.000E0	0.000E0	0.000E0
P22694	cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=2 - [KAPCB_HUMAN]	40.6	1.751E7	2.583E7	1.757E7	0.000E0	0.000E0	0.000E0
Q8NBM8	Preylcysteine oxidase-like OS=Homo sapiens GN=PCYOX1L PE=1 SV=2 - [PCYXL_HUMAN]	54.6	2.112E7	1.937E7	1.302E7	0.000E0	0.000E0	0.000E0
Q9NRX2	39S ribosomal protein L17, mitochondrial OS=Homo sapiens GN=MRPL17 PE=1 SV=1 - [RM17_HUMAN]	20.0	6.534E6	1.034E7	7.633E6	0.000E0	0.000E0	0.000E0
O15270	Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1 - [SPTC2_HUMAN]	62.9	5.706E7	8.205E7	5.371E7	0.000E0	0.000E0	0.000E0
Q9UM54	Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4 - [MYO6_HUMAN]	149.6	8.382E6	9.675E6	5.871E6	0.000E0	0.000E0	0.000E0
O15091	Mitochondrial ribonuclease P protein 3 OS=Homo sapiens GN=KIAA0391 PE=1 SV=2 - [MRRP3_HUMAN]	67.3	5.801E6	6.969E6	4.228E6	0.000E0	0.000E0	0.000E0

Q9BXK5	Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1 - [B2L13_HUMAN]	52.7	2.522E7	1.809E7	1.607E7	0.000E0	0.000E0	0.000E0
Q71SY5	Mediator of RNA polymerase II transcription subunit 25 OS=Homo sapiens GN=MED25 PE=1 SV=2 - [MED25_HUMAN]	78.1	5.045E6	5.387E6	3.312E6	0.000E0	0.000E0	0.000E0
P49427	Ubiquitin-conjugating enzyme E2 R1 OS=Homo sapiens GN=CDC34 PE=1 SV=2 - [UB2R1_HUMAN]	26.7	1.364E7	1.333E7	8.501E6	0.000E0	0.000E0	0.000E0
Q969V3	Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2 - [NCLN_HUMAN]	62.9	5.938E7	4.274E7	7.123E7	0.000E0	0.000E0	0.000E0
Q68EM7	Rho GTPase-activating protein 17 OS=Homo sapiens GN=ARHGAP17 PE=1 SV=1 - [RHG17_HUMAN]	95.4	1.140E8	9.610E7	6.818E7	0.000E0	0.000E0	0.000E0
P43007	Neutral amino acid transporter A OS=Homo sapiens GN=SLC1A4 PE=1 SV=1 - [SATT_HUMAN]	55.7	1.865E7	1.122E7	1.479E7	0.000E0	0.000E0	0.000E0
O00505	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 - [IMA4_HUMAN]	57.8	3.037E7	3.668E7	2.163E7	0.000E0	0.000E0	0.000E0
Q9UJX3	Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 - [APC7_HUMAN]	66.8	9.835E6	7.952E6	5.799E6	0.000E0	0.000E0	0.000E0
Q8N6T3	ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=2 - [ARFG1_HUMAN]	44.6	1.155E7	1.470E7	8.684E6	0.000E0	0.000E0	0.000E0
Q6P1J9	Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1 - [CDC73_HUMAN]	60.5	1.322E7	1.092E7	7.727E6	0.000E0	0.000E0	0.000E0
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens GN=PPP1R10 PE=1 SV=1 - [PP1RA_HUMAN]	99.0	1.711E7	1.074E7	1.814E7	0.000E0	0.000E0	0.000E0
Q9P253	Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2 - [VPS18_HUMAN]	110.1	8.921E6	7.616E6	5.186E6	0.000E0	0.000E0	0.000E0
Q6DKK2	Tetratricopeptide repeat protein 19, mitochondrial OS=Homo sapiens GN=TTC19 PE=1 SV=4 - [TTC19_HUMAN]	42.4	6.898E6	1.117E7	1.162E7	0.000E0	0.000E0	0.000E0
Q9HCM4	Band 4.1-like protein 5 OS=Homo sapiens GN=EPB41L5 PE=1 SV=3 - [E41L5_HUMAN]	81.8	7.145E6	6.942E6	4.215E6	0.000E0	0.000E0	0.000E0
Q8N999	Uncharacterized protein C12orf29 OS=Homo sapiens GN=C12orf29 PE=1 SV=2 - [CL029_HUMAN]	37.5	9.283E6	1.424E7	9.067E6	0.000E0	0.000E0	0.000E0
P04216	Thy-1 membrane glycoprotein OS=Homo sapiens GN=THY1 PE=1 SV=2 - [THY1_HUMAN]	17.9	2.110E7	2.460E7	1.401E7	0.000E0	0.000E0	0.000E0
Q8NB37	Parkinson disease 7 domain-containing protein 1 OS=Homo sapiens GN=PDDC1 PE=1 SV=1 - [PDDC1_HUMAN]	23.3	1.012E7	1.761E7	1.366E7	0.000E0	0.000E0	0.000E0
P51553	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 - [IDH3G_HUMAN]	42.8	1.147E7	7.188E6	1.261E7	0.000E0	0.000E0	0.000E0
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 - [PTN1_HUMAN]	49.9	3.933E7	3.805E7	2.269E7	0.000E0	0.000E0	0.000E0
Q08431	Lactadherin OS=Homo sapiens GN=OX=9606 GN=MFG8 PE=1 SV=3 - [MFGM_HUMAN]	43.1	3.088E7	1.948E7	1.977E7	0.000E0	0.000E0	0.000E0
Q96KG9	N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=1 SV=1 - [NTKL_HUMAN]	89.6	6.420E6	1.141E7	8.991E6	0.000E0	0.000E0	0.000E0
Q12846	Syntaxin-4 OS=Homo sapiens GN=STX4 PE=1 SV=2 - [STX4_HUMAN]	34.2	3.521E6	4.673E6	2.654E6	0.000E0	0.000E0	0.000E0
Q99943	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha OS=Homo sapiens GN=AGPAT1 PE=1 SV=2 - [PLCA_HUMAN]	31.7	3.987E7	3.031E7	2.253E7	0.000E0	0.000E0	0.000E0
P45985	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 - [MP2K4_HUMAN]	44.3	1.285E7	1.016E7	7.187E6	0.000E0	0.000E0	0.000E0
P09669	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2 - [COX6C_HUMAN]	8.8	4.101E7	2.321E7	3.072E7	0.000E0	0.000E0	0.000E0
Q9NZV5	Selenoprotein N OS=Homo sapiens GN=SELENON PE=1 SV=5 - [SELN_HUMAN]	65.8	7.325E6	7.437E6	4.275E6	0.000E0	0.000E0	0.000E0
Q92692	Nectin-2 OS=Homo sapiens GN=NECTIN2 PE=1 SV=1 - [NECT2_HUMAN]	57.7	3.699E7	2.126E7	2.660E7	0.000E0	0.000E0	0.000E0
Q13084	39S ribosomal protein L28, mitochondrial OS=Homo sapiens GN=MRPL28 PE=1 SV=4 - [RM28_HUMAN]	30.1	7.914E6	1.312E7	8.661E6	0.000E0	0.000E0	0.000E0
Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 OS=Homo sapiens GN=SMARCD1 PE=1 SV=2 - [SMRD1_HUMAN]	58.2	7.057E7	1.271E8	1.006E8	0.000E0	0.000E0	0.000E0
Q9H6R3	Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Homo sapiens GN=ACSS3 PE=1 SV=1 - [ACSS3_HUMAN]	74.7	3.467E7	3.599E7	2.040E7	0.000E0	0.000E0	0.000E0
O00186	Syntaxin-binding protein 3 OS=Homo sapiens GN=STXB3 PE=1 SV=2 - [STXB3_HUMAN]	67.7	9.205E6	6.481E6	5.263E6	0.000E0	0.000E0	0.000E0
Q9UF83	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2 - [YM012_HUMAN]	59.4	2.727E7	4.838E7	3.409E7	0.000E0	0.000E0	0.000E0
Q8IWA5	Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=3 - [CTL2_HUMAN]	80.1	3.674E7	5.768E7	3.471E7	0.000E0	0.000E0	0.000E0
P40763	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 - [STAT3_HUMAN]	88.0	8.574E6	4.775E6	8.405E6	0.000E0	0.000E0	0.000E0
Q15382	GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1 - [RHEB_HUMAN]	20.5	2.492E7	4.582E7	4.212E7	0.000E0	0.000E0	0.000E0
Q8IXH7	Negative elongation factor C/D OS=Homo sapiens GN=NELFCD PE=1 SV=2 - [NELFD_HUMAN]	66.2	6.446E6	1.099E7	7.179E6	0.000E0	0.000E0	0.000E0
Q9C040	Tripalmitolein-containing protein 2 OS=Homo sapiens GN=TRIM2 PE=1 SV=1 - [TRIM2_HUMAN]	81.5	6.450E6	1.190E7	8.872E6	0.000E0	0.000E0	0.000E0
O95487	Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2 - [SC24B_HUMAN]	137.3	5.717E6	4.705E6	8.357E6	0.000E0	0.000E0	0.000E0
P29992	Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2 - [GNA11_HUMAN]	42.1	1.903E7	1.666E7	1.010E7	0.000E0	0.000E0	0.000E0
Q9NZ32	Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1 - [ARP10_HUMAN]	46.3	1.305E7	1.508E7	7.965E6	0.000E0	0.000E0	0.000E0
O00170	AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2 - [AIP_HUMAN]	37.6	1.055E7	1.789E7	1.129E7	0.000E0	0.000E0	0.000E0
Q86YD1	Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1 - [PTOV1_HUMAN]	46.8	6.061E6	4.306E6	3.312E6	0.000E0	0.000E0	0.000E0
P35250	Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 - [RFC2_HUMAN]	39.1	1.581E7	1.726E7	9.135E6	0.000E0	0.000E0	0.000E0
P61011	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1 - [SRP54_HUMAN]	55.7	1.986E7	2.327E7	1.211E7	0.000E0	0.000E0	0.000E0
Q8NBN3	Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3 - [TM87A_HUMAN]	63.4	2.932E7	5.422E7	3.828E7	0.000E0	0.000E0	0.000E0
O60832	H/AcA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMAN]	57.6	1.374E7	1.039E7	7.237E6	0.000E0	0.000E0	0.000E0
P54753	Ephrin type-B receptor 3 OS=Homo sapiens GN=EPHB3 PE=1 SV=2 - [EPHB3_HUMAN]	110.3	3.162E7	5.500E7	6.020E7	0.000E0	0.000E0	0.000E0
P60201	Myelin proteolipid protein OS=Homo sapiens GN=PLP1 PE=1 SV=2 - [MYPR_HUMAN]	30.1	2.280E7	1.188E7	1.809E7	0.000E0	0.000E0	0.000E0
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN]	206.3	9.234E6	1.444E7	8.210E6	0.000E0	0.000E0	0.000E0
Q93034	Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4 - [CUL5_HUMAN]	90.9	6.069E6	1.119E7	7.684E6	0.000E0	0.000E0	0.000E0
Q96A65	Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1 - [EXOC4_HUMAN]	110.4	4.737E6	6.742E6	3.597E6	0.000E0	0.000E0	0.000E0
Q8IWX3	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [ANKH1_HUMAN]	269.3	1.235E7	2.442E7	1.974E7	0.000E0	0.000E0	0.000E0
P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2 - [PI42A_HUMAN]	46.2	8.898E6	1.570E7	9.729E6	0.000E0	0.000E0	0.000E0
Q96T76	MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2 - [MMS19_HUMAN]	113.2	2.334E7	1.306E7	1.441E7	0.000E0	0.000E0	0.000E0
O00192	Armadillo repeat protein deleted in velo-cardio-facial syndrome OS=Homo sapiens GN=ARVCF PE=1 SV=1 - [ARVC_HUMAN]	104.6	4.446E7	8.827E7	6.391E7	0.000E0	0.000E0	0.000E0
Q9Y399	28S ribosomal protein S2, mitochondrial OS=Homo sapiens GN=MRPS2 PE=1 SV=1 - [RT02_HUMAN]	33.2	1.725E7	1.479E7	8.463E6	0.000E0	0.000E0	0.000E0
Q712K3	Ubiquitin-conjugating enzyme E2 R2 OS=Homo sapiens GN=UBE2R2 PE=1 SV=1 - [UB2R2_HUMAN]	27.1	1.512E7	1.901E7	9.322E6	0.000E0	0.000E0	0.000E0
P18858	DNA ligase 1 OS=Homo sapiens GN=LIG1 PE=1 SV=1 - [DNL1_HUMAN]	101.7	3.244E7	5.453E7	3.083E7	0.000E0	0.000E0	0.000E0
Q9Y625	Glypican-6 OS=Homo sapiens GN=GPC6 PE=1 SV=1 - [GPC6_HUMAN]	62.7	7.912E7	4.146E7	5.200E7	0.000E0	0.000E0	0.000E0
Q96JJ3	Engulfment and cell motility protein 2 OS=Homo sapiens GN=ELMO2 PE=1 SV=2 - [ELMO2_HUMAN]	82.6	4.193E6	6.537E6	3.472E6	0.000E0	0.000E0	0.000E0
Q99986	Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 - [VRK1_HUMAN]	45.4	1.507E7	9.456E6	8.106E6	0.000E0	0.000E0	0.000E0
P35270	Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1 - [SPRE_HUMAN]	28.0	7.087E6	5.569E6	1.072E7	0.000E0	0.000E0	0.000E0
Q9UPT5	Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3 - [EXOC7_HUMAN]	83.3	6.611E6	8.801E6	4.318E6	0.000E0	0.000E0	0.000E0
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 - [AIMP2_HUMAN]	35.3	2.360E7	3.879E7	2.116E7	0.000E0	0.000E0	0.000E0
Q96DB5	Regulator of microtubule dynamics protein 1 OS=Homo sapiens GN=RMDN1 PE=1 SV=1 - [RMD1_HUMAN]	35.8	1.437E7	8.343E6	1.738E7	0.000E0	0.000E0	0.000E0
Q13501	Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1 - [SQSTM1_HUMAN]	47.7	3.431E6	5.524E6	2.944E6	0.000E0	0.000E0	0.000E0
Q9H6E4	Coiled-coil domain-containing protein 134 OS=Homo sapiens GN=CCDC134 PE=1 SV=1 - [CC134_HUMAN]	26.5	6.918E6	1.425E7	1.055E7	0.000E0	0.000E0	0.000E0
Q12873	Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3 - [CHD3_HUMAN]	226.4	4.673E7	3.934E7	2.221E7	0.000E0	0.000E0	0.000E0
O60684	Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1 - [IMA7_HUMAN]	60.0	2.000E7	2.723E7	1.317E7	0.000E0	0.000E0	0.000E0
Q722W9	39S ribosomal protein L21, mitochondrial OS=Homo sapiens GN=MRPL21 PE=1 SV=2 - [RM21_HUMAN]	22.8	3.032E7	2.805E7	1.452E7	0.000E0	0.000E0	0.000E0
Q727K6	Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1 - [CENPV_HUMAN]	29.9	7.322E7	4.451E7	9.396E7	0.000E0	0.000E0	0.000E0
Q9Y5Q8	General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=1 SV=2 - [TF3C5_HUMAN]	59.5	9.480E6	9.901E6	4.792E6	0.000E0	0.000E0	0.000E0
Q8WVC6	Dephospho-CoA kinase domain-containing protein OS=Homo sapiens GN=DCAKD PE=1 SV=1 - [DCAKD_HUMAN]	26.5	2.844E7	1.678E7	1.550E7	0.000E0	0.000E0	0.000E0
Q9GZM5	Protein YIPF3 OS=Homo sapiens GN=YIPF3 PE=1 SV=1 - [YIPF3_HUMAN]	38.2	3.175E7	2.462E7	1.503E7	0.000E0	0.000E0	0.000E0
O43681	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2 - [ASNA_HUMAN]	38.8	4.681E7	4.672E7	2.302E7	0.000E0	0.000E0	0.000E0
Q99720	Sigma non-opioid intracellular receptor 1 OS=Homo sapiens GN=SIGMAR1 PE=1 SV=1 - [SGMR1_HUMAN]	25.1	4.328E7	3.577E7	2.033E7	0.000E0	0.000E0	0.000E0
Q15904	V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2 - [VAS1_HUMAN]	52.0	2.012E7	1.709E7	9.341E6	0.000E0	0.000E0	0.000E0
Q9UPT9	Ubiquitin carboxyl-terminal hydrolase 22 OS=Homo sapiens GN=USP22 PE=1 SV=2 - [UBP22_HUMAN]	59.9	1.381E7	1.937E7	9.189E6	0.000E0	0.000E0	0.000E0
Q96SU4	Oxysterol-binding protein-related protein 9 OS=Homo sapiens GN=OSBPL9 PE=1 SV=2 - [OSBL9_HUMAN]	83.1	3.755E6	7.221E6	4.364E6	0.000E0	0.000E0	0.000E0
Q9BV20	Methylthioribose-1-phosphate isomerase OS=Homo sapiens GN=MR1 PE=1 SV=1 - [MTNA_HUMAN]	39.1	6.226E6	1.199E7	7.237E6	0.000E0	0.000E0	0.000E0
P51572	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3 - [BAP31_HUMAN]	28.0	1.590E8	7.751E7	1.053E8	0.000E0	0.000E0	0.000E0

Q9P2W9	Syntaxin-18 OS=Homo sapiens GN=STX18 PE=1 SV=1 - [STX18_HUMAN]	38.6	1.341E7	1.452E7	6.745E6	0.000E0	0.000E0	0.000E0
P33947	ER lumen protein-retaining receptor 2 OS=Homo sapiens GN=KDELRL2 PE=1 SV=1 - [ERD22_HUMAN]	24.4	8.000E6	6.087E6	3.683E6	0.000E0	0.000E0	0.000E0
Q96JB5	CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2 - [CK5P3_HUMAN]	56.9	1.627E7	1.224E7	7.509E6	0.000E0	0.000E0	0.000E0
Q9P003	Protein cornichon homolog 4 OS=Homo sapiens GN=CNH4 PE=1 SV=1 - [CNH4_HUMAN]	16.1	7.847E7	5.607E7	3.660E7	0.000E0	0.000E0	0.000E0
Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	180.5	1.120E7	6.929E6	5.642E6	0.000E0	0.000E0	0.000E0
Q9H330	Transmembrane protein 245 OS=Homo sapiens OX=9606 GN=TMEM245 PE=1 SV=3 - [TM245_HUMAN]	97.3	9.392E6	6.704E6	4.378E6	0.000E0	0.000E0	0.000E0
Q5VW32	BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1 - [BROX_HUMAN]	46.4	7.605E6	1.562E7	1.017E7	0.000E0	0.000E0	0.000E0
O15126	Secretory carrier-associated membrane protein 1 OS=Homo sapiens GN=SCAMP1 PE=1 SV=2 - [SCAM1_HUMAN]	37.9	1.393E7	1.098E7	6.325E6	0.000E0	0.000E0	0.000E0
P14209	CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1 - [CD99_HUMAN]	18.8	3.767E7	2.319E7	1.897E7	0.000E0	0.000E0	0.000E0
Q8IUR0	Trafficking protein particle complex subunit 5 OS=Homo sapiens GN=TRAPPC5 PE=1 SV=1 - [TPPC5_HUMAN]	20.8	3.839E6	8.141E6	8.088E6	0.000E0	0.000E0	0.000E0
Q8IUR7	Armado repeat-containing protein 8 OS=Homo sapiens GN=ARMC8 PE=1 SV=2 - [ARMC8_HUMAN]	75.5	4.483E6	7.581E6	3.909E6	0.000E0	0.000E0	0.000E0
Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	50.4	1.467E7	3.080E7	2.034E7	0.000E0	0.000E0	0.000E0
Q13636	Ras-related protein Rab-31 OS=Homo sapiens GN=RAB31 PE=1 SV=1 - [RAB31_HUMAN]	21.6	3.411E7	3.007E7	1.523E7	0.000E0	0.000E0	0.000E0
Q96IZ0	PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1 - [PAWR_HUMAN]	36.5	3.536E6	7.286E6	7.897E6	0.000E0	0.000E0	0.000E0
Q96IJ6	Mannose-1-phosphate guanylyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 - [GMPPA_HUMAN]	46.3	3.882E6	7.887E6	4.817E6	0.000E0	0.000E0	0.000E0
P52735	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2 PE=1 SV=2 - [VAV2_HUMAN]	101.2	6.244E6	1.112E7	5.828E6	0.000E0	0.000E0	0.000E0
Q9NZN8	CCR4-NOT transcription complex subunit 2 OS=Homo sapiens GN=CNOT2 PE=1 SV=1 - [CNOT2_HUMAN]	59.7	9.082E6	1.696E7	9.273E6	0.000E0	0.000E0	0.000E0
O14949	Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRCQ PE=1 SV=4 - [QCR8_HUMAN]	9.9	5.670E7	4.793E7	2.472E7	0.000E0	0.000E0	0.000E0
Q969Z0	Protein TBGR4 OS=Homo sapiens GN=TBGR4 PE=1 SV=1 - [TBGR4_HUMAN]	70.7	2.352E7	2.216E7	1.042E7	0.000E0	0.000E0	0.000E0
Q8NFO8	Torsin-1A-interacting protein 2 OS=Homo sapiens GN=TOR1AIP2 PE=1 SV=1 - [TOIP2_HUMAN]	51.2	1.094E7	7.294E6	5.013E6	0.000E0	0.000E0	0.000E0
Q8IWB7	WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDFY1 PE=1 SV=1 - [WDFY1_HUMAN]	46.3	1.426E7	3.315E7	2.471E7	0.000E0	0.000E0	0.000E0
Q9P2Q2	FERM domain-containing protein 4A OS=Homo sapiens GN=FRMD4A PE=1 SV=3 - [FRM4A_HUMAN]	115.4	5.964E7	4.368E7	2.569E7	0.000E0	0.000E0	0.000E0
Q9BQE5	Apolipoprotein L2 OS=Homo sapiens GN=APOL2 PE=1 SV=1 - [APOL2_HUMAN]	37.1	1.476E7	7.758E6	7.847E6	0.000E0	0.000E0	0.000E0
Q6UX04	Peptidyl-prolyl cis-trans isomerase CWC27 homolog OS=Homo sapiens GN=CWC27 PE=1 SV=1 - [CWC27_HUMAN]	53.8	1.232E7	2.134E7	1.033E7	0.000E0	0.000E0	0.000E0
P23258	Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2 - [TUBG1_HUMAN]	51.1	3.674E7	4.739E7	3.045E7	2.224E6	0.000E0	0.000E0
O95573	Long-chain-fatty-acid-CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 - [ACSL3_HUMAN]	80.4	9.981E7	7.584E7	4.479E7	0.000E0	5.937E6	0.000E0
Q9Y6B6	GTP-binding protein SAR1b OS=Homo sapiens GN=SAR1B PE=1 SV=1 - [SAR1B_HUMAN]	22.4	7.272E7	8.833E7	6.954E7	0.000E0	6.255E6	0.000E0
Q13740	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2 - [CD166_HUMAN]	65.1	1.789E8	2.869E8	2.206E8	0.000E0	1.186E7	9.509E6
Q9H6V9	UPF0554 protein C2orf43 OS=Homo sapiens GN=C2orf43 PE=1 SV=1 - [CB043_HUMAN]	37.3	3.835E7	2.817E7	1.649E7	0.000E0	0.000E0	2.639E6
P62487	DNA-directed RNA polymerase II subunit RPB7 OS=Homo sapiens GN=POLR2G PE=1 SV=1 - [RPB7_HUMAN]	19.3	1.506E7	1.147E7	1.801E7	0.000E0	1.438E6	0.000E0
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1 - [ACAD9_HUMAN]	68.7	4.400E7	4.434E7	2.016E7	0.000E0	3.606E6	0.000E0
O95772	MLN64 N-terminal domain homolog OS=Homo sapiens GN=STARD3NL PE=1 SV=1 - [MENTO_HUMAN]	26.6	1.301E7	1.383E7	6.410E6	0.000E0	1.145E6	0.000E0
Q14978	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HUMAN]	73.6	1.746E7	1.912E7	9.610E6	0.000E0	1.653E6	0.000E0
O95232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	51.4	1.594E7	1.668E7	1.425E7	0.000E0	0.000E0	1.717E6
Q9NR31	GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 - [SAR1A_HUMAN]	22.4	1.244E8	1.567E8	1.085E8	0.000E0	6.255E6	9.457E6
O43615	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2 - [TIM44_HUMAN]	51.3	6.820E7	6.990E7	3.756E7	5.341E6	0.000E0	2.138E6
O95741	Copine-6 OS=Homo sapiens GN=CPNE6 PE=1 SV=3 - [CPNE6_HUMAN]	62.0	8.904E7	6.417E7	4.995E7	0.000E0	8.686E6	0.000E0
Q9NVJ2	ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1 - [ARL8B_HUMAN]	21.5	7.541E7	7.022E7	4.705E7	0.000E0	8.570E6	0.000E0
Q9BXW7	Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 - [CECR5_HUMAN]	46.3	8.660E7	1.807E8	1.293E8	0.000E0	9.969E6	7.699E6
O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2 - [IDH3B_HUMAN]	42.2	1.497E7	1.149E7	1.467E7	0.000E0	0.000E0	1.885E6
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]	60.1	7.339E7	5.526E7	3.505E7	0.000E0	7.530E6	0.000E0
Q9BSK4	Protein fem-1 homolog A OS=Homo sapiens GN=FEM1A PE=1 SV=1 - [FEM1A_HUMAN]	73.6	2.998E8	2.733E8	2.224E8	4.032E7	0.000E0	0.000E0
Q8WXI9	Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1 - [P66B_HUMAN]	65.2	8.417E6	7.689E6	5.580E6	0.000E0	1.148E6	0.000E0
G2XKQ0	Small ubiquitin-related modifier 5 OS=Homo sapiens OX=9606 GN=SUMO1P1 PE=1 SV=2 - [SUMO5_HUMAN]	11.5	2.316E7	3.211E7	2.814E7	4.456E6	0.000E0	0.000E0
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	29.0	1.949E7	1.614E7	1.177E7	0.000E0	2.552E6	0.000E0
P51151	Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1 - [RAB9A_HUMAN]	22.8	1.829E7	1.034E7	1.791E7	0.000E0	0.000E0	2.666E6
Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1 - [DRG1_HUMAN]	40.5	9.577E6	1.009E7	1.321E7	0.000E0	0.000E0	1.917E6
Q9Y224	Tyrosine-tRNA ligase, mitochondrial OS=Homo sapiens GN=YARS2 PE=1 SV=2 - [SYYM_HUMAN]	53.2	2.680E7	2.347E7	1.258E7	0.000E0	3.707E6	0.000E0
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]	88.5	3.528E7	4.997E7	4.782E7	0.000E0	5.625E6	2.502E6
Q99805	Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1 - [TM9S2_HUMAN]	75.7	1.055E8	7.465E7	4.764E7	6.010E6	7.958E6	0.000E0
Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=2 - [REEP6_HUMAN]	23.4	1.889E7	2.117E7	1.212E7	0.000E0	0.000E0	3.239E6
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]	59.3	4.670E7	4.194E7	2.682E7	0.000E0	1.955E6	5.427E6
Q8TAQ2	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 - [SMRC2_HUMAN]	132.8	3.867E8	3.784E8	2.122E8	2.672E7	1.735E7	1.879E7
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 - [ILK_HUMAN]	51.4	1.594E7	2.887E7	1.737E7	0.000E0	0.000E0	4.044E6
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	70.3	6.980E7	5.224E7	6.205E7	0.000E0	1.218E7	0.000E0
O43847	Nardilysin OS=Homo sapiens OX=9606 GN=NRDC PE=1 SV=3 - [NRDC_HUMAN]	131.6	3.340E7	5.662E7	4.163E7	0.000E0	3.088E6	5.650E6
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	51.3	1.800E8	1.743E8	1.297E8	5.496E6	1.188E7	1.477E7
P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens OX=9606 GN=NDUFA6 PE=1 SV=4 - [NDUA6_HUMAN]	15.1	5.333E7	3.310E7	2.522E7	0.000E0	7.446E6	0.000E0
Q14160	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN]	174.8	4.339E7	3.206E7	4.012E7	1.334E6	4.219E6	2.229E6
Q5UJ48	Protein crumbs homolog 2 OS=Homo sapiens GN=CRB2 PE=1 SV=2 - [CRUM2_HUMAN]	134.2	9.609E7	5.222E7	5.716E7	0.000E0	4.175E6	9.666E6
O94874	E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2 - [UFL1_HUMAN]	89.5	2.405E7	1.628E7	1.207E7	0.000E0	3.568E6	0.000E0
Q9C0C4	Semaphorin-4C OS=Homo sapiens GN=SEMA4C PE=1 SV=2 - [SEM4C_HUMAN]	92.6	9.544E6	8.970E6	1.038E7	0.000E0	2.074E6	0.000E0
Q5XLA6	Caspase recruitment domain-containing protein 17 OS=Homo sapiens GN=CARD17 PE=1 SV=1 - [CAR17_HUMAN]	11.9	5.226E7	7.028E7	6.306E7	1.335E7	0.000E0	0.000E0
Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2 - [NSDHL_HUMAN]	41.9	1.443E8	1.144E8	1.020E8	4.168E6	1.266E7	9.341E6
Q92506	Estradiol 17-beta-dehydrogenase 8 OS=Homo sapiens GN=HSD17B8 PE=1 SV=2 - [DHB8_HUMAN]	27.0	2.194E6	1.827E6	1.676E6	0.000E0	4.184E5	0.000E0
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 - [USP9X_HUMAN]	292.1	1.918E7	2.985E7	3.867E7	0.000E0	3.675E6	2.824E6
Q9BYV8	Centrosomal protein of 41 kDa OS=Homo sapiens GN=CEP41 PE=1 SV=1 - [CEP41_HUMAN]	41.3	2.712E6	6.305E6	4.985E6	0.000E0	1.040E6	0.000E0
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	24.6	8.749E7	8.154E7	5.632E7	0.000E0	8.033E6	1.008E7
P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2 - [GNAI1_HUMAN]	40.3	2.595E8	2.519E8	1.467E8	1.560E7	3.354E7	4.365E6
Q12907	Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1 - [LMAN2_HUMAN]	40.2	1.396E8	1.011E8	6.120E7	1.821E6	2.300E7	0.000E0
Q5SQI0	Alpha-tubulin N-acetyltransferase 1 OS=Homo sapiens GN=ATAT1 PE=1 SV=1 - [ATAT_HUMAN]	46.8	6.481E6	9.230E6	5.531E6	0.000E0	0.000E0	1.771E6
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 - [IF2B_HUMAN]	38.4	1.591E7	2.664E7	2.534E7	0.000E0	0.000E0	5.666E6
P12931	Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC PE=1 SV=3 - [SRC_HUMAN]	59.8	5.176E7	1.020E8	5.989E7	0.000E0	0.000E0	1.804E7
Q8WYA6	Beta-catenin-like protein 1 OS=Homo sapiens GN=CTNBL1 PE=1 SV=1 - [CTBL1_HUMAN]	65.1	4.568E7	3.865E7	3.100E7	3.391E6	0.000E0	6.385E6
P78344	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN]	102.3	4.948E7	4.685E7	2.744E7	1.023E6	3.595E6	5.890E6
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [GNAI3_HUMAN]	40.5	2.595E8	2.519E8	1.467E8	1.660E7	3.354E7	6.050E6
Q14318	Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2 - [FKBP8_HUMAN]	44.5	6.618E7	5.612E7	3.864E7	0.000E0	4.751E6	9.108E6
Q96BM9	ADP-ribosylation factor-like protein 8A OS=Homo sapiens GN=ARL8A PE=1 SV=1 - [ARL8A_HUMAN]	21.4	7.541E7	7.022E7	4.705E7	0.000E0	6.666E6	9.961E6
P11172	Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1 - [UMPS_HUMAN]	52.2	5.033E7	3.943E7	5.500E7	3.490E6	3.689E6	5.479E6
P09234	U1 small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1 - [RU1C_HUMAN]	17.4	2.627E7	3.152E7	2.054E7	0.000E0	0.000E0	6.948E6
P08621	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2 - [RU17_HUMAN]	51.5	5.743E7	5.739E7	2.680E7	0.000E0	1.259E7	0.000E0

O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	43.6	3.097E7	2.677E7	2.160E7	0.000E0	0.000E0	7.113E6
Q969T4	Ubiquitin-conjugating enzyme E2 E3 OS=Homo sapiens GN=UBE2E3 PE=1 SV=1 - [UB2E3_HUMAN]	22.9	1.847E7	2.422E7	1.010E7	0.000E0	0.000E0	4.741E6
Q13616	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2 - [CUL1_HUMAN]	89.6	1.409E7	1.599E7	9.580E6	3.589E6	0.000E0	0.000E0
P48509	CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3 - [CD151_HUMAN]	28.3	1.899E7	1.302E7	1.315E7	0.000E0	4.096E6	0.000E0
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_HUMAN]	80.2	2.440E8	2.071E8	1.621E8	5.697E6	2.078E7	2.931E7
P52294	Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 - [IMA5_HUMAN]	60.2	1.895E7	2.078E7	9.196E6	0.000E0	2.678E6	1.841E6
Q15555	Microtubule-associated protein RP/EB family member 2 OS=Homo sapiens GN=MAPRE2 PE=1 SV=1 - [MARE2_HUMAN]	37.0	1.457E7	1.739E7	1.844E7	0.000E0	4.698E6	0.000E0
Q9NXR7	BRCA1-A complex subunit BRE OS=Homo sapiens GN=BRE PE=1 SV=2 - [BRE_HUMAN]	43.5	4.048E6	7.273E6	3.874E6	0.000E0	1.420E6	0.000E0
Q96HY6	DDRKG domain-containing protein 1 OS=Homo sapiens GN=DDRKG1 PE=1 SV=2 - [DDRKG_HUMAN]	35.6	2.760E7	1.821E7	1.320E7	0.000E0	3.024E6	2.520E6
P11233	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1 - [RALA_HUMAN]	23.6	6.126E7	5.169E7	3.178E7	0.000E0	1.366E7	0.000E0
Q13217	DnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3 PE=1 SV=1 - [DNJC3_HUMAN]	57.5	2.631E7	1.864E7	2.789E7	0.000E0	6.908E6	0.000E0
Q9UHN6	Transmembrane protein 2 OS=Homo sapiens GN=TMEM2 PE=1 SV=1 - [TMEM2_HUMAN]	154.3	1.833E8	9.885E7	1.938E8	0.000E0	4.589E7	0.000E0
P11234	Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1 - [RALB_HUMAN]	23.4	5.009E7	4.407E7	4.737E7	0.000E0	1.366E7	0.000E0
O15078	Centrosomal protein of 290 kDa OS=Homo sapiens GN=CEP290 PE=1 SV=2 - [CE290_HUMAN]	290.2	4.385E8	7.144E8	6.230E8	1.716E8	0.000E0	0.000E0
Q15041	ADP-ribosylation factor-like protein 6-interacting protein 1 OS=Homo sapiens GN=ARL6IP1 PE=1 SV=2 - [AR6P1_HUMAN]	23.3	1.360E8	1.411E8	1.140E8	8.802E6	1.930E7	9.744E6
Q00765	Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3 - [REEP5_HUMAN]	21.5	4.426E7	3.181E7	4.006E7	0.000E0	6.192E6	5.067E6
Q9BUB7	Transmembrane protein 70, mitochondrial OS=Homo sapiens GN=TMEM70 PE=1 SV=2 - [TMM70_HUMAN]	29.0	3.533E7	4.424E7	4.734E7	0.000E0	1.236E7	0.000E0
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	69.1	2.440E8	1.702E8	1.247E8	6.945E6	2.002E7	2.553E7
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRR59 PE=1 SV=1 - [LRC59_HUMAN]	34.9	1.284E8	1.291E8	7.729E7	0.000E0	3.268E7	0.000E0
O14787	Transportin-2 OS=Homo sapiens GN=TNPO2 PE=1 SV=3 - [TNPO2_HUMAN]	101.3	6.241E7	7.994E7	3.694E7	7.311E6	1.032E7	0.000E0
Q9BYD2	39S ribosomal protein L9, mitochondrial OS=Homo sapiens GN=MRPL9 PE=1 SV=2 - [RM09_HUMAN]	30.2	1.667E7	2.005E7	1.756E7	0.000E0	0.000E0	5.347E6
P40616	ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1 - [ARL1_HUMAN]	20.4	2.735E7	2.644E7	2.600E7	0.000E0	3.659E6	4.203E6
Q14677	Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1 - [EPN4_HUMAN]	68.2	1.237E7	1.834E7	1.192E7	0.000E0	0.000E0	4.224E6
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	40.4	2.595E8	2.519E8	1.467E8	1.854E7	3.391E7	1.317E7