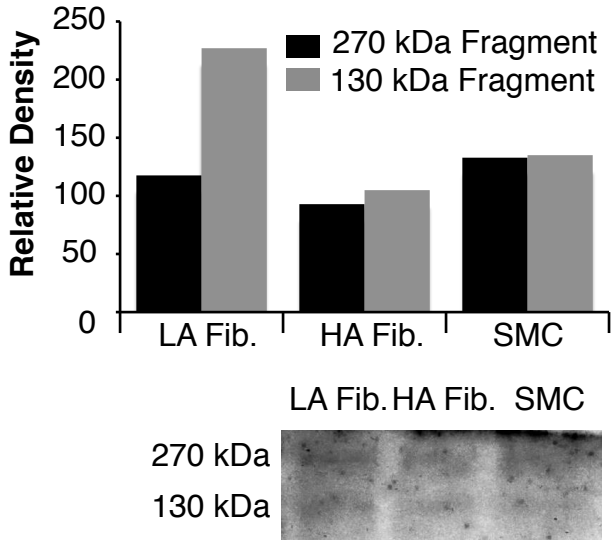
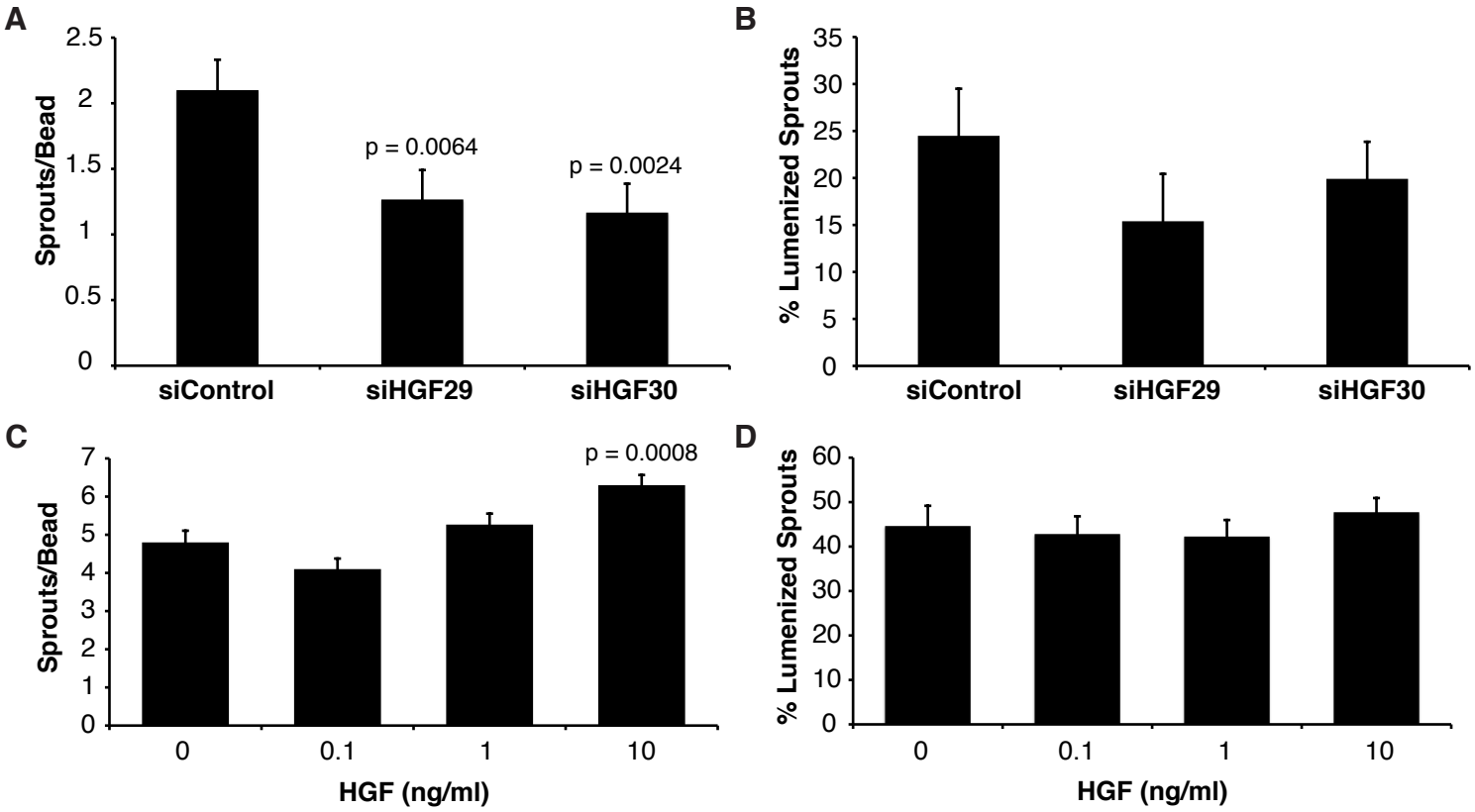
Supplemental Material

Supplemental Figure I



Supplemental Figure 1. Western blot showing levels of Collagen 1 in LA, HA and SMC supernatants.

Supplemental Figure II



Supplemental Table I

LA Fibroblasts	
Symbol	**Name**
A16L2_HUMAN	Autophagy-related protein 16-2 - Homo sapiens (Human)
A1AT_HUMAN	Alpha-1-antitrypsin precursor - Homo sapiens (Human)
A2MG_HUMAN	Alpha-2-macroglobulin precursor - Homo sapiens (Human)
ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
ACTB_HUMAN	Actin, cytoplasmic 1 - Homo sapiens (Human)
ACTN1_HUMAN	Alpha-actinin-1 - Homo sapiens (Human)
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1
ALBU_HUMAN	Serum albumin precursor - Homo sapiens (Human)
ALDOA_HUMAN	Fructose-bisphosphate aldolase A - Homo sapiens (Human)
ARFP1_HUMAN	Arfaptin-1 - Homo sapiens (Human)
ATP7A_HUMAN	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial precursor - Homo sapiens (Human)
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1
C1R_HUMAN	Complement C1r subcomponent precursor - Homo sapiens (Human)
C1S_HUMAN	Complement C1s subcomponent precursor - Homo sapiens (Human)
CAB45_HUMAN	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1
CALU_HUMAN	Calumenin precursor - Homo sapiens (Human)
CATB_HUMAN	Cathepsin B precursor - Homo sapiens (Human)
CD59_HUMAN	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1
CLC11_HUMAN	C-type lectin domain family 11 member A precursor - Homo sapiens (Human)
CLUS_HUMAN	Clusterin precursor - Homo sapiens (Human)
CO1A1_HUMAN	Collagen alpha-1(I) chain precursor - Homo sapiens (Human)
CO1A2_HUMAN	Collagen alpha-2(I) chain precursor - Homo sapiens (Human)
CO3A1_HUMAN	Collagen alpha-1(III) chain precursor - Homo sapiens (Human)
CO6A1_HUMAN	Collagen alpha-1(VI) chain precursor - Homo sapiens (Human)
CO6A2_HUMAN	Collagen alpha-2(VI) chain precursor - Homo sapiens (Human)
CO6A3_HUMAN	Collagen alpha-3(VI) chain precursor - Homo sapiens (Human)
COCA1_HUMAN	Collagen alpha-1(XII) chain precursor - Homo sapiens (Human)
CRIM1_HUMAN	Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3
CSTN1_HUMAN	Calsyntenin-1 precursor - Homo sapiens (Human)
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1
DHDDS_HUMAN	Dehydrodolichyl diphosphate synthase - Homo sapiens (Human)
DKK3_HUMAN	Dickkopf-related protein 3 precursor - Homo sapiens (Human)
EBI2_HUMAN	EBV-induced G-protein coupled receptor 2 - Homo sapiens (Human)
ECM1_HUMAN	Extracellular matrix protein 1 precursor - Homo sapiens (Human)
FAK2_HUMAN	Protein tyrosine kinase 2 beta - Homo sapiens (Human)
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 precursor - Homo sapiens (Human)
FETA_HUMAN	Alpha-fetoprotein precursor - Homo sapiens (Human)
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1
FINC_HUMAN	Fibronectin precursor - Homo sapiens (Human)
FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4
FMN1_HUMAN	Formin-1 - Homo sapiens (Human)
FST_HUMAN	Follistatin precursor - Homo sapiens (Human)
FSTL1_HUMAN	Follistatin-related protein 1 precursor - Homo sapiens (Human)
GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1

GALT5_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 5 - Homo sapiens (Human)
GAS6_HUMAN	Growth arrest-specific protein 6 precursor - Homo sapiens (Human)
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1
HSP76_HUMAN	Heat shock 70 kDa protein 6 - Homo sapiens (Human)
HSP7C_HUMAN	Heat shock cognate 71 kDa protein - Homo sapiens (Human)
IBP2_HUMAN	Insulin-like growth factor-binding protein 2 OS=Homo sapiens GN=IGFBP2 PE=1 SV=1
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 precursor - Homo sapiens (Human)
IC1_HUMAN	Plasma protease C1 inhibitor precursor - Homo sapiens (Human)
ITGBL_HUMAN	Integrin beta-like protein 1 precursor - Homo sapiens (Human)
ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 precursor - Homo sapiens (Human)
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=5
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
K2C1_HUMAN	Keratin, type II cytoskeletal 1 - Homo sapiens (Human)
K2C1B_HUMAN	Keratin, type II cytoskeletal 1b - Homo sapiens (Human)
K2C7_HUMAN	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=3
K2C73_HUMAN	Keratin, type II cytoskeletal 73 - Homo sapiens (Human)
KNG1_HUMAN	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2
LAMC1_HUMAN	Laminin subunit gamma-1 precursor - Homo sapiens (Human)
LDHB_HUMAN	L-lactate dehydrogenase B chain - Homo sapiens (Human)
LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
LTB1L_HUMAN	Latent-transforming growth factor beta-binding protein, isoform 1L precursor - Homo sapiens (Human)
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 precursor - Homo sapiens (Human)
LUM_HUMAN	Lumican precursor - Homo sapiens (Human)
LYOX_HUMAN	Protein-lysine 6-oxidase OS=Homo sapiens GN=LOX PE=1 SV=2
MASP1_HUMAN	Complement-activating component of Ra-reactive factor precursor - Homo sapiens (Human)
MFGM_HUMAN	Lactadherin precursor - Homo sapiens (Human)
MMP2_HUMAN	72 kDa type IV collagenase precursor - Homo sapiens (Human)
NID2_HUMAN	Nidogen-2 precursor - Homo sapiens (Human)
NUCB1_HUMAN	Nucleobindin-1 precursor - Homo sapiens (Human)
NUP93_HUMAN	Nuclear pore complex protein Nup93 - Homo sapiens (Human)
OPHN1_HUMAN	Oligophrenin 1 - Homo sapiens (Human)
PAI1_HUMAN	Plasminogen activator inhibitor 1 precursor - Homo sapiens (Human)
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 precursor - Homo sapiens (Human)
PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3
PGS1_HUMAN	Biglycan precursor - Homo sapiens (Human)
PGS2_HUMAN	Decorin precursor - Homo sapiens (Human)
PLTP_HUMAN	Phospholipid transfer protein precursor - Homo sapiens (Human)
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1
PTX3_HUMAN	Pentraxin-related protein PTX3 precursor - Homo sapiens (Human)
PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2
QSOX1_HUMAN	Sulfhydryl oxidase 1 precursor - Homo sapiens (Human)
RAB19_HUMAN	Ras-related protein Rab-19 - Homo sapiens (Human)
RARR2_HUMAN	Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1
RS28_HUMAN	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1

RXFP1_HUMAN	Relaxin receptor 1 - Homo sapiens (Human)
S10A6_HUMAN	Protein S100-A6 - Homo sapiens (Human)
SELN_HUMAN	Selenoprotein N precursor - Homo sapiens (Human)
SGSM2_HUMAN	Small G protein signaling modulator 2 - Homo sapiens (Human)
SLC2B_HUMAN	Slp homolog lacking C2 domains b - Homo sapiens (Human)
SMTN_HUMAN	Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=5
SNX9_HUMAN	Sorting nexin-9 OS=Homo sapiens GN=SNX9 PE=1 SV=1
SOX30_HUMAN	Transcription factor SOX-30 - Homo sapiens (Human)
SPON2_HUMAN	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=2
SPRC_HUMAN	SPARC precursor - Homo sapiens (Human)
STC2_HUMAN	Stanniocalcin-2 precursor - Homo sapiens (Human)
TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4
TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
TCEA3_HUMAN	Transcription elongation factor A protein 3 - Homo sapiens (Human)
TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2
THBG_HUMAN	Thyroxine-binding globulin precursor - Homo sapiens (Human)
TIG1_HUMAN	Retinoic acid receptor responder protein 1 - Homo sapiens (Human)
TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor - Homo sapiens (Human)
TIMP2_HUMAN	Metalloproteinase inhibitor 2 precursor - Homo sapiens (Human)
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2
TRFE_HUMAN	Serotransferrin precursor - Homo sapiens (Human)
TRFL_HUMAN	Lactotransferrin precursor - Homo sapiens (Human)
TRI55_HUMAN	Tripartite motif-containing protein 55 - Homo sapiens (Human)
UBE4B_HUMAN	Ubiquitin conjugation factor E4 B - Homo sapiens (Human)
UBIQ_HUMAN	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1
VIME_HUMAN	Vimentin - Homo sapiens (Human)
WDR87_HUMAN	WD repeat-containing protein 87 - Homo sapiens (Human)
ZYX_HUMAN	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

HA Fibroblasts	
Symbol	**Name**
1433Z_HUMAN	14-3-3 protein zeta/delta - Homo sapiens (Human)
A2MG_HUMAN	Alpha-2-macroglobulin precursor - Homo sapiens (Human)
ACTB_HUMAN	Actin, cytoplasmic 1 - Homo sapiens (Human)
ACTN1_HUMAN	Alpha-actinin-1 - Homo sapiens (Human)
ADML_HUMAN	ADM OS=Homo sapiens GN=ADM PE=1 SV=1
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
ALBU_HUMAN	Serum albumin precursor - Homo sapiens (Human)
ALDOA_HUMAN	Fructose-bisphosphate aldolase A - Homo sapiens (Human)
ALMS1_HUMAN	Alstrom syndrome protein 1 - Homo sapiens (Human)
APOH_HUMAN	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3
ARFP1_HUMAN	Arfaptin-1 OS=Homo sapiens GN=ARFIP1 PE=1 SV=2
ATP7A_HUMAN	Copper-transporting ATPase 1 - Homo sapiens (Human)
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1
C1R_HUMAN	Complement C1r subcomponent precursor - Homo sapiens (Human)
C1S_HUMAN	Complement C1s subcomponent precursor - Homo sapiens (Human)
CAB45_HUMAN	45 kDa calcium-binding protein precursor - Homo sapiens (Human)

CALR_HUMAN	Calreticulin precursor - Homo sapiens (Human)
CALU_HUMAN	Calumenin precursor - Homo sapiens (Human)
CATB_HUMAN	Cathepsin B precursor - Homo sapiens (Human)
CH3L1_HUMAN	Chitinase-3-like protein 1 precursor - Homo sapiens (Human)
CLC11_HUMAN	C-type lectin domain family 11 member A precursor - Homo sapiens (Human)
CLUS_HUMAN	Clusterin precursor - Homo sapiens (Human)
CO1A1_HUMAN	Collagen alpha-1(I) chain precursor - Homo sapiens (Human)
CO1A2_HUMAN	Collagen alpha-2(I) chain precursor - Homo sapiens (Human)
CO3A1_HUMAN	Collagen alpha-1(III) chain precursor - Homo sapiens (Human)
CO4A5_HUMAN	Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2
CO6A1_HUMAN	Collagen alpha-1(VI) chain precursor - Homo sapiens (Human)
CO6A2_HUMAN	Collagen alpha-2(VI) chain precursor - Homo sapiens (Human)
CO6A3_HUMAN	Collagen alpha-3(VI) chain precursor - Homo sapiens (Human)
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3
CTGF_HUMAN	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1
DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2
DKK3_HUMAN	Dickkopf-related protein 3 precursor - Homo sapiens (Human)
ECM1_HUMAN	Extracellular matrix protein 1 precursor - Homo sapiens (Human)
ENOA_HUMAN	Alpha-enolase - Homo sapiens (Human)
ENOG_HUMAN	Gamma-enolase - Homo sapiens (Human)
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 precursor - Homo sapiens (Human)
FBLN5_HUMAN	Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1
FETA_HUMAN	Alpha-fetoprotein precursor - Homo sapiens (Human)
FETUA_HUMAN	Alpha-2-HS-glycoprotein precursor - Homo sapiens (Human)
FINC_HUMAN	Fibronectin precursor - Homo sapiens (Human)
FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2
FLNA_HUMAN	Filamin-A - Homo sapiens (Human)
FSTL1_HUMAN	Follistatin-related protein 1 precursor - Homo sapiens (Human)
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase - Homo sapiens (Human)
GELS_HUMAN	Gelsolin precursor - Homo sapiens (Human)
HS90B_HUMAN	Heat shock protein HSP 90-beta - Homo sapiens (Human)
HSP76_HUMAN	Heat shock 70 kDa protein 6 - Homo sapiens (Human)
HSP7C_HUMAN	Heat shock cognate 71 kDa protein - Homo sapiens (Human)
HYAL4_HUMAN	Hyaluronidase-4 - Homo sapiens (Human)
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 precursor - Homo sapiens (Human)
IBP6_HUMAN	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 precursor - Homo sapiens (Human)
IC1_HUMAN	Plasma protease C1 inhibitor precursor - Homo sapiens (Human)
K1833_HUMAN	HEAT repeat-containing protein KIAA1833 - Homo sapiens (Human)
K1C10_HUMAN	Keratin, type I cytoskeletal 10 - Homo sapiens (Human)
K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=3
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
K1C16_HUMAN	Keratin, type I cytoskeletal 16 - Homo sapiens (Human)
K1C9_HUMAN	Keratin, type I cytoskeletal 9 - Homo sapiens (Human)
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal - Homo sapiens (Human)
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
K2C1B_HUMAN	Keratin, type II cytoskeletal 1b - Homo sapiens (Human)

K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A - Homo sapiens (Human)
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 - Homo sapiens (Human)
LAMC1_HUMAN	Laminin subunit gamma-1 precursor - Homo sapiens (Human)
LDHA_HUMAN	L-lactate dehydrogenase A chain - Homo sapiens (Human)
LDHB_HUMAN	L-lactate dehydrogenase B chain - Homo sapiens (Human)
LEG1_HUMAN	Galectin-1 - Homo sapiens (Human)
LG3BP_HUMAN	Galectin-3-binding protein precursor - Homo sapiens (Human)
LMNA_HUMAN	Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1
LMOD2_HUMAN	Leiomodin-2 - Homo sapiens (Human)
LRCC1_HUMAN	Leucine-rich repeat and coiled-coil domain-containing protein 1 - Homo sapiens (Human)
LTB1L_HUMAN	Latent-transforming growth factor beta-binding protein, isoform 1L precursor - Homo sapiens (Human)
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 precursor - Homo sapiens (Human)
LUM_HUMAN	Lumican precursor - Homo sapiens (Human)
MASP1_HUMAN	Complement-activating component of Ra-reactive factor precursor - Homo sapiens (Human)
MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor - Homo sapiens (Human)
MFAP4_HUMAN	Microfibril-associated glycoprotein 4 precursor - Homo sapiens (Human)
MIF_HUMAN	Macrophage migration inhibitory factor - Homo sapiens (Human)
MMP1_HUMAN	Interstitial collagenase precursor - Homo sapiens (Human)
MMP2_HUMAN	72 kDa type IV collagenase precursor - Homo sapiens (Human)
MOES_HUMAN	Moesin - Homo sapiens (Human)
MT1A_HUMAN	Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=1
NDKA_HUMAN	Nucleoside diphosphate kinase A - Homo sapiens (Human)
NUCB1_HUMAN	Nucleobindin-1 precursor - Homo sapiens (Human)
PAI1_HUMAN	Plasminogen activator inhibitor 1 precursor - Homo sapiens (Human)
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 precursor - Homo sapiens (Human)
PDIA1_HUMAN	Protein disulfide-isomerase precursor - Homo sapiens (Human)
PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor - Homo sapiens (Human)
PDIA4_HUMAN	Protein disulfide-isomerase A4 precursor - Homo sapiens (Human)
PEDF_HUMAN	Pigment epithelium-derived factor precursor - Homo sapiens (Human)
PGK1_HUMAN	Phosphoglycerate kinase 1 - Homo sapiens (Human)
PGS2_HUMAN	Decorin precursor - Homo sapiens (Human)
PKHG1_HUMAN	Pleckstrin homology domain-containing family G member 1 OS=Homo sapiens GN=PLEKHG1 PE=1 SV=2
PLTP_HUMAN	Phospholipid transfer protein precursor - Homo sapiens (Human)
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A - Homo sapiens (Human)
PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor - Homo sapiens (Human)
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase precursor - Homo sapiens (Human)
PTPRB_HUMAN	Receptor-type tyrosine-protein phosphatase beta OS=Homo sapiens GN=PTPRB PE=1 SV=1
PXDN_HUMAN	Peroxidasin homolog precursor - Homo sapiens (Human)
QSOX1_HUMAN	Sulfhydryl oxidase 1 precursor - Homo sapiens (Human)
RARR2_HUMAN	Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1
RNAS4_HUMAN	Ribonuclease 4 OS=Homo sapiens GN=RNASE4 PE=1 SV=3
RPGF3_HUMAN	Rap guanine nucleotide exchange factor 3 - Homo sapiens (Human)
S10A6_HUMAN	Protein S100-A6 - Homo sapiens (Human)
SEM3A_HUMAN	Semaphorin-3A precursor - Homo sapiens (Human)
SPON2_HUMAN	Spondin-2 precursor - Homo sapiens (Human)
SPRC_HUMAN	SPARC precursor - Homo sapiens (Human)
STC1_HUMAN	Stanniocalcin-1 OS=Homo sapiens GN=STC1 PE=1 SV=1
TCEA3_HUMAN	Transcription elongation factor A protein 3 - Homo sapiens (Human)

TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2
THBG_HUMAN	Thyroxine-binding globulin precursor - Homo sapiens (Human)
TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor - Homo sapiens (Human)
TIMP2_HUMAN	Metalloproteinase inhibitor 2 precursor - Homo sapiens (Human)
TPIS_HUMAN	Triosephosphate isomerase - Homo sapiens (Human)
TSP1_HUMAN	Thrombospondin-1 precursor - Homo sapiens (Human)
TYB10_HUMAN	Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2
UBE4B_HUMAN	Ubiquitin conjugation factor E4 B - Homo sapiens (Human)
UBIQ_HUMAN	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1
VASN_HUMAN	Vasorin precursor - Homo sapiens (Human)
VIME_HUMAN	Vimentin - Homo sapiens (Human)
VINC_HUMAN	Vinculin - Homo sapiens (Human)
WDR87_HUMAN	WD repeat-containing protein 87 - Homo sapiens (Human)

SMC	
Symbol	**Name**
1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3
1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1
1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4
1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2
1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1
1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1
1A01_HUMAN	HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4
A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3
A2AP_HUMAN	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3
A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=1
A4_HUMAN	Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3
ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2
ADA10_HUMAN	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1
ADK_HUMAN	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2
ADML_HUMAN	ADM OS=Homo sapiens GN=ADM PE=1 SV=1
AEBP1_HUMAN	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1
AGRIN_HUMAN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2
ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
AMD_HUMAN	Peptidyl-glycine alpha-amidating monooxygenase OS=Homo sapiens GN=PAM PE=1 SV=2
AMPD3_HUMAN	AMP deaminase 3 OS=Homo sapiens GN=AMPD3 PE=1 SV=1
ANGI_HUMAN	Angiogenin OS=Homo sapiens GN=ANG PE=1 SV=1
ANGL2_HUMAN	Angiopoietin-related protein 2 OS=Homo sapiens GN=ANGPTL2 PE=2 SV=1
ANKS3_HUMAN	Ankyrin repeat and SAM domain-containing protein 3 OS=Homo sapiens GN=ANKS3 PE=1 SV=1
ANT3_HUMAN	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1
ANX11_HUMAN	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1
ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2
ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2
APLP2_HUMAN	Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2

APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1
APOB_HUMAN	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=1
APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
ARHGI_HUMAN	Rho guanine nucleotide exchange factor 18 OS=Homo sapiens GN=ARHGEF18 PE=1 SV=2
ARL5C_HUMAN	Putative ADP-ribosylation factor-like protein 5C OS=Homo sapiens GN=ARL5C PE=2 SV=4
AT10A_HUMAN	Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2
ATS5_HUMAN	A disintegrin and metalloproteinase with thrombospondin motifs 5 OS=Homo sapiens GN=ADAMTS5 PE=1 SV=1
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1
B3GN1_HUMAN	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase OS=Homo sapiens GN=B3GNT1 PE=1 SV=1
B4GT1_HUMAN	Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5
B4GT5_HUMAN	Beta-1,4-galactosyltransferase 5 OS=Homo sapiens GN=B4GALT5 PE=2 SV=1
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1
BMP1_HUMAN	Bone morphogenetic protein 1 OS=Homo sapiens GN=BMP1 PE=1 SV=2
BST1_HUMAN	ADP-ribosyl cyclase 2 OS=Homo sapiens GN=BST1 PE=1 SV=2
BTD_HUMAN	Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2
C1R_HUMAN	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2
C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1
CAB45_HUMAN	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1
CAC1S_HUMAN	Voltage-dependent L-type calcium channel subunit alpha-1S OS=Homo sapiens GN=CACNA1S PE=1 SV=4
CAD11_HUMAN	Cadherin-11 OS=Homo sapiens GN=CDH11 PE=1 SV=2
CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1
CALU_HUMAN	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2
CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5
CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3
CATL1_HUMAN	Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2
CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3
CCBE1_HUMAN	Collagen and calcium-binding EGF domain-containing protein 1 OS=Homo sapiens GN=CCBE1 PE=2 SV=1
CCD37_HUMAN	Coiled-coil domain-containing protein 37 OS=Homo sapiens GN=CCDC37 PE=1 SV=1
CD109_HUMAN	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2
CD248_HUMAN	Endosialin OS=Homo sapiens GN=CD248 PE=1 SV=1
CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2
CD59_HUMAN	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1
CF115_HUMAN	UPF0727 protein C6orf115 OS=Homo sapiens GN=C6orf115 PE=1 SV=1
CFAD_HUMAN	Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5
CFAH_HUMAN	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4
CH3L1_HUMAN	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2
CHD1L_HUMAN	Chromodomain-helicase-DNA-binding protein 1-like OS=Homo sapiens GN=CHD1L PE=1 SV=1
CHID1_HUMAN	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1
CHM4A_HUMAN	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3
CHM4B_HUMAN	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1
CHST2_HUMAN	Carbohydrate sulfotransferase 2 OS=Homo sapiens GN=CHST2 PE=1 SV=2
CI051_HUMAN	Putative SIPAR-like protein C9orf51 OS=Homo sapiens GN=C9orf51 PE=5 SV=1
CI057_HUMAN	Uncharacterized protein C9orf57 OS=Homo sapiens GN=C9orf57 PE=2 SV=1
CLC11_HUMAN	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1
CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1
CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1
CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4
CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6
CO3_HUMAN	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

CO3A1_HUMAN	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4
CO4A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1
CO4A5_HUMAN	Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2
CO5A1_HUMAN	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3
CO5A2_HUMAN	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3
CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3
CO6A2_HUMAN	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4
CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=4
CO7A1_HUMAN	Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2
CO9_HUMAN	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2
COCA1_HUMAN	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2
COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3
COFA1_HUMAN	Collagen alpha-1(XV) chain OS=Homo sapiens GN=COL15A1 PE=1 SV=2
COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5
COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1
CQ080_HUMAN	Uncharacterized protein C17orf80 OS=Homo sapiens GN=C17orf80 PE=1 SV=1
CSF1_HUMAN	Macrophage colony-stimulating factor 1 OS=Homo sapiens GN=CSF1 PE=1 SV=1
CSPG2_HUMAN	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3
CSTN1_HUMAN	Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 PE=1 SV=1
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1
DAG1_HUMAN	Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2
DERM_HUMAN	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2
DKK3_HUMAN	Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1
DOCK3_HUMAN	Dedicator of cytokinesis protein 3 OS=Homo sapiens GN=DOCK3 PE=1 SV=1
DPOLA_HUMAN	DNA polymerase alpha catalytic subunit OS=Homo sapiens GN=POLA1 PE=1 SV=2
E41L5_HUMAN	Band 4.1-like protein 5 OS=Homo sapiens GN=EPB41L5 PE=1 SV=3
ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2
EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3
EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4
EMIL1_HUMAN	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2
ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2
ENPP2_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 OS=Homo sapiens GN=ENPP2 PE=1 SV=2
ENTP6_HUMAN	Ectonucleoside triphosphate diphosphohydrolase 6 OS=Homo sapiens GN=ENTPD6 PE=1 SV=2
EXT1_HUMAN	Exostosin-1 OS=Homo sapiens GN=EXT1 PE=1 SV=2
F180A_HUMAN	Protein FAM180A OS=Homo sapiens GN=FAM180A PE=2 SV=1
FAM3C_HUMAN	Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1
FAS_HUMAN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=2
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2
FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3
FBLN5_HUMAN	Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1
FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=2
FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3
FEM1B_HUMAN	Protein fem-1 homolog B OS=Homo sapiens GN=FEM1B PE=1 SV=1
FETA_HUMAN	Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1
FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3
FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4

FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3
FPGT_HUMAN	Fucose-1-phosphate guanylyltransferase OS=Homo sapiens GN=FPGT PE=1 SV=2
FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3
FST_HUMAN	Follistatin OS=Homo sapiens GN=FST PE=1 SV=2
FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1
FUCO2_HUMAN	Plasma alpha-L-fucosidase OS=Homo sapiens GN=FUCA2 PE=1 SV=2
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
G3ST1_HUMAN	Galactosylceramide sulfotransferase OS=Homo sapiens GN=GAL3ST1 PE=1 SV=1
G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4
GA2L3_HUMAN	GAS2-like protein 3 OS=Homo sapiens GN=GAS2L3 PE=1 SV=1
GALT2_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1
GALT5_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1
GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2
GDN_HUMAN	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1
GEMI5_HUMAN	Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=2
GLCM_HUMAN	Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3
GNPTG_HUMAN	N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens GN=GNPTG PE=1 SV=1
GP119_HUMAN	Glucose-dependent insulinotropic receptor OS=Homo sapiens GN=GPR119 PE=1 SV=1
GPC1_HUMAN	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=1
GREM1_HUMAN	Gremlin-1 OS=Homo sapiens GN=GREM1 PE=1 SV=1
GSCR1_HUMAN	Glioma tumor suppressor candidate region gene 1 protein OS=Homo sapiens GN=GLTSCR1 PE=1 SV=2
GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2
GTPB1_HUMAN	GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3
H2A1B_HUMAN	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2
HBB_HUMAN	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2
HGF_HUMAN	Hepatocyte growth factor OS=Homo sapiens GN=HGF PE=1 SV=2
HLAE_HUMAN	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens GN=HLA-E PE=1 SV=3
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3
HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5
HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1
HTRA1_HUMAN	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1
IBP2_HUMAN	Insulin-like growth factor-binding protein 2 OS=Homo sapiens GN=IGFBP2 PE=1 SV=1
IBP3_HUMAN	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1
IBP6_HUMAN	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1
IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2
IGF2_HUMAN	Insulin-like growth factor II OS=Homo sapiens GN=IGF2 PE=1 SV=1
IGSF1_HUMAN	Immunoglobulin superfamily member 1 OS=Homo sapiens GN=IGSF1 PE=1 SV=3
IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2
ISLR_HUMAN	Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=1 SV=1
ITB4_HUMAN	Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=4
ITGBL_HUMAN	Integrin beta-like protein 1 OS=Homo sapiens GN=ITGBL1 PE=2 SV=1
ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2
ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=5

K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=2
K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
K2C73_HUMAN	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1
K2C8_HUMAN	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7
KANK2_HUMAN	KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1
KIF3C_HUMAN	Kinesin-like protein KIF3C OS=Homo sapiens GN=KIF3C PE=1 SV=2
KRT82_HUMAN	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3
LAMA2_HUMAN	Laminin subunit alpha-2 OS=Homo sapiens GN=LAMA2 PE=1 SV=4
LAMA4_HUMAN	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=3
LAMA5_HUMAN	Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=7
LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1
LAMB2_HUMAN	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2
LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3
LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2
LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2
LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
LDLR_HUMAN	Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1
LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
LMNA_HUMAN	Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1
LMOD2_HUMAN	Leiomodin-2 OS=Homo sapiens GN=LMOD2 PE=2 SV=2
LOXL1_HUMAN	Lysyl oxidase homolog 1 OS=Homo sapiens GN=LOXL1 PE=2 SV=2
LOXL2_HUMAN	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1
LRP1_HUMAN	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=1
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=3
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=1 SV=2
LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2
LYAG_HUMAN	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=3
LYOX_HUMAN	Protein-lysine 6-oxidase OS=Homo sapiens GN=LOX PE=1 SV=2
MA1A1_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3
MA2A1_HUMAN	Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2
MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3
MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3
MFAP2_HUMAN	Microfibrillar-associated protein 2 OS=Homo sapiens GN=MFAP2 PE=2 SV=1
MFAP4_HUMAN	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2
MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2
MGT4B_HUMAN	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B OS=Homo sapiens GN=MGAT4B PE=1 SV=1
MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4
MIME_HUMAN	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1
MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1
MMP19_HUMAN	Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=1 SV=1
MMP2_HUMAN	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2
MRC2_HUMAN	C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=1
MT1G_HUMAN	Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2
MXRA5_HUMAN	Matrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=2

MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4
MYLK_HUMAN	Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=3
NAC1_HUMAN	Sodium/calcium exchanger 1 OS=Homo sapiens GN=SLC8A1 PE=1 SV=3
NAV3_HUMAN	Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=1 SV=2
NEBU_HUMAN	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=3
NEST_HUMAN	Nestin OS=Homo sapiens GN=NES PE=1 SV=2
NF2L1_HUMAN	Nuclear factor erythroid 2-related factor 1 OS=Homo sapiens GN=NFE2L1 PE=1 SV=1
NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3
NID2_HUMAN	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=2
NOTC3_HUMAN	Neurogenic locus notch homolog protein 3 OS=Homo sapiens GN=NOTCH3 PE=1 SV=1
NPC2_HUMAN	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1
NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4
NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3
OAF_HUMAN	Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=1
OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2
OLFL1_HUMAN	Olfactomedin-like protein 1 OS=Homo sapiens GN=OLFML1 PE=1 SV=1
OLFL3_HUMAN	Olfactomedin-like protein 3 OS=Homo sapiens GN=OLFML3 PE=2 SV=1
OR5H2_HUMAN	Olfactory receptor 5H2 OS=Homo sapiens GN=OR5H2 PE=2 SV=3
OS9_HUMAN	Protein OS-9 OS=Homo sapiens GN=OS9 PE=1 SV=1
OTU7A_HUMAN	OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=2 SV=1
PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1
PAMR1_HUMAN	Inactive serine protease PAMR1 OS=Homo sapiens GN=PAMR1 PE=1 SV=1
PAPP1_HUMAN	Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2
PCSK7_HUMAN	Proprotein convertase subtilisin/kexin type 7 OS=Homo sapiens GN=PCSK7 PE=1 SV=2
PDE6B_HUMAN	Rod cGMP-specific 3~,5~-cyclic phosphodiesterase subunit beta OS=Homo sapiens GN=PDE6B PE=1 SV=2
PDGFC_HUMAN	Platelet-derived growth factor C OS=Homo sapiens GN=PDGFC PE=1 SV=2
PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3
PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3
PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=3
PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2
PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3
PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3
PGS1_HUMAN	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2
PGS2_HUMAN	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=3
PLEC1_HUMAN	Plectin-1 OS=Homo sapiens GN=PLEC1 PE=1 SV=3
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1
PLTP_HUMAN	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1
POSTN_HUMAN	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2
PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2
PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1
PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3
PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3
PRIO_HUMAN	Major prion protein OS=Homo sapiens GN=PRNP PE=1 SV=1
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2

PRS23_HUMAN	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1
PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2
PSG4_HUMAN	Pregnancy-specific beta-1-glycoprotein 4 OS=Homo sapiens GN=PSG4 PE=2 SV=2
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1
PTK7_HUMAN	Tyrosine-protein kinase-like 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2
PTN_HUMAN	Pleiotrophin OS=Homo sapiens GN=PTN PE=1 SV=1
PTPRG_HUMAN	Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens GN=PTPRG PE=1 SV=4
PTX3_HUMAN	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=2
PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2
QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3
RA1L2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like protein 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2
RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3
RARR2_HUMAN	Retinoic acid receptor responder protein 2 OS=Homo sapiens GN=RARRES2 PE=1 SV=1
RBM42_HUMAN	RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=2 SV=1
RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1
RCN3_HUMAN	Reticulocalbin-3 OS=Homo sapiens GN=RCN3 PE=1 SV=1
RD23B_HUMAN	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1
RECK_HUMAN	Reversion-inducing cysteine-rich protein with Kazal motifs OS=Homo sapiens GN=RECK PE=1 SV=1
RENR_HUMAN	Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=1 SV=2
RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5
RNAS4_HUMAN	Ribonuclease 4 OS=Homo sapiens GN=RNASE4 PE=1 SV=3
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2
S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2
S10AG_HUMAN	Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1
SAP_HUMAN	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2
SCF_HUMAN	Kit ligand OS=Homo sapiens GN=KITLG PE=1 SV=1
SDF1_HUMAN	Stromal cell-derived factor 1 OS=Homo sapiens GN=CXCL12 PE=1 SV=1
SEM7A_HUMAN	Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1
SIA4A_HUMAN	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase OS=Homo sapiens GN=ST3GAL1 PE=2 SV=1
SIA4C_HUMAN	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase OS=Homo sapiens GN=ST3GAL4 PE=2 SV=1
SIAE_HUMAN	Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=1 SV=1
SIL1_HUMAN	Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1
SLIT3_HUMAN	Slit homolog 3 protein OS=Homo sapiens GN=SLIT3 PE=2 SV=2
SMAL1_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 OS=Homo sapiens GN=SMARCAL1 PE=1 SV=1
SNED1_HUMAN	Sushi, nidogen and EGF-like domain-containing protein 1 OS=Homo sapiens GN=SNED1 PE=1 SV=2
SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2
SODE_HUMAN	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2
SPON2_HUMAN	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=2
SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1
SRCRL_HUMAN	Scavenger receptor cysteine-rich domain-containing protein LOC284297 OS=Homo sapiens PE=2 SV=2
SRP14_HUMAN	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2
SRPX_HUMAN	Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1
SRPX2_HUMAN	Sushi repeat-containing protein SRPX2 OS=Homo sapiens GN=SRPX2 PE=1 SV=1
STC2_HUMAN	Stanniocalcin-2 OS=Homo sapiens GN=STC2 PE=1 SV=1
STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3
SVEP1_HUMAN	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=2
SYCP1_HUMAN	Synaptonemal complex protein 1 OS=Homo sapiens GN=SYCP1 PE=1 SV=2
TAD2B_HUMAN	Transcriptional adapter 2-beta OS=Homo sapiens GN=TADA2B PE=1 SV=2
TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4
TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3

TARSH_HUMAN	Target of Nesh-SH3 OS=Homo sapiens GN=ABI3BP PE=1 SV=1
TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
TCOF_HUMAN	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=2
TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2
TFPI1_HUMAN	Tissue factor pathway inhibitor OS=Homo sapiens GN=TFPI PE=1 SV=1
TGBR3_HUMAN	TGF-beta receptor type III OS=Homo sapiens GN=TGFBR3 PE=1 SV=2
THBG_HUMAN	Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2
THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3
THRB_HUMAN	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2
THY1_HUMAN	Thy-1 membrane glycoprotein OS=Homo sapiens GN=THY1 PE=1 SV=2
THYG_HUMAN	Thyroglobulin OS=Homo sapiens GN=TG PE=1 SV=5
TIMP1_HUMAN	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1
TIMP2_HUMAN	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2
TKT_HUMAN	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3
TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2
TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1
TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1
TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3
TPST1_HUMAN	Protein-tyrosine sulfotransferase 1 OS=Homo sapiens GN=TPST1 PE=2 SV=1
TR11B_HUMAN	Tumor necrosis factor receptor superfamily member 11B OS=Homo sapiens GN=TNFRSF11B PE=1 SV=2
TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3
TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=2
TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6
TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2
TSP2_HUMAN	Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2
TWSG1_HUMAN	Twisted gastrulation protein homolog 1 OS=Homo sapiens GN=TWSG1 PE=2 SV=1
UACA_HUMAN	Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=1 SV=2
UBE2O_HUMAN	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3
UBE4B_HUMAN	Ubiquitin conjugation factor E4 B OS=Homo sapiens GN=UBE4B PE=1 SV=1
UFO_HUMAN	Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL PE=1 SV=3
VAS1_HUMAN	V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1
VAV2_HUMAN	Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2 PE=1 SV=2
VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4
VTDB_HUMAN	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1
VTNC_HUMAN	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1
VWA1_HUMAN	von Willebrand factor A domain-containing protein 1 OS=Homo sapiens GN=VWA1 PE=2 SV=1
WBP4_HUMAN	WW domain-binding protein 4 OS=Homo sapiens GN=WBP4 PE=1 SV=1
WIPF2_HUMAN	WAS/WASL-interacting protein family member 2 OS=Homo sapiens GN=WIPF2 PE=1 SV=1
WNT2B_HUMAN	Protein Wnt-2b OS=Homo sapiens GN=WNT2B PE=1 SV=2
WNT5A_HUMAN	Protein Wnt-5a OS=Homo sapiens GN=WNT5A PE=1 SV=2
XKRY_HUMAN	Testis-specific XK-related protein, Y-linked OS=Homo sapiens GN=XKRY PE=2 SV=1
XPP1_HUMAN	Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3
ZDBF2_HUMAN	DBF4-type zinc finger-containing protein 2 OS=Homo sapiens GN=ZDBF2 PE=1 SV=3
ZN197_HUMAN	Zinc finger protein 197 OS=Homo sapiens GN=ZNF197 PE=2 SV=1

Supplemental Table II

LA Fibroblasts:HA Fibroblasts

Accession	Description	Sequence	# Indiv ceps	Pep SM ratio	Pep GM ratio	Pep ratio SDpep	# pep speceies	Prot SM of pep SMs	Prot weighted SM of pep SMs	Prot GM of pep SMs	Prot weighted GM of pep SMs	Prot GM of pep GMs	Prot weighted GM of pep GMs	Protein SDpep
1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	DSTLIMQLLR	2	7.1122	4.3925	4.4913	7	8.4536	7.6196	3.4802	3.6401		3.1045	5.0925
		IEAELQDICNDVLELLDK	0											
		NLLSVAYK	1	2.5993	2.5993									
		QTTVSNSQQAYQEAFEISK	2	0.9024	0.8999	1.1101								
		TAFDEAIAELDTLNEESYK	1	0.3619	0.3619									
		YDDMAAAMK	2	9.8407	7.8064	2.7183								
		YLSEVASGDNK	1	29.9051	29.9051									
1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	AAFDDAIAELDTLSEESYK	3	1.6744	1.4007	2.0248	7	2.319	2.2334	1.6519	1.5465		1.3314	2.3867
		DSTLIMQLLR	2	7.1122	4.3925	4.4913								
		EAAENSLVAYK	2	0.9136	0.9136	1.0096								
		HLIPAANTGESK	1	2.5072	2.5072									
		LICCDILDVLDK	2	0.9005	0.8982	1.1062								
		NLLSVAYK	1	2.5993	2.5993									
		QMVETELK	2	0.5258	0.4214	2.6542								
1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	DSTLIMQLLR	2	7.1122	4.3925	4.4913	6	3.9037	3.5672	2.1527	1.9648		1.7486	3.3567
		ELETVCNDVLSLLDK	2	0.783	0.7802	1.126								
		NLLSVAYK	1	2.5993	2.5993									
		NSVVEASEAAYK	2	0.7877	0.7574	1.4897								
		QAFDDAIAELDTLNEDSYK	1	0.7674	0.7674									
		YLAEVASGEK	1	11.3728	11.3728									
1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	DSTLIMQLLR	1	1.5185	1.5185		4	5.8193	6.3981	4.7983	5.7149		5.0783	2.2325
		TAFDDAIAELDTLNEDSYK	3	6.1486	5.8137	1.5377								
		YDDMAAAMK	2	9.8407	7.8064	2.7183								
		YLAEVATGEK	2	5.7696	4.9321	2.2544								
1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	DSTLIMQLLR	2	7.1122	4.3925	4.4913	2	4.8557	5.6079	4.2996	5.0849		3.6877	2.0375
		NLLSVAYK	1	2.5993	2.5993									
1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	DSTLIMQLLR	2	7.1122	4.3925	4.4913	7	2.7131	3.2333	1.9444	2.2949		1.8167	2.3507
		NLLSVAYK	1	2.5993	2.5993									
		QTIDNSQAAYQEAFDISK	1	0.9711	0.9711									
		SICTTVLELLDK	2	1.0462	1.034	1.2429								
		TAFDEAIAELDTLNEDSYK	2	5.1826	2.6393	6.2487								
		YDDMATCMK	1	0.9915	0.9915									
		YLANATNPESK	1	1.0888	1.0888									
1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	DICNDVLSLLEK	5	1.3559	1.3083	1.3301	10	1.6604	1.6409	0.8639	1.101		1.0365	3.9635
		DSTLIMQLLR	2	7.1122	4.3925	4.4913								
		EKIETELR	1	0.083	0.083									
		FLIPNASQAESK	1	1.3228	1.3228									
		GIVDQSQQAYQEAFEISK	2	1.1199	1.1196	1.0293								
		NLLSVAYK	1	2.5993	2.5993									
		TAFDEAIAELDTLSEESYK	6	1.1391	1.1229	1.2069								
		VVSSIEQK	2	0.7143	0.672	1.6467								
		YDDMAACMK	2	1.0715	1.0513	1.3188								
		YLAEVAAGEDK	1	0.0862	0.0862									
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	QLSQSLLPAIVELAEDAK	2	0.8657	0.8469	1.3463	1	0.8657	0.8657	0.8657	0.8657		0.8469	
2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	QLSQSLLPAIVELAEDAK	2	0.8657	0.8469	1.3463	1	0.8657	0.8657	0.8657	0.8657		0.8469	
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	AGQAVDDFIEK	1	1.22	1.22		3	0.8194	0.8712	0.6421	0.722		0.7134	2.6284
		NFELQNLLLDDFFK	2	1.0268	1.0024	1.3657								
		VGTGEPCCDWVGDEGAGHFVK	1	0.2113	0.2113									
AATM_HUMAN	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=2	ASAELALGENSEVLK	1	0.5882	0.5882		4	1.5523	1.9367	0.8645	1.1671		1.0139	3.5503
		EFSIYMTK	1	0.2098	0.2098									
		NLDKYLPIGGLAEFCK	2	4.3771	2.8736	4.0149								
		TCGFDFTGAVEDISK	2	1.034	1.0325	1.078								
ACBP_HUMAN	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2	QATVGDINTERPGMLDFTGK	1	0.8096	0.8096		1	0.8096	0.8096	0.8096	0.8096		0.8096	
ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	YGQAGLPLVILAGK	1	1.0911	1.0911		1	1.0911	1.0911	1.0911	1.0911		1.0911	
ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	AGFAGDDAPR	2	1.6895	1.6853	1.105	6	1.8353	1.8952	1.8196	1.8782		1.7923	1.1531
		DLTDYLMK	4	1.8785	1.8235	1.332								
		DSYVGDEAQSK	2	1.8195	1.8159	1.0936								
		EITALAPSTMK	4	2.3129	1.9743	1.9023								
		GILTLK	3	1.8121	1.8099	1.0615								
		LCYVALDFENEMATAASSSSLEK	2	1.4996	1.4764	1.284								
ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	AGFAGDDAPR	3	1.7944	1.7855	1.1303	12	1.7099	1.9012	1.3268	1.7266		1.6512	3.0842
		AVFPSIVGRPR	2	1.3725	1.362	1.191								
		DLTDYLMK	5	1.8245	1.7783	1.2898								
		DSYVGDEAQSK	2	1.8195	1.8159	1.0936								
		EITALAPSTMK	5	2.6436	2.2699	1.8934								
		GILTLK	5	2.1925	2.1372	1.2805								
		GYSFTTTAER	4	1.6561	1.6347	1.2092								
		HQGVMVGMGQK	1	0.0391	0.0391									
		IIAPPERK	1	2.0606	2.0606									
		LCYVALDFEQEMATAASSSSLEK	2	1.6776	1.6716	1.1265								
		QEYDESGPSIVHR	2	1.3322	1.3281	1.1175								
		VAPEEHPVLLTEAPLNPK	5	2.1059	1.8923	1.6284								
ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	DLTDYLMK	5	1.8245	1.7783	1.2898	4	1.381	1.6024	0.6964	1.1719		1.1499	6.839
		HQGVMVGMGQK	1	0.0391	0.0391									
		IIAPPERK	1	2.0606	2.0606									
		VAPDEHPILLTEAPLNPK	2	1.6	1.566	1.342								
ACTBM_HUMAN	Beta-actin-like protein 3 OS=Homo sapiens GN=ACTBL3 PE=1 SV=1	QEYDESGPSIVHR	2	1.3322	1.3281	1.1175	1	1.3322	1.3322	1.3322	1.3322		1.3281	
ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	AGFAGDDAPR	1	2.0044	2.0044		8	1.8811	1.9438	1.2324	1.4133		1.4039	4.1942
		AVFPSIVGRPR	2	1.3725	1.362	1.191								
		DLTDYLMK	1	1.6085	1.6085									
		EITALAPSTMK	1	3.9664	3.9664									
		GILTLK	3	2.4803	2.4329	1.2726								
		HQGVMVGMGQK	1	0.0391	0.0391									
		IIAPPERK	1	2.0606	2.0606									
		LCYVALDFENEMATAASSSSLEK	1	1.5168	1.5168									
ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	AGFAGDDAPR	3	1.7944	1.7855	1.1303	12	1.7099	1.9012	1.3268	1.7266		1.6512	3.0842
		AVFPSIVGRPR	2	1.3725	1.362	1.191								
		DLTDYLMK	5	1.8245	1.7783	1.2898								
		DSYVGDEAQSK	2	1.8195	1.8159	1.0936								
		EITALAPSTMK	5	2.6436	2.2699	1.8934								
		GILTLK	5	2.1925	2.1372	1.2805								
		GYSFTTTAER	4	1.6561	1.6347	1.2092								
		HQGVMVGMGQK	1	0.0391	0.0391									
		IIAPPERK	1	2.0606	2.0606									
		LCYVALDFEQEMATAASSSSLEK	2	1.6776	1.6716	1.1265								
		QEYDESGPSIVHR	2	1.3322	1.3281	1.1175								
		VAPEEHPVLLTEAPLNPK	5	2.1059	1.8923	1.6284								
ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	AGFAGDDAPR	1	1.5704	1.5704		5	2.1064	2.0053	1.8815	1.8117		1.8023	1.6353
		DLTDYLMK	1	1.2528	1.2528									
		EITALAPSTMK	1	4.3879	4.3879									
		GILTLK	1	1.8213	1.8213									
		LCYVALDFENEMATAASSSSLEK	2	1.4996	1.4764	1.284								
ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	1.2427	1.2289	1.2358	15	1.2375	1.2476	1.1925	1.2118		1.207	1.3137
		ASIHEAWTDGK	1	1.0175	1.0175									
		CQLEINFNTLQTK	1	1.0025	1.0025									
		DLLLDPAWEK	3	1.4875	1.4807	1.1235								
		FAIQDISVEETSAK	3	1.2497	1.2428	1.1367								
		GYEEWLLNEIR	1	1.4677	1.4677									
		ICDQWDNLGALTQK	2	0.8528	0.849	1.143								
		IDQLEGDHQLIQEALIFDNK	1	0.7608	0.7608									
		IVQTYHVNMAGTNPYTTITPQEINGK	1	1.0079	1.0079									
		LAILGIHNEVSK	1	2.3307	2.3307									
		LLETIDQLYLEYAK	2	1.5882	1.5881	1.004								
		QKDYETATLSEIK	2	1.0988	1.0849	1.2534								
		TINEVENQILTR	1	1.1052	1.1052									
		VGWEQLLTTIAR	1	1.2288	1.2288									
		VLAVNQENEQLMEDYEK	2	1.1225	1.1178	1.1375								
ACTN2_HUMAN	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	CQLEINFNTLQTK	1	1.0025	1.0025		5	1.0867	1.212	0.9082	1.088		1.0843	2.2121
		DLLLDPAWEK	3	1.4875	1.4807	1.1235								
		FAIQDISVEETSAK	3	1.2497	1.2428	1.1367								
		GYEEWLLNEIR	1	1.4677	1.4677									
		LEQAEKGYEEWLLNEIR	1	0.2259	0.2259									
ACTN3_HUMAN	Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	CQLEINFNTLQTK	1	1.0025	1.0025		3	1.2466	1.3163	1.2306	1.3049		1.2992	1.2187
		DLLLDPAWEK	3	1.4875	1.4807	1.1235								
		FAIQDISVEETSAK	3	1.2497	1.2428	1.1367								
ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	1.2427	1.2289	1.2358	14	1.4621	1.4548	1.3539	1.3734		1.3234	1.4477
		ASIHEAWTDGK	1	1.0175	1.0175									
		CQLEINFNTLQTK	1	1.0025	1.0025									
		DLLLDPAWEK	3	1.4875	1.4807	1.1235								
		EAILAIHK	2	1.9095	1.3526	3.4656								
		ETTDTADQVIASFK	1	1.9246	1.9246									
		FAIQDISVEETSAK	3	1.2497	1.2428	1.1367								
		GYEEWLLNEIR	1	1.4677	1.4677									
		ISIENWGTLEDQLSHLK	1	3.7604	3.7604									
		KDDPVTNLNNAFEVAEK	1	1.0013	1.0013									
		LSGSNPYTTVTPQIINSK	1	0.979	0.979									
		QFASQANVVGPWQTK	1	1.0927	1.0927									
		TINEVENQILTR	1	1.1052	1.1052									
		VGWEQLLTTIAR	1	1.2288	1.2288									
ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	AGFAGDDAPR	3	1.7944	1.7855	1.1303	9	1.6947	1.9143	1.2145	1.6848		1.6186	3.6802
		AVFPSIVGRPR	2	1.3725	1.362	1.191								
		DLTDYLMK	5	1.8245	1.7783	1.2898								
		DSYVGDEAQSK	2	1.8195	1.8159	1.0936								
		EITALAPSTMK	5	2.6436	2.2699	1.8934								
		GILTLK	5	2.1925	2.1372	1.2805								
		HQGVMVGMGQK	1	0.0391	0.0391									
		IIAPPERK	1	2.0606	2.0606									
		LCYVALDFENEMATAASSSSLEK	3	1.5053	1.4898	1.1942								
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1	DLLPEDFVVYTYNK	1	0.4814	0.4814		2	0.3813	0.3813	0.3679	0.3679		0.3679	1.4629
		QVSYVIQAEGK	1	0.2811	0.2811									
ADK_HUMAN	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2	ELFDELVK	1	0.6485	0.6485		1	0.6485	0.6485	0.6485	0.6485		0.6485	
AEBP1_HUMAN	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1	GEDEDEVSEAQETPDHAIFR	1	0.0883	0.0883		2	0.229	0.229	0.1807	0.1807		0.1807	2.7526
		YLSPDATVSTEVR	1	0.3697	0.3697									
AGRIN_HUMAN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4	SIESTLDDLFR	1	0.3848	0.3848		1	0.3848	0.3848	0.3848	0.3848		0.3848	
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	ADIDVSGPK	1	0.3816	0.3816		6	0.7771	0.7444	0.725	0.6967		0.695	1.5186
		AEGPEVDVNLPK	1	1.2556	1.2556									
		ISMPDIDLNLK	2	0.5485	0.5439	1.1998								
		ISMPDVDLHLK	1	0.956	0.956									
		VDINAPDVDVQGPDWHLK	1	0.7501	0.7501									
		VDVSAPDVEAHGPEWNLK	1	0.7707	0.7707									
AIBP_HUMAN	Apolipoprotein A-I-binding protein OS=Homo sapiens GN=APOA1BP PE=1 SV=2	GNAGSIQPDLLISLTAPK	1	1.2548	1.2548		1	1.2548	1.2548	1.2548	1.2548		1.2548	
AIMP1_HUMAN	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	GAEADQIEYLK	1	0.7391	0.7391		1	0.7391	0.7391	0.7391	0.7391		0.7391	
AINX_HUMAN	Alpha-internexin OS=Homo sapiens GN=INA PE=1 SV=2	EYGDLLNVK	4	1.4457	1.4104	1.2911	1	1.4457	1.4457	1.4457	1.4457		1.4104	
AK1A1_HUMAN	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	VFDFTFSPEEMK	2	1.0323	1.0309	1.0758	1	1.0323	1.0323	1.0323	1.0323		1.0309	
AKA12_HUMAN	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=3	VELPSEEQVSGSQGPSEEKPAPLATEVFDEK	2	1.0097	0.9347	1.755	1	1.0097	1.0097	1.0096	1.0096		0.9347	

AL1A1_HUMAN	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	1	5.7793	5.7793		6	1.638	1.6148	0.9782	1.0373	1.0373	2.9033
		IFINNEWHDSVSGK	1	0.8648	0.8648								
		LYSNAYLNDLAGCIK	2	1.4754	1.475	1.034							
		SLDDVIK	1	1.0649	1.0649								
		VAFTGSTEVGK	1	0.2408	0.2408								
		YILGNPLTPGVTQGPQIDKEQYDK	1	0.6027	0.6027								
ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	KVPQVSTPTLVEVSR	3	0.6768	0.6762	1.0519	2	0.6388	0.6334	0.6377	0.6323	0.6315	1.0878
		LVTDLTK	4	0.6009	0.5999	1.0675							
ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	AAGEEVLVK	1	1.0453	1.0453		8	1.1134	1.0773	1.0992	1.0686	1.016	1.1853
		ADDGRPFPQVIK	1	0.838	0.838								
		ALANSLACQGK	3	1.0429	0.9395	1.814							
		GGVVGIK	1	1.4703	1.4703								
		GILAADESTGSIAK	3	1.0378	0.9313	1.7724							
		VLAAVYK	1	1.1985	1.1985								
		VNPCIGGVILFHETLYQK	1	1.2674	1.2674								
		YASICQQNGIVPIVEPELPDGDHDLK	3	1.0068	0.9842	1.3066							
ALDOB_HUMAN	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2	VLAAVYK	1	1.1985	1.1985		1	1.1985	1.1985	1.1985	1.1985	1.1985	
ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	VLAAVYK	1	1.1985	1.1985		2	1.1027	1.0547	1.0985	1.0516	1.0339	1.1312
		YASICQQNGIVPIVEPELPDGDHDLK	3	1.0068	0.9842	1.3066							
AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	GLVLGIYSK	1	0.3751	0.3751		1	0.3751	0.3751	0.3751	0.3751	0.3751	
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	IKDLSTIEPLK	1	6.4198	6.4198		3	6.5501	6.5501	4.5067	4.5067	4.5067	3.32
		SLDLFNCEVTNLNDYR	1	12.0469	12.0469								
		VSGLEVLAEK	1	1.1835	1.1835								
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	IFGGLDMLAEK	1	0.7183	0.7183		2	3.5691	3.5691	2.1474	2.1474	2.1474	4.7056
		LKDISTLEPLK	1	6.4198	6.4198								
AN32C_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Homo sapiens GN=ANP32C PE=2 SV=1	IKDLSTIEPLK	1	6.4198	6.4198		2	3.8017	3.8017	2.7564	2.7564	2.7564	3.3057
		VSGGLEVLAEK	1	1.1835	1.1835								
AN32D_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member D OS=Homo sapiens GN=ANP32D PE=1 SV=2	IKDLSTIEPLK	1	6.4198	6.4198		1	6.4198	6.4198	6.4198	6.4198	6.4198	
ANM1_HUMAN	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	IVKANK	1	3.7221	3.7221		3	2.1601	2.1601	1.9122	1.9122	1.9122	1.7996
		VEDLTFTSPFCLQVK	1	1.2254	1.2254								
		VVLDVGSGTGILCMFAAK	1	1.5329	1.5329								
ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	GLGTDEDTLIEILASR	1	0.9499	0.9499		2	1.1866	1.1866	1.1628	1.1628	1.1628	1.331
		GVDEATIIDILTK	1	1.4233	1.4233								
ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	DALNIETAIK	1	1.8517	1.8517		2	1.8547	1.8547	1.8547	1.8547	1.8547	1.0023
		SALSQHLETVILGLLK	1	1.8577	1.8577								
ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	ETSGNLEQLLLAVVK	3	1.4606	1.4405	1.232	2	1.1384	1.2995	1.0919	1.2629	1.2498	1.5091
		LYDAYELK	1	0.8162	0.8162								
AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	TSVQFQNFSPTVVHPGDLQTQLAVQTK	1	0.7753	0.7753		1	0.7753	0.7753	0.7753	0.7753	0.7753	
API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=2	DAYGVILDGVK	1	0.4126	0.4126		1	0.4126	0.4126	0.4126	0.4126	0.4126	
APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	EQLGPVTQEFWDNLEK	2	1.2431	1.2382	1.1342	1	1.2431	1.2431	1.2431	1.2431	1.2382	
ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	DAVLLVFANK	1	1.657	1.657		1	1.657	1.657	1.657	1.657	1.657	
ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	DAVLLVFANK	2	1.4313	1.4171	1.2216	2	1.0569	1.1817	0.9884	1.1182	1.1108	1.6882
		NISFTVWDVGGQDK	1	0.6825	0.6825								
ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	DAVLLVFANK	3	1.5065	1.4929	1.1828	1	1.5065	1.5065	1.5065	1.5065	1.4929	
ARFP1_HUMAN		KYENILK	1	0.0344	0.0344		1	0.0344	0.0344	0.0344	0.0344	0.0344	
ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	FMEQVIFK	1	0.7363	0.7363		4	1.53	1.4282	1.1844	1.1977	1.1807	2.1953
		GVDDLDFFIGDEAIEKPTYATK	3	1.2245	1.1901	1.3493							
		TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1	3.543	3.543								
		YSYVCPDLVK	1	0.6161	0.6161								
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	DTDIVDEAIYYFK	1	1.0517	1.0517		1	1.0517	1.0517	1.0517	1.0517	1.0517	
ATX10_HUMAN		MEEQGLADASLLKK	1	0.1155	0.1155		1	0.1155	0.1155	0.1155	0.1155	0.1155	
ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	GINGGPSR	1	0.0417	0.0417		1	0.0417	0.0417	0.0417	0.0417	0.0417	
AXA2L_HUMAN	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2	DALNIETAIK	1	1.8517	1.8517		2	1.8547	1.8547	1.8547	1.8547	1.8547	1.0023
		SALSQHLETVILGLLK	1	1.8577	1.8577								
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	SNFLNCYVSGFHPSDIEVDLLK	1	0.2739	0.2739		3	0.2753	0.2756	0.2541	0.2503	0.2322	1.6569
		VEHSDLSFSK	2	0.1483	0.1406	1.5941							
		VNHVTLSQPK	2	0.4037	0.3531	2.1126							
BAF_HUMAN	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	AYVVLQGFLVLK	1	1.2936	1.2936		1	1.2936	1.2936	1.2936	1.2936	1.2936	
BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	ITDSEDK	1	0.2314	0.2314		1	0.2314	0.2314	0.2314	0.2314	0.2314	
BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase, cytosolic OS=Homo sapiens GN=BCAT1 PE=1 SV=3	ATLPVFDKEELECIQQLVK	1	7.7169	7.7169		1	7.7169	7.7169	7.7169	7.7169	7.7169	
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	DLLNNHILK	1	0.2866	0.2866		9	1.1142	0.8921	0.4272	0.3638	0.3553	3.0063
		EGVVTVFAPTNEAFR	1	7.5847	7.5847								
		ELANILK	1	0.2439	0.2439								
		GDELADSALEIFK	3	0.2097	0.1909	1.7646							
		LTLLAPLNSVFK	2	0.2579	0.2578	1.008							
		QAGLGNHLSGSER	1	0.3158	0.3158								
		SPYQLVLQHSR	1	0.4119	0.4119								
		VLTPPMGTVMDVLK	1	0.3979	0.3979								
		YLYHGQTLETLGGK	1	0.3191	0.3191								
BIG1_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	KGLECLVSILK	1	0.0299	0.0299		1	0.0299	0.0299	0.0299	0.0299	0.0299	
BIG2_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	KGLECLVSILK	1	0.0299	0.0299		1	0.0299	0.0299	0.0299	0.0299	0.0299	
BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	LNSDPQFVLAQNVGTTHDLLDICLK	1	1.8514	1.8514		1	1.8514	1.8514	1.8514	1.8514	1.8514	
BPNT1_HUMAN	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	LTDHIGNVLQYHK	1	0.5302	0.5302		1	0.5302	0.5302	0.5302	0.5302	0.5302	
BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	LMSERIK	1	2.4353	2.4353		1	2.4353	2.4353	2.4353	2.4353	2.4353	
BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=3	LMSERIK	1	2.4353	2.4353		1	2.4353	2.4353	2.4353	2.4353	2.4353	
C1R_HUMAN	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	ESEQGVYTCTAQGIWK	2	0.3919	0.3909	1.1045	7	1.9654	2.4541	1.029	1.1599	1.1554	3.1997
		GGGALLGDR	1	1.5913	1.5913								
		LPVANPQACENWLR	1	2.3335	2.3335								
		QDACQGDSGGVFAVR	1	0.4282	0.4282								
		QRPPDLDTSSNAVDLLFFTDESGDSR	1	0.7421	0.7421								
		TLDEFTIQPNLQPQYQFR	2	7.9377	7.8206	1.2769							
		YTTTMGVNTYK	1	0.3328	0.3328								
C1RL_HUMAN	Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	GGGALLGDR	1	1.5913	1.5913		1	1.5913	1.5913	1.5913	1.5913	1.5913	
C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	GFQVVYTLR	2	2.6108	1.3135	6.3745	8	1.2785	1.3045	0.6497	0.6659	0.5799	3.1702
		IIGGSDADIK	1	0.7541	0.7541								
		NYVDWIMK	2	0.2068	0.2059	1.1333							
		QFGPYCGHGFPGPLNIETK	1	5.2299	5.2299								
		SNALDIIFQTDLTGQK	1	0.4607	0.4607								
		SSNNPHSPIVEEFQVPYNK	1	0.3413	0.3413								
		TMQENSTPRED	1	0.363	0.363								
		TNFDNDIALVR	1	0.2613	0.2613								
C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	VRLSVLER	1	0.2199	0.2199		1	0.2199	0.2199	0.2199	0.2199	0.2199	
CAD13_HUMAN	Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1	DIQGSLQDIFK	1	0.5395	0.5395		1	0.5395	0.5395	0.5395	0.5395	0.5395	
CAD24_HUMAN		TLAELYGAK	1	0.7572	0.7572		1	0.7572	0.7572	0.7572	0.7572	0.7572	
CADH5_HUMAN	Cadherin-5 OS=Homo sapiens GN=CDH5 PE=1 SV=4	ELDSTGTPTGK	1	0.9651	0.9651		1	0.9651	0.9651	0.9651	0.9651	0.9651	
CALL3_HUMAN	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	EAFSLFDK	2	0.5059	0.4753	1.6573	1	0.5059	0.5059	0.5059	0.5059	0.4753	
CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	EAFSLFDK	2	0.5059	0.4753	1.6573	1	0.5059	0.5059	0.5059	0.5059	0.4753	
CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	IDNSQVESGSLEDDWDFLPPKK	2	0.9922	0.9907	1.0819	1	0.9922	0.9922	0.9922	0.9922	0.9907	
CALU_HUMAN	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	EEFTATLHPEEYDYMK	1	0.6686	0.6686		2	1.8086	1.8086	1.3166	1.3166	1.3166	3.2785
		EQFVEFR	1	3.0485	3.0485								
CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5	EFVILWTK	1	4.5174	4.5174		2	2.3382	2.3382	0.8472	0.8472	0.8472	10.6651
		SDGFSIETCK	1	0.1589	0.1589								
CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4	LSDLLAPISEQIK	2	0.9624	0.9588	1.1312	2	0.9384	0.9464	0.938	0.9461	0.9437	1.0369
		VENQENVSNLVIEDTELK	1	0.9143	0.9143								
CAPZB_HUMAN	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	LVEDMENK	1	0.7863	0.7863		2	0.4966	0.4966	0.4033	0.4033	0.4033	2.5704
		STLNEIYTGK	1	0.2069	0.2069								
CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	DIMAEIYK	4	1.5231	1.4822	1.3152	6	1.6385	1.5901	1.6008	1.5691	1.5489	1.2689
		DQGSCGSCWAFGAVEAISDR	1	1.1044	1.1044								
		EQWPQCPTIK	1	1.5257	1.5257								
		ICEPGYSPTYK	3	1.5455	1.5281	1.2062							
		NGPVEGAFSVYSDFLLYK	1	1.9016	1.9016								
		TDQYWEK	1	2.231	2.231								
CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	ISVNNVLPVFDNLMQQK	2	0.6147	0.5867	1.5451	2	0.5995	0.6046	0.5993	0.6044	0.5859	1.0363
		VSTLPAITLK	1	0.5844	0.5844								
CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	KIDGQQTIIACIESHQFQAK	1	0.733	0.733		1	0.733	0.733	0.733	0.733	0.733	
CB039_HUMAN		NKLISELQQELK	2	0.0553	0.0549	1.1804	1	0.0553	0.0553	0.0553	0.0553	0.0549	
CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	SETITEEELVGLMNK	1	0.8305	0.8305		2	0.7697	0.7697	0.7673	0.7673	0.7673	1.1185
		SPEEGAETPVYLALLPPDAEGPHGQFVSEK	1	0.7089	0.7089								
CCD57_HUMAN	Coiled-coil domain-containing protein 57 OS=Homo sapiens GN=CCDC57 PE=2 SV=1	AEVSELK	1	0.6682	0.6682		1	0.6682	0.6682	0.6682	0.6682	0.6682	
CCD58_HUMAN	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	NLDDLTLLK	1	1.5559	1.5559		1	1.5559	1.5559	1.5559	1.5559	1.5559	
CCL2_HUMAN	C-C motif chemokine 2 OS=Homo sapiens GN=CCL2 PE=1 SV=1	WVQDSMDHLDK	1	0.6728	0.6728		1	0.6728	0.6728	0.6728	0.6728	0.6728	
CD109_HUMAN	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	SNLIQQWLSQQSDLGVISK	1	0.5573	0.5573		1	0.5573	0.5573	0.5573	0.5573	0.5573	
CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2	YGFIEGHVVIPR	1	0.9233	0.9233		1	0.9233	0.9233	0.9233	0.9233	0.9233	
CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	CIDSGLWVPNSK	1	0.6365	0.6365		2	0.9713	0.9713	0.9118	0.9118	0.9118	1.6624
		QYMEGFNDLELEAFK	1	1.3061	1.3061								
CFAH_HUMAN	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	SIDVACHPGYALPK	1	73.4667	73.4667		1	73.4667	73.4667	73.4667	73.4667	73.4667	
CH10_HUMAN	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	DGDILGK	1	19.9954	19.9954		3	7.3712	7.3712	2.8174	2.8174	2.8174	5.4628
		VLLPEYGGTK	1	1.0026	1.0026								
		VVLDDKDYFLFR	1	1.1156	1.1156								
CH3L1_HUMAN	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2	EAGTLAYYEICDFLR	1	0.3905	0.3905		1	0.3905	0.3905	0.3905	0.3905	0.3905	
CING_HUMAN	Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	KVSLVLEK	1	0.0882	0.0882		1	0.0882	0.0882	0.0882	0.0882	0.0882	
CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	DLADLIPK	2	0.7413	0.6525	2.0738	1	0.7413	0.7413	0.7413	0.7413	0.6525	
CLC11_HUMAN	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	AALAPVNWPVWLGVHDR	1	0.3267	0.3267		3	0.2745	0.2909	0.2592	0.2774	0.2749	1.5469
		DAVQALQEAQGR	2	0.3401	0.334	1.3102							
		QQMEALTR	1	0.1567	0.1567								
CLCA_HUMAN		SVLISLK	1	0.6598	0.6598		1	0.6598	0.6598	0.6598	0.6598	0.6598	
CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	EADSYK	2	1.5765	1.5629	1.205	4	0.8792	1.0186	0.6652	0.7905	0.7878	2.6799
		EDKLECSEELGDLVK	1	1.0805	1.0805								
		LPVVIGGLLDVDCSEDVIK	1	0.6941	0.6941								
		TLQIFNIEMK	1	0.1656	0.1656								
CLH2_HUMAN	Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2	EDKLECSEELGDLVK	1	1.0805	1.0805		2	0.6231	0.6231	0.423	0.423	0.423	3.7669
		TLQIFNIEMK	1	0.1656	0.1656								
CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	EEFASTCPDDEIELAYEQVAK	1	6.6893	6.6893		5	2.416	2.0636	1.6669	1.5915	1.506	2.6266
		LAALNPESNTAGLDIFAK	2	1.3495	1.0866	2.6246							
		LCPGGQLPFLLYGTEVHTDTNK	1	2.0504	2.0504								
		LHIVQVVCK	1	0.4516	0.4516								
		NSNPALNDNLEK	3	1.5394	1.5351	1.0955							
CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	DEFTNTCPSDKEVEIAYSDVAK	1	2.7461	2.7461		3	17.0966	17.0966	5.5253	5.5253	5.5253	6.6572
		IEEFLEEVLCPPK	1	47.2435	47.2435								
		TDVNKIEEFLEEVLCPPK	1	1.3002	1.3002								
CLIC5_HUMAN	Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3	FLDGDELTLADCNLLPK	1	5.0325	5.0325		1	5.0325	5.0325	5.0325	5.0325	5.0325	
CLIC6_HUMAN	Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 PE=2 SV=3	FLDGDELTLADCNLLPK	1	5.0325	5.0325		1	5.0325	5.0325	5.0325	5.0325	5.0325	
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	ALQEYR	1	0.0758	0.0758		16	0.4784	0.2753	0.0937	0.0884	0.0719	3.535
		ASSIIDELFQDR	4	0.0456	0.0332	2.3671							
		EILSVDCSTNNPSQAK	4	0.082	0.071	1.873							
		EIQNAVNGVK	1	0.0668	0.0668								
		ELDESLQVAER	2	0.0495	0.0438	2.0374							
		FMETVAEK	4	0.0512	0.0479	1.4913							
		IDSLLENDR	3	0.0894	0.0542	3.3319							
		KTLLSNLEEAK	1	0.0787	0.0787								
		KYNELLK	1	0.0344	0.0344								
		LFDSDPITVTVPVEVSR	3	0.0563	0.0436	2.3473							
		QQTHMLDVMQDHFSR	1	0.0726	0.0726								
		RELDESLQVAER	1	0.2998	0.2998								
		SGSGLVGR	3	0.1217	0.1208	1.1624							
		TLLSNLEEAK	4	0.436	0.2076	3.9246							
		TLLSNLEEAKK	1	0.0434	0.0434								
		VTTVASHTSDSDVPSGVTEVVVK	3	0.0518	0.0516	1.1111							
CMBL_HUMAN	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	EVQVEHIK	1	7.1267	7.1267		1	7.1267	7.1267	7.1267	7.1267	7.1267	

CN153_HUMAN	UPF0671 protein C14orf153 OS=Homo sapiens GN=C14orf153 PE=2 SV=1	MVVLRAGK	1	0.0543	0.0543		1	0.0543	0.0543	0.0543	0.0543	0.0543	
CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	CYSCGEFGHIQK	1	0.1535	0.1535		1	0.1535	0.1535	0.1535	0.1535	0.1535	
CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	GNILIPGINEAVAVTEEEHK	1	4.7953	4.7953		2	6.4961	6.4961	6.2695	6.2695	6.2695	1.4609
		MMEVAAADVK	1	8.1968	8.1968								
CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	DGTILCTLMNK	2	0.4355	0.4265	1.3346	2	0.811	0.6858	0.7188	0.6082	0.5999	2.0317
		TWIEGLTGLSIGPDFQK	1	1.1866	1.1866								
CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4	ALLQGSNEIEIR	3	1.2969	0.7937	3.4608	20	4.0049	6.5884	0.6396	0.8709	0.7615	4.4671
		DLEVDTTLK	1	0.226	0.226								
		FTYSVTVDGCTSHTGAWGK	2	0.3251	0.3238	1.1301							
		GDAGPAGPK	1	1.3422	1.3422								
		GESGPSGPAGPTGAR	1	2.3695	2.3695								
		GFPGADGVAGPK	1	0.3074	0.3074								
		GFSGLDGAK	1	0.1665	0.1665								
		GLTGSPGSPGPDGK	1	0.1727	0.1727								
		GNSGEPGAPGSK	1	1.3636	1.3636								
		GPAGPPGPR	2	0.2408	0.2386	1.2124							
		GSEGPQGVR	3	0.274	0.2715	1.1812							
		GVPGPPGAVGPAGK	1	0.3152	0.3152								
		GVQGPPGPAGPR	2	0.6878	0.5521	2.6439							
		NSVAYMDQQTGNLK	1	0.4409	0.4409								
		NSVAYMDQQTGNLKK	2	0.2737	0.2711	1.2157							
		SGDRGETGPAGPAGPVGPVGAR	2	0.2163	0.2163	1.0033							
		SGEYWIDPNQGCNLDAIK	1	0.3871	0.3871								
		SLSQQIENIR	3	57.266	32.1038	4.5455							
		STGGISVPGPMGPSGPR	3	12.0656	9.7047	2.3525							
		VLCDVVICDETK	2	0.3602	0.3279	1.8629							
CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6	DGNPGNDGPPGR	1	0.3571	0.3571		25	2.2781	2.2083	0.6815	0.6142	0.5728	4.54
		DYEVDATLK	1	0.3006	0.3006								
		EMATQLAFMR	1	11.421	11.421								
		FTYTVLVDGCSK	1	0.3027	0.3027								
		GAAGIPGGK	3	0.0321	0.0308	1.4191							
		GAPGAVGAPGPAGATGDR	1	6.6582	6.6582								
		GASGPAGVR	1	0.3241	0.3241								
		GDGGPPGMTGFPGAAGR	1	0.2417	0.2417								
		GDQGPVGR	1	0.2296	0.2296								
		GEAGAAGPAGPAGPR	1	4.4224	4.4224								
		GETGPSGPVGPAGAVGPR	1	4.2206	4.2206								
		GFPGTPGLPGFK	1	0.5189	0.5189								
		GHAGLAGAR	2	0.319	0.3186	1.0643							
		GIPGPVGAAGATGAR	1	15.4319	15.4319								
		GPAGPSGPAGK	2	0.3087	0.3058	1.2117							
		GPNGDAGRPGEPGLMGPR	1	1.1254	1.1254								
		GPSGPPGPDGNK	1	0.9863	0.9863								
		GPSGPQGIR	2	0.3412	0.341	1.0434							
		GVGLGPGPMGLMGPR	4	7.4383	4.098	4.3513							
		GVVGPQGAR	2	0.3255	0.3244	1.1206							
		KTNEWGK	1	0.4134	0.4134								
		NSAYMDEETGNLKK	2	0.3277	0.3226	1.2842							
		SAPSLRPK	1	0.248	0.248								
		TGHPGTVGPAGIR	1	0.2819	0.2819								
		TIEYK	3	0.3762	0.3739	1.1421							
CO2A1_HUMAN	Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	FTYTALKDGCTK	1	0.0739	0.0739		1	0.0739	0.0739	0.0739	0.0739	0.0739	
CO3A1_HUMAN	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	DGNPGSDGLPGR	1	5.5004	5.5004		11	2.8644	3.1256	0.8646	0.9012	0.7159	5.5129
		FTYTVLEDGCTK	3	0.1589	0.1568	1.2182							
		GAPGPQGPR	2	0.2508	0.2469	1.2842							
		GESGPAGPAGAPGPAGSR	1	0.3615	0.3615								
		GPVGPSGPPGK	1	0.9025	0.9025								
		GRPGLPGAAGAR	1	4.8487	4.8487								
		INTDEIMTSLK	2	0.1567	0.1494	1.55							
		SGEYWVDPNQGCK	2	0.2715	0.2365	2.1377							
		SVNGQIESLISPDGSR	4	5.5672	1.9833	7.0742							
		TVFEYR	1	0.1849	0.1849								
		VFCNMETGETCISANPLNVPR	2	13.305	13.086	1.2948							
CO5A2_HUMAN	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	GSQFAYGDHQSPNTAITQMTFLR	2	11.0122	2.8926	17.215	5	2.9242	4.2722	1.079	1.5891	1.0177	4.9329
		NSVGYMDDQAK	1	0.9342	0.9342								
		QSGEYWIDPNQGSVEDAIK	1	0.3612	0.3612								
		SGLGSQVGLMPGSVGPVGPR	1	2.1287	2.1287								
		TVFEYR	1	0.1849	0.1849								
CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	DTTPLNVLCSPGKQVVSVGIK	4	1.797	1.1271	2.756	9	1.1724	1.208	0.8848	0.9934	0.8774	2.0313
		ENYAELLEDAFLK	2	0.6317	0.6316	1.0226							
		GLEQLLVGGSHLK	1	0.7038	0.7038								
		GTYTDCAIK	1	0.6365	0.6365								
		IALVITDGR	3	1.0264	0.9921	1.3689							
		LLLFSDGNSQGATPAAIEK	2	0.7009	0.6947	1.2062							
		NNVEQVCCSFECQPAR	1	4.1159	4.1159								
		SLQWMAGGTFTGEALQYTR	1	0.474	0.474								
		YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1	0.4656	0.4656								
CO6A2_HUMAN	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	DDDLNLR	1	0.4762	0.4762		3	0.4219	0.4118	0.42	0.41	0.4092	1.1205
		DVTVTAIGIDMFHEK	2	0.3815	0.3799	1.1366							
		HESENLYSIACDKPQQVR	1	0.4079	0.4079								
CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=4	AAPLQGMLPGLLAPLR	1	0.2067	0.2067		23	1.1462	1.1227	0.6872	0.6789	0.6602	2.7079
		ALILVGLER	1	3.9019	3.9019								
		DQNVFVAQK	1	0.3702	0.3702								
		EVITAVR	1	0.8783	0.8783								
		FWYGCGGGNENK	2	0.5984	0.4223	3.4923							
		IEEGVPQFLVLISSGK	1	0.2686	0.2686								
		ISLSPEYVFSVSTFR	1	0.2998	0.2998								
		ITEGVPQLILVLTADR	1	4.6189	4.6189								
		LLVLITGGK	1	3.4803	3.4803								
		NIDSEEVGK	1	0.5375	0.5375								
		NILVSSAGSR	1	0.4907	0.4907								
		NLQVALTSK	1	0.3181	0.3181								
		NNLFTSSAGYR	1	1.6676	1.6676								
		QINVGNALEVVSR	2	2.0355	2.0354	1.0121							
		QLQLQGDSGLNTGSALSYVYANHFTEAGGSR	1	0.4591	0.4591								
		QQSLETAMSFVAR	1	0.4607	0.4607								
		SQAPVLDAIR	1	1.9704	1.9704								
		SSGIVSLGVGDR	1	0.3813	0.3813								
		VAVIQFSDDPK	1	0.1903	0.1903								
		VEFSLTDYGSK	2	0.1945	0.1914	1.2891							
		VGVVQFSDEPR	1	2.0095	2.0095								
		VGVVQFSNDVFPEFYLK	1	0.5158	0.5158								
		VVESLDVGQDR	1	0.5079	0.5079								
CO7_HUMAN	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	SFFRSSSSSSR	3	0.6067	0.606	1.0602	1	0.6067	0.6067	0.6067	0.6067	0.606	
COCA1_HUMAN	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	ALALGALQNR	1	0.5462	0.5462		23	0.8071	0.813	0.5303	0.5323	0.5072	2.5628
		DLSFSEVTSYGFK	1	0.3999	0.3999								
		GEVQTVTFDTEEVK	1	0.7653	0.7653								
		GGNTLTGMALNFR	1	0.6397	0.6397								
		GGNTMTGDAIDYLVK	1	0.1492	0.1492								
		GSETSHCFTGLSPDTDYGVTVFVQTPNLEGPGVSVK	2	1.5105	0.9654	4.2197							
		GSPQDLVTK	1	3.5569	3.5569								
		IVDDLTINLCNSVK	1	0.9321	0.9321								
		LGELVVGPYDNTVVLEELR	1	0.472	0.472								
		NFASVQGVSLESGSSFPSYSAYR	1	0.334	0.334								
		NLPEDAIHTMIENLQPETK	1	0.2625	0.2625								
		NSDVEIFAVGVK	1	0.2043	0.2043								
		NTFTESAGAR	1	0.9643	0.9643								
		NVGVEVFSLGIK	2	0.2087	0.2038	1.3589							
		QVCEQLISGQMNR	1	0.4083	0.4083								
		SELEAIASPPAETHVFTVEDFDAFQR	1	2.1155	2.1155								
		SLYDDVDTGEK	1	0.1709	0.1709								
		TEFNLNQYYQR	2	1.9279	1.7348	1.9372							
		TNWSPAGENVFSYHITYK	1	0.3752	0.3752								
		TVGLLPPQNIHISDEWYTR	1	1.1387	1.1387								
		TYQIGWDTFCVK	1	0.0906	0.0906								
		VEDIIEAINTFPYR	3	0.2767	0.2593	1.5841							
		VMILITDGK	1	1.1138	1.1138								
COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	AVLFCLSEDKK	1	1.1866	1.1866		10	1.0974	1.0991	0.9683	1.007	1.0022	1.9529
		EILVGDVGQTVDDPYATFVK	2	1.2724	1.2361	1.407							
		HELQANCYEEVK	1	1.025	1.025								
		HELQANCYEEVKDR	2	1.2297	1.226	1.1149							
		LGGSAVISLEGKPL	3	0.8979	0.8962	1.0768							
		MIYASSK	1	1.1257	1.1257								
		MLPDKDCR	1	1.4634	1.4634								
		NIILEEGK	1	0.1505	0.1505								
		NIILEEGKEILVGDVGQTVDDPYATFVK	1	1.4068	1.4068								
		YALYDATYETK	2	1.2158	1.2141	1.0781							
COF2_HUMAN	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1	MIYASSK	1	1.1257	1.1257		3	1.1758	1.1945	1.1746	1.1932	1.1929	1.057
		QILVGDIGDTVEDPYTSFVK	2	1.2506	1.25	1.0431							
		YALYDATYETK	1	1.1512	1.1512								
COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	GLELEPGAGLFVAQAGGADPDKFGQVIAELK	1	0.4708	0.4708		1	0.4708	0.4708	0.4708	0.4708	0.4708	
COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	TALNLFFK	1	1.0287	1.0287		1	1.0287	1.0287	1.0287	1.0287	1.0287	
COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	NTLEWCLPVIDAK	1	1.3484	1.3484		1	1.3484	1.3484	1.3484	1.3484	1.3484	
COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	GMGYMPK	1	12.4893	12.4893		4	4.1534	3.4761	2.155	1.7527	1.7021	3.5813
		KSDLFQDDLYPDTAGPEAALEAEEWFEGK	1	0.9263	0.9263								
		NADPLILSLK	2	0.7669	0.7127	1.7299							
		YFEITDESPYVHYLNTFSSK	1	2.431	2.431								
COTL1_HUMAN	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	EFVISDR	1	0.6786	0.6786		3	1.9225	1.9225	1.384	1.384	1.384	2.6233
		ELEEDFIK	1	4.147	4.147								
		YDGSTVPGEQGAEYQHFIQQCTDDVR	1	0.942	0.942								
CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	SMVAVMDSDTTGK	1	0.2872	0.2872		1	0.2872	0.2872	0.2872	0.2872	0.2872	
CPPED_HUMAN	Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=2	TQAVAMNK	1	0.0468	0.0468		1	0.0468	0.0468	0.0468	0.0468	0.0468	
CRIP2_HUMAN	Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR	2	1.7491	1.6375	1.6806	2	1.1488	1.3489	0.9795	1.1883	1.1372	2.2705
		GVNTGAVGSYIYDRDPEGK	1	0.5485	0.5485								
CSN6_HUMAN	COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=1 SV=4	GYKPPDEGPSEYQTPLNK	1	0.1124	0.1124		1	0.1124	0.1124	0.1124	0.1124	0.1124	
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	GFGFGQGAGALVHSE	1	0.0698	0.0698		4	1.098	1.1597	1.055	1.1126	1.0682	1.3781
		GLESTTLADKDGEIYCK	2	1.6222	1.553	1.523							
		SCFLCMVCK	1	0.7562	0.7562								
		TVYFAEVQCEGNSFHK	2	0.944	0.8725	1.7659							
CTCFL_HUMAN		LEEEQEK	1	0.5371	0.5371		1	0.5371	0.5371	0.5371	0.5371	0.5371	
CTGF_HUMAN	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2	ANCLVQTTEWSACSK	1	1.0959	1.0959		4	1.391	1.3138	1.3312	1.2583	1.1326	1.3945
		CCEEWVCDEPK	1	2.1154	2.1154								
		SCESFQSSCK	1	1.3481	1.3481								
		TTTLPVEFK	2	1.0047	0.7722	2.9204							
CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	SQGMASLNLPAVSWK	1	0.1577	0.1577		1	0.1577	0.1577	0.1577	0.1577	0.1577	
CUTA_HUMAN	Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2	LAACVNLIPQITSIYEWK	1	0.8898	0.8898		2	1.0972	1.0972	1.0774	1.0774	1.0774	1.3107
		SVHPYEVAEVALPVEQGNFDYLQWVR	1	1.3045	1.3045								
CV028_HUMAN	UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1	GGGVGGFLPAMK	1	0.208	0.208		1	0.208	0.208	0.208	0.208	0.208	
CYBP_HUMAN	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	ISNYGWDQSDK	1	1.412	1.412		1	1.412	1.412	1.412	1.412	1.412	
CYC_HUMAN	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	ADLIAYLK	1	0.476	0.476		2	10.5859	10.5859	3.1387	3.1387	3.1387	14.4024
		TGQAPGYSYTAANK	1	20.6957	20.6957								
CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	GLECNFGASSTALK	2	1.3349	1.3218	1.2196	2	4.1571	4.1571	3.0523	3.0523	2.9282	3.2209
		VTGQCCEEWVCDEDSIKDPMEDQDGLLGK	2	6.9793	6.4867	1.7293							
CYTB_HUMAN	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	AKHDELTYF	1	0.5901	0.5901		2	1.2075	1.4133	1.0377	1.2526	1.2514	2.2218
		SQVVAGTNYFIK	2	1.8249	1.8223	1.0779							

CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	ALDFAVGEYNK	4	0.4006	0.4001	1.0571	4	0.5065	0.5056	0.4692	0.4739	0.4556	1.5702
		ALQVVR	1	0.2807	0.2807								
		LVGGPMDASVEEEGVR	2	0.8176	0.6999	2.2451							
		TQPNLDNCPFHDQPHLK	1	0.527	0.527								
DBPA_HUMAN	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4	SVGDGETVEFDVVEGEK	1	0.6601	0.6601		1	0.6601	0.6601	0.6601	0.6601	0.6601	
DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2	EAGLAPVPMIIFAK	1	1.313	1.313		1	1.313	1.313	1.313	1.313	1.313	
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	ELAQQVQQVADDYGK	1	0.4128	0.4128		1	0.4128	0.4128	0.4128	0.4128	0.4128	
DDX39_HUMAN	ATP-dependent RNA helicase DDX39 OS=Homo sapiens GN=DDX39 PE=1 SV=2	GLAITFVSDENDAK	1	0.8201	0.8201		1	0.8201	0.8201	0.8201	0.8201	0.8201	
DEOC_HUMAN	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	DSLAWLSLVK	1	1.1251	1.1251		1	1.1251	1.1251	1.1251	1.1251	1.1251	
DESM_HUMAN	Desmin OS=Homo sapiens GN=DES PE=1 SV=3	EYGDLLNVK	4	1.4457	1.4104	1.2911	5	1.2623	1.2856	1.2518	1.272	1.2584	1.157
		KLLEGEESR	1	1.2487	1.2487								
		LLEGEESR	2	1.4361	1.4267	1.1758							
		TNEKVELQELNDR	3	1.0283	1.0263	1.0811							
		VELQELNDR	1	1.1529	1.1529								
DEST_HUMAN	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	MIYASSK	1	1.1257	1.1257		1	1.1257	1.1257	1.1257	1.1257	1.1257	
DKK3_HUMAN	Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1	DQDGEILLPR	2	3.1169	1.1299	10.6587	6	0.7956	0.9635	0.4672	0.5524	0.4324	2.6369
		DSECCGDQLCVWGHCTK	1	0.3743	0.3743								
		EVEELMEDTQHK	1	0.1997	0.1997								
		LLDLITWELEPDGALDR	2	0.323	0.3229	1.009							
		QELEDLER	2	0.4578	0.4193	1.8249							
		SAVEEMEAEEAAAK	1	0.302	0.302								
DLRB1_HUMAN	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3	STMDNPTTTQYASLMHSFILK	1	3.5782	3.5782		1	3.5782	3.5782	3.5782	3.5782	3.5782	
DNJB4_HUMAN	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1	EIYDQFGEEGLK	1	0.2932	0.2932		1	0.2932	0.2932	0.2932	0.2932	0.2932	
DNJC9_HUMAN	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	ISLEDIQAFEK	1	2.3861	2.3861		1	2.3861	2.3861	2.3861	2.3861	2.3861	
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	GLVDGPVCEVSVTPK	1	1.3893	1.3893		2	7.3852	7.3852	4.3117	4.3117	4.3117	4.9611
		GSPLVVISQGK	1	13.3811	13.3811								
DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	GMTTVDDFFQGTK	1	0.0258	0.0258		1	0.0258	0.0258	0.0258	0.0258	0.0258	
DYH2_HUMAN	Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=1 SV=3	QELLAQANK	1	0.8972	0.8972		1	0.8972	0.8972	0.8972	0.8972	0.8972	
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	QLQNSLAAASGGAK	1	0.3293	0.3293		1	0.3293	0.3293	0.3293	0.3293	0.3293	
DYSF_HUMAN	Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1	DLAAMDK	1	0.7743	0.7743		1	0.7743	0.7743	0.7743	0.7743	0.7743	
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	ALNALCDGLIDELNQALK	1	3.6541	3.6541		1	3.6541	3.6541	3.6541	3.6541	3.6541	
ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	DILTIDIGR	2	3.0705	1.3927	7.5328	4	1.137	1.3268	0.7607	0.8402	0.6376	2.621
		LVWEEAMSR	1	0.627	0.627								
		NVALVSGDTENAK	2	0.3421	0.3296	1.474							
		VTPNLMGHLCGNQR	1	0.5086	0.5086								
EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	EALMTELSTVK	1	0.1569	0.1569		1	0.1569	0.1569	0.1569	0.1569	0.1569	
EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	MDSTEPPYSQKR	1	0.1932	0.1932		4	1.0951	1.0414	0.759	0.7915	0.7843	2.9395
		SGDAAVDMVPGKPMCVESFSDYPPLGR	2	0.571	0.5662	1.2012							
		STTTGHLIYK	2	1.2974	1.2732	1.3168							
		THNIVVIGHVDSGK	1	2.3187	2.3187								
EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	STTTGHLIYK	2	1.2974	1.2732	1.3168	2	1.808	1.6378	1.7344	1.5744	1.5548	1.5077
		THNIVVIGHVDSGK	1	2.3187	2.3187								
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1	EVSTYIK	1	1.2376	1.2376		2	1.5019	1.5019	1.4785	1.4785	1.4785	1.2859
		QTVAVGVIK	1	1.7662	1.7662								
EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	SPAGLQVLNDYLADK	2	0.8044	0.8027	1.0978	1	0.8044	0.8044	0.8044	0.8044	0.8027	
EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	GVVQELQQAISK	1	0.8705	0.8705		2	0.7765	0.7452	0.7708	0.7402	0.7399	1.1877
		SIQLDGLVWGASK	2	0.6825	0.6822	1.0415							
EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	AVLGEVK	2	37.9178	37.0701	1.3624	3	13.2683	15.7846	3.1497	4.2718	4.2218	8.783
		ILGLLDAYLK	2	1.2006	1.1924	1.1798							
		YSNEDTLSVALPYFWEHFDK	1	0.6864	0.6864								
EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EGIPALDNFLDKL	3	0.8268	0.8268	1.0814	9	0.8212	0.798	0.6003	0.6267	0.624	2.915
		ETVSEESNVLCLSK	1	1.9174	1.9174								
		GPLMMYISK	1	0.8997	0.8997								
		GVQYLNEIK	1	1.156	1.156								
		IWCFGPDGTGPNILTDITK	2	0.5274	0.5158	1.349							
		STLTDSLVCK	1	0.0448	0.0448								
		TFCQLILDPIFK	1	0.3941	0.3941								
		VFDAIMNFK	1	0.8253	0.8253								
		VFSGLVSTGLK	1	0.7979	0.7979								
EFHD1_HUMAN	EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1	DGFIDLMELK	1	2.5958	2.5958		1	2.5958	2.5958	2.5958	2.5958	2.5958	
EFHD2_HUMAN	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	DGFIDLMELK	1	2.5958	2.5958		1	2.5958	2.5958	2.5958	2.5958	2.5958	
EGLN_HUMAN	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2	GEVTYTTSQVSK	1	2.1186	2.1186		1	2.1186	2.1186	2.1186	2.1186	2.1186	
EHD2_HUMAN	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	DGMLDDEEFALASHLIEAK	2	1.0511	1.0484	1.1064	1	1.0511	1.0511	1.051	1.051	1.0484	
ELOB_HUMAN	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	LYKDDQLLDDGK	1	3.4636	3.4636		1	3.4636	3.4636	3.4636	3.4636	3.4636	
EMIL1_HUMAN	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	GLEEGQAQAGQCPSLEGR	1	0.1979	0.1979		3	0.1358	0.1358	0.0777	0.0777	0.0777	5.0419
		LVGSGLHTVEAAGEAR	1	0.012	0.012								
		QATLEGLQEVVGR	1	0.1976	0.1976								
ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	AVEHINK	1	0.2398	0.2398		17	2.4829	2.7343	1.0005	1.1471	1.0025	2.7164
		DATNVGDEGGFAPNILENK	1	0.3882	0.3882								
		DYPVVSIEDPFDQDDWGAWQK	1	0.4633	0.4633								
		EGLELLK	3	1.0722	0.9702	1.7129							
		FGANAILGVSLAVCK	2	1.1218	1.107	1.2594							
		FTASAGIQVVGDDLTVTNPK	1	0.7675	0.7675								
		GNPTVEVDLFTSK	3	0.7912	0.785	1.1654							
		HIADLAGNSEVILPVPAFNVINGGSHAGNK	1	0.6282	0.6282								
		IDKLMIEMDGTENK	1	0.8686	0.8686								
		IEEELGSK	2	0.8667	0.8184	1.6211							
		IGAEVYHNLK	1	1.4895	1.4895								
		KLNVTEGEK	1	0.7935	0.7935								
		LMIEMDGTENK	3	2.4166	1.6881	2.7512							
		SFIKDYPVVSIEDPFDQDDWGAWQK	1	1.1202	1.1202								
		TIAPALYSK	4	1.0362	0.9044	1.8477							
		VNQIGSVTESLQACK	2	27.4002	9.8583	10.7807							
		YISPDQLADLYK	3	0.748	0.7365	1.2377							
ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=4	FGANAILGVSLAVCK	2	1.1218	1.107	1.2594	5	4.7818	7.1553	1.9765	3	1.9033	3.9097
		HIADLAGNPDLILPVPAFNVINGGSHAGNK	2	1.6343	1.3243	2.5846							
		LAQSNGWGVMVSHR	1	1.8027	1.8027								
		SGETEDTFIADLVVGLCTGQIK	1	0.4838	0.4838								
		VNQIGSVTESIQACK	3	18.8664	5.5916	7.0088							
ENOG_HUMAN	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	FGANAILGVSLAVCK	2	1.1218	1.107	1.2594	3	0.7989	0.8502	0.7544	0.8189	0.8121	1.5258
		GNPTVEVDLYTAK	3	0.7912	0.785	1.1654							
		SGETEDTFIADLVVGLCTGQIK	1	0.4838	0.4838								
ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ELISNASDALDK	3	0.9544	0.9421	1.2161	1	0.9544	0.9544	0.9544	0.9544	0.9421	
EPCR_HUMAN	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1	EFLEDTCVQYVQK	2	0.997	0.9884	1.2052	1	0.997	0.997	0.997	0.997	0.9884	
ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	VNVAGLVLAGSADFK	1	3.2307	3.2307		2	8.5885	8.5885	6.7124	6.7124	6.7124	2.8127
		YFDESGQTGK	1	13.9482	13.9482								
ERH_HUMAN	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	ADTQTYQPYNK	1	1.0873	1.0873		1	1.0873	1.0873	1.0873	1.0873	1.0873	
ESYT3_HUMAN	Extended synaptotagmin-3 OS=Homo sapiens GN=ESYT3 PE=2 SV=1	VATNGQPK	2	0.8263	0.8255	1.0645	1	0.8263	0.8263	0.8263	0.8263	0.8255	
EVI5_HUMAN	Ecotropic viral integration site 5 protein homolog OS=Homo sapiens GN=EVI5 PE=1 SV=2	QHIAELEIQK	2	1.0639	1.0563	1.1843	1	1.0639	1.0639	1.0639	1.0639	1.0563	
EWS_HUMAN	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	AAVEWFDGK	1	5.8897	5.8897		1	5.8897	5.8897	5.8897	5.8897	5.8897	
EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	DNAMLEYLK	1	0.7526	0.7526		3	1.2479	1.4231	1.152	1.3137	1.2845	1.6217
		LFFLQVK	1	1.0424	1.0424								
		QLFDQVVK	2	1.9486	1.8627	1.5339							
F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	AIDLFTDAIK	2	2.7741	2.6652	1.496	4	2.2438	2.3499	1.4668	1.6661	1.6397	3.1906
		EWVESMGGK	1	4.8865	4.8865								
		LDYDEDASAMLK	1	0.3562	0.3562								
		VAAIEALNDGELQK	1	0.9586	0.9586								
F10A4_HUMAN	Protein FAM10A4 OS=Homo sapiens GN=FAM10A4 PE=1 SV=1	AIDLFTDAIK	2	2.7741	2.6652	1.496	2	1.8663	2.1689	1.6307	1.9467	1.8954	2.1199
		VAAIEALNDGELQK	1	0.9586	0.9586								
F10A5_HUMAN	Protein FAM10A5 OS=Homo sapiens GN=FAM10A5 PE=1 SV=1	AIDLFTDAIK	1	2.0046	2.0046		3	2.4158	2.4158	1.5167	1.5167	1.5167	3.7866
		EWVESMGGK	1	4.8865	4.8865								
		LDYDEDASAMLK	1	0.3562	0.3562								
FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	TQTVCNFTDGALVQHQEWDGK	2	15.6506	4.6796	14.2235	2	8.3137	10.7594	3.9101	6.2083	2.776	7.1095
		TTQFSCTLGEK	1	0.9769	0.9769								
FAKD2_HUMAN	FAST kinase domain-containing protein 2 OS=Homo sapiens GN=FASTKD2 PE=1 SV=1	MQSTDIIR	1	190.743	190.743		1	190.743	190.743	190.743	190.743	190.743	
FBSL3_HUMAN	Putative fatty acid-binding protein 5-like protein 3 OS=Homo sapiens GN=FABP5L3 PE=1 SV=1	TQTVCNFTDGALVQHQEWDGK	2	15.6506	4.6796	14.2235	1	15.6506	15.6506	15.6506	15.6506	4.6796	
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	CCHCCLLGR	1	1.231	1.231		10	4.8178	4.8178	1.6112	1.6112	1.6112	4.3798
		DCSLPYATESK	1	0.475	0.475								
		DSSCTGYELTEDNSCK	1	0.6709	0.6709								
		GYHLNEEGTR	1	0.6081	0.6081								
		IIEVEEEQEDPYLNDR	1	14.1919	14.1919								
		LEMNYVVGGVVSHR	1	0.7056	0.7056								
		SAATLQQEK	1	0.5867	0.5867								
		SQETGDLDVGGLQETDK	1	0.5844	0.5844								
		SQETGDLDVGGLQETDKIIEVEEEQEDPYLNDR	1	22.815	22.815								
		YMDGMTVGVVR	1	6.3096	6.3096								
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	ADQVCINLR	2	0.4017	0.4015	1.0487	10	0.3684	0.3839	0.3561	0.3765	0.3616	1.3339
		CVCPVSNAMCR	2	0.4976	0.453	1.8642							
		CVNHYGGYLCLPK	1	0.4299	0.4299								
		EHIVDLEMLTVSSIGTFR	1	0.2038	0.2038								
		ELPQSIVYK	3	0.4619	0.4274	1.5963							
		GSFACQCPPGYQK	4	0.3934	0.3726	1.4666							
		LNCEDIDECR	3	0.3353	0.3165	1.5159							
		QTSPVSAMLVLVK	4	0.3705	0.3597	1.3253							
		SGNENGEFYLR	2	0.36	0.3599	1.0279							
		TCQDINECETTNECR	1	0.2301	0.2301								
FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3	AGNSQGDFYIR	1	1.1854	1.1854		2	0.8989	0.8989	0.852	0.852	0.852	1.5952
		CVEPYQVSENR	1	0.6124	0.6124								
FBLN5_HUMAN	Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1	DMDVVSGR	2	0.3026	0.3023	1.056	3	0.8197	0.6272	0.5865	0.4696	0.4685	2.6339
		DQPFTILYR	2	0.3742	0.3722	1.157							
		SVPADIFQMQATTR	1	1.7825	1.7825								
FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=2	GFMTNGADIDECK	1	9.5199	9.5199		9	1.6792	1.6792	0.8076	0.8076	0.8076	2.9354
		GFQLDLR	1	0.7314	0.7314								
		GTCWQTVIDGR	1	1.8122	1.8122								
		GWGPHCEICPPGGTVAFK	1	0.7607	0.7607								
		GYILQEDGR	1	0.2897	0.2897								
		ILELLPALTTLTNHNR	1	0.2855	0.2855								
		TGCTDINECEIGAHNCGK	1	0.6025	0.6025								
		TGYTPDITGTSCVDLNECNQAPKPCNFICK	1	0.6081	0.6081								
		YLIESGNEDGFFK	1	0.5025	0.5025								
FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	GTCWLNIQDSR	1	0.1975	0.1975		1	0.1975	0.1975	0.1975	0.1975	0.1975	
FBN3_HUMAN	Fibrillin-3 OS=Homo sapiens GN=FBN3 PE=2 SV=2	ASCCQSLGR	1	1.3057	1.3057		1	1.3057	1.3057	1.3057	1.3057	1.3057	
FES_HUMAN	Proto-oncogene tyrosine-protein kinase Fes/Fps OS=Homo sapiens GN=FES PE=1 SV=3	QEMVTQLQQELR	2	0.0995	0.0935	1.6518	1	0.0995	0.0995	0.0995	0.0995	0.0935	
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	CDSSPDSAEDVR	1	0.7123	0.7123		3	0.677	0.6629	0.6765	0.6625	0.6536	1.0509
		CDSSPDSAEDVRK	4	0.6452	0.6302	1.2991							
		CNLLAEK	2	0.6736	0.6735	1.027							
FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3	AQITGYR	3	0.1656	0.1654	1.0561	31	0.2045	0.1983	0.2006	0.1958	0.1945	1.2146
		ATITGYR	4	0.189	0.1885	1.0865							
		DAPVNK	1	0.2902	0.2902								
		DLQFEVTDVK	1	0.1983	0.1983								
		ESKPLTAQQTTK	1	0.2372	0.2372								
		FTNIGPDTMR	2	0.1897	0.18	1.586							
		GATYNIVEALK	2	0.2021	0.2015	1.1132							
		GDSPASSKPISINYR	1	0.2926	0.2926								
		GEWTCKPIAEK	1	0.2884	0.2884								
		GLAFTDVDVDSK	1	0.1438	0.1438								
		HTSVQTTSSGSGPFTDVR	1	0.2735	0.2735								
		HYQINQQWER	1	0.1616	0.1616								
		IGDQWDK	1	0.2204	0.2204								
		IGDTWR	1	0.159	0.159								
		IGDTWSK	3	0.1982	0.198	1.0628							

		ISCTIANR	2	0.1773	0.1749	1.2639							
		ITGYIIK	1	0.2315	0.2315								
		IYLYTLNDNAR	1	0.1418	0.1418								
		LGVRPSQGGEAPR	1	0.2605	0.2605								
		QYNVGPSVSK	3	0.1901	0.1901	1.0115							
		SDTVPSPR	2	0.2434	0.2426	1.1199							
		SEPLIGR	3	0.1892	0.1874	1.1829							
		STTPDITGYR	4	0.2068	0.2019	1.2749							
		SYTITGLGPGTDTYK	1	0.1972	0.1972								
		TFYSCTTEGR	2	0.1835	0.1793	1.3532							
		TYHVGEQWQK	1	0.184	0.184								
		VDVIPVNLPGEHGQR	1	0.1829	0.1829								
		VFAVSHGR	2	0.1806	0.1797	1.1501							
		YEKPGSPPR	1	0.1809	0.1809								
		YEVSVYALK	4	0.1742	0.1736	1.0946							
		YTGNTYR	1	0.2048	0.2048								
FKBP3_HUMAN	FK506-binding protein 3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1	FLQEHGSDSFLAEHK	1	0.9892	0.9892		2	1.0755	1.1043	1.072	1.1012	1.1001	1.1204
		LEIEPEWAYGK	2	1.1618	1.1601	1.08							
FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	AGNNMLVGVHGPR	1	0.1743	0.1743		21	1.6277	1.7621	0.9333	1.0604	1.0193	3.4375
		AHVVPCFDASK	1	6.9864	6.9864								
		AWGPGLEGGVVGK	1	0.0621	0.0621								
		AYGPGIEPTGNMVK	1	0.1034	0.1034								
		DGSCGVAYVVQEPGDYEVSVK	1	1.1217	1.1217								
		DLAEDAPWK	2	6.0339	3.7022	4.5443							
		DVDIEHHDNTYTVK	1	1.8472	1.8472								
		EATTEFSVDAR	1	0.9249	0.9249								
		FVPAEMGTHTVSVK	1	0.1176	0.1176								
		GKLDVQFSGLTK	1	0.5698	0.5698								
		LDVQFSGLTK	1	1.455	1.455								
		LIALLEVLSQK	2	1.9028	1.9024	1.0288							
		LTVSSLQESGLK	1	1.1334	1.1334								
		LVSIDSK	2	1.1498	1.1279	1.3206							
		LYSVSYLLK	1	1.0198	1.0198								
		NDNDTFTVK	1	1.4607	1.4607								
		SAGQGEVLVYVEDPAGHQEEAK	2	0.903	0.8982	1.1568							
		SPFEVYVDK	1	1.5183	1.5183								
		SPFSVAVSPSLDLSK	2	1.6432	1.6428	1.0282							
		VEYTPYEEGLHSVDVTFDGSPVPSSPFQVPVTEGCDPSR	1	2.9839	2.9839								
		VTAGGPGLEPSGNIANK	1	1.071	1.071								
FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=1	AEITFDDHK	2	0.5101	0.2139	8.523	20	1.5851	1.617	1.2426	1.2271	1.1052	1.9097
		ALGALVDSCAPGLCPDWESWDPQKPVDNAR	1	1.1832	1.1832								
		DAGYGGISLAVEGPSK	1	1.0104	1.0104								
		DLAEDAPWK	2	6.0339	3.7022	4.5443							
		DLDIIDNYDYSHTVK	1	0.835	0.835								
		EAGAGGLSIAVEGPSK	2	0.8455	0.8213	1.4082							
		GAGTGGLGLTVEGPCEAK	1	1.6212	1.6212								
		GDYVLAVK	2	0.71	0.7092	1.068							
		GIEPTGNMVK	1	1.0408	1.0408								
		IEYNDQNDGSCDVK	1	1.9227	1.9227								
		LIALLEVLSQK	2	1.9028	1.9024	1.0288							
		LTVMSLQESGLK	2	0.8053	0.8007	1.1633							
		LVSIDSK	2	1.1498	1.1279	1.3206							
		MDGTYACSYTPVK	1	1.486	1.486								
		TFEMSDFIVDTR	1	5.1821	5.1821								
		VKVEPAVDTSR	1	0.603	0.603								
		VLQSFTVDSSK	1	1.497	1.497								
		VLSEDEDVDFDIIHNANDTFTVK	1	0.9519	0.9519								
		VTEAEIVPMGK	1	0.6154	0.6154								
		YMIGVTYGGDDIPLSPYR	1	1.7958	1.7958								
FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	AFGPGLEPTGCIVDKPAEFTIDAR	1	0.0684	0.0684		11	1.5949	1.8317	0.97	1.1485	1.0692	3.4887
		AWGPGLETGQVGK	1	1.4756	1.4756								
		DAGEGLLTVQILDPEGKPK	1	1.1084	1.1084								
		DFEIIDNHDYSYTVK	1	1.7389	1.7389								
		DLAEDAPWK	2	6.0339	3.7022	4.5443							
		EAGAGGLSIAVEGPSK	2	0.8455	0.8213	1.4082							
		GAGTGGLGLTVEGPCEAK	1	1.6212	1.6212								
		LIALLEVLSQK	2	1.9028	1.9024	1.0288							
		LVSIDSK	2	1.1498	1.1279	1.3206							
		LYAQDADGCPIDIK	1	0.1391	0.1391								
		NDNDTFTVK	1	1.4607	1.4607								
FRPD1_HUMAN	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1	DIILTVK	2	0.6435	0.6368	1.2259	1	0.6435	0.6435	0.6435	0.6435	0.6368	
FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	LSCFAQTVSPAEK	1	1.4054	1.4054		4	1.2485	1.3191	1.2216	1.297	1.2547	1.2811
		SSYDVFQLEFNDGAYNIK	2	1.2018	1.1986	1.1093							
		YLAADKDGNVTCER	1	0.8681	0.8681								
		YLTAEAFGFK	3	1.5188	1.4082	1.6116							
FST_HUMAN	Follistatin OS=Homo sapiens GN=FST PE=1 SV=2	EAACSSGVLLEVK	1	0.8673	0.8673		1	0.8673	0.8673	0.8673	0.8673	0.8673	
FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1	CLNPSFNPPEKK	1	1.0999	1.0999		9	0.6609	0.6036	0.6363	0.5829	0.5778	1.3356
		GAGTGTEEEMTR	3	0.3966	0.3908	1.228							
		GEPTCLCIEQCKPHK	1	0.7024	0.7024								
		GLCVDALIELSDENADWK	1	0.7564	0.7564								
		ICANVFCGAGR	2	0.697	0.6876	1.263							
		IIQWLEAEIIPDGWFSK	1	0.6844	0.6844								
		IQVDYDGHCK	1	0.5024	0.5024								
		LDSSEFLK	3	0.5522	0.5428	1.2624							
		LSFQEFLK	3	0.5573	0.5541	1.1422							
FTHFD_HUMAN	10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2	IGFTGSTEVGK	1	0.2408	0.2408		1	0.2408	0.2408	0.2408	0.2408	0.2408	
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	SELKDFQSYGNVVELR	1	0.9334	0.9334		4	0.9334	0.9334	0.9334	0.9334	0.9334	
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	AGAHLQGGAK	1	1.7034	1.7034		10	1.1533	1.1868	0.9429	1.0237	0.9614	2.1887
		GALQNIIPASTGAAK	4	0.9165	0.911	1.1332							
		IISNASCTTNCLAPLAK	3	1.1825	1.1776	1.118							
		LISWYDNEFGYSNR	1	1.057	1.057								
		QASEGPLK	1	0.1493	0.1493								
		TVDGPSGK	1	1.4992	1.4992								
		VIHDNFGIVEGLMTTVHAITATQK	2	1.328	1.3104	1.2603							
		VIISAPSADAPMFVMGVNHEK	2	0.4457	0.4009	1.94							
		VVDLMAHMASK	3	0.9236	0.8931	1.3792							
		WGDAGAEYVVESTGVFTTMEK	3	2.3275	1.699	2.5481							
G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	FAAFTGQQDMESNGK	2	0.7129	0.7101	1.1329	4	1.2357	1.1311	1.1263	1.0278	1.0262	1.6553
		HFVALSTNTTK	1	1.8433	1.8433								
		TFTTQETTNAETAK	1	0.7467	0.7467								
		VIVYVSNDGTHIAK	1	1.64	1.64								
GALT5_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1	WKEGNFNVYLSDLIPVDR	1	0.7171	0.7171		1	0.7171	0.7171	0.7171	0.7171	0.7171	
GALT6_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	NLGTNQCLDVGENNR	1	0.1426	0.1426		1	0.1426	0.1426	0.1426	0.1426	0.1426	
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	FSPNSSNPIIVSCGWDK	1	0.3453	0.3453		2	0.5024	0.5548	0.4772	0.5315	0.5169	1.5802
		YWLCAATGPSIK	2	0.6595	0.6324	1.511							
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	DVNVDLIPK	2	2.0075	1.6262	2.5869	3	2.3505	2.2648	2.1188	2.0904	1.8814	1.7473
		KFDLGQDVIDFTGHALALYR	1	3.7959	3.7959								
		MAGTAFDFENMK	1	1.2482	1.2482								
GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	DVNVDLIPK	2	2.0075	1.6262	2.5869	8	1.8369	1.6359	1.4109	1.2496	1.1549	2.1952
		FVSISDLLVPK	2	0.8669	0.8649	1.0984							
		KFDLGQDVIDFTGHALALYR	1	3.7959	3.7959								
		MTGSEFDFEEMK	2	0.4247	0.3405	2.6511							
		NPYYGGESASITPLEDLYK	1	0.9088	0.9088								
		TYDATTHFETTCDDIK	1	0.9531	0.9531								
		VICILSHPIK	1	1.5387	1.5387								
		VPSTEAEALASSLMGLFEK	1	4.2	4.2								
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	AEEYEFLTPVEEAPK	1	0.8941	0.8941		2	1.2814	1.2814	1.2214	1.2214	1.2214	1.5545
		IDKTDYMVGSYGPR	1	1.6686	1.6686								
GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	ATFMVGSYGPRPEEYEFLTPVEEAPK	1	0.7289	0.7289		2	0.7453	0.7453	0.7451	0.7451	0.7451	1.0316
		ELQEMDKDDESLIK	1	0.7617	0.7617								
GDN_HUMAN	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1	TIDSWMSIMVPK	2	1.7869	1.7472	1.3506	1	1.7869	1.7869	1.7868	1.7868	1.7472	
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	EVGGFESATFLGYFK	1	0.7153	0.7153		2	0.6953	0.6953	0.695	0.695	0.695	1.0415
		SEDCFLLDHGK	1	0.6753	0.6753								
GFAP_HUMAN	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	FLEQQNK	3	1.1935	1.19	1.0966	3	1.0996	1.0627	1.0621	1.023	1.0145	1.3945
		GTNESLER	3	1.3755	1.3535	1.2459							
		LADIEIATYR	4	0.7299	0.725	1.14							
GLBD3_HUMAN	Glycosyltransferase 8 domain-containing protein 3 OS=Homo sapiens GN=GLT8D3 PE=1 SV=1	LFLPLLK	3	1.0604	1.0317	1.3406	1	1.0604	1.0604	1.0604	1.0604	1.0317	
GLOD4_HUMAN	Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	ALLGYADNQCK	1	0.1721	0.1721		1	0.1721	0.1721	0.1721	0.1721	0.1721	
GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	WQTLLSVDDLVEK	1	1.2905	1.2905		1	1.2905	1.2905	1.2905	1.2905	1.2905	
GPC1_HUMAN	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=1	GANLHLEETLAEFWAR	1	0.2632	0.2632		4	0.514	0.514	0.4696	0.4696	0.4696	1.6524
		QLHFQLLLPDDYLDCLGK	1	0.3652	0.3652								
		SFVQGLGVASDVVR	1	0.6556	0.6556								
		VLQAMLATQLR	1	0.7718	0.7718								
GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	LYSPSQIQAFVLMK	1	0.4982	0.4982		1	0.4982	0.4982	0.4982	0.4982	0.4982	
GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	IINEPTAAAIAYGLDK	3	1.5844	1.5176	1.425	5	0.727	0.9689	0.3789	0.6076	0.5965	5.2649
		NELESYAYSLK	1	0.0251	0.0251								
		TFAPEEISAMVLTK	1	0.2504	0.2504								
		TWNDPSVQQDIK	2	0.9472	0.9389	1.2064							
		VEIANDQGNR	1	0.8278	0.8278								
GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	EDPTVSALLTSEK	2	0.3498	0.3491	1.0925	1	0.3498	0.3498	0.3497	0.3497	0.3491	
GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	ALPGQLKPFETLLSQNQGGK	1	0.9255	0.9255		4	0.9578	0.9578	0.9572	0.9572	0.9572	1.0413
		EEVTTVETWQEGSLK	1	0.9522	0.9522								
		TLGLYGK	1	1.0144	1.0144								
		TLGLYGKDQQEAALVDMVNDGVEDLR	1	0.9389	0.9389								
H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	DNIQGITKPAIR	1	0.7152	0.7152		2	0.695	0.6848	0.6947	0.6846	0.6813	1.0421
		TVTAMDVVYALK	3	0.6747	0.6703	1.1513							
H90B2_HUMAN	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2	ADLINNLGTIAK	1	1.0381	1.0381		5	1.2072	1.2636	1.1516	1.2135	1.1592	1.4264
		SIYYITGESK	1	0.6724	0.6724								
		SLVSVTK	1	1.5163	1.5163								
		YESLTDPSK	2	1.6482	1.6429	1.1197							
		YIDQEELNK	2	1.1611	0.9922	2.2563							
H90B3_HUMAN	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	EGLELPEDEEEKK	1	1.1874	1.1874		5	1.9587	1.8606	1.785	1.7347	1.7271	1.5676
		EGLELPEDEEEKK	1	3.8594	3.8594								
		EMLQQSK	2	1.5823	1.5633	1.2462							
		SLVSVTK	1	1.5163	1.5163								
		YESLTDPSK	2	1.6482	1.6429	1.1197							
H90B4_HUMAN	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1	EGLELPEDEEEK	1	1.1874	1.1874		4	2.6344	2.4371	2.321	2.1674	2.1647	1.8217
		EGLELPEDEEEKK	1	3.8594	3.8594								
		GFEVIYMSEPIDEYCVQQLK	1	3.8424	3.8424								
		YESLTDPSK	2	1.6482	1.6429	1.1197							
HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	MFLSFPTTK	3	1.1547	1.1367	1.249	1	1.1547	1.1547	1.1547	1.1547	1.1367	
HDGF_HUMAN	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	GPPQEEEEEDEEEATKEDAEAPGIR	2	6.0265	2.6585	7.8247	2	3.6053	4.4124	2.6714	3.5036	2.0354	3.1599
		YQVFFFGTHETAFLGPK	1	1.1842	1.1842								
HEXA_HUMAN	Beta-hexosaminidase subunit alpha OS=Homo sapiens GN=HEXA PE=1 SV=1	GLETFSQLVWK	1	0.3226	0.3226		1	0.3226	0.3226	0.3226	0.3226	0.3226	
HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	GSIVWQEVFDDK	1	0.7619	0.7619		3	0.6356	0.7247	0.487	0.5818	0.5817	2.7523
		LAPGTVVEVWK	2	0.9912	0.9912	1.0367							
		VLDIIATINK	1	0.1528	0.1528								
HGB1A_HUMAN	Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1L1 PE=5 SV=1	IKGEHPGLSIGDVAK	1	0.4372	0.4372		1	0.4372	0.4372	0.4372	0.4372	0.4372	
HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	IKGEHPGLSIGDVAK	1	0.4372	0.4372		3	0.749	0.873	0.675	0.7866	0.7841	1.7253
		KHPDASVNFSEFSK	2	1.2449	1.237	1.1729							
		LGEMWNNTAADDKQPYEK	1	0.565	0.565								
HMGLX_HUMAN	High mobility group protein 1-like 10 OS=Homo sapiens GN=HMG1L10 PE=1 SV=1	IKGEHPGLSIGDVAK	1	0.4372	0.4372		2	0.5011	0.5011	0.497	0.497	0.497	1.1988
		LGEMWNNTAADDKQPYEK	1	0.565	0.565								
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3	GFGFVLFK	1	0.1722	0.1722		1	0.1722	0.1722	0.1722	0.1722	0.1722	

HNRGT_HUMAN	RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens GN=RBMXL2 PE=1 SV=3	GFAFVTFESPADAK	1	0.7561	0.7561		2	3.4258	3.4258	2.1468	2.1468	2.1468	4.3746
		IVEVLLMK	1	6.0955	6.0955								
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	EYFGGFGEVESELPMDNK	2	0.4561	0.4455	1.3607	5	2.9974	3.6429	0.9708	1.265	0.9719	4.9721
		GFCFITFK	1	0.6587	0.6587								
		GFGFVLFK	1	0.1722	0.1722								
		IFVGGLSPDTPEEK	2	1.3499	1.3308	1.2702							
		MFIGGLSWDTTK	2	12.3501	4.4694	10.6857							
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	TEMDWVLK	1	1.4152	1.4152		1	1.4152	1.4152	1.4152	1.4152	1.4152	
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=RBMX PE=1 SV=3	GFAFVTFESPADAK	1	0.7561	0.7561		3	2.59	2.59	1.6176	1.6176	1.6176	3.1676
		IVEVLLMK	1	6.0955	6.0955								
		VEQATKPSFESGR	1	0.9184	0.9184								
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	ILLDLISESPIK	3	1.2374	1.2183	1.2363	2	0.9901	1.0396	0.9588	1.009	0.9773	1.4344
		ILSISADIETIGEILK	2	0.7429	0.7022	1.6151							
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	EFNEDGALAVLQQFK	1	1.4976	1.4976		1	1.4976	1.4976	1.4976	1.4976	1.4976	
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	EFNEEGALSVLQQFK	1	2.3121	2.3121		1	2.3121	2.3121	2.3121	2.3121	2.3121	
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	NVLIVEDIIDTGK	1	2.1584	2.1584		2	1.3377	1.3377	1.0563	1.0563	1.0563	2.7474
		VIGGDDLSTLTGK	1	0.5169	0.5169								
HPS6_HUMAN	Hermansky-Pudlak syndrome 6 protein OS=Homo sapiens GN=HPS6 PE=2 SV=1	LLLAEFAQHR	1	0.1095	0.1095		1	0.1095	0.1095	0.1095	0.1095	0.1095	
HS71L_HUMAN	Heat shock 70 kDa protein 1L OS=Homo sapiens GN=HSPA1L PE=1 SV=2	IINEPTAAAIAYGLDK	3	1.5844	1.5176	1.425	4	2.6937	2.3239	1.4509	1.4941	1.4623	3.5027
		NALESYAFNMK	1	7.9368	7.9368								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.4257	0.4257								
		VEIIANDQGNR	1	0.8278	0.8278								
HS902_HUMAN	Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2	ADLINNLGTIAK	1	1.0381	1.0381		4	1.3503	1.3124	1.1926	1.1862	1.114	1.7512
		ELHINLIPNK	1	0.6604	0.6604								
		ELISNSSDALDK	1	2.5416	2.5416								
		YIDQEELNK	2	1.1611	0.9922	2.2563							
HS904_HUMAN	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1	TLTVDTGIGMTK	5	1.4133	1.1178	2.116	1	1.4133	1.4133	1.4133	1.4133	1.1178	
HS905_HUMAN	Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1	EGLELPEDEEEK	1	1.1874	1.1874		3	2.0977	2.0977	1.7875	1.7875	1.7875	1.9484
		EGLELPEDEEEKK	1	3.8594	3.8594								
		HSQFIGYPITLFVEK	1	1.2463	1.2463								
HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	ADLINNLGTIAK	1	1.0381	1.0381		12	1.5114	1.4587	1.3418	1.3507	1.2515	1.6194
		EGLELPEDEEEK	1	1.1874	1.1874								
		EGLELPEDEEEKK	1	3.8594	3.8594								
		ELHINLIPNK	1	0.6604	0.6604								
		ELISNSSDALDK	1	2.5416	2.5416								
		EMLQQSK	2	1.5823	1.5633	1.2462							
		HSQFIGYPITLFVEK	1	1.2463	1.2463								
		NPDDITNEEYGEFYK	2	0.9918	0.9883	1.1268							
		SLTNDWEDHLAVK	1	0.8067	0.8067								
		TLTVDTGIGMTK	5	1.4133	1.1178	2.116							
		YESLTDPSK	2	1.6482	1.6429	1.1197							
		YIDQEELNK	2	1.1611	0.9922	2.2563							
HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	ADLINNLGTIAK	1	1.0381	1.0381		14	1.5624	1.4708	1.3574	1.3368	1.2493	1.6675
		CLELFSELAEDKENYK	1	1.2592	1.2592								
		EGLELPEDEEEK	1	1.1874	1.1874								
		EGLELPEDEEEKK	1	3.8594	3.8594								
		ELISNASDALDK	3	0.9544	0.9421	1.2161							
		EMLQQSK	2	1.5823	1.5633	1.2462							
		GFEVVYMTEPIDEYCVQQLK	1	3.8424	3.8424								
		NPDDITQEEYGEFYK	1	0.9327	0.9327								
		SIYYITGESK	1	0.6724	0.6724								
		SLTNDWEDHLAVK	1	0.8067	0.8067								
		SLVSVTK	1	1.5163	1.5163								
		TLTVDTGIGMTK	5	1.4133	1.1178	2.116							
		YESLTDPSK	2	1.6482	1.6429	1.1197							
		YIDQEELNK	2	1.1611	0.9922	2.2563							
HSP71_HUMAN	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5	AAAIGIDLGTTYSCVGVFQHGK	1	0.8679	0.8679		4	2.5146	2.5146	1.2482	1.2482	1.2482	3.58
		NALESYAFNMK	1	7.9368	7.9368								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.4257	0.4257								
		VEIIANDQGNR	1	0.8278	0.8278								
HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	DNNLLGK	2	1.3344	1.3333	1.0588	5	1.2431	1.3398	1.1935	1.2991	1.278	1.3844
		FEELNADLFR	1	0.86	0.86								
		IINEPTAAAIAYGLDK	3	1.5844	1.5176	1.425							
		IINEPTAAAIAYGLDKK	1	1.6089	1.6089								
		VEIIANDQGNR	1	0.8278	0.8278								
HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	LFEELGK	1	0.0804	0.0804		2	0.3649	0.3649	0.2285	0.2285	0.2285	4.3805
		SNLAYDIVQLPTGLTGIK	1	0.6494	0.6494								
HSP76_HUMAN	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	VEILANDQGNR	1	0.8278	0.8278		1	0.8278	0.8278	0.8278	0.8278	0.8278	
HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	CNEIINWLDK	2	1.0031	0.9926	1.2286	15	1.7212	1.643	1.4091	1.3788	1.316	1.82
		DNNLLGK	2	1.3344	1.3333	1.0588							
		EIAEAYLGK	1	0.9549	0.9549								
		FDDAVVQSDMK	1	1.2203	1.2203								
		FEELNADLFR	1	0.86	0.86								
		GPAVGIDLGTTYSCVGVFQHGK	2	3.2367	2.1304	3.9955							
		GTLDPVEK	1	5.4168	5.4168								
		IINEPTAAAIAYGLDK	3	1.5844	1.5176	1.425							
		IINEPTAAAIAYGLDKK	1	1.6089	1.6089								
		MVNHFIAEFK	1	0.9142	0.9142								
		NQVAMNPTNTVFDAK	1	0.9228	0.9228								
		RFDDAVVQSDMK	1	1.3702	1.3702								
		SFYPEEVSSMVLTK	3	0.7929	0.7832	1.2101							
		SINPDEAVAYGAAVQAAILSGDK	1	3.7705	3.7705								
		VEIIANDQGNR	1	0.8278	0.8278								
HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	AQLSGDPEAAK	1	1.0845	1.0845		3	1.0355	1.1304	0.9766	1.0715	1.0642	1.5419
		KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	2	1.4152	1.3961	1.2635							
		TKDGVVEITGK	1	0.6068	0.6068								
HTRA1_HUMAN	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	GACGQGQEDPNSLR	1	0.7233	0.7233		3	0.6515	0.6515	0.6294	0.6294	0.6294	1.3947
		SSELRPGEFVVGSPFSLQNTVTTGIVSTTQR	1	0.4306	0.4306								
		VTAGISFAIPSDK	1	0.8006	0.8006								
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2	EDARPVPQGSCQSELHR	1	0.72	0.72		2	0.6723	0.6723	0.6706	0.6706	0.6706	1.1057
		THEDLYIIPPNCDR	1	0.6246	0.6246								
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1	ALSMCPPSPLGCELVK	2	1.1619	1.0087	2.1593	5	0.7866	0.8215	0.7619	0.7921	0.7607	1.3159
		EHEEPTTSEMAEETYSPK	1	0.8656	0.8656								
		GICWCVDK	1	0.594	0.594								
		GVCLNEK	2	0.6556	0.6555	1.0186							
		HMEASLQELK	1	0.6557	0.6557								
IBP6_HUMAN	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1	APAVAEENPK	1	0.3528	0.3528		4	4.4692	4.2272	2.7226	2.8222	2.7918	4.1477
		EGQECGVYTPNCAPGLQCHPPKDDEAPLR	1	5.3757	5.3757								
		GAVLYVPNCDHR	2	3.2589	3.1718	1.3918							
		HLDSVLQQLQTEVYR	1	8.8896	8.8896								
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	AGAAAGGPGVSGVCVCK	1	0.8319	0.8319		8	0.9379	0.9099	0.9308	0.9015	0.8984	1.1414
		DACGCCPMCAR	1	0.7892	0.7892								
		EDAGEYECHASNSGQGASASAK	4	0.7807	0.7732	1.1787							
		GTCEQGPSIVTPPK	1	1.0025	1.0025								
		GYCAPGMECVK	1	0.9404	0.9404								
		HEVTGWVLVSPLSK	1	1.0421	1.0421								
		ITVVDALHEIPVK	2	1.0739	1.0723	1.0809							
		SRVPVCGSDGTTYPSGCQLR	1	1.0424	1.0424								
IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	LVLLNAIYLSAK	1	0.0382	0.0382		2	0.178	0.178	0.1102	0.1102	0.1102	4.472
		TNLESILSYPK	1	0.3177	0.3177								
ICAM2_HUMAN	Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2	GGNIFHK	1	0.9651	0.9651		3	1.2675	1.2675	1.2464	1.2464	1.2464	1.2563
		ILLDEQAQWK	1	1.4962	1.4962								
		QVILTLQPTLVAVGK	1	1.3411	1.3411								
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	GWPLYLSTK	1	3.0334	3.0334		1	3.0334	3.0334	3.0334	3.0334	3.0334	
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	TAIVFDDK	1	2.092	2.092		2	1.0549	1.0549	0.193	0.193	0.193	29.0945
		TEGLSVLSQAMAWVK	1	0.0178	0.0178								
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	EVEPEPTEDKDLEADEEDTR	1	7.7068	7.7068		1	7.7068	7.7068	7.7068	7.7068	7.7068	
IF2BL_HUMAN	Eukaryotic translation initiation factor 2 subunit 2-like protein OS=Homo sapiens PE=2 SV=1	EVEPEPTEDKDLEADEEDTR	1	7.7068	7.7068		1	7.7068	7.7068	7.7068	7.7068	7.7068	
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GVDVIAQAQSGTGK	1	0.6524	0.6524		1	0.6524	0.6524	0.6524	0.6524	0.6524	
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	GVDVIAQAQSGTGK	1	0.6524	0.6524		1	0.6524	0.6524	0.6524	0.6524	0.6524	
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	EDLRLPEGDLGK	1	1.1428	1.1428		4	0.8385	0.8385	0.7784	0.7784	0.7784	1.6117
		IVEMSTSK	1	0.3913	0.3913								
		KYEDICPSTHNMDVPNIK	1	0.9928	0.9928								
		YEDICPSTHNMDVPNIK	1	0.827	0.827								
IF5A2_HUMAN	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3	IVEMSTSK	1	0.3913	0.3913		2	0.6092	0.6092	0.5689	0.5689	0.5689	1.6975
		YEDICPSTHNMDVPNIK	1	0.827	0.827								
IF5AL_HUMAN	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=1 SV=2	KYEDICPSTHNMDVPNIK	1	0.9928	0.9928		1	0.9928	0.9928	0.9928	0.9928	0.9928	
IF6_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	QTVADQVLVSCVFSNQGGLVHPK	1	0.6662	0.6662		1	0.6662	0.6662	0.6662	0.6662	0.6662	
IFNG_HUMAN	Interferon gamma OS=Homo sapiens GN=IFNG PE=1 SV=1	SVETIK	1	2.6799	2.6799		1	2.6799	2.6799	2.6799	2.6799	2.6799	
ILEU_HUMAN	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	LVLVNAIYFK	1	0.941	0.941		1	0.941	0.941	0.941	0.941	0.941	
ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	GTMITTGHNVADLVVILK	1	0.232	0.232		2	0.5121	0.5121	0.4287	0.4287	0.4287	2.3828
		ILPTLEAVAALGNK	1	0.7921	0.7921								
ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	AVSDWIDEQEK	1	0.8652	0.8652		3	1.2439	1.2439	0.8531	0.8531	0.8531	3.057
		GDLDLELVLLCK	1	2.5893	2.5893								
		GWPLELLLCEK	1	0.2771	0.2771								
IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	LAATNALLNSLEFTK	2	0.3124	0.3121	1.0551	2	0.8719	0.9838	0.6686	0.7786	0.7768	2.9341
		SSAYESLMEIVK	3	1.4314	1.4268	1.1037							
IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	HFADLLPGFLQAVNDSCYQNDDSVLK	1	0.9474	0.9474		3	0.9172	0.9172	0.8898	0.8898	0.8898	1.36
		HIVENAVQK	1	1.1671	1.1671								
		QWGLCIFDDVIEHCGPASFK	1	0.6371	0.6371								
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	EQLSDMMMINK	1	10.2092	10.2092		5	2.9446	2.9446	1.6655	1.6655	1.6655	2.9475
		ILAIGLINEALDEGDAQK	1	0.5852	0.5852								
		LPYDVTPEQALAHEEVK	1	1.4337	1.4337								
		QSGQTDPLQKEELQSGVDAANSAAQQYQR	1	1.0023	1.0023								
		SWNQMESQTGEASK	1	1.4927	1.4927								
ISLR_HUMAN	Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=1 SV=1	EVPLLQSIWLAHNHIER	1	3.3729	3.3729		1	3.3729	3.3729	3.3729	3.3729	3.3729	
ITGBL_HUMAN	Integrin beta-like protein 1 OS=Homo sapiens GN=ITGBL1 PE=2 SV=1	NLCESADGILCSGK	1	0.3995	0.3995		1	0.3995	0.3995	0.3995	0.3995	0.3995	
K0020_HUMAN	Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3	QMWEILR	1	10.8096	10.8096		1	10.8096	10.8096	10.8096	10.8096	10.8096	
K0825_HUMAN	Uncharacterized protein KIAA0825 OS=Homo sapiens GN=KIAA0825 PE=2 SV=2	HIVPDCLLESMPK	1	0.6296	0.6296		1	0.6296	0.6296	0.6296	0.6296	0.6296	
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	AETECQNTEYQLLDIK	3	0.7489	0.742	1.1854	23	0.8953	0.8766	0.8806	0.8661	0.8633	1.1999
		ALEESNYELEGK	3	0.8605	0.8591	1.0711							
		DAEAWFNEK	2	0.9172	0.9156	1.0881							
		ELITEIDNNIEQISSYK	1	0.8827	0.8827								
		GSSGGGCFGSGSGGYGGLGGFGGGSFR	2	0.9807	0.9782	1.105							
		ISSSKGSLGGGFSSGGFSGGSFSR	1	1.0865	1.0865								
		LAADDFR	2	0.8198	0.8178	1.1032							
		LASYLDK	2	0.789	0.7848	1.1568							
		LENEIQTYR	1	0.7434	0.7434								
		LKYENEVALR	2	0.8657	0.8656	1.0207							
		NQILNLTTDNANILLQIDNAR	1	0.705	0.705								
		NVQALEIELQSQLALK	1	1.1542	1.1542								
		NVSTGDVNVEMNAAPGVDLTQLLNNMR	3	0.7844	0.7814	1.1136							
		QSLEASLAETEGR	1	1.1112	1.1112								
		QSVEADINGLR	1	0.6988	0.6988								
		QSVEADINGLRR	2	0.8348	0.8133	1.3832							
		RVLDELTLTK	1	0.8015	0.8015								
		SQYEQLAEQNR	3	0.9716	0.9711	1.0369							
		SQYEQLAEQNRK	1	1.0538	1.0538								
		TIDDLK	1	0.9046	0.9046								
		VLDELTLTK	1	1.4144	1.4144								
		VTMQNLNDR	2	0.7791	0.779	1.0012							
		YCVQLSQIQAQISALEEQLQQIR	1	0.6854	0.6854								
K1C12_HUMAN	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	LASYLDK	2	0.789	0.7848	1.1568	2	3.6533	2.6985	2.2677	1.595	1.5893	4.4507

		VLDELTLTR	1	6.5176	6.5176								
K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=3	QSVEADINGLR	1	0.6988	0.6988		2	0.7668	0.7895	0.7638	0.7868	0.7732	1.134
		QSVEADINGLRR	2	0.8348	0.8133	1.3832							
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	ADLEMQIESLKEELAYLK	1	0.0209	0.0209		7	2.5034	1.9912	0.8573	0.8384	0.8371	7.0261
		ASLENSLEETK	1	9.1222	9.1222								
		ISSVLAGGSCR	1	5.3282	5.3282								
		LAADDFR	2	0.8198	0.8178	1.1032							
		LASYLDK	2	0.789	0.7848	1.1568							
		VLDELTLAR	1	0.665	0.665								
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C15_HUMAN	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=2	LAADDFR	2	0.8198	0.8178	1.1032	3	0.7579	0.7765	0.7548	0.7742	0.7718	1.1178
		LASYLDK	2	0.789	0.7848	1.1568							
		VLDELTLAR	1	0.665	0.665								
K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	ASLENSLEETK	1	9.1222	9.1222		6	2.9172	2.2101	1.5921	1.2635	1.2613	3.1858
		ISSVLAGGSCR	1	5.3282	5.3282								
		LAADDFR	2	0.8198	0.8178	1.1032							
		LASYLDK	2	0.789	0.7848	1.1568							
		VLDELTLAR	1	0.665	0.665								
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	LAADDFR	2	0.8198	0.8178	1.1032	3	0.7579	0.7765	0.7548	0.7742	0.7718	1.1178
		LASYLDK	2	0.789	0.7848	1.1568							
		VLDELTLAR	1	0.665	0.665								
K1C18_HUMAN	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	LAADDFR	2	0.8198	0.8178	1.1032	2	0.4528	0.5751	0.2654	0.3865	0.3859	4.9288
		LASYLDR	1	0.0859	0.0859								
K1C19_HUMAN	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=3	LAADDFR	2	0.8198	0.8178	1.1032	3	0.7579	0.7765	0.7548	0.7742	0.7718	1.1178
		LASYLDK	2	0.789	0.7848	1.1568							
		VLDELTLAR	1	0.665	0.665								
K1C20_HUMAN	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1	MAMQNLNDR	1	0.8007	0.8007		1	0.8007	0.8007	0.8007	0.8007	0.8007	
K1C24_HUMAN	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1	LAADDFR	2	0.8198	0.8178	1.1032	3	2.7707	2.2829	1.5729	1.3364	1.3349	3.5591
		QSVEADINGLR	1	0.6988	0.6988								
		QSVEADINGLRK	1	6.7934	6.7934								
K1C25_HUMAN	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1	DAEAWFNEK	2	0.9172	0.9156	1.0881	2	0.8481	0.8481	0.8453	0.8453	0.8445	1.1224
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C26_HUMAN	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2	DAEAWFNER	1	0.0599	0.0599		2	0.4195	0.5393	0.216	0.3313	0.3313	6.135
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C27_HUMAN	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=1	DAEAWFNEK	2	0.9172	0.9156	1.0881	2	0.8481	0.8481	0.8453	0.8453	0.8445	1.1224
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C28_HUMAN	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=1	DAEAWFNEK	2	0.9172	0.9156	1.0881	3	0.8387	0.8387	0.8367	0.8367	0.8355	1.0871
		LAADDFR	2	0.8198	0.8178	1.1032							
		VTMQNLNDR	2	0.7791	0.779	1.0012							
K1C40_HUMAN	Keratin, type I cytoskeletal 40 OS=Homo sapiens GN=KRT40 PE=1 SV=2	ETMQFLNDR	1	0.8139	0.8139		1	0.8139	0.8139	0.8139	0.8139	0.8139	
K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	DIENQVETQITQIEHEVSSSGQEVQSSAK	3	0.5846	0.5726	1.2857	17	0.7887	0.7233	0.6904	0.6642	0.6586	1.5466
		EIETYHNLLEGQQEDFESSGAGK	1	0.6826	0.6826								
		FSSSGGGGGGGR	1	0.7023	0.7023								
		FSSSGYGGGSSR	3	0.6038	0.6019	1.0997							
		GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR	2	1.0375	0.9871	1.5685							
		GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK	1	0.5665	0.5665								
		GGSGGSYGGGGSGGGYGGGSGSR	2	0.5419	0.5388	1.1621							
		IKFEMEQNLR	1	3.1763	3.1763								
		LASYLDK	2	0.789	0.7848	1.1568							
		MTLDDFR	1	0.4521	0.4521								
		NYSPYYNTIDDLKDQIVDLTVGNNK	1	0.539	0.539								
		QEIECQNQEYSLLLSIK	2	0.6477	0.6358	1.3135							
		QVLDNLTMEK	1	0.5302	0.5302								
		SGGGGGGGLGSGGSIR	1	0.6589	0.6589								
		STMQELNSR	4	0.5712	0.5687	1.114							
		TLLDIDNTR	3	0.5842	0.5821	1.1114							
		VQALEEANNDLENK	2	0.7401	0.7381	1.109							
K1H1_HUMAN	Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	ETMQFLNDR	1	0.8139	0.8139		4	1.185	1.112	1.0828	1.0242	1.0232	1.5879
		LAADDFR	2	0.8198	0.8178	1.1032							
		LNVEVDAAPTVDLNR	1	2.1463	2.1463								
		SDLEAQVESLKEELLCLK	1	0.9601	0.9601								
K1H2_HUMAN	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=2	ETMQFLNDR	1	0.8139	0.8139		2	0.8168	0.8178	0.8168	0.8178	0.8165	1.0051
		LAADDFR	2	0.8198	0.8178	1.1032							
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	AQYEEIAQR	2	0.7457	0.7442	1.0935	14	1.1171	1.0674	0.7961	0.7547	0.7299	3.0117
		DVDNAYMIK	1	1.3647	1.3647								
		DYQELMNVK	2	0.0241	0.0164	3.7695							
		FASFIDK	1	0.7706	0.7706								
		FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK	1	0.8745	0.8745								
		FLEQQNQVLQTK	5	0.6902	0.6815	1.2013							
		IEISELNIR	2	1.1084	1.0743	1.4265							
		LNDLEEALQQAK	2	0.7891	0.7866	1.1175							
		NLDLDSIIAEVK	4	0.8368	0.8361	1.0467							
		STSSFSCLSR	1	1.1204	1.1204								
		TSQNSELNNMQDLVEDYKK	1	0.9153	0.9153								
		VDLLNQEIEFLK	3	1.0142	1.0065	1.1631							
		YEELQVTVGR	2	4.2796	4.2732	1.0798							
		YLDGLTAER	1	1.1063	1.1063								
K22O_HUMAN	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=1	DYQELMNVK	2	0.0241	0.0164	3.7695	3	0.6627	0.7332	0.2809	0.3021	0.2654	8.4824
		FASFIDK	1	0.7706	0.7706								
		FLEQQNK	3	1.1935	1.19	1.0966							
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	AEAESLYQSK	2	1.009	0.9706	1.4861	23	0.9224	1.1286	0.7738	0.8579	0.7585	1.6101
		AQYEDIAQK	3	0.5785	0.5784	1.0281							
		DVDGAYMTK	3	0.7312	0.6949	1.4651							
		DYQELMNTK	3	0.6289	0.6285	1.0434							
		FLEQQNQVLQTK	3	0.6857	0.6731	1.2738							
		FLEQQNQVLQTKWELLQQVDTSTR	1	0.6889	0.6889								
		FSSCGGGGSFGAGGGFGSR	1	0.7604	0.7604								
		GSGGGSSGGSIGGR	1	0.5859	0.5859								
		GSYGSGGSSYGSGGSGYGSGGGGGHGSYGSGSSSGGYR	1	0.6179	0.6179								
		IEISELNR	2	1.1084	1.0743	1.4265							
		LALDLEIATYR	4	0.7299	0.725	1.14							
		LNDLEDALQQAK	1	0.6813	0.6813								
		NKLNDLEDALQQAK	1	0.5933	0.5933								
		NMQDMVEDYR	4	5.162	1.4253	5.6383							
		SKAEAESLYQSK	1	1.1799	1.1799								
		SLDLDSIIAEVK	2	0.7823	0.7798	1.119							
		SLNNQFASFIDK	2	0.7421	0.7417	1.0452							
		SLVNLGGSKSISISVAR	1	0.7323	0.7323								
		TLLEGEESR	1	0.3644	0.3644								
		TNAENEFVTIK	2	0.7657	0.7647	1.074							
		WELLQQVDTSTR	3	0.7712	0.7708	1.0405							
		YEELQITAGR	1	0.6163	0.6163								
K2C1B_HUMAN		YQELQITAGR	2	0.6996	0.6983	1.0891							
K2C3_HUMAN	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=2	AQYEDIAQR	1	0.7474	0.7474		1	0.7474	0.7474	0.7474	0.7474	0.7474	
		DYQELMNVK	1	0.0969	0.0969		5	0.4218	0.5049	0.139	0.1519	0.1303	6.4159
		FASFIDK	2	0.0241	0.0164	3.7695							
		FLEQQNK	1	0.7706	0.7706								
		SLDLDSIIAEVR	3	1.1935	1.19	1.0966							
K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	AQYEEIAQR	2	0.0242	0.0179	3.1708							
		FASFIDK	2	0.7457	0.7442	1.0935	4	0.6979	0.6694	0.6916	0.6623	0.6391	1.1734
		LALDIEIATYR	1	0.7706	0.7706								
		NLDLDSIIAEVR	4	0.7299	0.725	1.14							
K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	AQYEEIANR	4	0.5454	0.4982	1.6393							
		FASFIDK	1	0.3897	0.3897		6	2.2115	1.6515	1.2248	1.0987	1.0975	2.8712
		FLEQQNK	1	0.7706	0.7706								
		NLDLDSIIAEVK	3	1.1935	1.19	1.0966							
		QLDSIVGER	4	0.8368	0.8361	1.0467							
		WTLLQEQGTK	1	1.2793	1.2793								
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	AQYEEVAQR	1	8.7993	8.7993								
		FASFIDK	2	0.7457	0.7442	1.0935	7	10.3504	6.9198	2.3499	1.6568	1.6551	5.2519
		FLEQQNK	1	0.7706	0.7706								
		ISIGGGSCAISGGYGSR	2	1.2374	1.2347	1.0989							
		NLDLDSIIAEVK	1	58.7795	58.7795								
		QLDSIVGER	3	0.8409	0.8401	1.0562							
		WTLLQEQGTK	1	1.2793	1.2793								
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	AQYEEIAQR	1	8.7993	8.7993								
		FASFIDK	1	0.7927	0.7927		5	0.8566	0.9023	0.8414	0.8827	0.8814	1.2273
		FLEQQNK	1	0.7706	0.7706								
		NLDLDSIIAEVK	3	1.1935	1.19	1.0966							
		YEELQITAGR	3	0.8267	0.8261	1.0487							
K2C8C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	AQYEEIAQR	2	0.6996	0.6983	1.0891							
		FASFIDK	1	0.7927	0.7927		6	0.9314	0.9422	0.9038	0.9176	0.9169	1.3026
		FLEQQNK	1	0.7706	0.7706								
		NLDLDSIIAEVK	2	1.2374	1.2347	1.0989							
		QLDSIVGER	3	0.8267	0.8261	1.0487							
		YEELQVTAGR	1	1.2793	1.2793								
K2C7_HUMAN	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=3	FASFIDK	1	0.6818	0.6818								
		FLEQQNK	1	0.7706	0.7706		5	1.0757	1.0356	1.0378	0.9961	0.9917	1.3564
		KLLEGEESR	3	1.1935	1.19	1.0966							
		LALDIEIATYR	1	1.2487	1.2487								
		LLEGEESR	4	0.7299	0.725	1.14							
K2C71_HUMAN	Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=2	FLEQQNQVLETK	2	1.4361	1.4267	1.1758							
K2C72_HUMAN	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	DLDLDSIIAEVR	1	0.8246	0.8246		1	0.8246	0.8246	0.8246	0.8246	0.8246	
		FASFIDK	4	0.5008	0.4637	1.5825	3	0.6987	0.5998	0.6827	0.5847	0.5555	1.3106
		FLEQQNQVLETK	1	0.7706	0.7706								
K2C73_HUMAN	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	FASFIDK	1	0.8246	0.8246								
		FLEQQNQVLETK	1	0.7706	0.7706		3	0.7135	0.6295	0.7024	0.6189	0.5827	1.2482
		NLDLDSIIAEVR	1	0.8246	0.8246								
K2C74_HUMAN	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2	DLDLDSIIAEVR	4	0.5454	0.4982	1.6393							
		FASFIDK	4	0.5008	0.4637	1.5825	3	0.6987	0.5998	0.6827	0.5847	0.5555	1.3106
		FLEQQNQVLETK	1	0.7706	0.7706								
K2C75_HUMAN	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2	FASFIDK	1	0.8246	0.8246								
		FLEQQNK	1	0.7706	0.7706		4	0.8707	0.9311	0.8511	0.9123	0.9111	1.272
		NLDLDSIIAEVK	3	1.1935	1.19	1.0966							
		YEELQVTAGR	4	0.8368	0.8361	1.0467							
K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	FLEQQNK	1	0.6818	0.6818								
K2C79_HUMAN	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=1	DYQELMNVK	2	1.1303	1.13	1.0314	1	1.1303	1.1303	1.1303	1.1303	1.13	
		FASFIDK	2	0.0241	0.0164	3.7695	5	0.8189	0.8196	0.4725	0.4986	0.4644	5.3526
		FLEQQNK	1	0.7706	0.7706								
		NLDLDSIIAEVK	3	1.1935	1.19	1.0966							
		YEELQVTAGK	4	0.8368	0.8361	1.0467							
K2C8_HUMAN	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	FASFIDK	1	1.2697	1.2697								
		FLEQQNK	1	0.7706	0.7706		5	1.0757	1.0356	1.0378	0.9961	0.9917	1.3564
		KLLEGEESR	3	1.1935	1.19	1.0966							
		LALDIEIATYR	1	1.2487	1.2487								
		LLEGEESR	4	0.7299	0.725	1.14							
K2C80_HUMAN	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	LALDIEIATYR	2	1.4361	1.4267	1.1758							
KCC2D_HUMAN	Calcium/calmodulin-dependent protein kinase type II delta chain OS=Homo sapiens GN=CAMK2D PE=1 SV=3	FTDEYQLFEELGK	4	0.7299	0.725	1.14	1	0.7299	0.7299	0.7299	0.7299	0.725	
KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1	FNFLEQAFDK	1	2.5447	2.5447		1	2.5447	2.5447	2.5447	2.5447	2.5447	
KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	EMDQTMAANAQK	1	1.9567	1.9567		1	1.9567	1.9567	1.9567	1.9567	1.9567	
		IVPVEITSLLK	1	0.2983	0.2983		2	0.2868	0.2868	0.2865	0.2865	0.2865	1.0586
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	DSLDPSFTHAMQLLTAEIEK	1	0.2752	0.2752								
			1	1.4837	1.4837		2	1.2126	1.2126	1.1818	1.1818	1.1818	1.3794

		KDDEENYLDLFSHK	1	0.9414	0.9414							
KIF14_HUMAN	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1	NFGGTVSIPVSEAKTYVNGK	1	0.2859	0.2859		1	0.2859	0.2859	0.2859	0.2859	0.2859	
KIF7_HUMAN	Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2	ELAINR	1	0.1094	0.1094		1	0.1094	0.1094	0.1094	0.1094	0.1094	
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	AEGSDVANAVLDGADCIMLSGETAK	1	1.3797	1.3797		13	2.5226	2.1733	1.5463	1.4477	1.4137	2.2015
		AGKPVICATQMLESMIK	2	0.8314	0.7532	1.8945							
		CDDNILVLDYK	1	16.6001	16.6001								
		GADFLVTEVENGGSLGSK	2	1.8947	1.7503	1.7695							
		GDLGEIPAEK	1	1.0899	1.0899								
		GDVVVLTGWRPGSGFTNTMR	1	0.8682	0.8682								
		GIFPVLCK	1	1.1281	1.1281								
		GSGTAEVELK	1	1.8301	1.8301								
		ITLDNAYMEK	1	0.8931	0.8931								
		IYVDDGLISLQVK	2	1.3221	1.3219	1.0228							
		LAPITSDPTEATAVGAVEASFK	2	1.1583	1.1567	1.0758							
		SVETLK	1	2.6799	2.6799								
		TATESFASDPILYRPVAVALDTK	2	1.1188	1.0809	1.453							
KPYR_HUMAN	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2	GDLGEIPAEK	1	1.0899	1.0899		1	1.0899	1.0899	1.0899	1.0899	1.0899	
KRT34_HUMAN	Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 PE=1 SV=2	ETMQFLNDR	1	0.8139	0.8139		1	0.8139	0.8139	0.8139	0.8139	0.8139	
KRT35_HUMAN	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=4	LAADDFR	2	0.8198	0.8178	1.1032	2	0.8899	0.8665	0.8872	0.8641	0.8627	1.1182
		SDLEAQVESLKEELLCLK	1	0.9601	0.9601								
KRT36_HUMAN	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1	ETMQFLNDR	1	0.8139	0.8139		2	0.8168	0.8178	0.8168	0.8178	0.8165	1.0051
		LAADDFR	2	0.8198	0.8178	1.1032							
KRT37_HUMAN	Keratin, type I cuticular Ha7 OS=Homo sapiens GN=KRT37 PE=2 SV=3	LAADDFR	2	0.8198	0.8178	1.1032	1	0.8198	0.8198	0.8198	0.8198	0.8178	
KRT38_HUMAN	Keratin, type I cuticular Ha8 OS=Homo sapiens GN=KRT38 PE=2 SV=3	ETMQFLNDR	1	0.8139	0.8139		2	0.7884	0.7884	0.788	0.788	0.788	1.0468
		LAADDFR	1	0.7629	0.7629								
KRT81_HUMAN	Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=2	FLEQQNK	3	1.1935	1.19	1.0966	1	1.1935	1.1935	1.1935	1.1935	1.19	
KRT82_HUMAN	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3	LAGLEEALQK	1	0.5473	0.5473		1	0.5473	0.5473	0.5473	0.5473	0.5473	
KRT83_HUMAN	Keratin, type II cuticular Hb3 OS=Homo sapiens GN=KRT83 PE=1 SV=2	FLEQQNK	2	1.1303	1.13	1.0314	1	1.1303	1.1303	1.1303	1.1303	1.13	
KRT84_HUMAN	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=1	FASFIDK	1	0.7706	0.7706		3	1.1334	1.2039	1.0972	1.1801	1.1759	1.3767
		FLEQQNK	3	1.1935	1.19	1.0966							
		LLEGEESR	2	1.4361	1.4267	1.1758							
KRT85_HUMAN	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	FLEQQNK	3	1.1935	1.19	1.0966	1	1.1935	1.1935	1.1935	1.1935	1.19	
KRT86_HUMAN	Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	FLEQQNK	2	1.1303	1.13	1.0314	1	1.1303	1.1303	1.1303	1.1303	1.13	
KT33A_HUMAN	Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT33A PE=1 SV=2	ETMQFLNDR	1	0.8139	0.8139		2	0.887	0.887	0.884	0.884	0.884	1.1239
		SDLEAQVESLKEELLCLK	1	0.9601	0.9601								
KT33B_HUMAN	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=1 SV=3	ETMQFLNDR	1	0.8139	0.8139		2	0.8168	0.8178	0.8168	0.8178	0.8165	1.0051
		LAADDFR	2	0.8198	0.8178	1.1032							
LA_HUMAN	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	EVTWEVLEGEVEK	3	0.8198	0.7784	1.4675	3	3.3128	2.3156	2.5734	1.6285	1.5786	2.6929
		GSIFVVFDSIESAK	1	4.5564	4.5564								
		LTTDFNVIVEALSK	1	4.5622	4.5622								
LAMA4_HUMAN	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=3	AHLPLDINFR	1	0.3823	0.3823		9	1.861	1.3155	0.5028	0.4222	0.4204	3.6774
		DAPSWDPVALK	1	0.389	0.389								
		DESENLLNQAR	1	0.2997	0.2997								
		ESMDTINHASQLVEQAHDMR	1	0.4398	0.4398								
		IPFTDIYIGGAPPEILQSR	1	0.4009	0.4009								
		LAALSIEEGK	2	0.1264	0.1264	1.0067							
		LSDLQEALDQALNHVR	1	13.94	13.94								
		SLLSDVEELVEK	3	0.3732	0.3684	1.2223							
		TLFPVALEQLDDYNAK	3	0.3975	0.3947	1.1601							
LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1	AAQNSGEAEYIEK	1	0.4176	0.4176		13	0.4897	0.4826	0.4483	0.4465	0.4455	1.4979
		ELAEQLEFIK	2	0.3337	0.3325	1.1249							
		ELDSLQTEAESLDNTVK	1	0.3578	0.3578								
		IEDPYSPR	1	0.7745	0.7745								
		KVDDICDSR	1	1.2132	1.2132								
		LNVEGEHCDVCK	1	0.3484	0.3484								
		NFLTQDSALDLDSIEAVANEVLK	2	0.425	0.4187	1.2772							
		NIGNLFEEAEK	1	0.3095	0.3095								
		SCACNPLGTIPGGNPCDSETGHCYCK	2	0.5973	0.5973	1.0019							
		TLDGELDEK	1	0.4983	0.4983								
		VESLSQVEVLQHSAADIAR	1	0.3754	0.3754								
		YFAYDCEASFPGISTGPMIK	1	0.4267	0.4267								
		YSDEPSTEGEVFFR	1	0.2883	0.2883								
LAMB2_HUMAN	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	GQVEQANQELQELIQSVK	1	0.3122	0.3122		1	0.3122	0.3122	0.3122	0.3122	0.3122	
LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	DIEEIMK	1	0.4077	0.4077		16	0.5388	0.5086	0.4974	0.4793	0.4744	1.4495
		DNVEGFNCER	1	0.46	0.46								
		EVMDLLR	2	0.4524	0.4522	1.0358							
		KQEAAIMDYNR	1	0.6394	0.6394								
		LCQCSDNIDPNAVGNCNR	1	0.505	0.505								
		LGNNEACSSCHCSPVGSLSTQCDSYGR	1	0.2841	0.2841								
		MEAENLEQLIDQK	2	0.3754	0.3739	1.1304							
		NTIEETGNLAEQAR	2	0.4294	0.4294	1.0193							
		QDAAVISDSYTFR	1	0.407	0.407								
		SQECYFDPELYR	2	0.4601	0.4555	1.2215							
		SWPGCQECPACYR	3	0.4683	0.4484	1.4509							
		SYYYAISDFAVGGR	2	0.557	0.5334	1.5202							
		TAAEEALR	1	1.5394	1.5394								
		TFAEVTDLDNEVNNMLK	2	0.3751	0.3751	1.0217							
		TGQCECQPGITGQHCER	1	0.6033	0.6033								
		TLPSGCPNTPSIEKP	1	0.658	0.658								
LDH6A_HUMAN	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1	VIGSGCNLDSAR	2	0.9829	0.9662	1.3002	1	0.9829	0.9829	0.9829	0.9829	0.9662	
LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	DLADELALVDVIEDK	6	1.2752	0.9585	2.7542	9	2.1684	2.0113	1.513	1.4699	1.2605	2.0845
		DQLIYNLLKEEQTPQNK	3	1.8395	1.8387	1.0364							
		DVNVTANSK	1	1.4334	1.4334								
		GLYGIKDDVFLSVPCILGQNGISDLVK	1	0.8321	0.8321								
		QIVESAYEVIK	1	1.4287	1.4287								
		SADTLWGIQK	2	9.6226	4.3672	7.5254							
		VIGSGCNLDSAR	4	0.9855	0.9728	1.1991							
		VTLTSEEEAR	2	0.9829	0.9662	1.3002							
			2	1.1154	1.1152	1.0289							
LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GEMMDLQHGSLFLQTPK	1	4.1256	4.1256		9	1.3178	1.1952	1.0876	1.0548	1.0435	1.8414
		GLTSVINQK	2	1.0875	1.0818	1.1555							
		ITVVGVGQVGMACAISILGK	2	1.1806	1.1563	1.336							
		IVADKDYSVTANSK	1	0.3754	0.3754								
		LIAPVAEEEATVPNNK	1	1.1936	1.1936								
		LKDDEVAQLK	1	1.0431	1.0431								
		SADTLWDIQK	2	9.9248	9.9141	1.2418							
		SLADELALVDVLEDK	3	0.9465	0.9301	1.257							
		VIGSGCNLDSAR	2	0.9829	0.9662	1.3002							
LDHC_HUMAN	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=2 SV=4	VIGSGCNLDSAR	2	0.9829	0.9662	1.3002	1	0.9829	0.9829	0.9829	0.9829	0.9662	
LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	DGGAWGTEQR	3	0.7065	0.7048	1.0893	6	1.0374	0.8895	0.8797	0.7925	0.6214	1.7654
		DSNNLCLHFNPR	1	0.5637	0.5637								
		FNAHGDANTIVCNSK	4	0.875	0.8672	1.1691							
		GEVAPDAK	2	2.6261	2.1289	2.582							
		LNLEAINYMAADGDFK	8	0.5805	0.3193	4.9944							
		SFVLNLGK	4	0.8726	0.8498	1.2952							
LEG3_HUMAN	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	MLTILGTVKPNANR	1	0.9375	0.9375		1	0.9375	0.9375	0.9375	0.9375	0.9375	
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	ELSEALGQIFDSQR	1	0.7795	0.7795		7	3.8974	3.8766	1.5279	1.7083	1.7068	5.2916
		GQWGTVCDNLWDLTDASVVCR	1	8.4585	8.4585								
		LASAYGAR	1	0.8288	0.8288								
		SLGWLK	1	0.1084	0.1084								
		STSSFPCPAGHFNGFR	1	0.6935	0.6935								
		TLQALEFHTVPFQLLAR	1	12.6818	12.6818								
		YSSDIYFQAPSDYFR	2	3.7311	3.7184	1.1239							
LGMN_HUMAN	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1	ESSYACYYDEK	1	0.5733	0.5733		1	0.5733	0.5733	0.5733	0.5733	0.5733	
LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	GLAFIQDPDGYWIEILNPNK	1	0.462	0.462		1	0.462	0.462	0.462	0.462	0.462	
LIMC1_HUMAN	LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=3	SDSLSPFR	1	0.2239	0.2239		1	0.2239	0.2239	0.2239	0.2239	0.2239	
LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	DLAAFDK	1	0.7928	0.7928		2	0.4972	0.4972	0.3998	0.3998	0.3998	2.6333
		LTYTAEVSVPK	1	0.2016	0.2016								
LMNA_HUMAN	Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	AAYEAELGDAR	1	0.7245	0.7245		7	2.1524	3.662	0.8006	1.282	1.048	3.3859
		AGQVVTIWAAGAGATHSPPTDLVWK	1	0.5303	0.5303								
		AQNTWGCGNSLR	1	0.3982	0.3982								
		EDLQELNDR	3	11.8893	5.8722	4.3405							
		IDSLSAQLSQLQK	3	0.7181	0.6944	1.3696							
		MQQQLDEYQELLDIK	1	0.3682	0.3682								
		TLEGELHDLR	1	0.4384	0.4384								
LOXL2_HUMAN	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	LGQGIGPHLNEIQCTGNEK	1	1.2126	1.2126		1	1.2126	1.2126	1.2126	1.2126	1.2126	
LRC67_HUMAN		TIDLSNNK	1	2.0225	2.0225		1	2.0225	2.0225	2.0225	2.0225	2.0225	
LRC59_HUMAN	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	LVNLQHLDLLNNK	1	2.0882	2.0882		2	1.3686	1.3686	1.1641	1.1641	1.1641	2.2852
		LVTLPVSFAQLK	1	0.6489	0.6489								
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=3	ASGLGDHCEDINECLEDK	2	0.2927	0.2922	1.0797	11	3.3442	3.6751	1.295	1.3201	1.0958	4.5791
		CEYCDSGYR	1	0.4263	0.4263								
		CVDIDECTQVQHLCSQGR	2	0.6678	0.6664	1.0947							
		DQCEDIDECQHR	2	7.4471	2.1569	14.9099							
		EAQPGQSQVSYQGLPVQK	1	0.3312	0.3312								
		EEPVEALTFSR	1	6.0281	6.0281								
		GFVPAGESSSEAGGENYKDADECLLFGQEICK	1	0.3734	0.3734								
		HPFEASVQIHQVSR	1	1.9146	1.9146								
		MTCVDVNECDELNNR	2	13.3527	10.7314	2.6363							
		QEDCCGTVGTSWGFNK	2	0.255	0.2478	1.4042							
		YTCICYEGYR	1	5.6976	5.6976								
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=1 SV=2	AISMLQGLCYR	1	0.3657	0.3657		13	0.2625	0.2521	0.2017	0.2138	0.2075	2.3267
		ALLEAPLK	3	0.2204	0.2127	1.4013							
		AQPGWGSPR	1	0.1672	0.1672								
		CEVIPDEEFDPQNSR	1	0.1479	0.1479								
		DCDGGYRPSPLGDSCEDVDECEDPQSSCLGGECK	1	0.2707	0.2707								
		EQDAPVAGLQPVER	1	0.1452	0.1452								
		GAGQGSMSEAPTGDHAPAPTR	1	0.5548	0.5548								
		GQSGSCVDVNECLTPGVCAHGK	1	0.343	0.343								
		SGAAPPTPPR	1	0.0183	0.0183								
		SSAAGEGTLAR	2	0.4433	0.4353	1.3088							
		SSEVYAQLCNVAR	2	0.1476	0.1473	1.0975							
		STPLGQQQPAPR	3	0.2689	0.247	1.6306							
		VTNDVCSEPLR	2	0.19	0.1724	1.883							
LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2	AGPDLASCLDVDECR	1	0.365	0.365		3	0.536	0.536	0.4875	0.4875	0.4875	1.674
		DVDECQLFR	1	0.3592	0.3592								
		GCQLCPPFGSEGFR	1	0.8837	0.8837								
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	FNALQYLR	1	7.5307	7.5307		6	6.4064	6.7867	1.4129	1.7907	0.7506	9.4768
		ISNIPDEYFK	1	0.2966	0.2966								
		LKEDAVSAAFK	2	0.169	0.1572	1.7232							
		LPSGLPVSLLTLYLDNNK	4	6.1954	0.7078	11.23							
		NIPTVNENLNYYLEVNQLEK	2	0.1411	0.1347	1.5436							
		SLEYLDLSFNQIAR	2	24.1059	11.2781	7.1695							
LYAR_HUMAN	Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2	SEEELLVIFNK	1	10.4717	10.4717		1	10.4717	10.4717	10.4717	10.4717	10.4717	
LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	STDYGIFQINSR	1	0.4026	0.4026		1	0.4026	0.4026	0.4026	0.4026	0.4026	
MA1A1_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	SSSGLTYIAEWK	1	0.3014	0.3014		1	0.3014	0.3014	0.3014	0.3014	0.3014	
MAP1A_HUMAN	Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=5	AVLDALLEGK	1	0.0815	0.0815		1	0.0815	0.0815	0.0815	0.0815	0.0815	
MAP1B_HUMAN	Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=1	AVLDALLEGK	1	0.0815	0.0815		1	0.0815	0.0815	0.0815	0.0815	0.0815	
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	EELQANGSAPAADKEEPAAAGSGAASPSAAEK	1	0.8801	0.8801		2	0.8359	0.8359	0.8347	0.8347	0.8347	1.0777
		VNGDASPAAAESGAK	1	0.7917	0.7917								
MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	VECSDNLFTQR	2	1.8105	1.5095	2.408	1	1.8105	1.8105	1.8104	1.8104	1.5095	
MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	IGPYQPNVPVGIDYVIPK	2	0.7827	0.7826	1.0171	1	0.7827	0.7827	0.7827	0.7827	0.7826	
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	NVIIWGNHSSTQYPDVNHAK	1	1.2596	1.2596		2	1.118	1.118	1.109	1.109	1.109	1.1973
		VIVVGNPANTNCLTASK	1	0.9764	0.9764								

MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	ANTFVAELK	2	0.9444	0.9421	1.1046	7	0.9154	0.8464	0.8465	0.7759	0.7627	1.6045
		FVFSLVDAMNGK	1	1.0556	1.0556								
		GYLGPEQLPDCLK	2	0.322	0.3064	1.5673							
		LTLYDIAHTPGVAADLSHIETK	1	1.1837	1.1837								
		SQETECTYFSTPLLLGK	2	0.6701	0.6652	1.1855							
		TIPLISQCTPK	1	1.2655	1.2655								
		VAVLGASGGIGQPLSLLLK	2	0.9666	0.9332	1.458							
MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	EVTGIITQGAR	1	0.6877	0.6877		2	0.673	0.673	0.6728	0.6728	0.6728	1.0314
		NLFETPILAR	1	0.6583	0.6583								
MGN_HUMAN	Protein mago nashi homolog OS=Homo sapiens GN=MAGOH PE=1 SV=1	VFYYLVQDLK	1	0.8746	0.8746		1	0.8746	0.8746	0.8746	0.8746	0.8746	
MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1	SSCTLFQDIFQHLDK	1	0.4809	0.4809		1	0.4809	0.4809	0.4809	0.4809	0.4809	
MK09_HUMAN	Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 PE=1 SV=2	EVMDWEER	1	0.9909	0.9909		1	0.9909	0.9909	0.9909	0.9909	0.9909	
ML12B_HUMAN	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	ATSNVFAMFDQSQIQEFK	1	1.7372	1.7372		2	3.1977	3.1977	2.8447	2.8447	2.8447	2.0086
		GNFNYIEFTR	1	4.6582	4.6582								
MLL3_HUMAN	Histone-lysine N-methyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	LEEQNGSK	1	1.2075	1.2075		1	1.2075	1.2075	1.2075	1.2075	1.2075	
MMP1_HUMAN	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	ADVDHAIEK	1	2.7805	2.7805		2	1.7563	1.7563	1.4267	1.4267	1.4267	2.5692
		IENYTPDLPR	1	0.7321	0.7321								
MMP2_HUMAN	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2	AFQVWSDVTPLR	2	0.1175	0.1154	1.3034	19	2.5523	1.4783	0.2898	0.2392	0.2291	3.5816
		DKPMGPLLVATFWPELPEK	1	0.1918	0.1918								
		ESCNLFVLK	4	0.2138	0.1982	1.5288							
		EYNSCTDTGR	1	0.2724	0.2724								
		FFGLPQTGDLDQNTIETMR	4	0.211	0.1915	1.673							
		FQGTSYDSCTTEGR	3	0.1992	0.1817	1.7283							
		GAYYLK	1	44.2502	44.2502								
		IDAVYEAPQEEK	2	0.2387	0.2224	1.7114							
		IHDGEADIMINFGR	1	0.4418	0.4418								
		IIGYTPDLDPETVDDAFAR	1	0.1402	0.1402								
		LIADAWNAIPDNLDAVVDLQGGGHSYFFK	1	0.2757	0.2757								
		MWCATTANYDDDRK	1	0.2851	0.2851								
		QDIVFDGIAQIR	1	0.1825	0.1825								
		TDKELAVQYLNTFYGCPK	2	0.2169	0.2032	1.6765							
		TYIFAGDK	3	0.1646	0.1567	1.4538							
		WCGTTEDYDR	3	0.1031	0.1022	1.1759							
		WEHGDGYPFDGK	1	0.275	0.275								
		YGFCPHEALFTMGGNAEGQPCK	1	0.2466	0.2466								
		YGNADGEYCK	2	0.4674	0.4542	1.4036							
MMP3_HUMAN	Stromelysin-1 OS=Homo sapiens GN=MMP3 PE=1 SV=2	GEDTSMNLVQK	1	0.1776	0.1776		1	0.1776	0.1776	0.1776	0.1776	0.1776	
MMRN1_HUMAN	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	EFQSLLK	1	1.3157	1.3157		7	1.3299	1.3299	1.126	1.126	1.126	1.864
		GLTEFVEPIQIK	1	1.5109	1.5109								
		IFGNDMQETVAQLFK	1	0.7184	0.7184								
		LSPTVILDNQVTYVPGGK	1	0.4486	0.4486								
		LVEENALAPDFSK	1	0.8159	0.8159								
		MTDQVNYQAMK	1	1.4297	1.4297								
		YNFVLQVAK	1	3.0702	3.0702								
MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	ALELEQER	2	1.2852	1.2731	1.2146	10	2.0462	1.8094	1.4493	1.4165	1.3581	2.3763
		AQMVQEDLEK	1	2.5957	2.5957								
		EDAVLEYLK	2	2.2228	1.8203	2.519							
		ESEAVEWQQK	2	1.3907	1.3905	1.0243							
		EVWFFGLQYQDTK	2	0.5641	0.5628	1.1023							
		GFSTWLK	3	1.4433	1.3493	1.5504							
		LFFLQVK	1	1.0424	1.0424								
		QLFDQVVK	2	1.9486	1.8627	1.5339							
		SGYLAGDK	1	7.6559	7.6559								
		VLEQHK	1	0.3132	0.3132								
MP3B2_HUMAN	Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens GN=MAP1LC3B2 PE=2 SV=1	FLVPDHVNMSELIK	1	0.3071	0.3071		1	0.3071	0.3071	0.3071	0.3071	0.3071	
MT1A_HUMAN	Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=1	CAQGCICK	2	0.4565	0.4564	1.0356	1	0.4565	0.4565	0.4565	0.4565	0.4564	
MT1E_HUMAN	Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1	SCCSCCPVGCAK	2	0.5063	0.4959	1.3357	1	0.5063	0.5063	0.5063	0.5063	0.4959	
MT1G_HUMAN	Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2	CAQGCICK	1	0.4452	0.4452		2	0.5718	0.614	0.5576	0.6011	0.5632	1.3749
		SCCSCCPVGCAK	2	0.6984	0.6334	1.888							
MT1H_HUMAN	Metallothionein-1H OS=Homo sapiens GN=MT1H PE=1 SV=1	CAQGCICK	2	0.4565	0.4564	1.0356	1	0.4565	0.4565	0.4565	0.4565	0.4564	
MT1M_HUMAN	Metallothionein-1M OS=Homo sapiens GN=MT1M PE=2 SV=2	SCCSCCPVGCAK	2	0.5063	0.4959	1.3357	1	0.5063	0.5063	0.5063	0.5063	0.4959	
MT1X_HUMAN	Metallothionein-1X OS=Homo sapiens GN=MT1X PE=1 SV=1	CAQGCICK	1	0.4678	0.4678		2	0.5382	0.5382	0.5335	0.5335	0.5335	1.2043
		SCCSCCPVGCAK	1	0.6085	0.6085								
MT2_HUMAN	Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1	CAQGCICK	2	0.4565	0.4564	1.0356	2	0.4814	0.4814	0.4808	0.4808	0.4757	1.076
		SCCSCCPVGCAK	2	0.5063	0.4959	1.3357							
MUC18_HUMAN	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2	CLADGNPPPHFSISK	1	2.4176	2.4176		4	1.2768	1.2768	1.1297	1.1297	1.1297	1.7345
		EDKDAQFYCELNYR	1	0.6621	0.6621								
		EVTVPVFVPTEK	1	0.9128	0.9128								
		GPVLQLHDLK	1	1.1146	1.1146								
MVP_HUMAN	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	DITPLQVVLPNTALHLK	1	1.9071	1.9071		1	1.9071	1.9071	1.9071	1.9071	1.9071	
MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	TQLEELEDELQATEDAK	1	0.7115	0.7115		1	0.7115	0.7115	0.7115	0.7115	0.7115	
MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	DLGEELEALK	1	1.0121	1.0121		4	1.0148	1.0148	0.9523	0.9523	0.9523	1.492
		KEEELQAALAR	1	1.6383	1.6383								
		QLLQANPILEAFGNAK	1	0.6971	0.6971								
		TQLEELEDELQATEDAK	1	0.7115	0.7115								
MYH14_HUMAN	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=1	EQADFALEALAK	2	1.4206	1.3943	1.3156	3	1.252	1.2942	1.175	1.2321	1.2207	1.5805
		KEEELQAALAR	1	1.6383	1.6383								
		QLLQANPILEAFGNAK	1	0.6971	0.6971								
MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	DLGEELEALK	1	1.0121	1.0121		14	1.4806	1.4027	1.0598	1.0557	1.0517	2.7399
		EQADFAIEALAK	2	1.4206	1.3943	1.3156							
		EQEVNILK	1	3.0108	3.0108								
		EQLEEEEEAK	1	4.8209	4.8209								
		IAEFTTNLTEEEEK	3	0.8876	0.8806	1.1645							
		KEEELQAALAR	1	1.6383	1.6383								
		KLEEEQIILEDQNCK	1	1.3389	1.3389								
		KLEGDSTDLSDDIAELQAQIAELK	1	0.9801	0.9801								
		LQVELDNVTGLLSQSDSK	1	1.6174	1.6174								
		QIATLHAQVADMK	1	0.0635	0.0635								
		QLLQANPILEAFGNAK	1	0.6971	0.6971								
		TDLLLEPYNK	0										
		TQLEELEDELQATEDAK	1	0.7115	0.7115								
		VISQVLQLGNVFFK	1	1.0491	1.0491								
MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	HVLVTLGEK	1	1.8738	1.8738		2	1.6582	1.6582	1.6441	1.6441	1.6441	1.2031
		VLDFEHFLPMLQTVAK	1	1.4426	1.4426								
MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	ILVDNLCDMEMVNK	1	0.1486	0.1486		1	0.1486	0.1486	0.1486	0.1486	0.1486	
NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	DPVPGYSVPAAEHSTITAWGK	1	0.868	0.868		6	3.3323	4.1878	1.2532	1.9095	1.2687	4.9819
		GWNYILEK	1	0.5706	0.5706								
		MWSIENIAFGSGGGLLQK	1	0.643	0.643								
		STQAPLIRPDSGNPLDTVLK	1	10.9939	10.9939								
		VIQCEGVDNTLQEIVEGMK	3	6.7544	2.2707	7.7516							
		YLLETSGNLDGLEYK	1	0.1638	0.1638								
NBL1_HUMAN	Neuroblastoma suppressor of tumorigenicity 1 OS=Homo sapiens GN=NBL1 PE=1 SV=1	ILHCSCQACGK	1	0.7857	0.7857		1	0.7857	0.7857	0.7857	0.7857	0.7857	
NDK8_HUMAN	Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1	DRPFFPGLVK	1	2.3671	2.3671		3	1.4864	1.2864	1.3719	1.2022	1.2017	1.6094
		VMLGETNPADSKPGTIR	1	1.1059	1.1059								
		YMNSGPVVAMVWEGLNVVK	3	0.9863	0.9856	1.0488							
NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	GLVGEIIK	2	1.4647	1.4642	1.0342	5	1.3702	1.4512	1.3133	1.4001	1.3877	1.3999
		GLVGEIIKR	1	0.7987	0.7987								
		NIIHGSDSVESAEK	2	1.843	1.7869	1.4239							
		VMLGETNPADSKPGTIR	1	1.1059	1.1059								
		YMHSGPVVAMVWEGLNVVK	1	1.6388	1.6388								
NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	DRPFFPGLVK	1	2.3671	2.3671		5	1.3445	1.27	1.2474	1.2001	1.1997	1.5215
		GLVGEIIK	2	1.4647	1.4642	1.0342							
		GLVGEIIKR	1	0.7987	0.7987								
		VMLGETNPADSKPGTIR	1	1.1059	1.1059								
		YMNSGPVVAMVWEGLNVVK	3	0.9863	0.9856	1.0488							
NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2	DIEEIIDELK	1	2.2503	2.2503		1	2.2503	2.2503	2.2503	2.2503	2.2503	
NEDD8_HUMAN	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1	EIEDIEPTDKVER	1	3.3505	3.3505		1	3.3505	3.3505	3.3505	3.3505	3.3505	
NELL1_HUMAN	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NELL1 PE=2 SV=3	GIIQDGK	1	0.3033	0.3033		1	0.3033	0.3033	0.3033	0.3033	0.3033	
NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	AELGALPDDFDSLEK	1	1.0245	1.0245		1	1.0245	1.0245	1.0245	1.0245	1.0245	
NFH_HUMAN	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	EYQDLLNVK	4	1.4457	1.4104	1.2911	1	1.4457	1.4457	1.4457	1.4457	1.4104	
NFL_HUMAN	Neurofilament light polypeptide OS=Homo sapiens GN=NEFL PE=1 SV=3	EYQDLLNVK	4	1.4457	1.4104	1.2911	1	1.4457	1.4457	1.4457	1.4457	1.4104	
NFM_HUMAN	Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=2	EYQDLLNVK	4	1.4457	1.4104	1.2911	1	1.4457	1.4457	1.4457	1.4457	1.4104	
NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	EVTDMNLNVINEGGIDK	1	1.495	1.495		2	2.3704	2.3704	2.2028	2.2028	2.2028	1.7301
		QWIQISDAVYHMVYEQAK	1	3.2458	3.2458								
NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	EDLSPSITQR	1	1.371	1.371		5	0.6979	0.6979	0.6167	0.6167	0.6167	1.7229
		GNLYWTDWNR	1	0.6619	0.6619								
		MNSVVALDLAISK	1	0.3681	0.3681								
		NIFWTDSNLDR	1	0.7154	0.7154								
		VLFETDLVNPR	1	0.3732	0.3732								
NID2_HUMAN	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=2	EDTSPAVLGLAAR	1	5.5138	5.5138		4	1.7555	1.7555	0.8935	0.8935	0.8935	3.4526
		ELYHYSDSTVTSTSSR	1	0.357	0.357								
		ETQYVDYDFTDFPAIAPFLADIDTSHGR	1	0.4892	0.4892								
		GNLYWTDWNR	1	0.6619	0.6619								
NNMT_HUMAN	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	IFCLDGVK	1	0.0555	0.0555		1	0.0555	0.0555	0.0555	0.0555	0.0555	
NOTC3_HUMAN	Neurogenic locus notch homolog protein 3 OS=Homo sapiens GN=NOTCH3 PE=1 SV=1	AGLGPQGPR	1	0.2562	0.2562		1	0.2562	0.2562	0.2562	0.2562	0.2562	
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	GIPEFNILYFK	1	0.9911	0.9911		1	0.9911	0.9911	0.9911	0.9911	0.9911	
NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	NVDNLSELVDEYDEPILK	1	1.4468	1.4468		1	1.4468	1.4468	1.4468	1.4468	1.4468	
NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	GPSSVEDIK	1	0.7232	0.7232		2	0.6785	0.6785	0.677	0.677	0.677	1.0978
		MTDQEAIQDLVWQWR	1	0.6338	0.6338								
NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	ADEDPIMGFHQMFLLK	1	0.7963	0.7963		1	0.7963	0.7963	0.7963	0.7963	0.7963	
NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	DLELLIQTATR	1	3.0028	3.0028		5	1.0083	1.0083	0.7195	0.7195	0.7195	2.2584
		EFGDTGEGWETVEMHPAYTEEELR	1	0.6075	0.6075								
		LSQETEALGR	1	0.5491	0.5491								
		LVTLEEFLASTQR	1	0.4874	0.4874								
		MDAEQDPNVQVDHLNLLK	1	0.3949	0.3949								
NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	ALELTGLK	2	1.0412	1.0387	1.1031	8	3.4102	3.8904	2.0731	2.2777	2.2399	2.9863
		EVEEDSEDEEMSEDEDDSSGEEVVIPQKK	1	5.1981	5.1981								
		FGYVDFESAEDLEK	1	0.8793	0.8793								
		GFGFVDFNSEEDAK	1	0.9959	0.9959								
		GIAYIEFK	2	10.5812	9.755	1.7825							
		GYAFIEFASFEDAK	1	5.5966	5.5966								
		KEDSDEEEDDDSEEDEEDEDEDEDEDEIEPAAMK	1	2.5037	2.5037								
		TGISDVFAK	1	0.4855	0.4855								
NUDC_HUMAN	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	VEESSWLIEDGK	1	1.0754	1.0754		1	1.0754	1.0754	1.0754	1.0754	1.0754	
OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	IPAFLNVVDIAGLVK	1	0.9649	0.9649		2	0.5297	0.5297	0.3018	0.3018	0.3018	5.1741
		NYIVEDGDIIFFK	1	0.0944	0.0944								
OSTF1_HUMAN	Osteoclast-stimulating factor 1 OS=Homo sapiens GN=OSTF1 PE=1 SV=2	TGLIPSNVVAEQAESIDNPLHEAAK	1	1.1051	1.1051		1	1.1051	1.1051	1.1051	1.1051	1.1051	
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2	AFGFSHLEALLDDGK	1	0.7241	0.7241		3	0.9152	0.9152	0.7537	0.7537	0.7537	2.1694
		EYAEDDNIYQQK	1	1.6667	1.6667								
		LELSVLYK	1	0.3547	0.3547								
P2RY4_HUMAN	P2Y purinoceptor 4 OS=Homo sapiens GN=P2RY4 PE=1 SV=1	ASTESSLLR	2	90.7683	20.7909	21.0225	1	90.7683	90.7683	90.7683	90.7683	20.7909	
PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	HELLQPFNVLYEK	1	0.5355	0.5355		2	0.557	0.5641	0.5566	0.5638	0.5498	1.0561
		SLVEASSSGVSVLSLCEK	2	0.5785	0.5571	1.4776							
PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	ALYDTFSAFGNILSCK	2	1.4814	1.4785	1.0934	1	1.4814	1.4814	1.4814	1.4814	1.4785	
PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	ALYDTFSAFGNILSCK	2	1.4814	1.4785	1.0934	1	1.4814	1.4814	1.4814	1.4814	1.4785	
PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1	DEISTTDAIFVQR	1	0.0654	0.0575	1.1883	17	0.9181	0.9257	0.9015	0.9099	0.9023	1.2163
		ELMGPWNKDEISTTDAIFVQR	2	0.6752	0.6751	1.024							
		EVPLSALTNILSAQLISHWK	1	0.9946	0.9946								
		FIINDWVK	4	1.3005	1.2837	1.2037							
		FSLETEVDLR	4	0.7862	0.7799	1.1568							
		GAVDQLTR	2	0.8436	0.8415	1.1046							

		GMAPALR	1	0.6553	0.6553								
		IGMISNLLGK	3	0.7471	0.7446	1.1058							
		IEVNESGTVASSSTAVIVSAR	2	1.151	1.1431	1.1807							
		KPLENLGMTDMFR	1	0.8125	0.8125								
		LLVLPK	1	1.2386	1.2386								
		LVLVNALYFNGQWK	2	0.9586	0.9515	1.1885							
		LVQGFMPHFFR	1	0.8082	0.8082								
		QFQADFTSLSDQEPLHVAQALQK	3	0.8188	0.7983	1.3297							
		QVDFSEVER	5	0.9264	0.9177	1.1672							
		SDGSTVSVPMMAQTNK	2	0.9239	0.9218	1.0996							
		VFQQVAQASK	4	0.9023	0.8876	1.2305							
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	EMTLDEVK	1	0.8397	0.8397		1	0.8397	0.8397	0.8397	0.8397	0.8397	
PAL4B_HUMAN	Peptidylprolyl cis-trans isomerase A-like 4B OS=Homo sapiens GN=PPIAL4B PE=1 SV=1	IIPGFMCQGGDFTR	1	1.1253	1.1253		2	0.898	0.898	0.8688	0.8688	0.8688	1.4418
		SIYGEK	1	0.6707	0.6707								
PARK7_HUMAN	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	ALVILAK	2	0.0319	0.031	1.3877	2	0.4059	0.2812	0.1576	0.0925	0.0908	9.5976
		GLIAAICAGPTALLAHEIGFGSK	1	0.78	0.78								
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	SDAYYCTGDVTAWTK	1	0.2115	0.2115		1	0.2115	0.2115	0.2115	0.2115	0.2115	
PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	IITLTGPTNAIFK	2	0.5153	0.5144	1.0864	1	0.5153	0.5153	0.5153	0.5153	0.5144	
PCD12_HUMAN	Protocadherin-12 OS=Homo sapiens GN=PCDH12 PE=2 SV=1	YTLTLLAQDGGLQPLSAK	1	0.1978	0.1978		1	0.1978	0.1978	0.1978	0.1978	0.1978	
PCNA_HUMAN	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	AEDNADTLALVFEAPNQEK	1	0.9367	0.9367		3	0.632	0.632	0.3512	0.3512	0.3512	5.3269
		DLSHIGDAVVISCAK	1	0.9085	0.9085								
		NLAMGVNLTSMSK	1	0.0509	0.0509								
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2	ATSGTEHQFCGGR	1	4.537	4.537		8	4.2601	5.0527	1.0986	1.172	1.1429	8.6489
		EPGEGLAVTVSLIGAYK	1	0.3795	0.3795								
		FDLEPDTYCR	1	0.0834	0.0834								
		GESGYVASEGFPNLYPPNK	2	0.1024	0.1017	1.1771							
		GFLLWYSGR	1	7.9471	7.9471								
		TEESPSAPDAPTCPK	2	0.1792	0.1773	1.2325							
		YDALEVFAGSGTSGQR	3	13.1349	12.0136	1.6954							
		YDSVSVFNGAVSDDSR	1	7.7175	7.7175								
PDC6I_HUMAN	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	LANQAADYFGDAFK	1	1.5756	1.5756		2	1.5972	1.5972	1.5971	1.5971	1.5971	1.0193
		SVIEQGGIQTVDQLIK	1	1.6188	1.6188								
PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	AGVNFSEFTGVWK	1	1.8317	1.8317		1	1.8317	1.8317	1.8317	1.8317	1.8317	
PDE8B_HUMAN	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B OS=Homo sapiens GN=PDE8B PE=1 SV=2	TLDDLK	1	0.9046	0.9046		1	0.9046	0.9046	0.9046	0.9046	0.9046	
PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	EADDIVNWLK	1	1.7904	1.7904		2	1.7495	1.7358	1.749	1.7354	1.7354	1.0337
		ENLLDFIK	2	1.7085	1.7085	1.0053							
PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	DASIVGFFDDSFSEAHSEFLK	1	1.2315	1.2315		2	1.2219	1.2219	1.2219	1.2219	1.2219	1.0112
		GFPTIYFSPANK	1	1.2123	1.2123								
PDLI5_HUMAN	PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=4	DFNMPLTISSLK	1	1.0614	1.0614		3	1.8281	1.8281	1.5354	1.5354	1.5354	2.0065
		IGDVVLSIDGINAQGMTHLEAQNK	1	0.9947	0.9947								
		NTMAYIGFVEEK	1	3.4282	3.4282								
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	APVAGTCYQAEWDDYVPK	1	1.2939	1.2939		3	0.9035	0.9035	0.8654	0.8654	0.8654	1.4196
		LYEQLSGK	1	0.7351	0.7351								
		NRPTSISWDGLDSGK	1	0.6815	0.6815								
PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=3	ALYYDLISSPDIHGTYK	1	0.2465	0.2465		9	0.7439	0.8196	0.4326	0.4193	0.3564	2.4472
		DTDTGALLFIGK	2	0.2284	0.2228	1.3707							
		EIPDEISLLLGVAHFK	1	0.67	0.67								
		ELLDTVTAPQK	1	0.3158	0.3158								
		LAAAVSNFGYDLYR	2	3.8824	1.368	11.1265							
		LDLQEINNWVQAQMK	1	0.4604	0.4604								
		LQSLFDSPDFSK	4	0.2227	0.215	1.3431							
		TSLEDFYLDEEK	1	0.3367	0.3367								
		YGLDSDLSCK	1	0.3323	0.3323								
PERI_HUMAN	Peripherin OS=Homo sapiens GN=PRPH PE=1 SV=2	KLLEGEESR	1	1.2487	1.2487		4	5.6206	7.1896	2.1134	2.8628	2.0461	4.5952
		LEEETRK	1	0.5788	0.5788								
		LLEGEESR	2	1.4361	1.4267	1.1758							
		MALDIEIATYR	2	19.219	7.0625	10.4402							
PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	ALPYWNEEIVPQIK	2	0.8888	0.888	1.0801	2	0.8907	0.8907	0.8907	0.8907	0.8902	1.0031
		YADLTEDQLPSCESLK	2	0.8926	0.8925	1.0181							
PGAM2_HUMAN	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	ALPFWNEEIVPQIK	2	0.8888	0.888	1.0601	1	0.8888	0.8888	0.8888	0.8888	0.888	
PGAM4_HUMAN	Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=1 SV=1	ALPFWNEEIVPQIK	1	0.8521	0.8521		1	0.8521	0.8521	0.8521	0.8521	0.8521	
PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3	AAGVPSATITWR	1	2.3149	2.3149		27	1.9377	1.7861	0.8138	0.8362	0.7329	2.8474
		AGFFGDAMK	1	0.9884	0.9884								
		AMDFNGILTIR	1	0.253	0.253								
		CSATGSPAPTIHWSK	1	0.5408	0.5408								
		ESDQGAYTCEAMNAR	1	0.3453	0.3453								
		EVSEAVVDTLESEYLK	4	0.5435	0.5319	1.2741							
		FDQPDDFK	3	0.5378	0.4534	2.1092							
		FSSGITGCVK	2	0.7568	0.7546	1.1135							
		GCVGEVSVNGK	1	0.8422	0.8422								
		GPSCQDCDTGYTR	1	0.5935	0.5935								
		LDVEPKPLAPDGVLLFSGGK	2	0.4436	0.3925	2.0412							
		LEGDTLIIPR	3	4.8814	1.2367	8.1351							
		LHHVSPADSGEYVCR	1	0.7457	0.7457								
		LHQMSVADSGEYVCR	1	0.5361	0.5361								
		LLSGPYFWSLPSR	1	12.4252	12.4252								
		LYQASPADSGEYVCR	1	0.4262	0.4262								
		GPQAITWYK	1	0.9991	0.9991								
		SGPVEDFVSLAMVGGHLEFR	1	0.602	0.602								
		SIGASVEFHCAVPSDR	1	0.3758	0.3758								
		SIVPQGGSHSLR	1	0.5622	0.5622								
		SPAYTLVWTR	2	1.2617	1.2334	1.353							
		SPVISIDPPSSTVQQGQDASFK	2	0.6217	0.6217	1.0087							
		SQSVRPGADVTFICTAK	1	0.3866	0.3866								
		TDEANCPTK	1	0.669	0.669								
		TSTASGLLLWQGVEVGEAGQGK	1	0.5444	0.5444								
		VAEGQTLDLK	1	0.2649	0.2649								
		VTSYCGGLR	1	18.8569	18.8569								
PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	ALMDEVVK	3	0.1464	0.1033	2.6815	8	1.0136	0.8402	0.8674	0.6077	0.5473	2.0988
		DCVGPEVEK	1	1.0819	1.0819								
		FHVEEEGK	1	1.5568	1.5568								
		GCITIIGGGDTATCCAK	1	1.3206	1.3206								
		ITLPVDFVTADK	1	1.016	1.016								
		ITLPVDFVTADKFDENAK	1	0.9212	0.9212								
		TGQATVASGIPAGWMGLDCGPESSKK	1	0.9063	0.9063								
		VLNNMEIGTSLFDEEGAK	1	1.1599	1.1599								
PGK2_HUMAN	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3	FHVEEEGK	1	1.5568	1.5568		1	1.5568	1.5568	1.5568	1.5568	1.5568	
PGS1_HUMAN	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	EISPDTTLDLQNNDISELRK	1	0.3695	0.3695		4	0.3392	0.3298	0.3166	0.3116	0.3037	1.5515
		ELHLDNNK	1	0.1809	0.1809								
		IQAIELEDLLR	2	0.2923	0.2741	1.6693							
		VGVNDFCPMGFGVK	1	0.5142	0.5142								
PGS2_HUMAN	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	AHEITK	1	0.3363	0.3363		12	11.2244	12.0777	0.5454	0.4878	0.4523	9.1012
		ASYSGVSLFSNPVQYWEIQPSTFR	1	26.7025	26.7025								
		DFEPSLGPVCPFR	2	105.512	65.6609	4.4302							
		DLPDTTLLDLQNNK	2	0.154	0.1526	1.2035							
		ELHLDNNK	1	0.1809	0.1809								
		GLNNLAK	3	0.2205	0.2204	1.0342							
		NLHALLVNNK	1	0.5398	0.5398								
		SSGIENGAFQGMK	3	0.2405	0.205	1.9778							
		VSPGAFTPLVK	2	0.143	0.1395	1.374							
		VTFNGLNGMPVELGTNPLK	1	0.4151	0.4151								
		VVQCSDLGLDK	2	0.1289	0.1279	1.1943							
		VVQCSDLGLDKVPK	1	0.1198	0.1198								
PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	AKYPDYEVTWANDGY	1	0.49	0.49		1	0.49	0.49	0.49	0.49	0.49	
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=3	VIGIDHK	1	0.7306	0.7306		1	0.7306	0.7306	0.7306	0.7306	0.7306	
PIR_HUMAN	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1	NLDPFLLFDEFK	1	0.915	0.915		1	0.915	0.915	0.915	0.915	0.915	
PLBL2_HUMAN	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	VLTILEQIPGMVVVADK	1	0.3466	0.3466		1	0.3466	0.3466	0.3466	0.3466	0.3466	
PLEC1_HUMAN	Plectin-1 OS=Homo sapiens GN=PLEC1 PE=1 SV=3	DYELQLVTYK	1	1.6309	1.6309		2	2.296	2.296	2.1976	2.1976	2.1976	1.5246
		TLLQGSCLAGIYLEDTK	1	2.9611	2.9611								
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	IFQNLDGALDEVVLK	1	0.665	0.665		1	0.665	0.665	0.665	0.665	0.665	
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	IFQNLNGALDEVVLK	1	0.6896	0.6896		1	0.6896	0.6896	0.6896	0.6896	0.6896	
PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5	LNNAKYAISMAR	2	0.7551	0.72	1.5529	1	0.7551	0.7551	0.7551	0.7551	0.72	
PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	AESMLQQADK	1	1.0926	1.0926		8	1.365	1.2863	1.125	1.0925	1.0732	1.8334
		DGETLEELMK	1	1.3775	1.3775								
		EGICALGGTSELSSEGTQHSYSEEEK	1	0.9694	0.9694								
		IDINMSGFNETDDLKR	1	0.7682	0.7682								
		LNLAFVANLFNK	1	1.1767	1.1767								
		VVALPEDLVEVKPK	1	0.4919	0.4919								
		YPALTKPENQDIDWTLEGETR	1	4.0722	4.0722								
		YTLNVLEDLGDGQK	3	0.9714	0.9154	1.5186							
PLTP_HUMAN	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	ATYFGSIVLLSPAVIDSPLK	1	0.2465	0.2465		7	1.1178	1.6312	0.4653	0.6296	0.4733	3.5969
		GAFFPLTER	1	0.2716	0.2716								
		GLREVIEK	1	0.1811	0.1811								
		SSVDELVGIDYSLMK	1	0.294	0.294								
		TGLELSR	1	1.4287	1.4287								
		TMLQIGVMPMLNER	1	0.1775	0.1775								
		VVDFLSTFITSGMR	2	5.2253	1.6695	12.8874							
PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens GN=NP PE=1 SV=2	HRPQVAIICGSGLGGLTDK	1	2.8721	2.8721		2	1.9308	1.9308	1.6857	1.6857	1.6857	2.1246
		VFGFSLITNK	1	0.9894	0.9894								
POSTN_HUMAN	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	AAATSDILEALGR	1	0.0806	0.0806		13	2.5032	2.1208	0.5501	0.5166	0.4999	4.4785
		DIVTNNGVIHLIDQVLIPDSAK	1	0.2715	0.2715								
		EGETITEVIHGEPIIK	1	0.2468	0.2468								
		ELTQPQEWTLFVPTNDAFK	1	0.1776	0.1776								
		FSTFLSLLEAADLK	1	0.2155	0.2155								
		GFEPGVTNILK	1	0.3856	0.3856								
		GSFTYFAPSNEAWDNLDSDIR	1	24.7162	24.7162								
		LLYPADTPVGNDQLLELNK	3	0.2661	0.2596	1.3064							
		NALQNILYHLTPGVFIGK	1	1.1058	1.1058								
		QVIELAGK	1	1.6642	1.6642								
		TTVLVECCPQGYMR	1	2.3335	2.3335								
		VGLNELYNGQILETIGGK	1	0.2182	0.2182								
		VLTQIGTSIQDFIEAEDLDLSSFR	2	0.8596	0.686	2.6806							
POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	AGFAGDDAPR	3	1.7944	1.7855	1.1303	5	1.7042	1.8163	1.6744	1.7859	1.7633	1.2342
		AVFPSIVGRPR	2	1.3725	1.362	1.191							
		GILTLK	5	2.1925	2.1372	1.2805							
		LCYVALDFEQEMATAASSSSLEK	3	1.8296	1.8133	1.1784							
		QEYDESGPSIVHR	2	1.3322	1.3281	1.1175							
POTEF_HUMAN	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	AGFAGDDAPR	3	1.7944	1.7855	1.1303	4	1.6729	1.8129	1.6377	1.7751	1.751	1.2664
		AVFPSIVGRPR	2	1.3725	1.362	1.191							
		GILTLK	5	2.1925	2.1372	1.2805							
		QEYDESGPSIVHR	2	1.3322	1.3281	1.1175							
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	1.3011	1.3011		1	1.3011	1.3011	1.3011	1.3011	1.3011	
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	TFTDCFNCLPIAAIVDEK	1	1.3011	1.3011		1	1.3011	1.3011	1.3011	1.3011	1.3011	
PPTG_HUMAN	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	1.3011	1.3011		1	1.3011	1.3011	1.3011	1.3011	1.3011	
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	EGMNIVEAMER	4	8.1315	4.9999	3.4973	11	1.4696	2.3038	0.9543	1.3012	1.1438	2.1762
		FEDENFILK	3	0.9526	0.9273	1.3205							
		HTGPGILSMANAGPNTNGSQFFICTAK	1	0.8241	0.8241								
		IIPGFMCQGGDFTR	1	1.1253	1.1253								
		KITIADCGQLE	2	0.8654	0.8539	1.2597							
		SIYGEK	1	0.6707	0.6707								
		SIYGEKFEDENFILK	1	0.3332	0.3332								
		TEWLDGK	1	0.7896	0.7896								
		VKEGMNIVEAMER	1	0.6719	0.6719								
		VNPTVFFDIAVDGEPLGR	1	0.886	0.886								

		VSFELFADK	4	0.9153	0.8026	1.9449								
PPM1F_HUMAN	Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=1 SV=3	AIGDVFQKPYVSGEADAASR	1	0.4318	0.4318		1	0.4318	0.4318	0.4318	0.4318	0.4318		
PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GLFIIDDK	4	1.4219	1.4166	1.1038	3	1.2328	1.2347	1.2242	1.2254	1.2097	1.1556	
		LVQAFQFTDK	3	1.211	1.2073	1.1003								
		TIAQDYGVLK	4	1.0654	1.0345	1.3177								
PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	KEGGLGPLNIPLLADVTR	1	0.924	0.924		1	0.924	0.924	0.924	0.924	0.924		
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	GLFIIDPNGVIK	2	0.6792	0.674	1.1906	1	0.6792	0.6792	0.6791	0.6791	0.674		
PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	GLFIIDDK	4	1.4219	1.4166	1.1038	1	1.4219	1.4219	1.4219	1.4219	1.4166		
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=3	GVLFGVPGAFTPGCSK	1	1.347	1.347		2	0.7779	0.7779	0.5302	0.5302	0.5302	3.7381	
		VNLAELFK	1	0.2087	0.2087									
PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	DINAYNCEEPTEK	1	2.2485	2.2485		5	11.2453	11.2453	2.0192	2.0192	2.0192	7.6454	
		ELAILLGMLDPAEKDEK	1	51.0889	51.0889									
		LIALSIDSVEDHLAWSK	1	0.2295	0.2295									
		VVFVFGPDKK	1	0.626	0.626									
		VVISLQLTAEK	1	2.0337	2.0337									
PRELP_HUMAN	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	NLMQLNLAHNILR	1	0.4022	0.4022		1	0.4022	0.4022	0.4022	0.4022	0.4022		
PREP_HUMAN	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=2	LLPDHTYSVVSGGDPLCIPELTVWEQLK	1	2.9006	2.9006		1	2.9006	2.9006	2.9006	2.9006	2.9006		
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	DSLLGDGEFSMDLR	1	1.0077	1.0077		7	1.0425	1.0075	1.0388	1.0037	0.986	1.095	
		DSPSVWAAVPGK	2	1.1776	1.1709	1.1631								
		EGVHGGLINK	1	1.131	1.131									
		SSFYVNGLTLGGQK	3	1.0218	1.0158	1.1432								
		STGGAPTFNVTVTK	2	1.0849	1.0847	1.0272								
		TFVNITPAEVGVLVGK	5	0.9077	0.8689	1.4088								
		TLVLLMGK	4	0.967	0.9495	1.2486								
PRS10_HUMAN	26S protease regulatory subunit S10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	ALQSVGQIVGEVLK	1	1.48	1.48		1	1.48	1.48	1.48	1.48	1.48		
PRS23_HUMAN	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1	DFLLNYPFSTSVK	1	1.4202	1.4202		2	1.1218	1.1218	1.0814	1.0814	1.0814	1.4703	
		FCDVKDETYDLLYQGCDAQPGASGSGVYVR	1	0.8234	0.8234									
PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	ATFDSLVVPK	1	0.0128	0.0128		2	2.8175	2.8175	0.2683	0.2683	0.2683	73.9032	
		TIQQCCENILLNAAWLK	1	5.6221	5.6221									
PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GYSFSLTTFSPSGK	1	1.2466	1.2466		2	0.9347	0.9347	0.8811	0.8811	0.8811	1.6336	
		YNEDLELEDAIHTAILTLK	1	0.6227	0.6227									
PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	ESLKEEDESDDDIMM	1	0.9437	0.9437		1	0.9437	0.9437	0.9437	0.9437	0.9437		
PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	LLDEVFFSEK	1	0.7021	0.7021		1	0.7021	0.7021	0.7021	0.7021	0.7021		
PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	LFQVEYAIEAIK	1	0.672	0.672		2	1.1466	1.1466	1.0438	1.0438	1.0438	1.864	
		SSLILK	1	1.6212	1.6212									
PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	CDPAGYYCGFK	1	0.155	0.155		3	0.2221	0.2221	0.1377	0.1377	0.1377	3.6817	
		LLDSSTVTHLFK	1	0.0354	0.0354									
		YGYEIPVDMLCK	1	0.476	0.476									
PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	LYQTDPSGTYHAWK	1	0.6532	0.6532		1	0.6532	0.6532	0.6532	0.6532	0.6532		
PSA7L_HUMAN	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	LYQTDPSGTYHAWK	1	0.6532	0.6532		1	0.6532	0.6532	0.6532	0.6532	0.6532		
PSAL_HUMAN	Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens GN=NPEPPSL1 PE=2 SV=3	ATFDSLVVPK	1	0.0128	0.0128		1	0.0128	0.0128	0.0128	0.0128	0.0128		
PSB3_HUMAN	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	DAVSGMGVIVHIIEK	1	1.3505	1.3505		2	6.4716	6.4716	3.9567	3.9567	3.9567	4.5732	
		LNLYELK	1	11.5926	11.5926									
PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	ATEGMVVADK	1	0.9159	0.9159		2	0.7385	0.7385	0.7168	0.7168	0.7168	1.4143	
		GTTAVLTEK	1	0.561	0.561									
PSG4_HUMAN	Pregnancy-specific beta-1-glycoprotein 4 OS=Homo sapiens GN=PSG4 PE=2 SV=2	SGENLYLSCFAESNPR	1	16.9315	16.9315		1	16.9315	16.9315	16.9315	16.9315	16.9315		
PSME1_HUMAN	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	IEDGNNFGVAVQEK	1	0.3488	0.3488		3	1.0299	1.0299	0.8638	0.8638	0.8638	2.2158	
		ISELDAFLK	1	1.1973	1.1973									
		TENLLGSYFPK	1	1.5436	1.5436									
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	NNQFQALLQYADPVSAQHAK	1	0.879	0.879		2	1.059	1.059	1.0435	1.0435	1.0435	1.2747	
		VTNLLMLK	1	1.2389	1.2389									
PTBP2_HUMAN	Polypyrimidine tract-binding protein 2 OS=Homo sapiens GN=PTBP2 PE=1 SV=1	VTNLMLK	1	1.2389	1.2389		1	1.2389	1.2389	1.2389	1.2389	1.2389		
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1	TMLLQPAGSLGSYSYR	2	2.0777	0.9418	7.5405	1	2.0777	2.0777	2.0777	2.0777	0.9418		
PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2	EVVEEAENGR	1	0.4916	0.4916		1	0.4916	0.4916	0.4916	0.4916	0.4916		
PTRF_HUMAN	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	SDQVNGVLVLSLLDK	3	0.8807	0.8207	1.569	1	0.8807	0.8807	0.8807	0.8807	0.8207		
PTX3_HUMAN	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=2	ALAAVLEELR	1	0.4661	0.4661		4	0.8891	0.8891	0.4527	0.4527	0.4527	4.8065	
		LTGFNIWDSVLSNEEIR	1	0.7185	0.7185									
		MLLQATDDVLR	1	2.3178	2.3178									
		TILFSYSTK	1	0.0541	0.0541									
PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	GYGFIEYEK	1	0.2451	0.2451		1	0.2451	0.2451	0.2451	0.2451	0.2451		
PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	ITSCIFQLLQEAGIK	1	0.7067	0.7067		1	0.7067	0.7067	0.7067	0.7067	0.7067		
PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	LDILDMFTEIK	1	0.7257	0.7257		1	0.7257	0.7257	0.7257	0.7257	0.7257		
PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	DAC7ICECK	1	0.9795	0.9795		6	0.7663	0.7663	0.7157	0.7157	0.7157	1.5462	
		LGPTLMCLLSTQFK	1	0.3202	0.3202									
		LNPHWDGDTIYYETR	1	0.7036	0.7036									
		LWYENPGVFSPAQLTQIK	1	0.7909	0.7909									
		SPNDLLALFR	1	0.6935	0.6935									
		VAEFPHGYGSCDEIPR	1	1.1103	1.1103									
QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	EVNYIDK	1	11.4836	11.4836		1	11.4836	11.4836	11.4836	11.4836	11.4836		
QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	AWRPALVLAALDCAEETNSAVCR	1	0.2855	0.2855		14	1.0333	0.9928	0.6531	0.6207	0.5604	2.4865	
		DVQNVAAAPELAMGALELESR	1	0.4341	0.4341									
		ELCSACHNER	1	2.1442	2.1442									
		EVALDLSQHK	1	0.4214	0.4214									
		FGVTDFPSCVLLFR	1	0.3951	0.3951									
		GGSYLGR	1	1.1872	1.1872									
		LAGAPSEDPQFPK	1	2.8188	2.8188									
		LDVGWDVEATLNFLK	3	0.6318	0.6317	1.021								
		LEEIDGFFAR	1	0.3684	0.3684									
		NGSGAVFPVAGADVQTLR	1	0.5495	0.5495									
		NNEEYLALIFEK	4	0.4322	0.4309	1.0949								
		SALYSPSDPLTLLQADTVR	3	0.2807	0.2805	1.0467								
		SFYTAYLQR	2	4.2542	1.3929	12.4249								
		VGSPNAVLWLWSSHNR	1	0.263	0.263									
RAL2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like protein 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	DYFEQYGK	3	0.4053	0.3584	1.836	1	0.4053	0.4053	0.4053	0.4053	0.3584		
RA1L3_HUMAN	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3 OS=Homo sapiens GN=HNRPA1L3 PE=5 SV=1	DYFEQYGK	1	0.202	0.202		1	0.202	0.202	0.202	0.202	0.202		
RAB28_HUMAN	Ras-related protein Rab-28 OS=Homo sapiens GN=RAB28 PE=1 SV=2	IVVLGDGASGK	1	0.7144	0.7144		1	0.7144	0.7144	0.7144	0.7144	0.7144		
RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	LVFLGEQSVGK	1	0.0227	0.0227		1	0.0227	0.0227	0.0227	0.0227	0.0227		
RAB6B_HUMAN	Ras-related protein Rab-6B OS=Homo sapiens GN=RAB6B PE=1 SV=1	LVFLGEQSVGK	1	0.0227	0.0227		1	0.0227	0.0227	0.0227	0.0227	0.0227		
RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	ATIGADFLTK	1	0.2653	0.2653		3	0.4824	0.4824	0.4449	0.4449	0.4449	1.6515	
		DPENFPFVVLGNK	1	0.7225	0.7225									
		GADCGLVFDVTAPNTFK	1	0.4595	0.4595									
RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1	EDSMMEYLK	1	2.1305	2.1305		4	1.3587	1.4767	1.079	1.2144	1.1927	2.4201	
		LFFLQVK	1	1.0424	1.0424									
		QLFDQVVK	2	1.9486	1.8627	1.5339								
		VLEQHK	1	0.3132	0.3132									
RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	HLTGEFEK	1	0.5588	0.5588		3	0.6073	0.5927	0.6028	0.5888	0.58	1.1588	
		LVLVGDGGTGK	1	0.7144	0.7144									
		NLQYYDISAK	2	0.5487	0.5325	1.4164								
RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	TLEEDEEELFK	1	0.7106	0.7106		1	0.7106	0.7106	0.7106	0.7106	0.7106		
RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	GAVGALLVVDIAK	1	0.9692	0.9692		1	0.9692	0.9692	0.9692	0.9692	0.9692		
RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	TPSSDVLVFDYTK	1	0.8163	0.8163		1	0.8163	0.8163	0.8163	0.8163	0.8163		
RBBP7_HUMAN	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	TPSSDVLVFDYTK	1	0.8163	0.8163		1	0.8163	0.8163	0.8163	0.8163	0.8163		
RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	TCLLIVFSK	1	1.1917	1.1917		1	1.1917	1.1917	1.1917	1.1917	1.1917		
RHOB_HUMAN	Rho-related GTP-binding protein RhoB OS=Homo sapiens GN=RHOB PE=1 SV=1	TCLLIVFSK	1	1.1917	1.1917		1	1.1917	1.1917	1.1917	1.1917	1.1917		
RHOC_HUMAN	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	TCLLIVFSK	1	1.1917	1.1917		1	1.1917	1.1917	1.1917	1.1917	1.1917		
RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	AVDIPHMDIEALK	1	0.6449	0.6449		2	2.2166	3.0024	1.563	2.4333	2.2307	3.4973	
		FSVCVLGDQQHCDEAK	3	3.7883	3.3735	1.8551								
RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	CTGGEVGATSALAPK	1	0.7543	0.7543		2	0.447	0.447	0.3246	0.3246	0.3246	3.2949	
		IGPLGLSPK	1	0.1397	0.1397									
RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	AVVLMGK	1	26.6825	26.6825		5	5.9003	3.4616	1.3246	0.753	0.6291	5.781	
		GHLENNPALEK	1	0.5744	0.5744									
		GTIEILSDVQLIK	1	1.1728	1.1728									
		IIQLLDDYPK	4	0.2901	0.1937	2.9311								
		TSFFQALGITTK	2	0.7819	0.7812	1.0617								
RLA0L_HUMAN	60S acidic ribosomal protein P0-like OS=Homo sapiens PE=2 SV=1	GHLENNPALEK	1	0.5744	0.5744		4	0.7048	0.5589	0.6252	0.4821	0.3938	1.803	
		GTIEILSDVQLIK	1	1.1728	1.1728									
		IIQLLDDYPK	4	0.2901	0.1937	2.9311								
		TSFFQALGITTK	2	0.7819	0.7812	1.0617								
RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	AAGVNVEPFWPGLFAK	2	0.6338	0.6333	1.056	2	0.6089	0.6172	0.6083	0.6167	0.6164	1.0597	
		KEESEESDDDMGFGLFD	1	0.5839	0.5839									
RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	KEESEESDDDMGFGLFD	2	0.5395	0.5377	1.1237	3	0.8877	0.9668	0.8329	0.8985	0.8926	1.552	
		NIEDVIAQGIGK	3	1.2993	1.2851	1.1952								
		YVASYLLAALGGNSSPSAK	1	0.8242	0.8242									
RMP_HUMAN	Unconventional prefoldin RPB5 interactor OS=Homo sapiens GN=RMP PE=1 SV=3	TIDDLK	1	0.9046	0.9046		1	0.9046	0.9046	0.9046	0.9046	0.9046		
RMXL3_HUMAN	RNA-binding motif protein, X-linked-like-3 OS=Homo sapiens GN=RBMXL3 PE=2 SV=2	GFAFVTFESPADAK	1	0.7561	0.7561		1	0.7561	0.7561	0.7561	0.7561	0.7561		
RNBP6_HUMAN	Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2	FMQDASNVMQLLLK	1	13.6849	13.6849		1	13.6849	13.6849	13.6849	13.6849	13.6849		
RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2	MTANSVLEPGNSEVSLVCEK	1	0.8098	0.8098		1	0.8098	0.8098	0.8098	0.8098	0.8098		
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=4	DYFEQYGK	2	0.4398	0.3699	2.353	3	0.5143	0.4957	0.5114	0.4925	0.4517	1.1399	
		GFAFVTFDDHDSVDK	1	0.5478	0.5478									
		LFIGGLSFETTDESLR	1	0.5553	0.5553									
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	DYFEEYGK	1	0.4553	0.4553		3	0.6139	0.6139	0.5972	0.5972	0.5972	1.3321	
		GFGFVTFDDHDPVDK	1	0.8062	0.8062									
		IDTIEIITDR	1	0.5802	0.5802									
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2	GFGFILFK	1	0.8618	0.8618		1	0.8618	0.8618	0.8618	0.8618	0.8618		
ROD1_HUMAN	Regulator of differentiation 1 OS=Homo sapiens GN=ROD1 PE=1 SV=2	VTNLLMLK	1	1.2389	1.2389		1	1.2389	1.2389	1.2389	1.2389	1.2389		
RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	DVIEEYFK	1	0.7802	0.7802		3	0.781	0.781	0.7474	0.7474	0.7474	1.4464	
		KVVGCSCVVVK	1	0.5067	0.5067									
		LVEALCAEHQINLIK	1	1.056	1.056									
RS20_HUMAN	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	LIDLHSPSEIVK	1	0.1486	0.1486		1	0.1486	0.1486	0.1486	0.1486	0.1486		
RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	DHASQMNVAEVDK	1	1.0949	1.0949		1	1.0949	1.0949	1.0949	1.0949	1.0949		
RS25_HUMAN	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	AALQELLSK	1	4.4389	4.4389		1	4.4389	4.4389	4.4389	4.4389	4.4389		
RSU1_HUMAN	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3	DNDLISLPK	1	0.6155	0.6155		1	0.6155	0.6155	0.6155	0.6155	0.6155		
S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	CIESLIAVFQK	3	1.4093	1.1688	2.0558	3	1.3762	1.3581	1.3753	1.357	1.2639	1.046	
		DGYNYTLSK	1	1.4135	1.4135									
		TEFLSFMNTELAAFTK	4	1.3057	1.3033	1.0728								
S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1	DVGSLDEK	1	0.6603	0.6603		1	0.6603	0.6603	0.6603	0.6603	0.6603		
SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1	EALEVDWSSEK	1	0.1967	0.1967		1	0.1967	0.1967	0.1967	0.1967	0.1967		
SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	GISEETTTGVHNLYK	1	0.7235	0.7235		2	0.9218	0.9218	0.4548	0.4548	0.4548	6.5809	
		VAVVAGYGDVGK	1	0.12	0.12									
SAP_HUMAN	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	DGGFCEVCK	2	0.6947	0.6759	1.3945	9	0.8858	0.8563	0.8211	0.8165	0.7135	1.514	
		DVVTAAGDMLK	1	1.7334	1.7334									
		EILDAFDK	3	1.0251	1.0205	1.1245								
		EIVDSYLPVILDIIK	6	0.8786	0.8715	1.1496								
		GCSFLPDPYQK	2	0.3888	0.2137	5.5016								
		LGPGMADICK	3	0.7768	0.4683	4.5574								
		QEILAALEK	2	0.9306	0.9305	1.0189								
		SDVYCEVCEFLVK	1	0.5726	0.5726									
		SLPCDICK	1	0.9719	0.9719									
SENP7_HUMAN	Sentrin-specific protease 7 OS=Homo sapiens GN=SENP7 PE=1 SV=3	TIDNDLR	1	0.0888	0.0888		1	0.0888	0.0888	0.0888	0.0888	0.0888		
SEPT11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3	STLMDTLFNTK	1	0.2449	0.2449		1	0.2449	0.2449	0.2449	0.2449	0.2449		
SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	LYPWGVVEVENPEHNDFLK	1	0.176	0.176		1	0.176	0.176	0.176	0.176	0.176		
SEPT6_HUMAN	Septin-6 OS=Homo sapiens GN=SEPT6 PE=1 SV=4	STLMDTLFNTK	1	0.2449	0.2449		1	0.2449	0.2449	0.2449	0.2449	0.2449		
SET_HUMAN	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	EFHLNESGDDPSSK	1	0.6195	0.6195		2	0.5328	0.5328	0.5256	0.5256	0.5256	1.2616	
		IDFYFDENPYFENK	1	0.446	0.446									
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1 OS=Homo sapiens GN=SFRS1 PE=1 SV=2	DIEDVFYK	1	1.8063	1.8063		1	1.8063	1.8063	1.8063	1.8063	1.8063		
SH3BG_HUMAN		QQEVVGFLEANK	1	0.4526	0.4526		1	0.4526	0.4526	0.4526	0.4526	0.4526		
SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	QQDVLGFLEANK	1	0.4526	0.4526		1	0.4526	0.4526	0.4526	0.4526	0.4526		
SKP1_HUMAN	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	RTDDIPVWDQEFLK	1	0.2251	0.2251		1	0.2251	0.2251	0.2251	0.2251	0.2251		

SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	LSHETVTIELK	1	0.1866	0.1866		1	0.1866	0.1866	0.1866	0.1866	0.1866	
SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	GDGPVQGIINFEQK	3	0.8406	0.8351	1.1509	1	0.8406	0.8406	0.8406	0.8406	0.8351	
SOX30_HUMAN	Transcription factor SOX-30 OS=Homo sapiens GN=SOX30 PE=1 SV=1	LGAVETGPR	2	0.0642	0.0642	1.0291	1	0.0642	0.0642	0.0642	0.0642	0.0642	
SPB6_HUMAN	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	ADFSGMSQTDLSLSK	1	2.5047	2.5047		2	1.8564	1.8584	1.7394	1.7394	1.7394	1.6747
		NLGMTDAFELGK	1	1.208	1.208								
SPB8_HUMAN	Serpin B8 OS=Homo sapiens GN=SERPINB8 PE=1 SV=2	LVLVNAIYFK	1	0.941	0.941		1	0.941	0.941	0.941	0.941	0.941	
SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1	AFQSLTEVNK	1	1.0079	1.0079		3	0.9259	0.9259	0.9229	0.9229	0.9229	1.1044
		LVLVNAIYFK	1	0.941	0.941								
		STEVEVLLPK	1	0.8287	0.8287								
SPI2_HUMAN	Serpin I2 OS=Homo sapiens GN=SERPINI2 PE=2 SV=1	LVLVNAIYFK	1	0.941	0.941		1	0.941	0.941	0.941	0.941	0.941	
SPON2_HUMAN	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=2	AFPPAPVLPSR	1	1.3778	1.3778		3	1.9636	2.7492	0.8261	1.2399	0.8682	7.2663
		GEAWALMK	2	0.0926	0.0915	1.2338							
		IVPSPDWFVGVDSLDLCDGDR	4	4.4205	2.3829	4.0791							
SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	DEDNNLLTEK	1	0.8292	0.8292		9	0.8612	0.9004	0.856	0.8936	0.8884	1.1225
		DIDKDLVI	2	0.811	0.8074	1.1428							
		FFETCDLDNDK	3	1.0055	1.0029	1.0918							
		FFETCDLDNDKYILDEWAGCFGIK	1	0.8925	0.8925								
		LEAGDHPVELLAR	1	0.7801	0.7801								
		LHLDYIGPCK	1	0.796	0.796								
		TFDSSCHFFATK	2	0.8148	0.8039	1.2614							
		YILDEWAGCFGIK	3	1.0595	1.0443	1.228							
		YIPPCLDSELTEFPLR	1	0.7624	0.7624								
SPSY_HUMAN	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	DVLILGGGDGGILCEIVK	1	0.7384	0.7384		1	0.7384	0.7384	0.7384	0.7384	0.7384	
SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	DLAALEDK	1	1.2102	1.2102		10	1.7653	2.2844	0.8997	1.1702	1.1382	4.2233
		DLTSWVTEMK	1	2.3995	2.3995								
		DTEQVDNWMSK	1	0.1677	0.1677								
		DVDEIEAWISEK	1	1.3511	1.3511								
		DVDETISWIK	1	1.3067	1.3067								
		LDENSAFLQFNWK	2	7.0819	5.9987	2.3107							
		LIQEQHPEEELIK	1	0.4914	0.4914								
		MNEVISLWK	1	0.919	0.919								
		QWELLLEK	2	2.6779	2.6779	1.0069							
		VNEVNQFAAK	1	0.0472	0.0472								
SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	ENEVLEAWK	1	0.8215	0.8215		6	1.18	1.0942	0.7992	0.7633	0.7233	2.3667
		MFSEADACLWIDEK	1	0.4053	0.4053								
		NDSFTTCIELGK	1	4.0153	4.0153								
		QAEAFLNNGEYVLAHTEMPTTLEGAEAAIK	1	0.8729	0.8729								
		TAASGIPYHSEVPVSLK	2	0.5795	0.48	2.4477							
		VDTVNHLADELINSGHSDAATIAEWK	1	0.3853	0.3853								
SRGN_HUMAN	Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=2	GPMFELLPGESNK	2	0.718	0.7159	1.1123	2	1.7855	1.7855	1.4312	1.4312	1.4273	2.6528
		TDLFPK	2	2.853	2.8455	1.1075							
SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	VTDDLVCLVYK	2	1.085	1.0832	1.0829	1	1.085	1.085	1.0849	1.0849	1.0832	
SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1	LLGMGDIEGLIDK	1	0.1824	0.1824		1	0.1824	0.1824	0.1824	0.1824	0.1824	
SRPX_HUMAN	Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1	DTADGILTDVILK	1	0.2591	0.2591		1	0.2591	0.2591	0.2591	0.2591	0.2591	
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	SEISQVFEALK	1	0.2994	0.2994		1	0.2994	0.2994	0.2994	0.2994	0.2994	
STC2_HUMAN	Stanniocalcin-2 OS=Homo sapiens GN=STC2 PE=1 SV=1	VIVEMIHFK	1	0.4765	0.4765		1	0.4765	0.4765	0.4765	0.4765	0.4765	
STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	ALSVGNIDDALQCYSEAIK	1	0.7184	0.7184		7	0.8737	0.9589	0.7104	0.7835	0.7834	2.1662
		DCEECIQLEPTFIK	1	0.8339	0.8339								
		DPQALSEHLK	1	0.1717	0.1717								
		ELDPTNMTYITNQAAVYFEK	2	1.5556	1.5549	1.0422							
		FMNPFNMPNLYQK	1	0.4107	0.4107								
		LAYINPDLALEEPK	1	0.9273	0.9273								
		LLEFQLALK	1	1.4981	1.4981								
STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	AIEENNNFSK	1	1.2713	1.2713		4	0.9242	0.9242	0.7671	0.7671	0.7671	2.1466
		DLSLEEIQK	1	0.6582	0.6582								
		ESVPEPPLSPPK	1	0.2778	0.2778								
		KLEAAEER	1	1.4893	1.4893								
STMN2_HUMAN	Stathmin-2 OS=Homo sapiens GN=STMN2 PE=1 SV=3	ALEENNNFSK	1	1.2713	1.2713		3	1.1396	1.1396	1.0761	1.0761	1.0761	1.5419
		DLSLEEIQK	1	0.6582	0.6582								
		KLEAAEER	1	1.4893	1.4893								
STMN4_HUMAN	Stathmin-4 OS=Homo sapiens GN=STMN4 PE=2 SV=1	KLEAAEER	1	1.4893	1.4893		1	1.4893	1.4893	1.4893	1.4893	1.4893	
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	YDYNSGEELESYK	1	0.7959	0.7959		1	0.7959	0.7959	0.7959	0.7959	0.7959	
STRBP_HUMAN	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	GWPLELICEK	1	0.2771	0.2771		1	0.2771	0.2771	0.2771	0.2771	0.2771	
SUMO2_HUMAN	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=1	TENNDHINLK	1	0.5544	0.5544		2	0.3401	0.2686	0.264	0.2062	0.2054	2.855
		VAGQDGSVVQFK	2	0.1258	0.125	1.1693							
SUMO3_HUMAN	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	VAGQDGSVVQFK	2	0.1258	0.125	1.1693	1	0.1258	0.1258	0.1258	0.1258	0.125	
SUMO4_HUMAN	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2	VAGQDGSVVQFK	1	0.1119	0.1119		1	0.1119	0.1119	0.1119	0.1119	0.1119	
SVEP1_HUMAN	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=2	AFCLACPFYGTTPFAGSR	1	2.4785	2.4785		2	1.7834	1.7834	1.6423	1.6423	1.6423	1.7897
		TTGPNVVYSCNR	1	1.0882	1.0882								
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=4	LGVENCYFPMFVSQSALEK	1	0.8606	0.8606		1	0.8606	0.8606	0.8606	0.8606	0.8606	
SYG_HUMAN	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=2	TFSSFWVAPFK	1	1.0934	1.0934		1	1.0934	1.0934	1.0934	1.0934	1.0934	
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	IFDSEEILAGYK	1	1.2602	1.2602		1	1.2602	1.2602	1.2602	1.2602	1.2602	
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	FLGDIEVWDQAEK	1	1.3397	1.3397		1	1.3397	1.3397	1.3397	1.3397	1.3397	
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	DIIACGFDINK	1	0.2802	0.2802		2	0.8353	0.8353	0.6242	0.6242	0.6242	3.1039
		DMNQVLDAYENIK	1	1.3904	1.3904								
TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	AAEDYGVIK	1	1.5204	1.5204		6	1.4327	1.4327	1.4306	1.4306	1.4306	1.0609
		DMAAVQR	1	1.3053	1.3053								
		GDPNWFMK	1	1.3986	1.3986								
		LVNSLYPDGSKPVK	1	1.523	1.523								
		TDMFQTVDLFEGK	1	1.3942	1.3942								
		TLMALGSLAVTK	1	1.4544	1.4544								
TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	DDGLFSGDPNWFPK	2	0.7381	0.7367	1.0925	7	1.7484	2.0674	1.3298	1.4821	1.3463	2.089
		DGTVLCELINALYPEGQAPVKK	2	0.7997	0.7942	1.1815							
		ENFQNWLK	2	2.55	2.5261	1.2147							
		IQASTMAFK	1	1.3211	1.3211								
		NFSDNQLQEGK	2	0.8349	0.8272	1.213							
		TLMNLGGLAVAR	4	5.1319	3.4759	3.3976							
		YGINTTDIFQTVDLWEGK	4	0.8631	0.8589	1.1214							
TAGL3_HUMAN	Transgelin-3 OS=Homo sapiens GN=TAGLN3 PE=1 SV=2	DMAAVQR	1	1.3053	1.3053		1	1.3053	1.3053	1.3053	1.3053	1.3053	
TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	AAQASDLEK	1	1.0789	1.0789		5	1.1716	1.1306	0.9797	0.9341	0.819	1.854
		ALAGCDFLTSPK	2	2.7576	2.7555	1.0565							
		LLGELLQDNAK	2	6.6041	0.3369	5.3666							
		LSSTWEGIQAGK	4	0.6954	0.6705	1.3543							
		WLHNEDQMAVEK	1	0.7222	0.7222								
TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	DVNAAIATIK	1	2.2331	2.2331		4	1.0312	1.0312	0.3922	0.3922	0.3922	10.5509
		EDMAALEK	1	1.0247	1.0247								
		TIGGGDDSFNTFFSETGAGK	1	0.8548	0.8548								
		TIQFVDWCPTGFK	1	0.0121	0.0121								
TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	LISQIVSSITASLR	1	0.6932	0.6932		4	3.4433	4.2306	1.8231	2.2202	2.0618	3.3607
		QLFHPEQLITGK	1	1.4699	1.4699								
		SIQFVDWCPTGFK	2	10.586	8.5962	2.5717							
		TIGGGDDSFNTFFSETGAGK	2	1.0242	1.0101	1.2662							
TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	DVNAAIATIK	1	2.2331	2.2331		6	1.0762	1.0688	0.5539	0.6048	0.6024	6.7826
		EDMAALEK	1	1.0247	1.0247								
		LISQIVSSITASLR	1	0.6932	0.6932								
		QLFHPEQLITGK	1	1.4699	1.4699								
		TIGGGDDSFNTFFSETGAGK	2	1.0242	1.0101	1.2662							
		TIQFVDWCPTGFK	1	0.0121	0.0121								
TBA3C_HUMAN	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3	DVNAAIATIK	1	2.2331	2.2331		4	1.1848	1.1527	0.4491	0.5296	0.5267	11.3624
		QLFHPEQLITGK	1	1.4699	1.4699								
		TIGGGDDSFNTFFSETGAGK	2	1.0242	1.0101	1.2662							
		TIQFVDWCPTGFK	1	0.0121	0.0121								
TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	EDMAALEK	1	1.0247	1.0247		2	5.8053	7.3989	3.2935	4.8606	4.2306	5.2132
		SIQFVDWCPTGFK	2	10.586	8.5962	2.5717							
TBA4B_HUMAN	Putative tubulin-like protein alpha-4B OS=Homo sapiens GN=TUBA4B PE=5 SV=2	LISQIVSSITASLR	1	0.6932	0.6932		2	1.0816	1.0816	1.0094	1.0094	1.0094	1.7015
		QIFHPEQLITGK	1	1.4699	1.4699								
TBA8_HUMAN	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	LISQIVSSITASLR	1	0.6932	0.6932		3	0.7251	0.7251	0.231	0.231	0.231	13.219
		QLFHPEQLITGK	1	1.4699	1.4699								
		TIQFVDWCPTGFK	1	0.0121	0.0121								
TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	EIVHIQAGQCGNQIGAK	1	2.5491	2.5491		3	1.8404	1.5913	1.7593	1.5185	1.4346	1.447
		MSATFIGNSTAIQELFK	3	1.2175	1.1076	1.6824							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	1.7546	1.7546								
TBB2C_HUMAN	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	EAESCDLQGFQLTHSLGGGTGSGMGTLLISK	2	0.7049	0.6881	1.3654	5	1.3039	1.2074	1.024	1.0205	0.9791	2.3271
		EIVHLQAGQCGNQIGAK	1	2.5491	2.5491								
		IMNTFSVVPSPK	1	0.2934	0.2934								
		MSATFIGNSTAIQELFK	3	1.2175	1.1076	1.6824							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	1.7546	1.7546								
TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	EIVHIQAGQCGNQIGAK	1	2.5491	2.5491		3	1.4343	1.4409	1.0299	1.1239	1.0856	3.0726
		IMNTFSVVPSPK	1	0.2934	0.2934								
		MSSTFIGNSTAIQELFK	2	1.4605	1.3628	1.7027							
TBB4_HUMAN	Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	0.7049	0.6881	1.3654	5	1.2067	1.1231	0.9249	0.8839	0.8769	2.3379
		EIVHLQAGQCGNQIGAK	1	2.5491	2.5491								
		IMNTFSVVPSPK	1	0.2934	0.2934								
		MAATFIGNSTAIQELFK	1	0.7316	0.7316								
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	1.7546	1.7546								
TBB4Q_HUMAN	Putative tubulin beta-4q chain OS=Homo sapiens GN=TUBB4Q PE=5 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	0.7049	0.6881	1.3654	1	0.7049	0.7049	0.7049	0.7049	0.6881	
TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	ALTVPELTQQVFDAK	1	1.2213	1.2213		7	1.3135	1.2054	1.0915	1.0237	1.0162	2.0525
		EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	0.7049	0.6881	1.3654							
		EIVHIQAGQCGNQIGAK	1	2.5491	2.5491								
		IMNTFSVVPSPK	1	0.2934	0.2934								
		ISVYYNEATGGK	1	1.7222	1.7222								
		MAVTFIGNSTAIQELFK	2	0.949	0.9403	1.2114							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	1.7546	1.7546								
TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	MASTFIGNSTAIQELFK	3	1.2175	1.1076	1.6824	1	1.2175	1.2175	1.2175	1.2175	1.1076	
TBB8_HUMAN	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	2	0.7049	0.6881	1.3654	1	0.7049	0.7049	0.7049	0.7049	0.6881	
TBB8B_HUMAN	Tubulin beta-8 chain B OS=Homo sapiens PE=1 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	0.7049	0.6881	1.3654	1	0.7049	0.7049	0.7049	0.7049	0.6881	
TBC8B_HUMAN	TBC1 domain family member 8B OS=Homo sapiens GN=TBC1D8B PE=2 SV=2	SVIISIK	1	0.6598	0.6598		1	0.6598	0.6598	0.6598	0.6598	0.6598	
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	DDNMFQIGK	1	7.0898	7.0898		2	3.8062	3.8062	1.9249	1.9249	1.9249	6.3208
		GISLNPEQWSQLK	1	0.5226	0.5226								
TCPA_HUMAN	T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1	ICDDELILIK	1	0.9865	0.9865		2	1.7218	1.9669	1.5569	1.8127	1.7338	1.9066
		SLLVIPNTLAVNAAQDSTDLVAK	2	2.4572	2.2986	1.686							
TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	DALSDLALHFLNK	1	0.4793	0.4793		2	0.2877	0.2877	0.2145	0.2145	0.2145	3.1174
		KLGGTIDDCELVEGLVLTQK	1	0.096	0.096								
TCPG_HUMAN	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	IVLLDSSLEYK	2	1.1656	1.1646	1.0604	1	1.1656	1.1656	1.1656	1.1656	1.1646	
TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	QQLLIGAYAK	1	1.5651	1.5651		1	1.5651	1.5651	1.5651	1.5651	1.5651	
TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	DMLEAGILDTYLGK	2	1.1646	1.1436	1.3099	2	1.0276	1.0733	1.0185	1.065	1.0522	1.2087
		LVPGGGATEIELAK	1	0.8907	0.8907								
TCTP_HUMAN	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	DLISHDEMFSDIYK	3	2.0669	1.2912	3.1752	3	1.629	1.8042	1.5518	1.7403	1.3123	1.4886
		EIADGLCLEVEGK	1	1.8349	1.8349								
		VKPFMTGAAEQIK	1	0.9853	0.9853								
TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1	LNWLSVDFNNWK	1	1.194	1.194		1	1.194	1.194	1.194	1.194	1.194	
TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	AIANECQANFISIK	1	2.0165	2.0165		9	1.1713	1.138	0.903	0.9334	0.9219	2.2117
		DVDLEFLAK	1	0.2778	0.2778								
		ETVVEVPQVTWEDIGGLEDVKR	1	0.4513	0.4513								
		GDDLSTAILK	1	1.1916	1.1916								
		IVSQLLTLMDGLK	1	1.2678	1.2678								
		LDQLIYRLPQDEK	1	2.9853	2.9853								
		NAPAIIFIDELDAIAPK	3	1.1213	1.0814	1.408							
		QAAPCVLFFDELDSIAK	2	0.8716	0.8542	1.3294							
		QLAQIK	1	0.3583	0.3583								
TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2	LDTLAQEVALLK	1	0.407	0.407		1	0.407	0.407	0.407	0.407	0.407	

TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	NEFGEIQGDK	1	0.015	0.015		2	0.7253	0.7253	0.1467	0.1467	0.1467	25.1603
		YLLNLNLEPFSEK	1	1.4355	1.4355								
THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	TAFQEALDAAGDK	2	1.3472	1.3416	1.1382	1	1.3472	1.3472	1.3472	1.3472	1.3416	
THIOM_HUMAN	Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2	VVNSETPVVVDFHAQWCGPCK	1	0.1509	0.1509		1	0.1509	0.1509	0.1509	0.1509	0.1509	
TICN1_HUMAN	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	DSLGWMFNK	2	0.9791	0.8468	2.1827	5	0.6971	0.6535	0.5481	0.4885	0.4294	2.4746
		FDTSILPICK	2	0.1539	0.1208	2.7831							
		LSNNEWCYCFQKPGGLPCQNEMNR	1	0.534	0.534								
		SLATLCDGPCPCLPEPEPPK	0										
		VCVTGDYQTALCVSR	1	1.1213	1.1213								
TICN3_HUMAN	Testican-3 OS=Homo sapiens GN=SPOCK3 PE=1 SV=2	DSLGWMFNR	1	0.2137	0.2137		2	0.1838	0.1738	0.1814	0.1717	0.1461	1.2613
		FDTSILPICK	2	0.1539	0.1208	2.7831							
TIMP1_HUMAN	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	EPGLCTWQSLR	2	5.7338	1.9808	11.4638	8	27.7092	20.2285	3.1139	3.0384	1.3696	12.7879
		FVYTPAMESVCGYYFHR	3	17.6098	1.548	21.6134							
		GFQALGDAADIR	5	44.9867	8.9448	18.148							
		HLACLPR	1	0.2926	0.2926								
		LQDGLLHITTCSFVAPWNSLSLAQR	1	151.9924	151.9924								
		LQSGTHCLWTDQLLQGSEK	3	0.3766	0.3751	1.1163							
		SEEFLIAGK	4	0.3366	0.3365	1.0327							
		TVTVCGEECTVFPCLSIPCK	3	0.3453	0.3429	1.1553							
TIMP2_HUMAN	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	DIEFIYVPSAVCGVSLDVGGK	1	0.4504	0.4504		5	0.4237	0.4179	0.4201	0.4144	0.4109	1.158
		EVDSGNDIYGNPIK	1	0.3909	0.3909								
		EVDSGNDIYGNPIKR	5	0.4246	0.4214	1.1455							
		EYLIAGK	2	0.5085	0.4963	1.3664							
		SDGSCAWYR	3	0.3444	0.3426	1.1313							
TKT_HUMAN	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	AVELAANTK	1	8.0633	8.0633		7	2.8418	2.6639	1.8918	1.825	1.6102	2.7264
		IIALDGDTK	1	0.7455	0.7455								
		LGQSDPAPLQHQMDIYQK	1	0.5955	0.5955								
		NMAEQIIQEIYSQIQSK	2	0.7853	0.7832	1.1082							
		NSTFSEIFK	1	2.2529	2.2529								
		QAFTDVATGSLGGGLGAACGMAYTGK	1	4.153	4.153								
		TSRPENAIIYNNNEDFQVGQAK	2	3.2973	1.8822	5.1582							
TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	AQEACGPLEMDSALSVQNLEK	1	0.7226	0.7226		10	2.0717	1.8854	1.2597	1.1088	1.0789	2.5176
		EADESLNFEEQILEAAK	1	0.9782	0.9782								
		GVGAAATAVTQALNELLQHVK	1	1.0637	1.0637								
		ILAQATSDLVNAIK	1	0.7197	0.7197								
		SIAATSALVK	3	0.3508	0.3496	1.1077							
		TEDSGLQTQVMAATQCALSTSQLVACTK	1	1.5301	1.5301								
		TLAESALQLLYTAK	1	10.1168	10.1168								
		TYGVSFFLVK	1	0.8673	0.8673								
		VAGSVTELQAAEAMK	2	3.0916	2.6026	2.3488							
		VSQMAGYFEPLTLAAVGAASK	1	1.2767	1.2767								
TLN2_HUMAN	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	SIAATSALVK	3	0.3508	0.3496	1.1077	2	0.6091	0.48	0.5516	0.4399	0.4388	1.8964
		TYGVSFFLVK	1	0.8673	0.8673								
TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2	VEEEIQTLSQVLAAK	1	6.662	6.662		1	6.662	6.662	6.662	6.662	6.662	
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	EAGITEK	1	1.5111	1.5111		10	1.3486	1.3346	1.2175	1.2129	1.1316	1.5787
		ELASQPDVDGFLVGGASLKPEFVDIINAK	2	1.2006	1.1962	1.1289							
		HVFGESDELIGQK	1	2.8287	2.8287								
		IAVAAQNCYK	1	0.962	0.962								
		IIYGGSVTGATCK	1	0.8147	0.8147								
		QSLGELIGTLNAAK	3	1.3982	1.3612	1.3234							
		TATPQQAQEVHEK	3	2.3118	1.6122	2.7274							
		VTNGAFTGEISPGMIK	3	0.7965	0.7623	1.4447							
		VVFEQTK	1	0.833	0.833								
		VVLAYEPVWAIGTGK	3	0.8294	0.8246	1.1445							
TPISL_HUMAN	Putative triosephosphate isomerase-like protein LOC286016 OS=Homo sapiens PE=1 SV=2	EAGITEK	1	1.5111	1.5111		2	1.1721	1.1721	1.1219	1.1219	1.1219	1.5237
		VVFEQTK	1	0.833	0.833								
TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	IQLVEEELDR	1	1.9976	1.9976		3	1.2341	1.1659	1.1259	1.0823	1.0719	1.6702
		LATALQK	1	0.7433	0.7433								
		MEIQEIQLK	2	0.9613	0.9429	1.3211							
TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	IQLVEEELDR	1	1.9976	1.9976		3	1.2316	1.2316	1.123	1.123	1.123	1.6722
		LATALQK	1	0.7433	0.7433								
		MELQEMQLK	1	0.9539	0.9539								
TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	IQLVEEELDR	1	1.9976	1.9976		3	1.2341	1.1659	1.1259	1.0823	1.0719	1.6702
		LATALQK	1	0.7433	0.7433								
		MELQEIQLK	2	0.9613	0.9429	1.3211							
TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like protein OS=Homo sapiens PE=5 SV=2	MELQEIQLK	2	0.9613	0.9429	1.3211	1	0.9613	0.9613	0.9613	0.9613	0.9429	
TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	AEVSELK	2	12.3155	4.0015	12.5687	8	2.6867	3.7565	0.9665	1.2823	0.9988	8.1482
		EENVGLHQTLDQTLNELNCI	1	1.4061	1.4061								
		EKAEGDVAALNR	1	1.3366	1.3366								
		IQLVEEELDR	1	1.9976	1.9976								
		KIQALQGQADEAEDR	1	2.7317	2.7317								
		LATALQK	1	0.7433	0.7433								
		MEIQEMQLK	1	0.9539	0.9539								
		TIDDLEEK	1	0.0085	0.0085								
TPT1L_HUMAN	TPT1-like protein OS=Homo sapiens PE=1 SV=1	VKPFMTGAAEQIK	1	0.9853	0.9853		1	0.9853	0.9853	0.9853	0.9853	0.9853	
TR150_HUMAN	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	GSFSDTGLGDGK	1	1.2942	1.2942		1	1.2942	1.2942	1.2942	1.2942	1.2942	
TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=2	GDVAFVK	2	0.667	0.6666	1.0524	1	0.667	0.667	0.667	0.667	0.6666	
TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	CGLVPVLAENYK	1	0.7424	0.7424		1	0.7424	0.7424	0.7424	0.7424	0.7424	
TRI14_HUMAN		LLLDEEEALAK	1	1.1795	1.1795		1	1.1795	1.1795	1.1795	1.1795	1.1795	
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	SYDYDLIIIGGGSGGLAAAK	1	1.1467	1.1467		1	1.1467	1.1467	1.1467	1.1467	1.1467	
TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	AGTLDLSLTVQGK	3	2.0113	1.9343	1.408	24	1.4387	1.2978	1.1672	1.1156	1.0923	1.8567
		AQGYSGLSVK	2	1.1704	1.1653	1.142							
		AQLYIDCEK	2	1.2974	1.29	1.163							
		CTSYPDGSWK	2	1.0733	1.0712	1.0912							
		DCVGDVTENQICNK	2	0.7622	0.7289	1.5305							
		DHSGQVFSVVSNGK	1	1.3335	1.3335								
		FQMIPLDPK	1	1.2257	1.2257								
		FTGSQPFGQGVEHATANK	5	1.1715	1.1555	1.2075							
		GDACKDDFDHDSVPDIDDICPENVDISETDFR	1	5.9464	5.9464								
		GTLLALER	1	1.0348	1.0348								
		GTSQNDPNWVVR	2	1.8339	1.8181	1.2047							
		IEDANLIPPVPDGKFQDLVDAVR	1	1.4173	1.4173								
		IMADSGPIYDK	3	0.8488	0.7987	1.5664							
		KDHSGQVFSVVSNGK	1	0.7851	0.7851								
		LCNNPTPGFGGK	5	0.8553	0.7893	1.6121							
		LCNSPSPQMNGKPCEGEAR	1	0.621	0.621								
		MENAELDVPIQSVFTR	1	4.099	4.099								
		NPCTDGTHDCNK	1	1.1991	1.1991								
		QVTQSYWDTNPTR	1	1.5979	1.5979								
		SITLFVQEDR	1	1.2401	1.2401								
		TIVTTLQDSIR	2	1.5244	1.5121	1.1973							
		TKDLQAICGISCDELSSMVLELR	1	0.6468	0.6468								
		VTEENKELANELR	3	0.5434	0.5415	1.1082							
		VVMYEGKK	1	0.2894	0.2894								
TXD15_HUMAN		TLETLK	1	0.9084	0.9084		1	0.9084	0.9084	0.9084	0.9084	0.9084	
TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	ALAPTWEQLALGLEHSETVK	2	1.0179	1.0155	1.1031	3	2.1168	2.2574	1.78	1.8639	1.8453	2.0195
		EFPGLAGVK	2	3.9186	3.8304	1.3537							
		TLAPTWEELSK	1	1.414	1.414								
TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	SEPTQALELTEDDIKEDGGIVPLR	1	0.7213	0.7213		1	0.7213	0.7213	0.7213	0.7213	0.7213	
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	ELLTSFGPLK	1	0.1502	0.1502		2	0.4621	0.4621	0.3409	0.3409	0.3409	3.1876
		LFIGGLPNYLNDDQVK	1	0.7739	0.7739								
UAP56_HUMAN	Spliceosome RNA helicase BAT1 OS=Homo sapiens GN=BAT1 PE=1 SV=1	GLAITFVSDENDAK	1	0.8201	0.8201		1	0.8201	0.8201	0.8201	0.8201	0.8201	
UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	GQVCLPVISAENWKPATK	1	4.5214	4.5214		2	2.7069	2.7069	2.0087	2.0087	2.0087	3.15
		IEINFPAEYPFKPPK	1	0.8924	0.8924								
UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1	NPDGTMNLMNWECAIPGK	1	1.2092	1.2092		2	0.7345	0.7345	0.5605	0.5605	0.5605	2.9665
		NPDGTMNLMNWECAIPGKK	1	0.2598	0.2598								
UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	LELFLPEEYPMAAPK	1	0.9167	0.9167		1	0.9167	0.9167	0.9167	0.9167	0.9167	
UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	LGFEDGSVLK	1	0.679	0.679		5	1.0664	1.0664	1.0047	1.0047	1.0047	1.4824
		MPFPVNHGASSEDTLLK	1	0.6513	0.6513								
		MQLKPMEINPEMLNK	1	1.4934	1.4934								
		QFLSETEK	1	1.1027	1.1027								
		QTIGNSCGTIGLIHAVANNQDK	1	1.4054	1.4054								
UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	TLDGGLNVQLETAVGAAIK	1	0.6146	0.6146		2	0.9273	0.9273	0.873	0.873	0.873	1.6426
		TYNTDVPLVLMNSFNTDEDTKK	1	1.2399	1.2399								
ULK4_HUMAN	Serine/threonine-protein kinase ULK4 OS=Homo sapiens GN=ULK4 PE=2 SV=2	EQKLLLR	1	2.3741	2.3741		1	2.3741	2.3741	2.3741	2.3741	2.3741	
UVRAG_HUMAN		ALGREVALLHK	1	0.0752	0.0752		1	0.0752	0.0752	0.0752	0.0752	0.0752	
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1	LAGLGLQQLDEGLFSR	1	2.3435	2.3435		1	2.3435	2.3435	2.3435	2.3435	2.3435	
VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	DNLAEDIMR	3	1.1219	1.1161	1.1348	23	1.2813	1.3635	1.2335	1.3195	1.2823	1.3213
		EEAENTLQSFR	1	1.3216	1.3216								
		EKLQEEMLQR	3	2.7174	1.9639	2.5982							
		EYQDLLNVK	4	1.4457	1.4104	1.2911							
		FADLSEAANR	2	1.4546	1.4518	1.0925							
		FANYIDK	4	1.3691	1.3579	1.1588							
		FLEQQNK	3	1.1935	1.19	1.0966							
		GTNESLER	3	1.3755	1.3535	1.2459							
		ILLAELEQLK	5	1.1701	1.1536	1.2139							
		ILLAELEQLKQQK	1	1.0508	1.0508								
		ISLPLPNFSSLNLR	1	1.0261	1.0261								
		KLLEGEESR	1	1.2487	1.2487								
		KVESLQEEIAFLK	3	1.6135	1.5665	1.3377							
		LLEGEESR	2	1.4361	1.4267	1.1758							
		LQDEIQNMK	4	1.2667	1.2617	1.1101							
		LQEEMLQR	1	0.8445	0.8445								
		MALDIEIATYR	1	1.3447	1.3447								
		QDVDNASLAR	1	1.0338	1.0338								
		QQYESVAAK	2	1.2952	1.2952	1.0012							
		QVDQLTNDK	3	1.4579	1.4172	1.3337							
		RQVDQLTNDK	1	0.59	0.59								
		TNEKVELQELNDR	1	0.9394	0.9394								
		VELQELNDR	1	1.1529	1.1529								
VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	AAVHLEGK	1	1.0533	1.0533		5	1.043	1.043	0.9916	0.9916	0.9916	1.426
		AVAGNISDPGLQK	1	1.6338	1.6338								
		ELLPVLISAMK	1	0.6138	0.6138								
		SLGEISALTSK	1	0.8679	0.8679								
		TNISDEESEQATEMLVHNAQNLMQSVK	1	1.046	1.046								
VTA1_HUMAN	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	QLGDNEAITQEIVQCAHLENYALK	1	0.674	0.674		1	0.674	0.674	0.674	0.674	0.674	
VWF_HUMAN	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=2	GLRPSCPNSQSPVK	1	0.5936	0.5936		7	2.3569	2.3569	1.574	1.574	1.574	2.479
		GLWEQCQLLK	1	0.615	0.615								
		IEDLPTMVTLGNSFLHK	1	8.3285	8.3285								
		ILTSDVFQDCNK	1	1.4843	1.4843								
		LSEAEFEVLK	1	2.2316	2.2316								
		NSQWICSNEECPGECLVTGQSHFK	1	1.1156	1.1156								
		VEDFGNAWK	1	2.13	2.13								
WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	DYSQQGVVK	1	2.0936	2.0936		5	0.9933	0.977	0.8674	0.872	0.8661	1.7421
		FATASADGQIIYIYDGK	1	0.8738	0.8738								
		LYSILGTTLKDEGK	1	0.6216	0.6216								
		YAPSGFYIASGDVSGK	1	0.4825	0.4825								
		YEYQPFAGK	2	0.8952	0.877	1.3323							
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	SVGDGETVEFDVVEGEK	1	0.6601	0.6601		1	0.6601	0.6601	0.6601	0.6601	0.6601	
		SVGDGETVEFDVVEGEK	1	0.6601	0.6601								
		MLLSQNSK	1	0.0153	0.0153								

HUVEC:HA Fibroblasts

Accession	Description	Sequence	# Indiv oeos	Pep SM ratio	Pep GM ratio	Pep ratio SDoeo	# pep soecies	Prot SM of pep SMs	Prot weighted SM of pep SMs	Prot GM of pep SMs	Prot weighted GM of pep SMs	Prot GM of pep GMs	Prot weighted GM of pep GMs	Protein SDoeo
1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	DSTLIMQLLR	2	10.8265	1.8463	32.1785	7	9.7346	8.2734	4.8383	4.1651		2.8088	3.6888
		IEAELQDICNDVLELLDK	1	7.4579	7.4579									
		NLLSVAYK	1	38.7517	38.7517									
		QTTVSNSQQAYQEAFEISK	2	2.9807	2.9551	1.2045								
		TAFDEAIAELDTLNEESYK	1	1.4367	1.4367									
		YDDMAAAMK	2	0.7846	0.6471	2.4745								
		YLSEVASGDNK	1	5.9044	5.9044									
1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	AAFDDAIAELDTLSEESYK	3	3.9631	2.3689	3.7607	7	13.3845	10.3759	9.8133	7.8691		4.2515	2.3282
		DSTLIMQLLR	2	10.8265	1.8463	32.1785								
		EAAENSLVAYK	2	8.3089	6.8848	2.4463								
		HLIPAANTGESK	1	17.7078	17.7078									
		LICCDILDVLDK	2	10.8237	10.7267	1.2093								
		NLLSVAYK	1	38.7517	38.7517									
		QMVETELK	2	3.31	0.935	15.471								
1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	DSTLIMQLLR	2	10.8265	1.8463	32.1785	6	10.8038	9.5558	6.183	6.2151		4.1662	2.9809
		ELETVCNDVLSLLDK	2	7.1571	6.9699	1.3869								
		NLLSVAYK	1	38.7517	38.7517									
		NSVVEASEAAYK	2	3.196	3.1813	1.1456								
		QAFDDAIAELDTLNEDSYK	1	2.8455	2.8455									
		YLAEVASGEK	1	2.046	2.046									
1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	DSTLIMQLLR	1	21.4943	21.4943		4	6.7681	4.1776	2.6886	1.7734		1.6213	4.8933
		TAFDDAIAELDTLNEDSYK	3	0.7701	0.6949	1.8158								
		YDDMAAAMK	2	0.7846	0.6471	2.4745								
		YLAEVATGEK	2	4.0235	3.9757	1.245								
1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	DSTLIMQLLR	2	10.8265	1.8463	32.1785	2	24.7891	20.1349	20.4828	16.561		5.0929	2.4638
		NLLSVAYK	1	38.7517	38.7517									
1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	DSTLIMQLLR	2	10.8265	1.8463	32.1785	7	12.0644	10.747	8.7114	8.1259		5.0568	2.2662
		NLLSVAYK	1	38.7517	38.7517									
		QTIDNSQGAYQEAFDISK	1	5.325	5.325									
		SICTTVLELLDK	2	8.6872	8.5271	1.3147								
		TAFDEAIAELDTLNEDSYK	2	3.5057	1.9545	5.371								
		YDDMATCMK	1	13.0748	13.0748									
		YLIANATNPESK	1	4.2798	4.2798									
1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	DICNDVLSLLEK	5	15.7164	15.5327	1.1911	10	10.0539	9.9303	5.4958	7.2544		5.9698	3.9142
		DSTLIMQLLR	2	10.8265	1.8463	32.1785								
		EKIETELR	1	0.9004	0.9004									
		FLIPNASQAESK	1	5.672	5.672									
		GIVDQSQQAYQEAFEISK	2	10.6094	10.2378	1.4621								
		NLLSVAYK	1	38.7517	38.7517									
		TAFDEAIAELDTLSEESYK	6	4.4604	5.7494	1.7168								
		VVSSIEQK	2	6.1677	6.1458	1.1267								
		YDDMAACMK	2	5.0875	4.8192	1.5996								
		YLAEVAAGDDK	1	0.3471	0.3471									
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	QLSQSLLPAIVELAEDAK	2	4.7258	4.6178	1.3569	1	4.7258	4.7258	4.7258	4.7258		4.6178	
2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	QLSQSLLPAIVELAEDAK	2	4.7258	4.6178	1.3569	1	4.7258	4.7258	4.7258	4.7258		4.6178	
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	ACGAVDDFIEK	1	5.2635	5.2635		3	4.2007	4.9007	2.3389	3.0764		3.0696	5.2408
		NPELQNLLLDDFFK	2	7.0007	6.9696	1.1427								
		VGTGEPCCDWVGDEGAGHFVK	1	0.3479	0.3479									
AATM_HUMAN	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=2	ASAELALGENSEVLK	1	3.0215	3.0215		4	2.3095	2.5	1.8352	2.1316		2.0525	2.5418
		EFSIYMTK	1	0.454	0.454									
		NLDKEYLPIGGLAEFCK	2	2.7024	2.4254	1.9535								
		TCGFDFTGAVEDISK	2	3.06	3.0437	1.1571								
ACBP_HUMAN	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2	QATVGDINTERPGMLDFTGK	1	2.5013	2.5013		1	2.5013	2.5013	2.5013	2.5013		2.5013	
ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	YQQAGLPLIVLAGK	1	8.0023	8.0023		1	8.0023	8.0023	8.0023	8.0023		8.0023	
ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	AGFAGDDAPR	2	13.0826	13.0767	1.0435	6	10.7085	10.6121	10.1153	10.1138		9.5525	1.4828
		DLTDYLMK	4	11.8814	11.2814	1.461								
		DSYVGDEAQSK	2	13.6029	13.2836	1.3627								
		EITALAPSTMK	4	7.6095	6.6485	1.7972								
		GILTLK	3	12.9222	12.6262	1.3117								
		LCYVALDFENEMATAASSSSLEK	2	5.1523	4.8875	1.5895								
ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	AGFAGDDAPR	3	13.8928	13.843	1.1086	12	8.8485	9.9449	5.8887	8.4072		7.658	4.626
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691								
		DLTDYLMK	5	11.5915	11.1061	1.3912								
		DSYVGDEAQSK	5	9.5721	8.0612	1.9461								
		GILTLK	5	14.6377	14.2916	1.292								
		GYSFTTTAER	4	10.9043	10.7225	1.2461								
		HQGVMVGMGQK	1	0.0523	0.0523									
		IIAPPERK	1	5.1687	5.1687									
		LCYVALDFEQEMATAASSSSLEK	2	5.9483	5.9259	1.1243								
		QEYDESGPSIVHR	2	6.5412	6.506	1.1582								
		VAPEEHPVLLTEAPLNPK	5	5.9046	4.2011	3.0895								
ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	DLTDYLMK	5	11.5915	11.1061	1.3912	4	6.2361	8.8269	2.2467	5.3744		5.2228	12.535
		HQGVMVGMGQK	1	0.0523	0.0523									
		IIAPPERK	1	5.1687	5.1687									
		VAPDEHPILLTEAPLNPK	2	8.1319	7.9567	1.3448								
ACTBM_HUMAN	Beta-actin-like protein 3 OS=Homo sapiens GN=ACTBL3 PE=1 SV=1	QEYDESGPSIVHR	2	6.5412	6.506	1.1582	1	6.5412	6.5412	6.5412	6.5412		6.506	
ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	AGFAGDDAPR	1	15.5131	15.5131		8	9.8654	10.8962	5.2647	6.7426		6.4866	6.8279
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691								
		DLTDYLMK	1	10.432	10.432									
		EITALAPSTMK	1	17.4225	17.4225									
		GILTLK	3	16.2835	16.2282	1.1074								
		HQGVMVGMGQK	1	0.0523	0.0523									
		IIAPPERK	1	5.1687	5.1687									
		LCYVALDFENEMATAASSSSLEK	1	5.6826	5.6826									
ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	AGFAGDDAPR	3	13.8928	13.843	1.1086	12	8.8485	9.9449	5.8887	8.4072		7.658	4.626
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691								
		DLTDYLMK	5	11.5915	11.1061	1.3912								
		DSYVGDEAQSK	2	13.6029	13.2836	1.3627								
		EITALAPSTMK	5	9.5721	8.0612	1.9461								
		GILTLK	5	14.6377	14.2916	1.292								
		GYSFTTTAER	4	10.9043	10.7225	1.2461								
		HQGVMVGMGQK	1	0.0523	0.0523									
		IIAPPERK	1	5.1687	5.1687									
		LCYVALDFEQEMATAASSSSLEK	2	5.9483	5.9259	1.1243								
		QEYDESGPSIVHR	2	6.5412	6.506	1.1582								
		VAPEEHPVLLTEAPLNPK	5	5.9046	4.2011	3.0895								
ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	AGFAGDDAPR	1	12.6892	12.6892		5	9.4329	8.7194	8.702	7.9741		7.8351	1.5655
		DLTDYLMK	1	6.9321	6.9321									
		EITALAPSTMK	1	7.2926	7.2926									
		GILTLK	1	15.0981	15.0981									
		LCYVALDFENEMATAASSSSLEK	2	5.1523	4.8875	1.5895								
ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	5.2805	3.7257	3.4932	15	6.5878	6.6938	5.994	6.1037		5.8178	1.5974
		ASHEAWTDGK	1	6.1789	6.1789									
		CQLEINFNTLQTK	1	7.4101	7.4101									
		DLLLDPAWEK	3	10.4895	10.4555	1.1042								
		FAIQDISVEETSAK	3	6.6055	6.5606	1.1521								
		GYEEWLLNEIR	1	11.0595	11.0595									
		ICDQWDNLGALTQK	2	4.2197	4.1185	1.3671								
		IDLEGDHQLIQEALIFDNK	1	4.1769	4.1769									
		IVQTYHVNMAGTNPYTTITPQEINGK	1	2.5997	2.5997									
		LAILGIHNEVSK	1	6.6636	6.6636									
		LLETDQLYLEYAK	2	9.6091	9.5695	1.1372								
		QKDYETATLSEIK	2	2.4794	2.2548	1.8702								
		TINEVENQILTR	1	5.3191	5.3191									
		VGWEQLLTTIAR	1	10.6699	10.6699									
		VLAVNQENEQLMEDYEK	2	6.0556	5.5426	1.8292								
ACTN2_HUMAN	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	CQLEINFNTLQTK	1	7.4101	7.4101		5	7.1487	7.7704	3.9945	5.5358		5.5173	5.7519
		DLLLDPAWEK	3	10.4895	10.4555	1.1042								
		FAIQDISVEETSAK	3	6.6055	6.5606	1.1521								
		GYEEWLLNEIR	1	11.0595	11.0595									
		LEQAEKGYEEWLLNEIR	1	0.1791	0.1791									
ACTN3_HUMAN	Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	CQLEINFNTLQTK	1	7.4101	7.4101		3	8.1684	8.385	8.0075	8.1868		8.1516	1.2723
		DLLLDPAWEK	3	10.4895	10.4555	1.1042								
		FAIQDISVEETSAK	3	6.6055	6.5606	1.1521								
ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	5.2805	3.7257	3.4932	14	5.8821	6.222	4.946	5.3346		4.9752	1.9659
		ASHEAWTDGK	1	6.1789	6.1789									
		CQLEINFNTLQTK	1	7.4101	7.4101									
		DLLLDPAWEK	3	10.4895	10.4555	1.1042								
		EAILAHHK	2	2.6206	1.8774	3.3879								
		ETTDTDTADQVIASFK	1	4.4245	4.4245									
		FAIQDISVEETSAK	3	6.6055	6.5606	1.1521								
		GYEEWLLNEIR	1	11.0595	11.0595									
		ISIEMNGTLEDQLSHLK	1	0.9425	0.9425									
		KDDPVTNLNNAFEVAEK	1	3.6112	3.6112									
		LSGSNPYTTVTPQIINSK	1	5.3952	5.3952									
		QFASQANVVGPWIQTK	1	2.3418	2.3418									
		TINEVENQILTR	1	5.3191	5.3191									
		VGWEQLLTTIAR	1	10.6699	10.6699									
ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	AGFAGDDAPR	3	13.8928	13.843	1.1086	9	9.135	10.5865	5.3678	8.5812		8.0352	5.9302
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691								
		DLTDYLMK	5	11.5915	11.1061	1.3912								
		DSYVGDEAQSK	2	13.6029	13.2836	1.3627								
		EITALAPSTMK	5	9.5721	8.0612	1.9461								
		GILTLK	5	14.6377	14.2916	1.292								
		HQGVMVGMGQK	1	0.0523	0.0523									
		IIAPPERK	1	5.1687	5.1687									
		LCYVALDFENEMATAASSSSLEK	3	5.329	5.1393	1.4036								
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1	DLLPEDFVVVTYNK	1	0.5116	0.5116		2	0.3736	0.3736	0.3472	0.3472		0.3472	1.7303
		QVSYVQAEGK	1	0.2356	0.2356									
ADK_HUMAN	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2	ELFDELVK	1	0.5023	0.5023		1	0.5023	0.5023	0.5023	0.5023		0.5023	
AEBP1_HUMAN	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1	GEDEDEVSEAQETPDHAIFR	1	0.4089	0.4089		2	0.4672	0.4672	0.4635	0.4635		0.4635	1.1939
		YLSPDATVSTEVR	1	0.5254	0.5254									
AGRIN_HUMAN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4	SIESTLDDLFR	1	0.655	0.655		1	0.655	0.655	0.655	0.655		0.655	
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	ADIDVSGPK	1	0.1183	0.1183		6	1.542	1.5935	1.1396	1.2261		1.2243	3.0861
		AEGPEVDVNLPK	1	2.3554	2.3554									
		ISMPDIDLNLK	2	1.9022	1.8922	1.156								
		ISMPDVDLHLK	1	1.6037	1.6037									
		VDINAPDVDVQGPDWHLK	1	1.9542	1.9542									
		VDVSAPDVEAHGPEWNLK	1	1.3185	1.3185									
AIBP_HUMAN	Apolipoprotein A-I-binding protein OS=Homo sapiens GN=APOA1BP PE=1 SV=2	GNAGGIQPDLLISLTAPK	1	6.4323	6.4323		1	6.4323	6.4323	6.4323	6.4323		6.4323	
AIMP1_HUMAN	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	GAEADQIIEYLK	1	2.1055	2.1055		1	2.1055	2.1055	2.1055	2.1055		2.1055	
AINX_HUMAN	Alpha-internexin OS=Homo sapiens GN=INA PE=1 SV=2	EYQDLLNVK	4	12.6181	12.3633	1.264	1	12.6181	12.6181	12.6181	12.6181		12.3633	
AK1A1_HUMAN	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	VFDTTFSPEEMK	2	6.8854	6.7184	1.3698	1	6.8854	6.8854	6.8854	6.8854		6.7184	
AKAP2_HUMAN	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=3	VELPSEEQVSGSQGPSEEKPAPLATEVFDEK	2	7.5513	4.9875	3.9696	1	7.5513	7.5513	7.5513	7.5513		4.9875	
AL1A1_HUMAN	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	1	0.9228	0.9228		6	5.5518	6.224	2.3126	2.861		2.8015	5.5333
		IFINNEWHDSVSGK	1	0.6042	0.6042									

		LYSNAYLNDLAGCIK	2	10.2573	9.5292	1.7322							
		SLDDVIK	1	9.2423	9.2423								
		VAFTGSTEVGK	1	0.2403	0.2403								
		YILGNPLTPGVTQGPQIDKEQYDK	1	12.044	12.044								
ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	KVPQVSTPTLVEVSR	3	0.7796	0.7788	1.0595	2	0.7169	0.7079	0.7141	0.7052	0.7045	1.1321
		LVTDLTK	4	0.6542	0.6534	1.0584							
ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	AAQEEYVK	1	7.5227	7.5227		8	5.3322	5.2095	5.1125	5.0205	4.8535	1.3738
		ADDGRPFPQVIK	1	3.0942	3.0942								
		ALANSLACQGIK	3	5.0352	4.9038	1.3365							
		GGVVGIK	1	4.3213	4.3213								
		GILAADESTGSIAK	3	6.5149	6.1111	1.5651							
		VLAAVYK	1	5.9101	5.9101								
		VNPCIGGVILFHETLYQK	1	6.6714	6.6714								
		YASICQQNGIVPIVEPEILPDGDHDLK	3	3.5875	3.3534	1.5487							
ALDOB_HUMAN	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2	VLAAVYK	1	5.9101	5.9101		1	5.9101	5.9101	5.9101	5.9101	5.9101	
ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	VLAAVYK	1	5.9101	5.9101		2	4.7488	4.1681	4.6046	4.0643	3.8638	1.4233
		YASICQQNGIVPIVEPEILPDGDHDLK	3	3.5875	3.3534	1.5487							
AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	GLVLGIYSK	1	0.2917	0.2917		1	0.2917	0.2917	0.2917	0.2917	0.2917	
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	IKDLSTIEPLK	1	2.7125	2.7125		3	2.6197	2.6197	1.9539	1.9539	1.9539	2.8481
		SLDLFNCEVTNLNDYR	1	0.6056	0.6056								
		VSGGLEVLAEK	1	4.5411	4.5411								
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	IFGGLDMLAEK	1	8.3987	8.3987		2	5.5556	5.5556	4.773	4.773	4.773	2.2237
		LKDISTLEPLK	1	2.7125	2.7125								
AN32C_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Homo sapiens GN=ANP32C PE=2 SV=1	IKDLSTIEPLK	1	2.7125	2.7125		2	3.6268	3.6268	3.5097	3.5097	3.5097	1.4396
		VSGGLEVLAEK	1	4.5411	4.5411								
AN32D_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member D OS=Homo sapiens GN=ANP32D PE=1 SV=2	IKDLSTIEPLK	1	2.7125	2.7125		1	2.7125	2.7125	2.7125	2.7125	2.7125	
ANM1_HUMAN	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	IVKANK	1	145.7659	145.7659		3	50.8405	50.6405	10.834	10.834	10.834	9.6749
		VEDLTFTSPFCLQVK	1	2.2124	2.2124								
		VVLDVGSGTGILCMFAAK	1	3.9432	3.9432								
ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	GLGTDEDTLIEILASR	1	4.661	4.661		2	4.9482	4.9482	4.9398	4.9398	4.9398	1.0856
		GVDEATIDILTK	1	5.2353	5.2353								
ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	DALNIETAIK	1	4.3042	4.3042		2	4.3547	4.3547	4.3544	4.3544	4.3544	1.0165
		SALSGHLETVILGLLK	1	4.4052	4.4052								
ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	ETSGNLEQLLLAVVK	3	3.7544	3.6908	1.2611	2	3.2157	3.4851	3.1703	3.45	3.4061	1.2702
		LVDAYELK	1	2.677	2.677								
AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	TSVQFQNFSPTVVHPGDLQTQLAVQTK	1	2.1657	2.1657		1	2.1657	2.1657	2.1657	2.1657	2.1657	
API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=2	DAYQVILDGVK	1	3.9013	3.9013		1	3.9013	3.9013	3.9013	3.9013	3.9013	
APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	EQLGPVTQEFWDNLEK	2	1.3862	1.3732	1.2148	1	1.3862	1.3862	1.3862	1.3862	1.3732	
ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	DAVLLVFANK	1	5.1745	5.1745		1	5.1745	5.1745	5.1745	5.1745	5.1745	
ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	DAVLLVFANK	2	11.2682	9.5131	2.3311	2	7.4758	8.7399	6.4425	7.7623	6.9338	2.2048
		NISFTVWDVGGQDK	1	3.6835	3.6835								
ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	DAVLLVFANK	3	9.2369	7.7655	2.0019	1	9.2369	9.2369	9.2369	9.2369	7.7655	
ARPP1_HUMAN		KYENILK	1	0.1213	0.1213		1	0.1213	0.1213	0.1213	0.1213	0.1213	
ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	FMEQVIFK	1	1.6232	1.6232		4	3.1053	4.1555	2.5887	3.4739	3.4378	1.9792
		GVDDLDFFIGDEAIEKPTYATK	3	6.256	6.1266	1.2785							
		TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1	1.4138	1.4138								
		YSYVCPDLVK	1	3.1282	3.1282								
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	DTDIVDEAIYYFK	1	4.5876	4.5876		1	4.5876	4.5876	4.5876	4.5876	4.5876	
ATX10_HUMAN		MEEQGLADASLLKK	1	0.1261	0.1261		1	0.1261	0.1261	0.1261	0.1261	0.1261	
ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	GINGGPSR	1	0.2175	0.2175		1	0.2175	0.2175	0.2175	0.2175	0.2175	
AXA2L_HUMAN	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2	DALNIETAIK	1	4.3042	4.3042		2	4.3547	4.3547	4.3544	4.3544	4.3544	1.0165
		SALSGHLETVILGLLK	1	4.4052	4.4052								
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	SNFLNCYVSGFHPSDIEVDLLK	1	0.7169	0.7169		3	0.6805	0.6732	0.6405	0.6263	0.5952	1.5539
		VEHSDLSFSK	2	0.3939	0.3735	1.5924							
		VNHVTLSQPK	2	0.9306	0.8642	1.7344							
BAF_HUMAN	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	AYVVLGQFLVLK	1	7.2666	7.2666		1	7.2666	7.2666	7.2666	7.2666	7.2666	
BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	ITDSEDK	1	0.2404	0.2404		1	0.2404	0.2404	0.2404	0.2404	0.2404	
BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase, cytosolic OS=Homo sapiens GN=BCAT1 PE=1 SV=3	ATLPVFDKEELECIQQLVK	1	1.1639	1.1639		1	1.1639	1.1639	1.1639	1.1639	1.1639	
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	DLLNHHLK	1	0.0457	0.0457		9	0.4094	0.3382	0.2211	0.1915	0.1822	2.928
		EGVYTVFAPTNEAFR	1	1.9807	1.9807								
		ELANILK	1	0.2678	0.2678								
		GDELADSALEIFK	3	0.1221	0.1134	1.5855							
		LTLLAPLNSVFK	2	0.1291	0.1071	2.4396							
		QAGLGNHLSGISER	1	0.2097	0.2097								
		SPYQLVLQHSR	1	0.6004	0.6004								
		VLTPPMGTVMDVLK	1	0.1946	0.1946								
		YLYHGQTLETLGGK	1	0.1348	0.1348								
BIG1_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	KGLECLVSILK	1	0.049	0.049		1	0.049	0.049	0.049	0.049	0.049	
BIG2_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	KGLECLVSILK	1	0.049	0.049		1	0.049	0.049	0.049	0.049	0.049	
BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	LNSDPQFVLAQNVGTTHDLLDICLK	1	0.4025	0.4025		1	0.4025	0.4025	0.4025	0.4025	0.4025	
BPNT1_HUMAN	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	LTDIHGNVLQYHK	1	0.5594	0.5594		1	0.5594	0.5594	0.5594	0.5594	0.5594	
BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	LMSERIK	1	3.8396	3.8396		1	3.8396	3.8396	3.8396	3.8396	3.8396	
BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=3	LMSERIK	1	3.8396	3.8396		1	3.8396	3.8396	3.8396	3.8396	3.8396	
C1R_HUMAN	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	ESEQGVYTCTAQGIWK	2	0.4156	0.4095	1.2739	7	0.6661	0.6784	0.5554	0.5758	0.5724	1.9364
		GGGALLGDR	1	0.2443	0.2443								
		LPVANPQACENWLR	1	1.1623	1.1623								
		QDACQGDSGGVFAVR	1	0.3484	0.3484								
		QRPPDLDTSSNAVDLLFFTDESGDSR	1	1.1204	1.1204								
		TLDEFTIQNLQPQYQFR	2	1.0274	1.0149	1.2485							
		VTTTMGVNTYK	1	0.3446	0.3446								
C1RL_HUMAN	Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	GGGALLGDR	1	0.2443	0.2443		1	0.2443	0.2443	0.2443	0.2443	0.2443	
C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	GFQVVVTLR	2	0.8527	0.7217	2.3153	8	3.7206	3.0838	0.669	0.6134	0.5891	5.0089
		IIGGSDADIK	1	26.3101	26.3101								
		NYVDWIMK	2	0.2204	0.2127	1.4585							
		QFGPYCGHGFPGPLNIETK	1	1.2175	1.2175								
		SNALDIIFQTDLTGQK	1	0.2987	0.2987								
		SSNNPHSPIVEEFQVPYNK	1	0.3824	0.3824								
		TMQENSTPRED	1	0.2416	0.2416								
		TNFDNDIALVR	1	0.2415	0.2415								
C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	VRLSVLER	1	0.1386	0.1386		1	0.1386	0.1386	0.1386	0.1386	0.1386	
CAD13_HUMAN	Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1	DIQGSLQDIFK	1	1.3996	1.3996		1	1.3996	1.3996	1.3996	1.3996	1.3996	
CAD24_HUMAN		TLAELYGAK	1	2.2731	2.2731		1	2.2731	2.2731	2.2731	2.2731	2.2731	
CADH5_HUMAN	Cadherin-5 OS=Homo sapiens GN=CDH5 PE=1 SV=4	ELDSTGTPTGK	1	7.7999	7.7999		1	7.7999	7.7999	7.7999	7.7999	7.7999	
CALL3_HUMAN	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	EAFSLFDK	2	2.7405	2.6828	1.3398	1	2.7405	2.7405	2.7404	2.7404	2.6828	
CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	EAFSLFDK	2	2.7405	2.6828	1.3398	1	2.7405	2.7405	2.7404	2.7404	2.6828	
CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	IDNSQVESGSLEDDWDFLPPKK	2	1.3489	1.347	1.0776	1	1.3489	1.3489	1.3489	1.3489	1.347	
CALU_HUMAN	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	EEFTAFLHPEEYDYMK	1	0.6712	0.6712		2	1.2324	1.2324	1.0972	1.0972	1.0972	2.0037
		EQFVEFR	1	1.7935	1.7935								
CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5	EFYILWTK	1	13.2538	13.2538		2	6.8384	6.8384	2.3675	2.3675	2.3675	11.4263
		SDGFSIETCK	1	0.4229	0.4229								
CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4	LSDLLAPISEQIK	2	7.0757	6.5718	1.7339	2	3.774	4.8746	1.8281	2.8702	2.7323	6.7802
		VENQENVSNLVIEDTELK	1	0.4723	0.4723								
CAPZB_HUMAN	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	LVEDMENK	1	4.8107	4.8107		2	3.1212	3.1212	2.6243	2.6243	2.6243	2.3562
		STLNEIYFGK	1	1.4316	1.4316								
CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	DIMAEIYK	4	4.4685	4.1925	1.5417	6	2.9058	3.5957	2.0983	2.945	2.8283	2.8594
		DQGSCGSCWAFGAVEAISDR	1	1.018	1.018								
		EQWPQCPTIK	1	4.4566	4.4566								
		ICEPGYSPTYK	3	4.3562	4.0893	1.5816							
		NGPVEGAFSVYSDFLLYK	1	2.7887	2.7887								
		TDQYWEK	1	0.3466	0.3466								
CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	ISVNNVLPVFDNLMQQK	2	1.66	1.6591	1.0479	2	3.202	2.688	2.8063	2.3557	2.3549	2.1012
		VSTLPAITLK	1	4.744	4.744								
CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	KIDGQGTIACESHQFQAK	1	0.5278	0.5278		1	0.5278	0.5278	0.5278	0.5278	0.5278	
CB039_HUMAN		NKLISELQQELK	2	0.0637	0.0631	1.2134	1	0.0637	0.0637	0.0637	0.0637	0.0631	
CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	SETITEEELVGLMNK	1	1.2088	1.2088		2	2.1996	2.1996	1.9638	1.9638	1.9638	1.9862
		SPEEGAETPVYLALLPPDAEGPHGQFVSEK	1	3.1903	3.1903								
CCD57_HUMAN	Coiled-coil domain-containing protein 57 OS=Homo sapiens GN=CCDC57 PE=2 SV=1	AEVSEIK	1	1.8067	1.8067		1	1.8067	1.8067	1.8067	1.8067	1.8067	
CCD58_HUMAN	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	NLDDLTLLK	1	5.8401	5.8401		1	5.8401	5.8401	5.8401	5.8401	5.8401	
CCL2_HUMAN	C-C motif chemokine 2 OS=Homo sapiens GN=CCL2 PE=1 SV=1	WVQDSMDHLDK	1	1.7696	1.7696		1	1.7696	1.7696	1.7696	1.7696	1.7696	
CD109_HUMAN	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	SNLIQQWLSQQSDLGVISK	1	3.818	3.818		1	3.818	3.818	3.818	3.818	3.818	
CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2	YGFIEGHVVIPR	1	0.6968	0.6968		1	0.6968	0.6968	0.6968	0.6968	0.6968	
CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	CIDSGLWVPNSK	1	1.1217	1.1217		2	1.7047	1.7047	1.6019	1.6019	1.6019	1.6552
		QYMEGFNDELEAFK	1	2.2876	2.2876								
CFAH_HUMAN	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	SIDVACHPGYALPK	1	11.5781	11.5781		1	11.5781	11.5781	11.5781	11.5781	11.5781	
CH10_HUMAN	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	DGDILGK	1	0.7985	0.7985		3	2.8836	2.8836	2.2859	2.2859	2.2859	2.5277
		VLLPEYGGTK	1	3.2505	3.2505								
		VVLDDKDYFLFR	1	4.6019	4.6019								
CHI3L1_HUMAN	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2	EAGTLAYYEICDFLR	1	0.3353	0.3353		1	0.3353	0.3353	0.3353	0.3353	0.3353	
CING_HUMAN	Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	KVSLVLEK	1	0.1034	0.1034		1	0.1034	0.1034	0.1034	0.1034	0.1034	
CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	DLADLIPK	2	3.8265	3.687	1.4738	1	3.8265	3.8265	3.8265	3.8265	3.687	
CLC11_HUMAN	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	AALAPYNWPVWLGVHDR	1	0.2656	0.2656		3	0.249	0.2586	0.2455	0.2554	0.2454	1.2314
		DAVQALQEAQGR	2	0.2874	0.2654	1.7695							
		QQMEALTR	1	0.1939	0.1939								
CLCA_HUMAN		SVLISLK	1	3.4654	3.4654		1	3.4654	3.4654	3.4654	3.4654	3.4654	
CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	EAIDSYIK	2	7.7359	7.3085	1.6181	4	2.9268	3.8886	1.2822	1.8369	1.7956	6.4639
		EDKLECSEELGDLVK	1	2.0425	2.0425								
		LPVVIGGLLDVDCSEDVIK	1	1.8356	1.8356								
		TLQIFNIEMK	1	0.0932	0.0932								
CLH2_HUMAN	Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2	EDKLECSEELGDLVK	1	2.0425	2.0425		2	1.0679	1.0679	0.4363	0.4363	0.4363	8.8726
		TLQIFNIEMK	1	0.0932	0.0932								
CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	EEFASTCPDDEIELAYEQVAK	1	0.6437	0.6437		5	4.3893	5.3253	3.1011	4.1688	3.2242	2.9234
		LAALNPESNTAGLDIFAK	2	5.6502	3.1499	5.3715							
		LCPGGQLPFLLYGTEVHTDTNK	1	6.5439	6.5439								
		LHIVQVVCK	1	1.6062	1.6062								
		NSNPALNDNLEK	3	7.5027	5.5825	2.7685							
CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	DEFTNTCPSDKEVEIAYSDVAK	1	0.8867	0.8867		3	3.3145	3.3145	2.2974	2.2974	2.2974	2.8719
		IEEFLEEVLCPPK	1	1.9148	1.9148								
		TDVNKIEEFLEEVLCPPK	1	7.1419	7.1419								
CLIC5_HUMAN	Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3	FLDGDELTLADCNLLPK	1	1.0108	1.0108		1	1.0108	1.0108	1.0108	1.0108	1.0108	
CLIC6_HUMAN	Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 PE=2 SV=3	FLDGDELTLADCNLLPK	1	1.0108	1.0108		1	1.0108	1.0108	1.0108	1.0108	1.0108	
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	ALQEYR	1	0.1469	0.1469		16	0.2678	0.221	0.2151	0.197	0.1933	1.7868
		ASSIIDELFQDR	4	0.1685	0.1623	1.3548							
		EILSVDCSTNNPSQAK	4	0.1873	0.1859	1.1488							
		EIQNAVNGVK	1	0.1888	0.1888								
		ELDESLQVAER	2	0.1388	0.1386	1.0691							
		FMETVAEK	4	0.176	0.1744	1.1661							
		IDSLLENDR	3	0.1755	0.1674	1.4432							
		KTLLSNLEEAK	1	0.167	0.167								
		KYNELLK	1	0.1213	0.1213								
		LFDSDPITVTVPVEVSR	3	0.1726	0.1697	1.2517							
		QQTHMLDVMQDHFSR	1	0.2122	0.2122								
		RELDESLQVAER	1	0.911	0.911								
		SGSGLVGR	3	0.2221	0.2161	1.3349							
		TLLSNLEEAK	4	0.1972	0.1879	1.4118							
		TLLSNLEEAKK	1	0.8865	0.8865								
		VTTVASHTSDSDVPSGVTEVVVK	3	0.2131	0.2125	1.0974							
CMBL_HUMAN	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	EVQVEHIK	1	0.5916	0.5916		1	0.5916	0.5916	0.5916	0.5916	0.5916	
CN153_HUMAN	UPF0671 protein C14orf153 OS=Homo sapiens GN=C14orf153 PE=2 SV=1	MVVLRAGK	1	0.0407	0.0407		1	0.0407	0.0407	0.0407	0.0407	0.0407	
CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	CYSCGEFGHIQK	1	0.2582	0.2582		1	0.2582	0.2582	0.2582	0.2582	0.2582	

CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	GNILIPGINEAVAAVTEEEEHK	1	1.5331	1.5331		2	2.6984	2.6984	2.4338	2.4338	2.4338	1.9224
		MMEVAAADVK	1	3.8636	3.8636								
CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	DGTILCTLMNK	2	0.4515	0.4054	1.9501	2	2.8622	2.0586	1.5429	1.0243	0.9534	5.6858
		TWIEGLTGLSIGPDFQK	1	5.2729	5.2729								
CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4	ALLLQGSNEIEIR	3	8.7638	1.1108	20.777	20	1.616	2.421	0.4617	0.7055	0.4943	4.5886
		DLEVDTTLK	1	0.0714	0.0714								
		FTYSVTVDGCTSHTGAWGK	2	0.1908	0.1683	2.0596							
		GDAGPAGPK	1	0.184	0.184								
		GESGPSGPAGPTGAR	1	0.9806	0.9806								
		GPFGADGVAGPK	1	0.5755	0.5755								
		GFSGLDGAK	1	0.3596	0.3596								
		GLTGSPGSPGPDGK	1	0.0917	0.0917								
		GNSGEPGAPGSK	1	0.7519	0.7519								
		GPAGPQGPR	2	0.256	0.2559	1.0064							
		GSEGPQGVR	3	0.8548	0.7436	1.9358							
		GVPGPPGAVGPAGK	1	0.2546	0.2546								
		GVQGPPGPAGPR	2	6.6444	1.3203	25.8246							
		NSVAYMDQQTGNLK	1	0.158	0.158								
		NSVAYMDQQTGNLKK	2	0.1263	0.1203	1.5602							
		SGDRGETGPAGPAGPVGPVGAR	2	0.2305	0.2289	1.18							
		SGEYWIDPNQGCNLDAIK	1	0.1326	0.1326								
		SLSQIENIR	3	8.8605	5.1187	4.2896							
		STGGISVPGPMGPSGPR	3	2.7354	2.5763	1.5577							
		VLCDDVICDETK	2	0.1175	0.1139	1.422							
CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6	DGNPGNDGPPGR	1	0.1527	0.1527		25	1.2195	1.0664	0.3674	0.3006	0.2933	5.4983
		DYEVDATLK	1	0.0583	0.0583								
		EMATQLAFMR	1	4.9639	4.9639								
		FTYTVLVDGCSK	1	0.0846	0.0846								
		GAAGIPGGK	3	0.0461	0.0461	1.0494							
		GAPGAVGAPGPAGATGDR	1	3.5949	3.5949								
		GASGPAGVR	1	0.1848	0.1848								
		GDGGPPGMTGFPGAAGR	1	0.1111	0.1111								
		GDQGPVGR	1	1.1199	1.1199								
		GEAGAAGPAGPAGPR	1	1.6893	1.6893								
		GETGPSGPVGPAGAVGPR	1	1.8895	1.8895								
		GFPGTPGLPGFK	1	0.3689	0.3689								
		GHAGLAGAR	2	0.2811	0.2804	1.1016							
		GIPGPVGAAGATGAR	1	4.9729	4.9729								
		GPAGPSGPAGK	2	0.3202	0.3196	1.0915							
		GPNGDAGRPGEPGLMGPR	1	4.8242	4.8242								
		GPSGPPGPDGNK	1	2.28	2.28								
		GPSGPQGIR	2	0.2213	0.2129	1.4845							
		GVGLGPGPMGLMGPR	4	2.6194	2.2631	1.9978							
		GVVGPQGAR	2	0.0786	0.0784	1.0943							
		KTNEWGK	1	0.31	0.31								
		NSIAYMDEETGNLKK	2	0.0344	0.0319	1.738							
		SAPSLRPK	1	0.0402	0.0402								
		TGHPGTVGPAGIR	1	0.1986	0.1986								
		TIIEYK	3	0.0419	0.0407	1.3388							
CO2A1_HUMAN	Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	FTYTALKDGCTK	1	0.0614	0.0614		1	0.0614	0.0614	0.0614	0.0614	0.0614	
CO3A1_HUMAN	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	DGNPGSDGLPGR	1	1.2266	1.2266		11	0.9807	0.8325	0.497	0.424	0.3866	3.769
		FTYTVLEDGCTK	3	0.0931	0.0916	1.2542							
		GAPGPQGPR	2	0.2589	0.2588	1.0025							
		GESGPAGPAGAPGAGSR	1	0.4914	0.4914								
		GPVGPSGPPGK	1	2.9617	2.9617								
		GRPGLPGAAGAR	1	2.2629	2.2629								
		INTDEIMTSLK	2	0.0978	0.0919	1.6504							
		SGEYWVDPNQGCK	2	0.1556	0.1186	2.9721							
		SVNGQIESLISPDGSR	4	1.0297	0.7766	2.8688							
		TVFEYR	1	0.1449	0.1449								
		VFCNMETGETCISANPLNVPR	2	2.0753	2.0724	1.0783							
CO5A2_HUMAN	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	GSQFAYGDHQSPNTAITQMTFLR	2	0.5061	0.5046	1.1115	5	2.6107	2.2599	0.792	0.735	0.7343	4.943
		NSVGYMDDQAK	1	0.6055	0.6055								
		QSGEYWIDPNQGSVEDAIK	1	0.6285	0.6285								
		SGLGSIQVGLMPGSVGPVGPR	1	11.1685	11.1685								
		TVFEYR	1	0.1449	0.1449								
CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	DTTPLNVLCSPGIQVVSVGIK	4	1.169	0.3801	4.9747	9	0.6851	0.7932	0.3704	0.4871	0.2899	3.1588
		ENYKLLEDAFLK	2	0.183	0.1764	1.4718							
		GLEQLLVGGSHLK	1	0.0973	0.0973								
		GTYTDCAIK	1	0.2075	0.2075								
		IALVITDGR	3	1.3454	0.3837	7.1915							
		LLLFSDGNSQGATPAAIEK	2	0.1445	0.1409	1.3736							
		NNVEQVCCSFECQPAR	1	2.5031	2.5031								
		SLQWMAGGTFTGEALQYTR	1	0.3231	0.3231								
		YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1	0.1932	0.1932								
CO6A2_HUMAN	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	DDDLNLR	1	0.0829	0.0829		3	0.1444	0.1565	0.136	0.1484	0.1465	1.5534
		DVTVTAIGIDMFHEK	2	0.1928	0.1878	1.3821							
		HESENLYSIACDKPQQVR	1	0.1574	0.1574								
CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=4	AAPLQGMLPGLLAPLR	1	0.1006	0.1006		23	4.5619	4.3024	0.6031	0.6358	0.5692	5.0645
		ALILVGLER	1	1.1664	1.1664								
		DQNVFVAQK	1	4.1131	4.1131								
		EVITAVR	1	0.6021	0.6021								
		FWYGGCGGNENK	2	5.8602	1.4069	19.6322							
		IEEGVPQFLVLISSGK	1	0.1339	0.1339								
		ISLSPEYVFSVSTFTR	1	0.0847	0.0847								
		ITEGVPQLLIVLTADR	1	1.7314	1.7314								
		LLVLITGGK	1	82.2366	82.2366								
		NIDSEEVGK	1	0.216	0.216								
		NILVSSAGSR	1	2.7883	2.7883								
		NLQVALTSK	1	0.0888	0.0888								
		NNLFTSSAGYR	1	1.2629	1.2629								
		QINVGNALEYVSR	2	0.9177	0.9086	1.2214							
		QLQLQGGSGLNTGSALSYVYANHFTEAGGSR	1	0.2632	0.2632								
		QQSLETAMSFVAR	1	0.2378	0.2378								
		SQAPVLDAIR	1	0.9868	0.9868								
		SSGIVSLGVGDR	1	0.2374	0.2374								
		VAVGFSDDFK	1	0.6105	0.6105								
		VEFSLTDYGSK	2	0.1608	0.1608	1.0258							
		VGVVQFSDEPR	1	0.663	0.663								
		VGVVQFSNDVFPEPYLK	1	0.21	0.21								
		VVESLDVGQDR	1	0.2622	0.2622								
CO7_HUMAN	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	SFRRSSSSSSR	3	0.532	0.5314	1.06	1	0.532	0.532	0.532	0.532	0.5314	
COCA1_HUMAN	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	ALALGALQNIR	1	0.5738	0.5738		23	1.6688	1.4547	0.6601	0.5996	0.5852	3.4299
		DLSFSEVTSYGFK	1	1.4729	1.4729								
		GEVQTVTFDTEEVK	1	2.6463	2.6463								
		GGNTLTGMALNFIR	1	0.6177	0.6177								
		GGNTMTGDAIDYLVK	1	0.1499	0.1499								
		GSETSHCFTGLSPDTDYGVTVFVQTPNLEGPGVSVK	2	0.6688	0.5381	2.6286							
		GSPQDLVTK	1	14.2309	14.2309								
		IVDDLTINLCNSVK	1	2.9751	2.9751								
		LGELVVGPYDNTVVLEELR	1	0.4256	0.4256								
		NFASVGGVSLESGSFPSYSAYR	1	0.3867	0.3867								
		NLPEDAIHTMIENLQPETK	1	0.3118	0.3118								
		NSDVEIFAVGVK	1	0.2284	0.2284								
		NTFTESAGAR	1	7.9951	7.9951								
		NVGVEVFSLGIK	2	0.2046	0.1934	1.612							
		QVCEQLISGQMNNR	1	0.2905	0.2905								
		SELEAIASPPAETHVFTVEDFDAFQR	1	1.6013	1.6013								
		SLYDDVDTGEK	1	0.2076	0.2076								
		TEFNLNQYYQR	2	0.9708	0.9701	1.0527							
		TNWSPAGENVFSYHITYK	1	0.51	0.51								
		TVGLLPPQNIHISDEWYTR	1	1.2374	1.2374								
		TYQIGWDTFCVK	1	0.1609	0.1609								
		VEDIEAINTFPYR	3	0.2529	0.2418	1.4581							
		VMILITDGK	1	0.2627	0.2627								
COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	AVLFCLSEDKK	1	14.065	14.065		10	12.0262	12.6044	10.3176	11.0803	10.7016	1.9558
		EILVGDVGQTVDDPYATFVK	2	17.7039	15.7258	2.018							
		HELQANCYEEVK	1	6.6314	6.6314								
		HELQANCYEEVKDR	2	5.9997	5.9216	1.2578							
		LGSSAVSLEGKPL	3	12.8808	11.824	1.7122							
		MIYASSK	1	12.657	12.657								
		MLPDKDCR	1	16.9374	16.9374								
		NILEEGK	1	2.1765	2.1765								
		NILEEGKEILVGDVGQTVDDPYATFVK	1	11.8726	11.8726								
		YALYDATYETK	2	19.3382	19.3227	1.0583							
COF2_HUMAN	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1	MIYASSK	1	12.657	12.657		3	11.6943	9.3489	8.3812	6.0744	6.0522	3.1233
		QILVGDIGDTVEDPYTSFVK	2	2.3126	2.2957	1.187							
		YALYDATYETK	1	20.1132	20.1132								
CO1A1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	GLELEPGAGLFVAQAGGADPDKFGGVIAELK	1	2.0552	2.0552		1	2.0552	2.0552	2.0552	2.0552	2.0552	
COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	TALNLFFK	1	6.097	6.097		1	6.097	6.097	6.097	6.097	6.097	
COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	NTLEWCLPVIDAK	1	4.1957	4.1957		1	4.1957	4.1957	4.1957	4.1957	4.1957	
COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	GMGYMPK	1	7.3471	7.3471		4	3.4992	3.1682	2.5841	2.4155	2.4152	2.5776
		KSDLFQDDLYPDTAGPEAALEAEEWFEGK	1	3.9782	3.9782								
		NADPLISLK	2	1.8444	1.8438	1.0381							
		YFEITDESPYVHYLNTFSSK	1	0.8271	0.8271								
COTL1_HUMAN	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	EFVISDR	1	3.0863	3.0863		3	3.3119	3.3119	3.2435	3.2435	3.2435	1.2814
		ELEEDFIK	1	4.2447	4.2447								
		YDGSTIVPGEQQAEYQHFIQQCTDDVR	1	2.6046	2.6046								
CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	SMVAVMDSDTTGK	1	0.1169	0.1169		1	0.1169	0.1169	0.1169	0.1169	0.1169	
CPPED_HUMAN	Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=2	LTEQAVQAINK	1	0.0342	0.0342		1	0.0342	0.0342	0.0342	0.0342	0.0342	
CRIP2_HUMAN	Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	GVNIGGACSYIYEKPLAEGPQVTGPIEVPAAR	2	3.4033	2.0461	4.7117	2	3.5168	3.4789	3.5149	3.4773	2.477	1.0467
		GVNTGAVGSYIYGRDPEGK	1	3.6303	3.6303								
CSN5_HUMAN	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	GYKPPDEGPSEYQTIPLNK	1	0.2142	0.2142		1	0.2142	0.2142	0.2142	0.2142	0.2142	
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	GFGFGQGAGALVHSE	1	5.8566	5.8566		4	3.9725	3.7565	3.8471	3.6643	3.4102	1.3237
		GLESTTLAGKDGEIYCK	2	3.3579	2.7369	2.5484							
		SCFLCMVCK	1	3.384	3.384								
		TVYFAEEVQCEGNSFHK	2	3.2915	3.2549	1.2359							
CTCFL_HUMAN		LEEEQEK	1	16.5065	16.5065		1	16.5065	16.5065	16.5065	16.5065	16.5065	
CTGF_HUMAN	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2	ANCLVQTTEWSACSK	1	9.6269	9.6269		4	10.7588	12.2039	9.8717	11.1299	9.166	1.6151
		CCEEWVCDEPK	1	9.5597	9.5597								
		SGESFGSSCK	1	5.5645	5.5645								
		TTTLPVEFK	2	17.9842	11.0689	4.5191							
CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	SQGMASLNLPAVSWK	1	0.174	0.174		1	0.174	0.174	0.174	0.174	0.174	
CUTA_HUMAN	Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2	LAACVNLIPQITSIYEWK	1	2.5885	2.5885		2	3.0825	3.0825	3.0426	3.0426	3.0426	1.2568
		SVHPYEVAEVIALPVEQGNFPYLQWVR	1	3.5764	3.5764								
CV028_HUMAN	UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1	GGQVGGFLPMIK	1	0.0908	0.0908		1	0.0908	0.0908	0.0908	0.0908	0.0908	
CYBP_HUMAN	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	ISNYGWDQSDK	1	3.8756	3.8756		1	3.8756	3.8756	3.8756	3.8756	3.8756	
CYC_HUMAN	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	ADLIAYLK	1	4.6074	4.6074		2	3.0993	3.0993	2.7076	2.7076	2.7076	2.1208
		TGQAPGYSYTAANK	1	1.5912	1.5912								
CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	GLECNFGASSTALK	2	9.3996	9.3704	1.118	2	5.4766	5.4766	3.8214	3.8214	3.7921	3.571
		VTGQCCEEWVCDEDSIKDPMEDQDGLLGK	2	1.5536	1.5346	1.2488							
CYTB_HUMAN	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	AKHDELTYF	1	4.3786	4.3786		2	4.9552	5.1474	4.9215	5.1171	5.0852	1.1798
		SQVVAGTNYFIK	2	5.5318	5.4801	1.2143							
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	ALDFAVGEYNK	4	0.557	0.5553	1.0953	4	1.0161	0.9955	0.844	0.8154	0.7383	1.9168
		ALQVVR	1	0.6518	0.6518								

		LVGGPMDASVEEEGVR	2	2.2284	1.5068	3.7961							
		TQPNLDNCPFHDQPHLK	1	0.6273	0.6273								
DBPA_HUMAN	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4	SVGDGETVEFDVVEGEK	1	1.8794	1.8794		1	1.8794	1.8794	1.8794	1.8794	1.8794	
DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2	EAGLAPVPMIIFAK	1	4.5562	4.5562		1	4.5562	4.5562	4.5562	4.5562	4.5562	
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	ELAQQVQGVADDYGK	1	1.146	1.146		1	1.146	1.146	1.146	1.146	1.146	
DDX39_HUMAN	ATP-dependent RNA helicase DDX39 OS=Homo sapiens GN=DDX39 PE=1 SV=2	GLAITFVSDENDAK	1	2.298	2.298		1	2.298	2.298	2.298	2.288	2.298	
DEOC_HUMAN	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	DSLAWLSLVK	1	3.1128	3.1128		1	3.1128	3.1128	3.1128	3.1128	3.1128	
DESM_HUMAN	Desmin OS=Homo sapiens GN=DES PE=1 SV=3	EYQDLLNVK	4	12.6181	12.3633	1.264	5	10.2392	10.1221	9.7538	9.4761	9.3094	1.4572
		KLLEGEESR	1	11.2815	11.2815								
		LLEGEESR	2	12.1651	12.1517	1.0685							
		TNEKVELQELNDR	3	5.0639	4.8792	1.4125							
		VELQELNDR	1	10.0673	10.0673								
DEST_HUMAN	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	MIYASSK	1	12.657	12.657		1	12.657	12.657	12.657	12.657	12.657	
DKK3_HUMAN	Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1	DQDGELLPR	2	0.84	0.5661	3.8208	6	0.3897	0.4216	0.3475	0.3702	0.3322	1.6389
		DSECCGDQLCVWGHCTK	1	0.3701	0.3701								
		EVEELMEDTQHK	1	0.2193	0.2193								
		LLDLITWELEPDGALDR	2	0.2266	0.2266	1.0246							
		QELEDLER	2	0.3896	0.355	1.857							
		SAVEEMEAEEAAAK	1	0.2927	0.2927								
DLRB1_HUMAN	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3	STMDNPTTTQYASLMHSFILK	1	1.299	1.299		1	1.299	1.299	1.299	1.299	1.299	
DNJB4_HUMAN	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1	EIYDQFGEEGLK	1	0.1017	0.1017		1	0.1017	0.1017	0.1017	0.1017	0.1017	
DNJC9_HUMAN	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	ISLEDIQAFEK	1	3.254	3.254		1	3.254	3.254	3.254	3.254	3.254	
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	GLYDGPVCEVSVTPK	1	5.4363	5.4363		2	3.0212	3.0212	1.815	1.815	1.815	4.7179
		GSPLVVISQGK	1	0.606	0.606								
DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	GMTTVDDFFQGTK	1	0.0778	0.0778		1	0.0778	0.0778	0.0778	0.0778	0.0778	
DYH2_HUMAN	Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=1 SV=3	QELLAQANK	1	13.1184	13.1184		1	13.1184	13.1184	13.1184	13.1184	13.1184	
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	QLQNISLAAASGGAK	1	0.2061	0.2061		1	0.2061	0.2061	0.2061	0.2061	0.2061	
DYSF_HUMAN	Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1	DLAAMDK	1	2.9644	2.9644		1	2.9644	2.9644	2.9644	2.9644	2.9644	
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	ALNALCDGLIDELNQALK	1	1.2123	1.2123		1	1.2123	1.2123	1.2123	1.2123	1.2123	
ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	DILTEDGR	2	1.2474	0.4443	10.947	4	0.6579	0.6799	0.5437	0.5286	0.374	2.1258
		LVWEEAMSR	1	0.618	0.618								
		NVALVSGDTENAK	2	0.2002	0.199	1.1635							
		VTPNLMGHLCGNQR	1	0.5662	0.5662								
EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	EALMTELSTVK	1	0.7537	0.7537		1	0.7537	0.7537	0.7537	0.7537	0.7537	
EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	MDSTEPPYSQKR	1	0.2988	0.2988		4	4.9342	5.2051	2.5369	2.9956	2.9381	5.0114
		SGDAAIVDMVPGKPMCVESFSDYPPLGR	2	1.7999	1.793	1.1317							
		STTTGHLIYK	2	9.6935	9.1806	1.6008							
		THINIVVIGHVDSGK	1	7.9448	7.9448								
EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	STTTGHLIYK	2	9.6935	9.1806	1.6008	2	8.8191	9.1106	8.7757	9.0715	8.7487	1.151
		THINIVVIGHVDSGK	1	7.9448	7.9448								
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1	EVSTYIK	1	11.9983	11.9983		2	10.6553	10.6553	10.5703	10.5703	10.5703	1.1963
		QTVAVGVIK	1	9.3122	9.3122								
EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	SPAGLQVLNDYLADK	2	10.1913	10.1751	1.083	1	10.1913	10.1913	10.1913	10.1913	10.1751	
EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	GVVGELQQAISK	1	8.3025	8.3025		2	6.951	6.5004	6.8183	6.385	5.8786	1.3212
		SIQLDGLVVGASK	2	5.5994	4.9466	2.052							
EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	AVLGEVK	2	1.7088	1.6292	1.5529	3	4.8874	4.8683	4.079	3.9189	3.8154	2.2018
		ILGLLDAYLK	2	7.9705	7.8187	1.3208							
		YSNEDTLSVALPYFWEHFDK	1	4.983	4.983								
EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EGIPALDNFLDKL	3	7.1275	6.9108	1.3687	9	6.6518	6.6405	4.6635	5.0794	5.0394	3.8105
		ETVSEESNVLCLSK	1	10.3856	10.3856								
		GPLMMYSK	1	5.6735	5.6735								
		GVQYLNEIK	1	10.7984	10.7984								
		IWCFGPDGTGPNILTDITK	2	5.5652	5.5589	1.0695							
		STLTDSLVCK	1	0.1403	0.1403								
		TFCQLILDPIFK	1	7.5958	7.5958								
		VFDAIMNFK	1	7.1669	7.1669								
		VFSGLVSTGLK	1	5.4126	5.4126								
EFHD1_HUMAN	EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1	DGFIDLMELK	1	0.5467	0.5467		1	0.5467	0.5467	0.5467	0.5467	0.5467	
EFHD2_HUMAN	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	DGFIDLMELK	1	0.5467	0.5467		1	0.5467	0.5467	0.5467	0.5467	0.5467	
EGLN_HUMAN	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2	GEVTYTTSQVSK	1	4.7267	4.7267		1	4.7267	4.7267	4.7267	4.7267	4.7267	
EHD2_HUMAN	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	DGMLDDEEFALASHLIEAK	2	2.8743	2.8629	1.1348	1	2.8743	2.8743	2.8743	2.8743	2.8629	
ELOB_HUMAN	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	LYKDDQLLDDGK	1	7.0907	7.0907		1	7.0907	7.0907	7.0907	7.0907	7.0907	
EMIL1_HUMAN	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	GLEEGQAQAGQCPSLEGR	1	0.3479	0.3479		3	0.3212	0.3212	0.1813	0.1813	0.1813	4.9661
		LVGSGLHTVEAAGEAR	1	0.0292	0.0292								
		QATLEGLQEVVGR	1	0.5864	0.5864								
ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	AVEHINK	1	0.0987	0.0987		17	11.1263	12.1921	7.5617	9.5322	8.5525	3.5615
		DATNVGDEGGFAPNILENK	1	8.7228	8.7228								
		DYPVVSIEDPFDQDDWGAWQK	1	4.8382	4.8382								
		EGLELLK	3	12.6119	9.9195	2.6151							
		FGANAILGVSLAVCK	2	4.111	4.1109	1.009							
		FTASAGIQVVGDDLTVTNPK	1	10.1223	10.1223								
		GNPTVEVDLFTSK	3	18.0463	17.3679	1.4203							
		HIADLAGNSEVILPVPAFNVINGGSHAGNK	1	3.8314	3.8314								
		IDKLMIEMDGTENK	1	4.9765	4.9765								
		IEEELGSK	2	17.3549	17.3533	1.0197							
		IGAEVYHNLK	1	30.6013	30.6013								
		KLNVTEQEK	1	17.2213	17.2213								
		LMIEMDGTENK	3	12.8099	7.5729	4.6019							
		SFIKDYPVVSIEDPFDQDDWGAWQK	1	6.279	6.279								
		TIAPALVSK	4	12.3097	10.603	1.9813							
		VNQIGSVTESLQACK	2	6.944	6.7672	1.3806							
		YSPDQLADLYK	3	18.2671	16.5226	1.7884							
ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=4	FGANAILGVSLAVCK	2	4.111	4.1109	1.009	5	4.4328	5.31	3.5106	4.3007	4.0296	2.2413
		HIADLAGNPDLILPVPAFNVINGGSHAGNK	2	2.5548	2.1551	2.3361							
		LAQSNGWGVMVSHR	1	1.0859	1.0859								
		SGETEDTFIADLVVGLCTGQIK	1	4.932	4.932								
		VNQIGSVTESIQACK	3	9.4803	8.7349	1.6445							
ENOG_HUMAN	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	FGANAILGVSLAVCK	2	4.111	4.1109	1.009	3	9.0298	11.2155	7.1524	8.8786	8.7101	2.2404
		GNPTVEVDLVTAK	3	18.0463	17.3679	1.4203							
		SGETEDTFIADLVVGLCTGQIK	1	4.932	4.932								
ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ELISNASDALDK	3	9.0362	7.9112	1.8714	1	9.0362	9.0362	9.0362	9.0362	7.9112	
EPCR_HUMAN	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1	EFLEDTCVQYVQK	2	9.0674	6.5103	3.3725	1	9.0674	9.0674	9.0674	9.0674	6.5103	
ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	VNVAGLVLAGSADFK	1	2.6684	2.6684		2	1.5416	1.5416	1.0519	1.0519	1.0519	3.73
		YFDEISQDTGK	1	0.4147	0.4147								
ERH_HUMAN	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	ADTQTYQPYNK	1	7.8046	7.8046		1	7.8046	7.8046	7.8046	7.8046	7.8046	
ESYT3_HUMAN	Extended synaptotagmin-3 OS=Homo sapiens GN=ESYT3 PE=2 SV=1	VATNGGPK	2	0.034	0.0292	2.4413	1	0.034	0.034	0.034	0.034	0.0292	
EVI5_HUMAN	Ecotropic viral integration site 5 protein homolog OS=Homo sapiens GN=EVI5 PE=1 SV=2	QHAELEIDK	2	9.5921	9.5921	1.5195	1	10.0149	10.0149	10.0149	10.0149	9.5921	
EWS_HUMAN	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	AAVEWFDGK	1	0.8441	0.8441		1	0.8441	0.8441	0.8441	0.8441	0.8441	
EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	DNAMLEYLK	1	2.347	2.347		3	7.6342	7.9648	6.2473	6.836	6.8327	2.3576
		LFFLQVK	1	11.5991	11.5991								
		QLFDQVVK	2	8.9565	8.9477	1.0649							
F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	AIDLFTDAIK	2	6.0927	5.3597	2.0781	4	3.9134	4.3493	3.2715	3.7047	3.5196	2.1942
		EWVESMGGK	1	1.0346	1.0346								
		LDYDEDASAMLK	1	4.2086	4.2086								
		VAAIEALNDGELQK	1	4.3177	4.3177								
F10A4_HUMAN	Protein FAM10A4 OS=Homo sapiens GN=FAM10A4 PE=1 SV=1	AIDLFTDAIK	2	6.0927	5.3597	2.0781	2	5.2052	5.501	5.129	5.432	4.9871	1.2757
		VAAIEALNDGELQK	1	4.3177	4.3177								
F10A5_HUMAN	Protein FAM10A5 OS=Homo sapiens GN=FAM10A5 PE=1 SV=1	AIDLFTDAIK	1	3.1954	3.1954		3	2.8129	2.8129	2.4052	2.4052	2.4052	2.1032
		EWVESMGGK	1	1.0346	1.0346								
		LDYDEDASAMLK	1	4.2086	4.2086								
FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	TQTVCNFTDGALVQHQEWDGK	2	11.4093	5.9044	6.0856	2	8.6836	9.5921	8.2447	9.1876	5.9222	1.5831
		TTQFSCTLGEK	1	5.9579	5.9579								
FAKD2_HUMAN	FAST kinase domain-containing protein 2 OS=Homo sapiens GN=FASTKD2 PE=1 SV=1	MQSTDIIR	1	6.447	6.447		1	6.447	6.447	6.447	6.447	6.447	
FBL3_HUMAN	Putative fatty acid-binding protein 5-like protein 3 OS=Homo sapiens GN=FABP5L3 PE=1 SV=1	TQTVCNFTDGALVQHQEWDGK	2	11.4093	5.9044	6.0856	1	11.4093	11.4093	11.4093	11.4093	5.9044	
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	CCHCCLLGR	1	2.5609	2.5609		10	2.7903	2.7903	1.1822	1.1822	1.1822	4.3503
		DCSLPYATESK	1	0.2055	0.2055								
		DSSCGTGYELTEDNSCK	1	0.2993	0.2993								
		GYHLNEEGTR	1	0.4392	0.4392								
		IIEVEEQEDPYLNDR	1	7.0089	7.0089								
		LEMNYVVGGVVSHR	1	3.9036	3.9036								
		SAATLQQEK	1	0.5072	0.5072								
		SQETGDLDVGGLQETDK	1	0.2464	0.2464								
		SQETGDLDVGGLQETDKIIEVEEEQEDPYLNDR	1	10.606	10.606								
		YMDGMTVGVVR	1	2.1261	2.1261								
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	ADGVCINLR	2	5.8372	5.8371	1.007	10	4.0741	4.1211	3.8885	3.9861	3.9628	1.4102
		CVCPVSNAMCR	2	4.266	4.2424	1.1609							
		CVNHYGGYLCLPK	1	4.9375	4.9375								
		EHIVDLEMLTVSSIGTFR	1	1.7443	1.7443								
		ELPGSIVYK	3	3.6707	3.6449	1.1565							
		GSFACQCPPGYQK	4	4.3953	4.3503	1.1817							
		LNCEDIDECR	3	5.2291	5.2119	1.105							
		QTSPVSAMLVLVK	4	2.9533	2.9282	1.1675							
		SGNENGEFYLR	2	4.0962	4.0599	1.208							
		TCQDINECETTNECR	1	3.6111	3.6111								
FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3	AGNSQGDFYIR	1	0.5409	0.5409		2	0.6025	0.6025	0.5993	0.5993	0.5993	1.156
		CVEPYIQVSENR	1	0.664	0.664								
FBLN5_HUMAN	Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1	DMDVVSGR	2	0.1283	0.1148	1.9694	3	2.3894	1.4943	0.5359	0.3218	0.2991	9.1524
		DQFFTILYR	2	0.1748	0.1627	1.7211							
		SVPADIFQMQATTR	1	6.8652	6.8652								
FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=2	GFMTNGADIDECK	1	3.062	3.062		9	0.7548	0.7548	0.4843	0.4843	0.4843	2.5159
		GFQLDLR	1	0.4301	0.4301								
		GTCWQTVEDGR	1	1.2704	1.2704								
		GWGPHCEICPFGQTVAFK	1	0.4183	0.4183								
		GYILQEDGR	1	0.1353	0.1353								
		ILELLPALTTLTNHHNR	1	0.2029	0.2029								
		TGCTDINECEIGAHNCGK	1	0.4381	0.4381								
		TGYTPDITGTSCVDLNECNQAPKPCNFICK	1	0.4421	0.4421								
		YLIESGNEDDFFK	1	0.3941	0.3941								
FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	GTGWLNIQDSR	1	0.1431	0.1431		1	0.1431	0.1431	0.1431	0.1431	0.1431	
FBN3_HUMAN	Fibrillin-3 OS=Homo sapiens GN=FBN3 PE=2 SV=2	ASCCCSLGR	1	0.6447	0.6447		1	0.6447	0.6447	0.6447	0.6447	0.6447	
FES_HUMAN	Proto-oncogene tyrosine-protein kinase Fes/Fps OS=Homo sapiens GN=FES PE=1 SV=3	QEMVTQLQQELR	2	0.8228	0.8206	1.1082	1	0.8228	0.8228	0.8227	0.8227	0.8206	
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	CDSSPDSAEDVR	1	0.8722	0.8722		3	0.8671	0.8552	0.8666	0.8546	0.8401	1.0436
		CDSSPDSAEDVRK	4	0.828	0.8043	1.3225							
		CNLLAEK	2	0.9011	0.8996	1.0863							
FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3	AQITGYR	3	0.1483	0.148	1.0687	31	0.2044	0.1939	0.1974	0.189	0.1877	1.2856
		ATITGYR	4	0.1582	0.1576	1.1038							
		DAPIVNK	1	0.1519	0.1519								
		DLGFVEVTDVK	1	0.1825	0.1825								
		ESKPLTAQQQTTK	1	0.1645	0.1645								
		FTNIGPDTMR	2	0.1707	0.1668	1.3548							
		GATYNIIVEALK	2	0.1751	0.1709	1.3644							
		GDSPASSKPISINYR	1	0.444	0.444								
		GEWTCKPAEK	1	0.2664	0.2664								
		GLAFTDVDVDSIK	1	0.1635	0.1635								
		HTSVQTTSSGSGPFTDVR	1	0.3712	0.3712								
		HYQINQQWER	1	0.1574	0.1574								
		IGDQWDK	1	0.2126	0.2126								
		IGDTWR	1	0.1809	0.1809								
		IGDTWSK	3	0.1944	0.1933	1.1378							
		ISCTIANR	2	0.1653	0.1652	1.0021							
		ITGYIIK	1	0.2014	0.2014								

		IYLYTLNDNAR	1	0.1918	0.1918								
		LGVRPSQGGEAPR	1	0.2688	0.2688								
		QYNVGPSVSK	3	0.1737	0.1724	1.1627							
		SDTVPSPR	2	0.1564	0.1562	1.0688							
		SERLIGR	3	0.1952	0.1913	1.2753							
		STTPDITGYR	4	0.1731	0.1724	1.106							
		SYTITGLQPGTDYK	1	0.2261	0.2261								
		TFYSCTTEGR	2	0.2319	0.2205	1.5715							
		TYHVGEQWQK	1	0.222	0.222								
		VDVIPVNLPGEHGQR	1	0.2379	0.2379								
		VFAVSHGR	2	0.1608	0.16	1.1491							
		YEKPGSPPR	1	0.1782	0.1782								
		YEVSVYALK	4	0.2187	0.2165	1.18							
		YTGNTYR	1	0.1945	0.1945								
FKBP3_HUMAN	FK506-binding protein 3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1	FLQEHGSDSFLAEHK	1	3.2798	3.2798		2	3.5308	3.6145	3.5219	3.6065	3.5779	1.106
		LEIEPEWAYGK	2	3.7819	3.737	1.2448							
FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	AGNNMLLVGVHGPR	1	0.2403	0.2403		21	4.2243	4.6138	2.2185	2.6192	2.6112	4.5798
		AHVVPCFDASK	1	1.2746	1.2746								
		AWGPGLEGGVVGK	1	0.1211	0.1211								
		AYGPGIEPTGNMVK	1	0.1033	0.1033								
		DGSCGVAYVVQEPGDYEVSVK	1	1.6829	1.6829								
		DLAEDAPWK	2	4.6534	4.5598	1.3312							
		DVDIIDHHDNTYTVK	1	11.2058	11.2058								
		EATTEFSVDAR	1	5.9853	5.9853								
		FVPAEMGTHTVSVK	1	0.0963	0.0963								
		GKLDVQFSGLTK	1	3.7485	3.7485								
		LDVQFSGLTK	1	2.651	2.651								
		LIALLEVLSGK	2	14.925	14.9243	1.0131							
		LTVSSLQESGLK	1	3.7286	3.7286								
		LVSIDSK	2	3.7408	3.7044	1.2188							
		LYSVSYLLK	1	5.6349	5.6349								
		NDNDTFTVK	1	8.9733	8.9733								
		SAGQGEVLYVVEDPAGHQEEAK	2	4.4193	4.3999	1.1419							
		SPFEVYVDK	1	4.6742	4.6742								
		SPFSVAVSPSLDLSK	2	3.5098	3.491	1.1578							
		VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	1	2.7282	2.7282								
		VTAGQPGLEPSGNIANK	1	4.6133	4.6133								
FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=1	AEITFDDHK	2	0.8383	0.3537	8.4376	20	6.1183	5.8812	4.8972	4.6178	4.2177	2.1157
		ALGALVDSCAPGLCPDWESWDPQKPVDNAR	1	4.4401	4.4401								
		DAGYGGISLAVEGPSK	1	5.9122	5.9122								
		DLAEDAPWK	2	4.6534	4.5598	1.3312							
		DLDIIDNYDYSHTVK	1	11.8116	11.8116								
		EAGAGGLSIAVEGPSK	2	2.9677	2.4905	2.368							
		GAGTGGLGLTVEGPCEAK	1	10.1002	10.1002								
		GDYVLAVK	2	5.1343	5.1238	1.0944							
		GIEPTGNMVK	1	5.072	5.072								
		IEYNDQNDGSCDVK	1	9.0075	9.0075								
		LIALLEVLSGK	2	14.925	14.9243	1.0131							
		LTVMSLQESGLK	2	4.1667	3.5748	2.2322							
		LVSIDSK	2	3.7408	3.7044	1.2188							
		MDGTYACSYTPVK	1	12.1287	12.1287								
		TFEMSDFIVDTR	1	1.6672	1.6672								
		VKVEPAVDTSR	1	7.4522	7.4522								
		VLQSFTVDSSK	1	6.885	6.885								
		VLSEDEEDVDFDIIHNANDTFTVK	1	3.8628	3.8628								
		VTEAEIVPMGK	1	7.3346	7.3346								
		YMIGVTVGGDDIPLSPYR	1	1.2667	1.2667								
FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	AFGPGLEPTGCIVDIKPAEFTIDAR	1	0.104	0.104		11	4.7423	5.2301	2.3673	2.9303	2.8512	4.7606
		AWGPGLETGQVGK	1	1.5985	1.5985								
		DAGEGLLTVQILDPEGKPK	1	2.6503	2.6503								
		DFEIDNHDYSYTVK	1	2.2641	2.2641								
		DLAEDAPWK	2	4.6534	4.5598	1.3312							
		EAGAGGLSIAVEGPSK	2	2.9677	2.4905	2.368							
		GAGTGGLGLTVEGPCEAK	1	10.1002	10.1002								
		LIALLEVLSGK	2	14.925	14.9243	1.0131							
		LVSIDSK	2	3.7408	3.7044	1.2188							
		LYAQDADGCPIDIK	1	0.1877	0.1877								
		NDNDTFTVK	1	8.9733	8.9733								
FRPD1_HUMAN	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1	DIILTVK	2	4.6638	0.8197	30.8154	1	4.6638	4.6638	4.6638	4.6638	0.8197	
FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	LSCFAQTVSPAEK	1	5.3198	5.3198		4	5.6738	6.1906	5.323	5.9198	5.6544	1.5372
		SSYDVFQLEFNDGAYNIK	2	8.1909	7.7702	1.5892							
		YLAADKDGNVTCER	1	2.9602	2.9602								
		YLTAEAFGFK	3	6.2242	5.7926	1.593							
FST_HUMAN	Follistatin OS=Homo sapiens GN=FST PE=1 SV=2	EAACSSCVLLEVK	1	0.3119	0.3119		1	0.3119	0.3119	0.3119	0.3119	0.3119	
FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1	CLNPSFNPPEKK	1	5.6042	5.6042		9	1.1941	0.9445	0.7978	0.7074	0.7024	2.1473
		GAQTQTEEEMTR	3	0.5571	0.5424	1.3269							
		GEPTCLCIEQCKPHK	1	0.7722	0.7722								
		GLCVDALIELSDENADWK	1	0.548	0.548								
		ICANVFCGAGR	2	1.0431	1.0406	1.1032							
		IIQWLEAEIPDGWFSK	1	0.5432	0.5432								
		IQVDYDGHCK	1	0.5749	0.5749								
		LDSSEFLK	3	0.5679	0.5666	1.0859							
		LSFQEFLK	3	0.536	0.5321	1.158							
FTHFD_HUMAN	10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2	IGFTGSTEVGK	1	0.2403	0.2403		1	0.2403	0.2403	0.2403	0.2403	0.2403	
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	SELKDFFQSYGNVVELR	1	3.1055	3.1055		1	3.1055	3.1055	3.1055	3.1055	3.1055	
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	AGAHLQGGAK	1	3.6279	3.6279		10	7.3315	8.3893	4.779	6.4036	5.4169	3.5027
		GALQNIIPASTGAAK	4	13.8804	11.344	2.3362							
		IISNASCTTNCLAPLAK	3	11.7005	10.5634	1.7929							
		LISWYDNEFGYSNR	1	16.7635	16.7635								
		QASEGPLK	1	0.2154	0.2154								
		TVDGPSGK	1	3.398	3.398								
		VIHDNFGIVEGLMTTVHAITATQK	2	2.8966	2.2053	2.9814							
		VIISAPSADAPMFVMGVNHEK	2	6.7437	5.4571	2.5934							
		VVDLMAHMASK	3	9.4151	8.2088	1.8714							
		WGDAGAEYVVESTGVFTTMEK	3	4.6741	3.3269	3.2126							
G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	FAAYFQQGDMESNGK	2	2.571	2.5582	1.1521	4	8.1969	7.0717	6.7861	5.5888	5.5776	2.1214
		HFVALSTNTTK	1	14.8262	14.8262								
		TFTTQETITNAETAK	1	5.8026	5.8026								
		VWYVSNIDGTHIAK	1	9.5879	9.5879								
GALT5_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1	WKEGNFNVYLSDLIPVDR	1	6.7399	6.7399		1	6.7399	6.7399	6.7399	6.7399	6.7399	
GALT6_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	NLGTNQCLDVGENNR	1	0.5278	0.5278		1	0.5278	0.5278	0.5278	0.5278	0.5278	
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	FSPNSSNPIVVSCSWDK	1	3.1178	3.1178		2	3.1153	3.1144	3.1153	3.1144	3.1119	1.0011
		YWLCAATGPSIK	2	3.1128	3.109	1.0723							
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	DWNVDLIPK	2	9.648	8.4029	2.1397	3	4.8051	6.0158	3.5743	4.5814	4.2756	2.6203
		KFDLGQDVIDFTGHALALYR	1	1.4095	1.4095								
		MAGTAFDFENMK	1	3.3578	3.3578								
GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	DWNVDLIPK	2	9.648	8.4029	2.1397	8	6.7334	7.0865	4.7473	5.13	3.8314	2.774
		FVSIDDLLVPK	2	12.3255	12.3254	1.0056							
		KFDLGQDVIDFTGHALALYR	1	1.4095	1.4095								
		MTGSEFDFEEMK	2	2.1112	0.4868	20.818							
		NPYYGGESASITPLEDLYK	1	11.1286	11.1286								
		TYDATTHFETTCDDIK	1	7.5785	7.5785								
		VICILSHPIK	1	8.669	8.669								
		VPSTEAEALASSLMGLFEK	1	0.9971	0.9971								
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	AEEYEFLTPVEEAPK	1	9.7324	9.7324		2	9.8325	9.8325	9.8319	9.8319	9.8319	1.0145
		IDKTDYMYGSYGPR	1	9.9325	9.9325								
GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	ATFMVGSYGPRPEEYEFLTPVEEAPK	1	3.0547	3.0547		2	5.6805	5.6805	5.0372	5.0372	5.0372	2.0286
		ELQEMDKDDESLIK	1	8.3062	8.3062								
GDN_HUMAN	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1	TIDSWMSMVPK	2	0.6616	0.6595	1.119	1	0.6616	0.6616	0.6616	0.6616	0.6595	
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	EVQGFESATFLGYFK	1	2.7354	2.7354		2	1.6852	1.6852	1.3179	1.3179	1.3179	2.8085
		SEDCFILDHGK	1	0.635	0.635								
GFAP_HUMAN	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	FLEQQNK	3	9.9734	9.9349	1.1139	3	6.8137	6.1935	3.9186	3.2547	3.224	4.9916
		GTNESLER	3	9.8554	9.7679	1.1803							
		LALDIEIATYR	4	0.6122	0.6036	1.21							
GLBD3_HUMAN	Glycosyltransferase 8 domain-containing protein 3 OS=Homo sapiens GN=GLT8D3 PE=1 SV=1	LFLPLILK	3	12.7813	12.2354	1.4345	1	12.7813	12.7813	12.7813	12.7813	12.2354	
GLOD4_HUMAN	Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	ALLGYADNGCK	1	0.2093	0.2093		1	0.2093	0.2093	0.2093	0.2093	0.2093	
GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	WQTLLSVDDLVEK	1	4.0406	4.0406		1	4.0406	4.0406	4.0406	4.0406	4.0406	
GPC1_HUMAN	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=1	GANLHLEETLAEFWAR	1	0.2696	0.2696		4	0.4003	0.4003	0.3809	0.3809	0.3809	1.4248
		QLHPQLLLPDDYLDCLGK	1	0.3743	0.3743								
		SFVQGLGVASDVVR	1	0.3354	0.3354								
		VLQAMLATQLR	1	0.6217	0.6217								
GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	LYSPSQIGAFVLMK	1	0.5899	0.5899		1	0.5899	0.5899	0.5899	0.5899	0.5899	
GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	IINEPTAAAIAYGLDK	3	6.0371	5.997	1.151	5	3.5368	3.9957	1.2159	1.9555	1.95	7.949
		NELESYAYSLK	1	0.0642	0.0642								
		TAPEESAMVLTK	1	0.3439	0.3439								
		TWNDPSVQQDIK	2	2.2079	2.2051	1.0738							
		VEIANDQGNR	1	9.0307	9.0307								
GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	EDPTVSALLTSEK	2	0.6266	0.6168	1.286	1	0.6266	0.6266	0.6266	0.6266	0.6168	
GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	ALPGQLKPFETLLSQNQGGK	1	9.5181	9.5181		4	8.4406	8.4406	7.7708	7.7708	7.7708	1.642
		EEVVTVETWQEGSLK	1	3.9118	3.9118								
		TLGLYGK	1	12.4945	12.4945								
		TLGLYGKDQQEAALVDMVNDGVEDLR	1	7.8381	7.8381								
H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	DNIQGITKPAIR	1	3.3521	3.3521		2	3.7188	3.9022	3.7007	3.8883	3.8489	1.1502
		TVTAMDVVYALK	3	4.0855	4.0303	1.2285							
H90B2_HUMAN	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2	ADLINNLGTIAK	1	16.8853	16.8853		5	14.7593	15.6925	13.659	14.7743	13.3544	1.6311
		SIYYITGESK	1	5.7756	5.7756								
		SLVSVTK	1	15.0808	15.0808								
		YESLTDPSK	2	19.3384	17.4884	1.9057							
		YIDQEELNK	2	16.7128	12.9754	2.8552							
H90B3_HUMAN	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	EGLELPEDEEEK	1	7.904	7.904		5	11.4921	12.4708	10.2342	11.2489	10.8916	1.7483
		EGLELPEDEEEKK	1	4.6399	4.6399								
		EMLGGSK	2	10.4972	10.3675	1.2504							
		SLVSVTK	1	15.0808	15.0808								
		YESLTDPSK	2	19.3384	17.4884	1.9057							
H90B4_HUMAN	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1	EGLELPEDEEEK	1	7.904	7.904		4	8.2784	10.4904	5.4363	7.0069	6.7307	3.1641
		EGLELPEDEEEKK	1	4.6399	4.6399								
		GFEVIYMSEPIDEYCVQQLK	1	1.2315	1.2315								
		YESLTDPSK	2	19.3384	17.4884	1.9057							
HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	MFLSFPTTK	3	1.3329	1.331	1.0676	1	1.3329	1.3329	1.3329	1.3329	1.331	
HDGF_HUMAN	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	GPPQEEEEEEEDEEEEATKEDAEEAPGIR	2	3.242	3.2407	1.0397	2	3.0238	3.0965	3.0159	3.0894	3.0886	1.1076
		YQVFFFGTHETAFLGPK	1	2.8056	2.8056								
HEXA_HUMAN	Beta-hexosaminidase subunit alpha OS=Homo sapiens GN=HEXA PE=1 SV=1	GLETFSQLVWK	1	0.7687	0.7687		1	0.7687	0.7687	0.7687	0.7687	0.7687	
HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	GSIVWQEVFDDK	1	6.2807	6.2807		3	4.5077	5.1408	2.0772	2.8184	2.719	7.5089
		LAPGTIVEVWK	2	7.0398	6.5522	1.7199							
		VLDIAITINK	1	0.2027	0.2027								
HGB1A_HUMAN	Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1L1 PE=5 SV=1	IKGEHPGLSIGDVAK	1	2.811	2.811		1	2.811	2.811	2.811	2.811	2.811	
HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	IKGEHPGLSIGDVAK	1	2.811	2.811		3	3.5405	3.7498	3.4827	3.6876	3.6603	1.2484
		KHPDASVNFSEFSK	2	4.3776	4.313	1.2769							
		LGEMWNNTAADDKQPYEK	1	3.4328	3.4328								
HMGL1_HUMAN	High mobility group protein 1-like 10 OS=Homo sapiens GN=HMG1L10 PE=1 SV=1	IKGEHPGLSIGDVAK	1	2.811	2.811		2	3.1219	3.1219	3.1064	3.1064	3.1064	1.1518
		LGEMWNNTAADDKQPYEK	1	3.4328	3.4328								
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3	GFGFVLFK	1	8.3806	8.3806		1	8.3806	8.3806	8.3806	8.3806	8.3806	
HNRGT_HUMAN	RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens GN=RBMXL2 PE=1 SV=3	GFAFVTFESPADAK	1	3.6019	3.6019		2	2.226	2.226	1.7499	1.7499	1.7499	2.7759

		IVEVLLMK	1	0.8501	0.8501								
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	EYFGGFGEVESIELPMDNK	2	5.3932	5.3931	1.0065	5	5.182	4.7675	4.7606	4.3766	4.3377	1.6244
		GFCFITFK	1	5.2994	5.2994								
		GFGFVLFK	1	8.3806	8.3806								
		IFVGGLSPDTPEEK	2	4.6337	4.5494	1.3124							
		MFIGGLSWDTTK	2	2.2031	2.1652	1.3022							
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	TEMDWVLK	1	5.0132	5.0132		1	5.0132	5.0132	5.0132	5.0132	5.0132	
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=RBMX PE=1 SV=3	GFAFVTFESPADAK	1	3.6019	3.6019		3	2.2342	2.2342	1.903	1.903	1.903	2.0884
		IVEVLLMK	1	0.8501	0.8501								
		VEQATKPSFESGR	1	2.2507	2.2507								
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	IILDLISESPIK	3	6.2546	5.9628	1.4611	2	4.5944	4.9264	4.2839	4.6207	4.4628	1.7078
		ILSISADIETIGEILK	2	2.9341	2.8896	1.2811							
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	EFNEQGALAVLQQFK	1	2.5775	2.5775		1	2.5775	2.5775	2.5775	2.5775	2.5775	
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	EFNEEGALSVLQQFK	1	1.2739	1.2739		1	1.2739	1.2739	1.2739	1.2739	1.2739	
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	NVLIVEDIIDTGK	1	7.7613	7.7613		2	4.2314	4.2314	2.3332	2.3332	2.3332	5.4726
		VIGGDDLSTLTGK	1	0.7014	0.7014								
HPS6_HUMAN	Hermansky-Pudlak syndrome 6 protein OS=Homo sapiens GN=HPS6 PE=2 SV=1	LLLAEFAQHR	1	1.3886	1.3886		1	1.3886	1.3886	1.3886	1.3886	1.3886	
HS71L_HUMAN	Heat shock 70 kDa protein 1L OS=Homo sapiens GN=HSPA1L PE=1 SV=2	IINEPTAAAIAYGLDK	3	6.0371	5.997	1.151	4	4.0709	4.7263	2.0639	2.9517	2.9419	4.5032
		NALESYAFNMK	1	0.7995	0.7995								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.4163	0.4163								
		VEIIANDQGNR	1	9.0307	9.0307								
HS902_HUMAN	Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2	ADLINNLGTIAK	1	16.8893	16.8893		4	10.5281	11.765	8.446	9.6812	8.749	2.2166
		ELHINLIPNK	1	3.9746	3.9746								
		ELISNSSDALDK	1	4.5358	4.5358								
		YDQEELNK	2	16.7126	12.9754	2.8552							
HS904_HUMAN	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1	TLTIVDTGIGMTK	5	6.8501	5.42	2.2351	1	6.8501	6.8501	6.8501	6.8501	5.42	
HS905_HUMAN	Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1	EGLELPEDEEEK	1	7.904	7.904		3	7.9852	7.9852	7.48	7.48	7.48	1.5722
		EGLELPEDEEEKK	1	4.6399	4.6399								
		HSQFIGYPITLFVEK	1	11.4116	11.4116								
HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	ADLINNLGTIAK	1	16.8893	16.8893		12	10.0191	10.2882	8.7523	9.1651	8.333	1.736
		EGLELPEDEEEK	1	7.904	7.904								
		EGLELPEDEEEKK	1	4.6399	4.6399								
		ELHINLIPNK	1	3.9746	3.9746								
		ELISNSSDALDK	1	4.5358	4.5358								
		EMLQQSK	2	10.4972	10.3675	1.2504							
		HSQFIGYPITLFVEK	1	11.4116	11.4116								
		NPDDITNEEYGEFYK	2	11.5876	11.5841	1.0353							
		SLTNDWEDHLAVK	1	5.8881	5.8881								
		TLTIVDTGIGMTK	5	6.8501	5.42	2.2351							
		YESLTDPSK	2	19.3384	17.4884	1.9057							
		YDQEELNK	2	16.7126	12.9754	2.8552							
HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	ADLINNLGTIAK	1	16.8893	16.8893		14	9.9921	10.083	8.3635	8.7785	7.9425	2.0258
		CLELFSELAEDKENYK	1	9.1658	9.1658								
		EGLELPEDEEEK	1	7.904	7.904								
		EGLELPEDEEEKK	1	4.6399	4.6399								
		ELISNASDALDK	3	9.0362	7.9112	1.8714							
		EMLQQSK	2	10.4972	10.3675	1.2504							
		GFEVVYMTEPIDEYCVQQLK	1	1.2315	1.2315								
		NPDDITQEEYGEFYK	1	10.8798	10.8798								
		SIYYITGESK	1	5.7756	5.7756								
		SLTNDWEDHLAVK	1	5.8881	5.8881								
		SLVSVTK	1	15.0808	15.0808								
		TLTLVDTGIGMTK	5	6.8501	5.42	2.2351							
		YESLTDPSK	2	19.3384	17.4884	1.9057							
		YDQEELNK	2	16.7126	12.9754	2.8552							
HSP71_HUMAN	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5	AAAIGIDLGTTYSCVGVFQHGK	1	5.5276	5.5276		4	3.9435	3.9435	2.0189	2.0189	2.0189	4.412
		NALESYAFNMK	1	0.7995	0.7995								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.4163	0.4163								
		VEIIANDQGNR	1	9.0307	9.0307								
HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	DNNLLGK	2	10.8734	10.3565	1.5604	5	9.4544	8.7775	9.2419	8.4792	8.3557	1.2838
		FEELNADLFR	1	10.5416	10.5416								
		IINEPTAAAIAYGLDK	3	6.0371	5.997	1.151							
		IINEPTAAAIAYGLDKK	1	10.7894	10.7894								
		VEIIANDQGNR	1	9.0307	9.0307								
HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	LFEELGK	1	0.0662	0.0662		2	1.374	1.374	0.4213	0.4213	0.4213	13.7001
		SNLAYDIVQLPTGLTGIK	1	2.6818	2.6818								
HSP76_HUMAN	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	VEILANDQGNR	1	9.0307	9.0307		1	9.0307	9.0307	9.0307	9.0307	9.0307	
HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	CNEIINWLDK	2	13.3968	13.2843	1.2018	15	7.3638	7.294	5.9309	6.1109	5.9088	2.2259
		DNNLLGK	2	10.8734	10.3565	1.5604							
		EIAEAYLGK	1	7.815	7.815								
		FDDAVVQSDMK	1	2.7906	2.7906								
		FEELNADLFR	1	10.5416	10.5416								
		GPAVGIDLGTTYSCVGVFQHGK	2	4.1173	3.1349	2.981							
		GTLDPVEK	1	1.3962	1.3962								
		IINEPTAAAIAYGLDK	3	6.0371	5.997	1.151							
		IINEPTAAAIAYGLDKK	1	10.7894	10.7894								
		MVNHFIAEFK	1	8.5167	8.5167								
		NQVAMNPTNTVFDAK	1	10.1138	10.1138								
		RFDDAVVQSDMK	1	9.3566	9.3566								
		SFYPEEVSSMVLTK	3	4.7745	4.6791	1.2845							
		SINPDEAVAYGAAVQAALSGDK	1	0.907	0.907								
		VEIIANDQGNR	1	9.0307	9.0307								
HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	AQLGGPEAAK	1	0.4747	0.4747		3	2.5065	2.8788	1.795	2.1925	2.0852	3.1892
		KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	2	3.9954	3.614	1.9044							
		TKDGVVEITGK	1	3.0495	3.0495								
HTRA1_HUMAN	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	GACGQQQEDPNSLR	1	1.3417	1.3417		3	3.3037	3.3037	2.1929	2.1929	2.1929	2.9303
		SSELRPGEFVVAIGSPFSLQNTVTTGIVSTTQR	1	1.0445	1.0445								
		VTAGISFAIPSDK	1	7.525	7.525								
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2	EDARPVPQGSCQSELHR	1	0.2479	0.2479		2	0.3534	0.3534	0.3372	0.3372	0.3372	1.5454
		THEDLYIIPIPNCDR	1	0.4588	0.4588								
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1	ALSMCPPSPLGCELVK	2	6.4925	1.8312	15.5051	5	1.5536	2.0969	0.524	0.7268	0.506	4.5843
		EHEEPTTSEMEETYSPK	1	0.3572	0.3572								
		GICWCVDK	1	0.3984	0.3984								
		GVCLNEK	2	0.4176	0.4169	1.0862							
		HMEASLQELK	1	0.1024	0.1024								
IBP6_HUMAN	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1	APAVAEENPK	1	0.1372	0.1372		4	1.4215	1.3896	0.8947	0.9584	0.9584	3.7563
		EGQECGVYTPNCAPGLQCHPPKDDEAPLR	1	3.0886	3.0886								
		GAQTLVYVPNCDHR	2	1.262	1.2618	1.0275							
		HLDSVLQQLQTEVYR	1	1.1982	1.1982								
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	AGAAAGGPGVSGVCVCK	1	1.5053	1.5053		8	2.3639	2.2523	2.1626	2.115	2.1046	1.5021
		DACGCCPMCAR	1	2.2748	2.2748								
		EDACYECVHASNSGQGQASASAK	4	1.9341	1.9204	1.1487							
		GTCEQGPSIVTPPK	1	1.9419	1.9419								
		GYCAPGMECVK	1	5.5279	5.5279								
		HEVTGWLVSPLSK	1	1.7629	1.7629								
		ITVVDALHEIPVK	2	2.315	2.2793	1.284							
		SRYPVCGSDGTTYPSGCQLR	1	1.649	1.649								
IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	LVLLNAIYLSAK	1	0.0128	0.0128		2	0.124	0.124	0.0549	0.0549	0.0549	7.8309
		TNLESLSYPK	1	2.2351	2.2351								
ICAM2_HUMAN	Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2	GGNIFHK	1	5.3519	5.3519		3	12.2362	12.2362	9.4389	9.4389	9.4389	2.3407
		ILLDEQAQWK	1	6.2612	6.2612								
		QVILTLQPTLVAVGK	1	25.0955	25.0955								
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	GWPLYLSTK	1	7.5774	7.5774		1	7.5774	7.5774	7.5774	7.5774	7.5774	
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	TAWVFDDK	1	2.1783	2.1783		2	1.1035	1.1035	0.25	0.25	0.25	21.3564
		TEGLSVLSQAMAVIK	1	0.0287	0.0287								
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	EVEPEPTEDKDLEADEEDTR	1	1.4607	1.4607		1	1.4607	1.4607	1.4607	1.4607	1.4607	
IF2BL_HUMAN	Eukaryotic translation initiation factor 2 subunit 2-like protein OS=Homo sapiens PE=2 SV=1	EVEPEPTEDKDLEADEEDTR	1	1.4607	1.4607		1	1.4607	1.4607	1.4607	1.4607	1.4607	
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GYDVIAQAQSGTGK	1	3.6921	3.6921		1	3.6921	3.6921	3.6921	3.6921	3.6921	
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	GYDVIAQAQSGTGK	1	3.6921	3.6921		1	3.6921	3.6921	3.6921	3.6921	3.6921	
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	EDLRLPEGDLGK	1	5.4312	5.4312		4	3.9141	3.9141	3.8178	3.8178	3.8178	1.2861
		IVEMSTSK	1	3.0815	3.0815								
		KYEDICPSTHNMDVPNIK	1	3.3174	3.3174								
		YEDICPSTHNMDVPNIK	1	3.8264	3.8264								
IF5A2_HUMAN	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3	IVEMSTSK	1	3.0815	3.0815		2	3.454	3.454	3.4338	3.4338	3.4338	1.1654
		YEDICPSTHNMDVPNIK	1	3.8264	3.8264								
IF5AL_HUMAN	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=1 SV=2	KYEDICPSTHNMDVPNIK	1	3.3174	3.3174		1	3.3174	3.3174	3.3174	3.3174	3.3174	
IF8_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	QTVADQVLVGSYCVFSNQGGLVHPK	1	1.6916	1.6916		1	1.6916	1.6916	1.6916	1.6916	1.6916	
IFNG_HUMAN	Interferon gamma OS=Homo sapiens GN=IFNG PE=1 SV=1	SVETIK	1	0.0856	0.0856		1	0.0856	0.0856	0.0856	0.0856	0.0856	
ILEU_HUMAN	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	LVLVNAIYFK	1	5.9377	5.9377		1	5.9377	5.9377	5.9377	5.9377	5.9377	
ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	GTMTTGHNVADLVVILK	1	0.4687	0.4687		2	1.6813	1.6813	1.1646	1.1646	1.1646	3.6227
		ILPTLEAVAALGNK	1	2.8939	2.8939								
ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	AVSDWDEQEK	1	3.8038	3.8038		3	3.5145	3.5145	3.3513	3.3513	3.3513	1.4784
		GDLDLELVLLCK	1	4.5781	4.5781								
		GWPLELLCEK	1	2.1615	2.1615								
IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	LAATNALLNSLEFTK	2	1.0611	0.6943	4.0397	2	2.7258	3.0588	2.1584	2.4878	2.0381	2.7298
		SSAYESLMEIVK	3	4.3906	4.1784	1.4789							
IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	HFADLLPGFLQAVNDSCYQNDDSVLK	1	2.8847	2.8847		3	4.0288	4.0288	3.4423	3.4423	3.4423	1.9628
		HIVENAVQK	1	7.252	7.252								
		QWGLCIFDDVIEHCSPASFK	1	1.9498	1.9498								
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	EQLSDMMMINK	1	0.9197	0.9197		5	2.1927	2.1927	1.875	1.875	1.875	1.9179
		ILAIGLINEALDEGDAQK	1	2.1877	2.1877								
		LPYDVTPEQALAWEEVK	1	0.9758	0.9758								
		QSGQTDPLQKEELQSGVDAANSAAQQYQR	1	3.6196	3.6196								
		SWVNQMESQTGEASK	1	3.2606	3.2606								
ISLR_HUMAN	Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=1 SV=1	EVPLLQSLWLAHNEIR	1	1.406	1.406		1	1.406	1.406	1.406	1.406	1.406	
ITGB1_HUMAN	Integrin beta-like protein 1 OS=Homo sapiens GN=ITGBL1 PE=2 SV=1	NLCESADGILCSGK	1	0.1468	0.1468		1	0.1468	0.1468	0.1468	0.1468	0.1468	
K0020_HUMAN	Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3	QMWEILR	1	4.2261	4.2261		1	4.2261	4.2261	4.2261	4.2261	4.2261	
K0825_HUMAN	Uncharacterized protein KIAA0825 OS=Homo sapiens GN=KIAA0825 PE=2 SV=2	HIVPDCLLESMPK	1	0.138	0.138		1	0.138	0.138	0.138	0.138	0.138	
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=5	AETECQNTEYQQLLDIK	3	0.5738	0.5711	1.128	23	0.7084	0.717	0.6949	0.7069	0.7038	1.2357
		ALEESNYELEGK	3	0.7474	0.7468	1.0518							
		DAEAWFNEK	2	0.7422	0.7403	1.1055							
		ELTTEIDNNIEQISSYK	1	0.6739	0.6739								
		GSSGGGCFGSGSGGYGGLGGFGGGGSFR	2	0.7443	0.7442	1.0156							
		ISSSKGSLGGGFSSGGFSGGSFSR	1	0.3474	0.3474								
		LAADDFR	2	0.7209	0.7208	1.024							
		LASYLDK	2	0.6162	0.6147	1.1024							
		LENEIQTYR	1	0.9283	0.9283								
		LKYENEVALR	2	0.8212	0.8169	1.1549							
		NQILNLTTDNANILLQIDNAR	1	0.6447	0.6447								
		NVQALEIELQSQLALK	1	0.7944	0.7944								
		NVSTGDVNVEMNAAPGVDLTQLLNNMR	3	0.7856	0.7593	1.3734							
		QSLEASLAETEGR	1	0.7937	0.7937								
		QSVEADINGLR	1	0.5996	0.5996								
		QSVEADINGLRR	2	0.8074	0.8054	1.1037							
		RVLDELTLTK	1	0.4773	0.4773								
		SQYEQLAEQNR	3	0.8024	0.7969	1.1574							
		SQYEQLAEQNRK	1	0.8054	0.8054								
		TIDDLK	1	0.649	0.649								
		VLDELTLTK	1	0.8411	0.8411								
		VTMQNLNDR	2	0.6842	0.6832	1.078							
		YCVQLSQIQAQISALEEQLQQIR	1	0.6921	0.6921								
K1C12_HUMAN	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	LASYLDK	2	0.6162	0.6147	1.1024	2	6.2031	4.3408	2.6954	1.6481	1.6454	8.0605
		VLDELTLTR	1	11.79	11.79								

K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=3	QSVEADINGLR	1	0.5996	0.5996		2	0.7035	0.7381	0.6958	0.7311	0.73	1.2341
		QSVEADINGLRR	2	0.8074	0.8054	1.1037							
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	ADLEMQIESLKEELAYLK	1	0.0323	0.0323		7	0.6171	0.6341	0.4533	0.5102	0.5098	3.243
		ASLENSLEETK	1	0.9988	0.9988								
		ISSVLAGGSCR	1	0.6433	0.6433								
		LAADDFR	2	0.7209	0.7208	1.024							
		LASYLDK	2	0.6162	0.6147	1.1024							
		VLDELTLAR	1	0.6237	0.6237								
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C15_HUMAN	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=2	LAADDFR	2	0.7209	0.7208	1.024	3	0.6536	0.6596	0.6519	0.6577	0.657	1.0912
		LASYLDK	2	0.6162	0.6147	1.1024							
		VLDELTLAR	1	0.6237	0.6237								
K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	ASLENSLEETK	1	0.9988	0.9988		6	0.7145	0.7009	0.7041	0.6933	0.6927	1.1987
		ISSVLAGGSCR	1	0.6433	0.6433								
		LAADDFR	2	0.7209	0.7208	1.024							
		LASYLDK	2	0.6162	0.6147	1.1024							
		VLDELTLAR	1	0.6237	0.6237								
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	LAADDFR	2	0.7209	0.7208	1.024	3	0.6536	0.6596	0.6519	0.6577	0.657	1.0912
		LASYLDK	2	0.6162	0.6147	1.1024							
		VLDELTLAR	1	0.6237	0.6237								
K1C18_HUMAN	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	LAADDFR	2	0.7209	0.7208	1.024	2	0.8076	0.7787	0.8029	0.7746	0.7745	1.1645
		LASYLDR	1	0.8942	0.8942								
K1C19_HUMAN	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=3	LAADDFR	2	0.7209	0.7208	1.024	3	0.6536	0.6596	0.6519	0.6577	0.657	1.0912
		LASYLDK	2	0.6162	0.6147	1.1024							
		VLDELTLAR	1	0.6237	0.6237								
K1C20_HUMAN	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1	MAMQNLNDR	1	0.7445	0.7445		1	0.7445	0.7445	0.7445	0.7445	0.7445	
K1C24_HUMAN	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1	LAADDFR	2	0.7209	0.7208	1.024	3	1.9048	1.6088	1.2384	1.0817	1.0816	3.0059
		QSVEADINGLR	1	0.5996	0.5996								
		QSVEADINGLRK	1	4.3938	4.3938								
K1C25_HUMAN	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1	DAEAWFNEK	2	0.7422	0.7403	1.1055	2	0.7132	0.7132	0.7126	0.7126	0.7112	1.0592
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C26_HUMAN	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2	DAEAWFNER	1	1.0228	1.0228		2	0.8535	0.7971	0.8365	0.7823	0.7816	1.3288
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C27_HUMAN	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=1	DAEAWFNEK	2	0.7422	0.7403	1.1055	2	0.7132	0.7132	0.7126	0.7126	0.7112	1.0592
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C28_HUMAN	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=1	DAEAWFNEK	2	0.7422	0.7403	1.1055	3	0.7158	0.7158	0.7153	0.7153	0.7144	1.0421
		LAADDFR	2	0.7209	0.7208	1.024							
		VTMQNLNDR	2	0.6842	0.6832	1.078							
K1C40_HUMAN	Keratin, type I cytoskeletal 40 OS=Homo sapiens GN=KRT40 PE=1 SV=2	ETMQFLNDR	1	3.1326	3.1326		1	3.1326	3.1326	3.1326	3.1326	3.1326	
K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	DIENQYETQITQIEHEVSSSGQEVQSSAK	3	0.4004	0.3981	1.1405	17	0.7207	0.7653	0.5951	0.6254	0.5619	1.7799
		EIETYHNLLEGQEDFESSGAGK	1	0.4917	0.4917								
		FSSSGGGGGGGR	1	0.4668	0.4668								
		FSSSSGYGGGSSR	3	0.5257	0.5255	1.0395							
		GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR	2	1.1942	1.0552	2.0507							
		GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK	1	0.6284	0.6284								
		GGSGGSYGGGGSGGGYGGGSGSR	2	0.4582	0.4581	1.0067							
		IKFEMEQNLR	1	2.3907	2.3907								
		LASYLDK	2	0.6162	0.6147	1.1024							
		MTLDDFR	1	0.2406	0.2406								
		NYSPYYNTIDLKDQIVDLTVGNNK	1	0.4353	0.4353								
		QEIECQNQEYSLLSIK	2	0.5402	0.5371	1.1634							
		QVLDNLTMEK	1	0.5328	0.5328								
		SGGGGGGLGSGGSIR	1	0.6267	0.6267								
		STMQELNSR	4	1.8729	0.8975	3.6574							
		TLLDIDNTR	3	0.3621	0.3593	1.1612							
		VQALEEANNDLENK	2	0.4696	0.4529	1.4664							
K1H1_HUMAN	Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	ETMQFLNDR	1	3.1326	3.1326		4	7.6182	6.2387	2.6038	2.014	2.0139	5.3178
		LAADDFR	2	0.7209	0.7208	1.024							
		LNVEVDAAPTVDLNR	1	0.788	0.788								
		SDLEAQVESLKEELLCLK	1	25.8312	25.8312								
K1H2_HUMAN	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=2	ETMQFLNDR	1	3.1326	3.1326		2	1.9268	1.5248	1.5028	1.1764	1.1763	2.8259
		LAADDFR	2	0.7209	0.7208	1.024							
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	AQYEEIAQR	2	0.82	0.8174	1.1191	14	1.2985	1.0212	0.7685	0.6662	0.6573	3.5012
		DVDNAYMIK	1	0.9577	0.9577								
		DYQELMNVK	2	0.0177	0.0151	2.2524							
		FASFIDK	1	0.9668	0.9668								
		FGGFGGPGGVGGLGGPGGGYPGGIHEVSVNQSLLQPLNVK	1	0.9765	0.9765								
		FLEQQNQVLQTK	5	0.5503	0.5461	1.1455							
		IEISELNR	2	0.5939	0.5925	1.1017							
		LNDLEEALQQAK	2	0.7674	0.7654	1.1049							
		NLDLDSIIAEVK	4	0.8027	0.8024	1.0322							
		STSSFSQLSR	1	7.2166	7.2166								
		TSQNSELNNMQDLVEDYKK	1	0.8269	0.8269								
		VDLLNQEIEFLK	3	0.9033	0.9003	1.1044							
		YEELQVTVGR	2	1.7991	1.799	1.0018							
		YLDGLTAER	1	0.9805	0.9805								
K22O_HUMAN	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=1	DYQELMNVK	2	0.0177	0.0151	2.2524	3	3.6526	5.1537	0.5542	0.8176	0.7747	24.6535
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	3	9.9734	9.9349	1.1139							
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	AEAESLYQSK	2	19.6443	5.4064	16.0758	23	1.374	1.3838	0.629	0.6219	0.5795	2.1466
		AQYEDIAQK	3	0.4419	0.4404	1.1061							
		DVDGAYMTK	3	0.58	0.5061	1.8682							
		DYQELMNTK	3	0.4655	0.4613	1.1778							
		FLEQQNQVLQTK	3	0.5829	0.5781	1.1693							
		FLEQQNQVLQTKWELLQQVDTSTR	1	0.7275	0.7275								
		FSSCGGGGCGSFGAGGGFGSR	1	0.544	0.544								
		GSGGGSSSGGSGSIGGR	1	0.5162	0.5162								
		GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSSGGYR	1	0.4867	0.4867								
		IEISELNR	2	0.5939	0.5925	1.1017							
		LALDLEIATYR	4	0.6122	0.6036	1.21							
		LNDLEDALQQAK	1	0.6507	0.6507								
		NKLNDLEDALQQAK	1	0.4445	0.4445								
		NMQDMVEDYR	4	0.4485	0.4457	1.1397							
		SKAEAESLYQSK	1	0.6545	0.6545								
		SLDLDSIIAEVK	2	0.5815	0.5779	1.1709							
		SLNNQFASFIDK	2	0.5011	0.5008	1.0492							
		SLVNLGGSK	1	0.616	0.616								
		SLVNLGGSKSISISVAR	1	0.5475	0.5475								
		TLLEGEESR	2	0.5415	0.5389	1.1484							
		TNAENEFVTIK	3	0.4788	0.4762	1.1369							
		WELLQQVDTSTR	1	0.4148	0.4148								
		YEELQITAGR	2	0.528	0.527	1.092							
K2C1B_HUMAN		YQELQITAGR	1	0.5521	0.5521		1	0.5521	0.5521	0.5521	0.5521	0.5521	
K2C3_HUMAN	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=2	AQYEDIAQR	1	0.5538	0.5538		5	2.4538	3.6657	0.5898	0.7698	0.7413	9.6845
		DYQELMNVK	2	0.0177	0.0151	2.2524							
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	3	9.9734	9.9349	1.1139							
		SLDLDSIIAEVR	2	0.7575	0.7515	1.1949							
K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	AQYEEIAQR	2	0.82	0.8174	1.1191	4	0.8055	0.7589	0.795	0.7495	0.7446	1.2097
		FASFIDK	1	0.9668	0.9668								
		LALDIEIATYR	4	0.6122	0.6036	1.21							
		NLDLDSIIAEVR	4	0.8231	0.8212	1.0815							
K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	AQYEEIANR	1	0.6502	0.6502		6	2.4089	3.3462	1.3221	1.6662	1.6642	2.7343
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	3	9.9734	9.9349	1.1139							
		NLDLDSIIAEVK	4	0.8027	0.8024	1.0322							
		QLDSIVGER	1	1.0437	1.0437								
		WTLLQEQGTK	1	1.0167	1.0167								
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	AQYEEIAQR	2	0.82	0.8174	1.1191	7	4.0522	3.7526	1.9106	1.7616	1.7599	3.4859
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	2	10.5013	10.4861	1.0789							
		ISIGGGSCAISGGYGSR	1	13.2213	13.2213								
		NLDLDSIIAEVK	3	0.7958	0.7955	1.033							
		QLDSIVGER	1	1.0437	1.0437								
		WTLLQEQGTK	1	1.0167	1.0167								
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	AQYEEIAQR	1	0.8851	0.8851		5	2.6312	3.5236	1.2932	1.6172	1.6144	3.2068
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	3	9.9734	9.9349	1.1139							
		NLDLDSIIAEVK	3	0.8025	0.8021	1.0395							
		YEELQITAGR	2	0.528	0.527	1.092							
K2C8C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	AQYEEIAQR	1	0.8851	0.8851		6	2.6202	3.092	1.5014	1.6215	1.6207	2.6588
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	2	10.5013	10.4861	1.0789							
		NLDLDSIIAEVK	3	0.8025	0.8021	1.0395							
		QLDSIVGER	1	1.0437	1.0437								
		YEELQVTAGR	1	1.522	1.522								
K2C7_HUMAN	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=3	FASFIDK	1	0.9668	0.9668		5	6.9998	6.2679	3.8169	3.0658	3.0463	4.3611
		FLEQQNK	3	9.9734	9.9349	1.1139							
		KLLEGEESR	1	11.2815	11.2815								
		LALDIEIATYR	4	0.6122	0.6036	1.21							
		LLEGEESR	2	12.1651	12.1517	1.0685							
K2C71_HUMAN	Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=2	FLEQQNQVLETK	1	0.5677	0.5677		1	0.5677	0.5677	0.5677	0.5677	0.5677	
K2C72_HUMAN	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	DLDLDSIIAEVR	4	0.8314	0.8287	1.0992	3	0.7886	0.81	0.7699	0.8001	0.7983	1.3157
		FASFIDK	1	0.9668	0.9668								
		FLEQQNQVLETK	1	0.5677	0.5677								
K2C73_HUMAN	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	FASFIDK	1	0.9668	0.9668		3	0.7859	0.8045	0.7673	0.7947	0.7935	1.314
		FLEQQNQVLETK	1	0.5677	0.5677								
		NLDLDSIIAEVR	4	0.8231	0.8212	1.0815							
K2C74_HUMAN	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2	DLDLDSIIAEVR	4	0.8314	0.8287	1.0992	3	0.7886	0.81	0.7699	0.8001	0.7983	1.3157
		FASFIDK	1	0.9668	0.9668								
		FLEQQNQVLETK	1	0.5677	0.5677								
K2C75_HUMAN	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2	FASFIDK	1	0.9668	0.9668		4	3.3162	3.9578	1.8526	2.0378	2.0349	3.1707
		FLEQQNK	3	9.9734	9.9349	1.1139							
		NLDLDSIIAEVK	4	0.8027	0.8024	1.0322							
		YEELQVTAGR	1	1.522	1.522								
K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	FLEQQNK	2	9.4278	9.414	1.0796	1	9.4278	9.4278	9.4278	9.4278	9.414	
K2C79_HUMAN	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=1	DYQELMNVK	2	0.0177	0.0151	2.2524	5	2.48	3.1612	0.6142	0.7942	0.7711	9.6988
		FASFIDK	1	0.9668	0.9668								
		FLEQQNK	3	9.9734	9.9349	1.1139							
		NLDLDSIIAEVK	4	0.8027	0.8024	1.0322							
		YEELQVTAGK	1	0.6396	0.6396								
K2C8_HUMAN	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	FASFIDK	1	0.9668	0.9668		5	6.9998	6.2679	3.8169	3.0658	3.0463	4.3611
		FLEQQNK	3	9.9734	9.9349	1.1139							
		KLLEGEESR	1	11.2815	11.2815								
		LALDIEIATYR	4	0.6122	0.6036	1.21							
		LLEGEESR	2	12.1651	12.1517	1.0685							
K2C80_HUMAN	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	LALDIEIATYR	4	0.6122	0.6036	1.21	1	0.6122	0.6122	0.6122	0.6122	0.6036	
KCC2D_HUMAN	Calcium/calmodulin-dependent protein kinase type II delta chain OS=Homo sapiens GN=CAMK2D PE=1 SV=3	FTDEYQLFEELGK	1	1.1839	1.1839		1	1.1839	1.1839	1.1839	1.1839	1.1839	
KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1	FNFLEQAFDK	1	2.1255	2.1255		1	2.1255	2.1255	2.1255	2.1255	2.1255	
KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	EMDQTMAANAQK	1	0.2027	0.2027		2	0.2432	0.2432	0.2398	0.2398	0.2398	1.2684
		IVPVEITSLLK	1	0.2837	0.2837								
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	DSLDPSFTHMQLLTAEIEK	1	4.1935	4.1935		2	3.3894	3.3894	3.2926	3.2926	3.2926	1.4078
		KDDEENYLDLFSHK	1	2.5852	2.5852								

KIF14_HUMAN	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1	NFGGTVSIIPVGEAKTYVNGK	1	0.416	0.416		1	0.416	0.416	0.416	0.416	0.416	
KIF7_HUMAN	Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2	ELAINR	1	0.2604	0.2604		1	0.2604	0.2604	0.2604	0.2604	0.2604	
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	AEGSDVANAVLDGADCIMLSGETAK	1	4.3875	4.3875		13	6.0384	6.103	5.62	5.7867	5.6258	1.5544
		AGKPVICATQMLESMIK	2	6.1886	4.9019	2.7277							
		CDENILWLDYK	1	4.7221	4.7221								
		GADFLVTEVENGGSLGSK	2	6.2343	6.1248	1.306							
		GDLGIEIPAEK	1	8.3366	8.3366								
		GDVVIVLTGWRPGSGFTNTMR	1	1.6069	1.6069								
		GIFPVLCK	1	9.7074	9.7074								
		GSGTAEVELK	1	7.5448	7.5448								
		ITLDNAYMEK	1	4.7541	4.7541								
		IVVDDGLISLLQVK	2	7.0711	7.0058	1.2127							
		LAPITSDPTEATAVGAVEASFK	2	6.557	6.556	1.0255							
		SVETLK	1	6.0856	6.0856								
		TATESFASDPILYRPVAVALDTK	2	5.3037	4.5425	2.2426							
KPYR_HUMAN	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2	GDLGIEIPAEK	1	8.3366	8.3366		1	8.3366	8.3366	8.3366	8.3366	8.3366	
KRT34_HUMAN	Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 PE=1 SV=2	ETMQFLNDR	1	3.1326	3.1326		1	3.1326	3.1326	3.1326	3.1326	3.1326	
KRT35_HUMAN	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=4	LAADDFR	2	0.7209	0.7208	1.024	2	13.2761	9.091	4.3153	2.3766	2.3764	12.5613
		SDLEAQVESLKEELLCLK	1	25.8312	25.8312								
KRT36_HUMAN	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1	ETMQFLNDR	1	3.1326	3.1326		2	1.9268	1.5248	1.5028	1.1764	1.1763	2.8259
		LAADDFR	2	0.7209	0.7208	1.024							
KRT37_HUMAN	Keratin, type I cuticular Ha7 OS=Homo sapiens GN=KRT37 PE=2 SV=3	LAADDFR	2	0.7209	0.7208	1.024	1	0.7209	0.7209	0.7209	0.7209	0.7208	
KRT38_HUMAN	Keratin, type I cuticular Ha8 OS=Homo sapiens GN=KRT38 PE=2 SV=3	ETMQFLNDR	1	3.1326	3.1326		2	1.9207	1.9207	1.4901	1.4901	1.4901	2.8599
		LAADDFR	1	0.7088	0.7088								
KRT81_HUMAN	Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=2	FLEQQNK	3	9.9734	9.9349	1.1139	1	9.9734	9.9734	9.9734	9.9734	9.9349	
KRT82_HUMAN	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3	LAGLEEALQK	1	0.6307	0.6307		1	0.6307	0.6307	0.6307	0.6307	0.6307	
KRT83_HUMAN	Keratin, type II cuticular Hb3 OS=Homo sapiens GN=KRT83 PE=1 SV=2	FLEQQNK	2	9.4278	9.414	1.0796	1	9.4278	9.4278	9.4278	9.4278	9.414	
KRT84_HUMAN	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=1	FASFEIK	1	0.9668	0.9668		3	7.7018	9.2029	4.8951	7.2224	7.2058	4.0886
		FLEQQNK	3	9.9734	9.9349	1.1139							
		LLEGEESR	2	12.1651	12.1517	1.0685							
KRT85_HUMAN	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	FLEQQNK	3	9.9734	9.9349	1.1139	1	9.9734	9.9734	9.9734	9.9734	9.9349	
KRT86_HUMAN	Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	FLEQQNK	2	9.4278	9.414	1.0796	1	9.4278	9.4278	9.4278	9.4278	9.414	
KT33A_HUMAN	Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT33A PE=1 SV=2	ETMQFLNDR	1	3.1326	3.1326		2	14.4819	14.4819	8.9955	8.9955	8.9955	4.4451
		SDLEAQVESLKEELLCLK	1	25.8312	25.8312								
KT33B_HUMAN	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=1 SV=3	ETMQFLNDR	1	3.1326	3.1326		2	1.9268	1.5248	1.5028	1.1764	1.1763	2.8259
		LAADDFR	2	0.7209	0.7208	1.024							
LA_HUMAN	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	EVTWEVLEGEVEK	3	5.7806	5.7323	1.1713	3	5.3824	5.5417	2.7485	3.7004	3.6818	5.9551
		GSIFVVFDSIESAK	1	0.3589	0.3589								
		LTTDFNWIVEALSK	1	10.0078	10.0078								
LAMA4_HUMAN	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=3	AHLPLDINFR	1	0.3956	0.3956		9	0.6892	0.5809	0.4628	0.4022	0.4	2.5974
		DAPSWDPVALK	1	0.4547	0.4547								
		DESENLLNQAR	1	0.5248	0.5248								
		ESMDTINHASQLVEQAHDMR	1	0.5592	0.5592								
		IPFTDIYIGGAPPEILQSR	1	0.484	0.484								
		LAALSIEEGK	2	0.0629	0.0613	1.3838							
		LSDLQEALDQALNHVR	1	2.7879	2.7879								
		SLLSDVEELVEK	3	0.4499	0.4483	1.1089							
		TLFPVVLEQLDDYNAK	3	0.4835	0.4812	1.125							
LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1	AAQNSQEAEYIEK	1	0.5067	0.5067		13	2.5334	2.1628	0.825	0.7554	0.7521	3.3218
		ELAEQLEFIK	2	0.321	0.3203	1.093							
		ELDSLQTEAESLDNTVK	1	0.5127	0.5127								
		IEDPYSPR	1	21.5888	21.5888								
		KVDDIICDSR	1	5.5087	5.5087								
		LNVEGEHCDVCK	1	0.5083	0.5083								
		NFLTQDSADLDSIEAVANEVLK	2	0.5051	0.4947	1.3357							
		NIGNLFEEAEK	1	0.4114	0.4114								
		SCACNPLGTIPGGNPCDSETGHCYCK	2	0.8454	0.8353	1.2454							
		TLDGELDEK	1	0.541	0.541								
		VESLSQVEVELQHSAADIAR	1	0.6808	0.6808								
		YFAYDCEASFPGISTGPMIK	1	0.5303	0.5303								
		YSDIEPSTEGEVIFR	1	0.4741	0.4741								
LAMB2_HUMAN	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	GQVEQANGELQELIQSVK	1	0.1214	0.1214		1	0.1214	0.1214	0.1214	0.1214	0.1214	
LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	DIEEIMK	1	0.343	0.343		16	0.7307	0.6558	0.614	0.5738	0.5691	1.7248
		DNVEGFNCER	1	2.0712	2.0712								
		EVMDLLR	2	0.4403	0.439	1.1119							
		KQEAAIMDYNR	1	0.6324	0.6324								
		LCQCSDNIDPNAVGNCNR	1	0.4978	0.4978								
		LGNNEACSSCHCSPVGSLSTQCDSYGR	1	0.4238	0.4238								
		MEAENLEQLIDQK	2	0.5026	0.5025	1.0262							
		NTIEETGNLAEQAR	2	0.4368	0.4367	1.0188							
		QDIAVISDSYFPR	1	0.4017	0.4017								
		SQECYFDPELYR	2	0.4515	0.4294	1.5715							
		SWPGCQECPACYR	3	0.597	0.5791	1.3438							
		SYYYAISDFAVGGR	2	0.5851	0.585	1.0074							
		TAAEEALR	1	2.1293	2.1293								
		TFAEVTDLDNEVNNMLK	2	0.4379	0.4378	1.0063							
		TGQCECQPGITGQHCER	1	0.8039	0.8039								
		TLPSGCPNTPSIEKP	1	0.9378	0.9378								
LDH6A_HUMAN	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1	VIGSGCNLDSAR	2	10.2623	10.2238	1.1305	1	10.2623	10.2623	10.2622	10.2622	10.2238	
LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	DLADELALVDVIEDK	6	6.7235	3.9349	5.0828	9	6.036	6.6761	5.3501	6.1713	5.1941	1.7
		DQLIYNLLKEEQTPQNK	3	11.0047	10.487	1.488							
		DYNVTANSK	1	2.5007	2.5007								
		GLYGIKDDVFLSVPCILGQNGISDLVK	1	2.868	2.868								
		QVVESAYEVIK	2	5.8763	5.7383	1.3627							
		SADTLWGIQK	4	4.5914	4.2471	1.5465							
		VIGSGCNLDSAR	2	10.2623	10.2238	1.1305							
		VTLTSEEEAR	2	7.0103	6.7796	1.4447							
LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GEMIDLQHGSLFLQTPK	1	1.4825	1.4825		9	6.7579	7.7717	5.5088	6.4825	6.4392	2.0741
		GLTSVINQK	2	6.0917	6.0082	1.2656							
		ITVVGVGQVGMACAISILGK	2	2.8606	2.8219	1.2635							
		IVADKDYSVTANSK	1	3.2559	3.2559								
		LIAPVAEEEATVPNNK	1	4.467	4.467								
		LKDDEVAQLK	1	8.5896	8.5896								
		SADTLWDIQK	2	11.082	11.0032	1.1842							
		SLADELALVDVLEDK	3	12.7294	12.6281	1.1657							
		VIGSGCNLDSAR	2	10.2623	10.2238	1.1305							
LDHC_HUMAN	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=2 SV=4	VIGSGCNLDSAR	2	10.2623	10.2238	1.1305	1	10.2623	10.2623	10.2622	10.2622	10.2238	
LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	DGSAWGTEQR	3	6.4382	6.4339	1.0457	6	5.1686	4.9833	5.0095	4.8411	3.2306	1.3293
		DSNNLCLHFNPR	1	5.7319	5.7319								
		FNAHGDANTIVCNSK	4	5.904	5.7258	1.3244							
		GEVAPDAK	2	3.1744	1.7962	5.2364							
		LNLEAINYMAADGDFK	8	3.8919	1.5017	9.7429							
		SFVLNLGK	4	5.8716	5.8473	1.1109							
LEG3_HUMAN	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	MLTILGTVKPNANR	1	0.5974	0.5974		1	0.5974	0.5974	0.5974	0.5974	0.5974	
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	ELSEALGQIFDSQR	1	0.8646	0.8646		7	2.2208	2.2192	1.1442	1.2421	1.2053	4.027
		GQWGTVCDNLWDLTDASVVCR	1	1.3884	1.3884								
		LASAYGAR	1	0.628	0.628								
		SLGWLK	1	0.0901	0.0901								
		STSSFPCPAGHFNGFR	1	8.3061	8.3061								
		TLQALEFHTVPFQLLAR	1	2.0612	2.0612								
		YSSDYFQAPSDYR	2	2.2075	1.9572	2.0295							
LGMN_HUMAN	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1	ESSYACYYDEK	1	1.9944	1.9944		1	1.9944	1.9944	1.9944	1.9944	1.9944	
LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	GLAFIQDPDGYWIEILNPNK	1	2.4357	2.4357		1	2.4357	2.4357	2.4357	2.4357	2.4357	
LIMC1_HUMAN	LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=3	SDSLSPPR	1	0.1637	0.1637		1	0.1637	0.1637	0.1637	0.1637	0.1637	
LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	DLAAFDK	1	3.0653	3.0653		2	1.7341	1.7341	1.1112	1.1112	1.1112	4.1998
		LTVTAEVSVPK	1	0.4028	0.4028								
LMNA_HUMAN	Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	AAYEAELGDAR	1	1.7635	1.7635		7	2.5699	2.4387	2.2287	1.9989	1.8655	1.8635
		AGQVVTIWAAGAGATHSPPTDLVWK	1	2.512	2.512								
		AQNTWCQNSLR	1	4.0676	4.0676								
		EDLQELNDR	3	0.7427	0.6205	2.0906							
		IDSLSAQLSQLQK	3	3.6758	3.4155	1.6199							
		MQQLDEYQELLDIK	1	1.4825	1.4825								
		TLEGELHDLR	1	3.7449	3.7449								
LOXL2_HUMAN	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	LGQGIGPIHLNEIQCTGNEK	1	2.0769	2.0769		1	2.0769	2.0769	2.0769	2.0769	2.0769	
LRC57_HUMAN	Leucine-rich repeat-containing protein 57 OS=Homo sapiens GN=LRRC57 PE=1 SV=1	TIDLSNNK	1	19.6386	19.6386		1	19.6386	19.6386	19.6386	19.6386	19.6386	
LRC59_HUMAN	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	LVNLQHLDLLNNK	1	11.7205	11.7205		2	9.1822	9.1822	8.8244	8.8244	8.8244	1.4939
		LVTLPVSFAQLK	1	6.6439	6.6439								
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=3	ASGLGDHCEDINECLEDK	2	0.1915	0.191	1.1046	11	0.9379	0.9533	0.5934	0.5853	0.5451	2.9091
		CEYCDSGYR	1	0.542	0.542								
		CVDIDECTQVQHLCSQGR	2	0.5041	0.5041	1.0187							
		DQCEDIDECQHR	2	1.2861	0.861	3.8697							
		EAQPGQSGVSYQGLPVQK	1	0.206	0.206								
		EEPVEALTFSR	1	1.6852	1.6852								
		GFVPAGESSSEAGGENYKDADECLLFGQEICK	1	0.1511	0.1511								
		HPPEASVQIHQVSR	1	1.1895	1.1895								
		MTCVDVNECDELNNR	2	2.7832	2.5642	1.7867							
		QEDCCGTVGTSWGFNK	2	0.1712	0.1574	1.7973							
		YTCICYEGYR	1	1.6068	1.6068								
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=1 SV=2	AISMLQGLCYR	1	0.3601	0.3601		13	0.454	0.4622	0.3551	0.3926	0.3911	3.0892
		ALLEAPLK	3	0.5582	0.5566	1.0971							
		AQPGWGSPR	1	0.3994	0.3994								
		CEEVIPDEEFDPQNSR	1	0.452	0.452								
		DCDGGYRPSPLGDSCEDVDECEDPQSSCLGGECK	1	0.5828	0.5828								
		EQDAPVAGLQPVER	1	0.5162	0.5162								
		GAGGQSMSEAPTGDHAPAPTR	1	0.6793	0.6793								
		GQSGSCVDVNECLTPGVCAHGK	1	0.5135	0.5135								
		SGAAPPTPPR	1	0.0087	0.0087								
		SSAAGEGTLAR	2	0.4533	0.4529	1.0634							
		SSEVTAQLCNVAR	2	0.5212	0.5179	1.1714							
		STPLGQQQPAPR	3	0.393	0.3912	1.1243							
		VTNDVCSEPLR	2	0.4648	0.4566	1.3072							
LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2	AGPDLASCLDVDECR	1	0.4871	0.4871		3	4.821	4.821	1.5384	1.5384	1.5384	6.5335
		DVDECQLFR	1	0.557	0.557								
		GCQLCPPFGSEGFR	1	13.4188	13.4188								
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	FNALQYLR	1	0.7889	0.7889		6	0.716	0.7853	0.4736	0.5241	0.3119	2.9468
		ISNIPDEYFK	1	0.3728	0.3728								
		LKEDAVSAAFK	2	0.0947	0.0784	2.4497							
		LPSGLPVSLLTLYLDNNK	4	0.9966	0.2891	6.4767							
		NIPTVNENLENYYLEVNQLEK	2	0.2235	0.1764	2.752							
		SLEYLDLSFNQIAR	2	1.8198	1.4682	2.6121							
LYAR_HUMAN	Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2	SEEELLVIFNK	1	1.3915	1.3915		1	1.3915	1.3915	1.3915	1.3915	1.3915	
LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	STDYGIFQINSR	1	0.5384	0.5384		1	0.5384	0.5384	0.5384	0.5384	0.5384	
MA1A1_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	SSSGLTYIAEWK	1	0.1353	0.1353		1	0.1353	0.1353	0.1353	0.1353	0.1353	
MAP1A_HUMAN	Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=5	AVLDALLEGK	1	0.0745	0.0745		1	0.0745	0.0745	0.0745	0.0745	0.0745	
MAP1B_HUMAN	Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=1	AVLDALLEGK	1	0.0745	0.0745		1	0.0745	0.0745	0.0745	0.0745	0.0745	
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	EELQANGSAPAADKEEPAAAGSGAASPSAAEK	1	5.8011	5.8011		2	5.293	5.293	5.2686	5.2686	5.2686	1.1459
		VNGDASPAAAESGAK	1	4.7849	4.7849								
MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	VECSDNLTQR	2	2.3609	2.1937	1.7309	1	2.3609	2.3609	2.3609	2.3609	2.1937	
MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	IGPYQPNVPVGIDYVIPK	2	3.2247	3.0981	1.4962	1	3.2247	3.2247	3.2247	3.2247	3.0981	
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	NVIIWGNHSSTQYPDVNHAK	1	5.5764	5.5764		2	3.8542	3.8542	3.448	3.448	3.448	1.9736
		VIVVGNPANTNCLTASK	1	2.132	2.132								
MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	ANTPVAELK	2	2.9393	2.9199	1.1768	7	3.7312	3.8161	3.5979	3.657	3.1463	1.327

		FVFSLVDAMNGK	1	3.808	3.808									
		GYLGPEQLPDCLK	2	2.898	1.2296	7.4753								
		LTLYDIAHTPGVAADLSHIETK	1	2.7956	2.7956									
		SQETECTYFSTPLLLGK	2	4.1964	4.0527	1.4556								
		TIPLISQCTPK	1	3.6566	3.6566									
		VAVLGASGGIGQPLSLLLK	2	0.0247	6.024	1.0222								
MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	EVTGIITQGAR	1	0.3331	0.3331		2	0.2821	0.2821	0.2774	0.2774	0.2774	1.2954	
		NLFETPILAR	1	0.231	0.231									
MGN_HUMAN	Protein mago nashi homolog OS=Homo sapiens GN=MAGOH PE=1 SV=1	VFYYLVQDLK	1	1.8235	1.8235		1	1.8235	1.8235	1.8235	1.8235	1.8235		
MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1	SSCTLFQDIFQHLDK	1	0.5434	0.5434		1	0.5434	0.5434	0.5434	0.5434	0.5434		
MK09_HUMAN	Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 PE=1 SV=2	EVMDWEER	1	3.8682	3.8682		1	3.8682	3.8682	3.8682	3.8682	3.8682		
ML12B_HUMAN	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	ATSNVFAMFDQSQIQEFK	1	3.6848	3.6848		2	5.6816	5.6816	5.3191	5.3191	5.3191	1.6806	
		GNFNYIEFTR	1	7.6783	7.6783									
MLL3_HUMAN	Histone-lysine N-methyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	LEEQNGSK	1	18.779	18.779		1	18.779	18.779	18.779	18.779	18.779		
MMP1_HUMAN	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	ADVDHAIEK	1	2.139	2.139		2	1.9823	1.9823	1.9761	1.9761	1.9761	1.1185	
		IENYTPDLPR	1	1.8256	1.8256									
MMP2_HUMAN	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2	AFQVWSDVTPLR	2	0.3347	0.3344	1.0592	19	0.5094	0.507	0.4518	0.4445	0.415	1.5792	
		DKPMGPLLVATFWPELPEK	1	0.3507	0.3507									
		ESCNLFVLK	4	1.1756	0.6765	3.0327								
		EYNSCTDTGR	1	0.412	0.412									
		FFGLPQTGDLDQNTIETMR	4	0.3505	0.3425	1.2815								
		FQGTSYDSCTTEGR	3	0.3756	0.3733	1.1438								
		GAYYLK	1	1.4885	1.4885									
		IDAVYEAPQEEK	2	0.3583	0.3471	1.429								
		IHDGEADIMINFGR	1	0.4989	0.4989									
		IIGYTPDLDPETVDDAFAR	1	0.7096	0.7096									
		LIADAWNAIPDNLDAVVDLQGGGHSYFFK	1	0.3706	0.3706									
		MWCATTANYDDDRK	1	0.4545	0.4545									
		QDIVFDGIAQIR	1	0.2566	0.2566									
		TDKELAVQYLNTFYGCPK	2	0.3113	0.3105	1.1033								
		TYIFAGDK	3	0.306	0.3055	1.0773								
		WCGTTEDYDR	3	0.3221	0.3207	1.1249								
		WEHGDGYPFDGK	1	0.6397	0.6397									
		YGFCPHEALFTMGGNAEGQPCK	1	0.4842	0.4842									
		YGNADGEYCK	2	0.4785	0.4784	1.0208								
MMP3_HUMAN	Stromelysin-1 OS=Homo sapiens GN=MMP3 PE=1 SV=2	GEDTSMNLVQK	1	0.1938	0.1938		1	0.1938	0.1938	0.1938	0.1938	0.1938		
MMRN1_HUMAN	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	EFQSLLK	1	6.7812	6.7812		7	6.7342	6.7342	3.7368	3.7368	3.7368	4.2236	
		GLTEFVEPIIQIK	1	15.2243	15.2243									
		IFGNDMQETVAQLFK	1	13.035	13.035									
		LSPTVILDNQVTVVPGGK	1	0.3419	0.3419									
		LVEENALAPDFSK	1	4.2352	4.2352									
		MTDQVNYQAMK	1	6.748	6.748									
		YNFVLQVAK	1	0.7737	0.7737									
MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	ALELEGER	2	13.9912	13.9911	1.0038	10	7.2665	8.0713	5.0818	6.3545	6.1242	3.0583	
		AQMVQEDLEK	1	5.1305	5.1305									
		EDAVLEYLK	2	10.7266	10.0444	1.6792								
		ESEAVEWGQK	2	6.1435	5.8938	1.5071								
		EVWFFGLQYQDTK	2	4.6683	4.5952	1.2866								
		GFSTWLK	3	10.1805	8.9709	1.9515								
		LFFLQVK	1	11.5991	11.5991									
		QLFDQVVK	2	8.9565	8.9477	1.0649								
		SGYLAGDK	1	1.1204	1.1204									
		VLEQHK	1	0.4486	0.4486									
MP3B2_HUMAN	Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens GN=MAP1LC3B2 PE=2 SV=1	FLVPDHVNMSELIK	1	0.68	0.68		1	0.68	0.68	0.68	0.68	0.68		
MT1A_HUMAN	Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=1	CAQGCICK	2	3.6961	3.6948	1.0372	1	3.6961	3.6961	3.696	3.696	3.6948		
MT1E_HUMAN	Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1	SCCSCCPVGCAK	2	3.521	3.516	1.0779	1	3.521	3.521	3.521	3.521	3.516		
MT1G_HUMAN	Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2	CAQGCICK	1	3.6007	3.6007		2	3.5753	3.5668	3.5752	3.5667	3.5643	1.0101	
		SCCSCCPVGCAK	2	3.5498	3.5463	1.0649								
MT1H_HUMAN	Metallothionein-1H OS=Homo sapiens GN=MT1H PE=1 SV=1	CAQGCICK	2	3.6961	3.6948	1.0372	1	3.6961	3.6961	3.696	3.696	3.6948		
MT1M_HUMAN	Metallothionein-1M OS=Homo sapiens GN=MT1M PE=2 SV=2	SCCSCCPVGCAK	2	3.521	3.516	1.0779	1	3.521	3.521	3.521	3.521	3.516		
MT1X_HUMAN	Metallothionein-1X OS=Homo sapiens GN=MT1X PE=1 SV=1	CAQGCICK	1	3.7914	3.7914		2	3.5629	3.5629	3.5555	3.5555	3.5555	1.0951	
		SCCSCCPVGCAK	1	3.3343	3.3343									
MT2_HUMAN	Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1	CAQGCICK	2	3.6961	3.6948	1.0372	2	3.6085	3.6085	3.6074	3.6074	3.6043	1.0349	
		SCCSCCPVGCAK	2	3.521	3.516	1.0779								
MUC18_HUMAN	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2	CLAQGNPPPHFSISK	1	0.7445	0.7445		4	5.9959	5.9959	4.124	4.124	4.124	3.2955	
		EDKDAQFYCELNYR	1	7.1066	7.1066									
		EVTVPVFYPTEK	1	4.8425	4.8425									
		GPVLQLHDLK	1	11.2901	11.2901									
MVP_HUMAN	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	DITPLQVVLPNTALHLK	1	71.4281	71.4281		1	71.4281	71.4281	71.4281	71.4281	71.4281		
MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	TQLEELEDELQATEDAK	1	4.3079	4.3079		1	4.3079	4.3079	4.3079	4.3079	4.3079		
MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	DLGEELEALK	1	4.5521	4.5521		4	5.4458	5.4458	4.8392	4.8392	4.8392	1.7238	
		KEEELQAALAR	1	10.1746	10.1746									
		QLLQANPLEAFGNAK	1	2.7486	2.7486									
		TQLEELEDELQATEDAK	1	4.3079	4.3079									
MYH14_HUMAN	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=1	EQADFALEALAK	2	0.2307	0.2125	1.7864	3	4.3846	3.3461	1.8615	1.1044	1.0601	6.843	
		KEEELQAALAR	1	10.1746	10.1746									
		QLLQANPLEAFGNAK	1	2.7486	2.7486									
MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	DLGEELEALK	1	4.5521	4.5521		14	4.5411	4.4694	3.0626	2.8518	2.8046	3.6099	
		EQADFAIEALAK	2	0.2307	0.2125	1.7864								
		EQEVNILK	1	6.5417	6.5417									
		EQLEEEEEAK	1	4.9832	4.9832									
		IAEFTTNLTEEEEK	3	6.0872	5.8488	1.4092								
		KEEELQAALAR	1	10.1746	10.1746									
		KLEEEQIILEDQNCK	1	3.9451	3.9451									
		KLEGDSTDLSDQIAELQAQIAELK	1	4.9613	4.9613									
		LQVELDNVTGLLSQSDSK	1	3.43	3.43									
		QIATLHAQVADMK	1	0.1181	0.1181									
		QLLQANPLEAFGNAK	1	2.7486	2.7486									
		TDLLLEPYNK	1	6.7163	6.7163									
		TQLEELEDELQATEDAK	1	4.3079	4.3079									
		VISGVLQLGNIVFK	1	4.778	4.778									
MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	HVLVTLGEK	1	7.0721	7.0721		2	7.0892	7.0892	7.0891	7.0891	7.0891	1.0034	
		VLDFEHFLPMLQTVAK	1	7.1062	7.1062									
MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	ILVDNLCDMEMVNK	1	0.1069	0.1069		1	0.1069	0.1069	0.1069	0.1069	0.1069		
NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	DPVPGYSVPAAEHSTITAWGK	1	2.7799	2.7799		6	2.473	4.0037	1.3772	2.1768	1.1751	3.2278	
		GWNYLEK	1	0.6803	0.6803									
		MWSIENIAFGSGGGLLQK	1	1.6571	1.6571									
		STQAPLIIRPDSGNPLDTVLK	1	0.813	0.813									
		VIQGDGVDINTLQEIVEGMK	3	8.596	1.661	10.5965								
		YLLETSGNLDGLEYK	1	0.3115	0.3115									
NBL1_HUMAN	Neuroblastoma suppressor of tumorigenicity 1 OS=Homo sapiens GN=NBL1 PE=1 SV=1	ILHCSCQACGK	1	0.5804	0.5804		1	0.5804	0.5804	0.5804	0.5804	0.5804		
NDK8_HUMAN	Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1	DRPFFPGLVK	1	16.69	16.69		3	7.9901	6.0269	5.9996	4.5964	4.5595	2.4582	
		VMLGETNPADSKPGTIR	1	4.1983	4.1983									
		YMNSGPVVAMVWEGLNVVK	3	3.0821	3.041	1.2276								
NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	GLVGEIIK	2	6.6877	6.2211	1.7235	5	5.0768	5.5278	4.8975	5.346	5.2276	1.3519	
		GLVGEIIKR	1	3.3432	3.3432									
		NIHGSDSVESAEK	2	6.6229	6.583	1.1685								
		VMLGETNPADSKPGTIR	1	4.1983	4.1983									
		YMHSGPVVAMVWEGLNVVK	1	4.532	4.532									
NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	DRPFFPGLVK	1	16.69	16.69		5	6.8003	5.8567	5.4546	4.8512	4.7403	2.0016	
		GLVGEIIK	2	6.6877	6.2211	1.7235								
		GLVGEIIKR	1	3.3432	3.3432									
		VMLGETNPADSKPGTIR	1	4.1983	4.1983									
		YMNSGPVVAMVWEGLNVVK	3	3.0821	3.041	1.2276								
NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2	DIEEIIDELK	1	1.6641	1.6641		1	1.6641	1.6641	1.6641	1.6641	1.6641		
NEDD8_HUMAN	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1	EIEIDIEPTDKVER	1	0.9059	0.9059		1	0.9059	0.9059	0.9059	0.9059	0.9059		
NELL1_HUMAN	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NELL1 PE=2 SV=3	GIIQDGK	1	0.1832	0.1832		1	0.1832	0.1832	0.1832	0.1832	0.1832		
NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	AELGALPDFDSLEK	1	6.0001	6.0001		1	6.0001	6.0001	6.0001	6.0001	6.0001		
NFH_HUMAN	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	EYQDLLNVK	4	12.6181	12.3633	1.264	1	12.6181	12.6181	12.6181	12.6181	12.6181	12.3633	
NFL_HUMAN	Neurofilament light polypeptide OS=Homo sapiens GN=NEFL PE=1 SV=3	EYQDLLNVK	4	12.6181	12.3633	1.264	1	12.6181	12.6181	12.6181	12.6181	12.6181	12.3633	
NFM_HUMAN	Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=2	EYQDLLNVK	4	12.6181	12.3633	1.264	1	12.6181	12.6181	12.6181	12.6181	12.6181	12.3633	
NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	EVTDMNLNVNEGGIDK	1	4.5741	4.5741		2	2.7179	2.7179	1.9852	1.9852	1.9852	3.2558	
		QWIQISDAVYHMVYEQAK	1	0.8616	0.8616									
NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	EDLSPSITQR	1	1.5941	1.5941		5	4.6689	4.6689	1.6798	1.6798	1.6798	4.6379	
		GNLYWTDWNR	1	0.4216	0.4216									
		MNSVALDLAISK	1	2.2886	2.2886									
		NIFWTDSNLDR	1	18.5721	18.5721									
		VLFETDLVNPR	1	0.4682	0.4682									
NID2_HUMAN	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=2	EDTSPWLGLAAR	1	2.1793	2.1793		4	0.8815	0.8815	0.6486	0.6486	0.6486	2.3425	
		ELYHYSDSTVTSTSSR	1	0.3164	0.3164									
		ETQYVDYDFPTDFPAIAPFLADIDTSHGR	1	0.6088	0.6088									
		GNLYWTDWNR	1	0.4216	0.4216									
NNMT_HUMAN	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	IFCLDGVK	1	0.059	0.059		1	0.059	0.059	0.059	0.059	0.059		
NOTC3_HUMAN	Neurogenic locus notch homolog protein 3 OS=Homo sapiens GN=NOTCH3 PE=1 SV=1	AGLGPQGPR	1	0.2108	0.2108		1	0.2108	0.2108	0.2108	0.2108	0.2108		
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	GIPEFWLTVFK	1	8.2131	8.2131		1	8.2131	8.2131	8.2131	8.2131	8.2131		
NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	NVDMLSELVQEYDEPILK	1	7.1199	7.1199		1	7.1199	7.1199	7.1199	7.1199	7.1199		
NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	GPSSVEDIK	1	11.8702	11.8702		2	8.9517	8.9517	8.4625	8.4625	8.4625	1.6137	
		MTDQEAIQDLWQWR	1	6.0331	6.0331									
NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	ADEDPIMGFHQMFLLK	1	3.1887	3.1887		1	3.1887	3.1887	3.1887	3.1887	3.1887		
NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	DLELLIQTATR	1	0.6117	0.6117		5	0.864	0.864	0.8414	0.8414	0.8414	1.2956	
		EFGDTGEGWETVEMHPAYTEEELR	1	1.0486	1.0486									
		LSQETEALGR	1	0.694	0.694									
		LVTLEEFLASTQR	1	0.8473	0.8473									
		MDAEQDPNVQVDHLNLLK	1	1.1183	1.1183									
NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	ALELTGLK	2	12.5125	12.0375	1.4859	8	18.8574	16.7617	5.0768	5.4575	5.4136	4.6376	
		EVEEDSEDEEMSEDEEDDSSGEEVVIPQKK	1	1.5415	1.5415									
		FGYVDFESAEDLEK	1	3.0244	3.0244									
		GFGFVDFNSEEDAK	1	2.0866	2.0866									
		GIAYIEFK	2	4.2449	4.2377	1.0861								
		GYAFIEFASFEDAK	1	118.4987	118.4987									
		KEDSDEEEDDDSEEDEDDEDEDEDEDEIEPAAMK	1	0.8946	0.8946									
		TGISDVFAK	1	8.0564	8.0564									
NUDC_HUMAN	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	VEESSWLIEDGK	1	5.5472	5.5472		1	5.5472	5.5472	5.5472	5.5472	5.5472		
OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	IPAFLNVVDIAGLVK	1	2.9776	2.9776		2	1.5516	1.5516	0.6115	0.6115	0.6115	9.3796	
		NYIVEDGDIIFFK	1	0.1256	0.1256									
OSTF1_HUMAN	Osteoclast-stimulating factor 1 OS=Homo sapiens GN=OSTF1 PE=1 SV=2	TGLIPSNYVAEQAESIDNPLHEAAK	1	1.8004	1.8004		1	1.8004	1.8004	1.8004	1.8004	1.8004		
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2	AFGFSHLEALLDDSK	1	3.3995	3.3995		3	2.1706	2.1706	1.7419	1.7419	1.7419	2.4625	
		EYAEDDNIYQQK	1	0.6251	0.6251									
		LELSVLYK	1	2.4871	2.4871									
P2RY4_HUMAN	P2Y purinoceptor 4 OS=Homo sapiens GN=P2RY4 PE=1 SV=1	ASTESSLLR	2	5.0934	2.401	7.0836	1	5.0934	5.0934	5.0933	5.0933	2.401		
PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	HELLQPFNVLYEK	1	0.4928	0.4928		2	2.4224	3.0656	1.4645	2.1055	2.1028	4.6659	
		SLVEASSSQVSVLSLCEK	2	4.3521	4.3438	1.0912								
PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	ALYDTFSAFGNILSCK	2	6.9927	6.9515	1.1663	1	6.9927	6.9927	6.9927	6.9927	6.9915		
PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	ALYDTFSAFGNILSCK	2	6.9927	6.9515	1.1663	1	6.9927	6.9927	6.9927	6.9927	6.9515		
PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1	DEISTTDAIFVQR	2	2.9533	2.9438	1.1202	17	3.2277	3.2604	3.1746	3.2142	3.1223	1.2068	
		ELMGPWNKDEISTTDAIFVQR	2	2.6537	2.642	1.1418								
		EVPLSALTNILSAQLISHWK	1	3.4377	3.4377									
		FIINDWVK	4	3.979	3.1818	2.445								
		FSLETEVDLR	4	3.3295	3.3003	1.1647								
		GAVDQLTR	2	3.234	3.2319	1.0515								
		GMAPALR	1	2.9395	2.9395									

		GMISNLLGK	3	3.2824	3.2823	1.0109							
		IEVNESGTVASSSTAVAVSAR	2	2.2878	2.2854	1.0656							
		KPLENLGMTDMFR	1	2.5528	2.5528								
		LLVLPK	1	4.5768	4.5768								
		LVLVNALYFNGQWK	2	2.8414	2.8266	1.1556							
		LVQGFMPHFFR	1	3.7843	3.7843								
		QFQADFTSLSDQEPLHVAQALQK	3	2.387	2.2938	1.4333							
		QVDFSEVER	5	3.7428	3.733	1.0849							
		SDGSTVSVPMMAQTNK	2	3.6622	3.6605	1.0443							
		VFQQVAQASK	4	3.2263	3.1725	1.2438							
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	EMTLDEWK	1	6.0861	6.0861		1	6.0861	6.0861	6.0861	6.0861	6.0861	
PAL4B_HUMAN	Peptidylprolyl cis-trans isomerase A-like 4B OS=Homo sapiens GN=PPIAL4B PE=1 SV=1	IIPGFMCQGGDFTR	1	19.2145	19.2145		2	18.4965	18.4965	18.4826	18.4826	18.4826	1.0565
		SIYGEK	1	17.7785	17.7785								
PARK7_HUMAN	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	ALVILAK	2	0.0787	0.0785	1.1161	2	1.4772	1.011	0.4757	0.2612	0.2607	12.736
		GLIAAICAGPTALLAHEIGFGSK	1	2.8756	2.8756								
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	SDAYYCTGDVTAWTK	1	0.4253	0.4253		1	0.4253	0.4253	0.4253	0.4253	0.4253	
PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	IITLTGPTNAIFK	2	0.3501	0.3022	2.1938	1	0.3501	0.3501	0.3501	0.3501	0.3022	
PCD12_HUMAN	Protocadherin-12 OS=Homo sapiens GN=PCDH12 PE=2 SV=1	YTLTLLAQDGGLQPLSAK	1	0.2054	0.2054		1	0.2054	0.2054	0.2054	0.2054	0.2054	
PCNA_HUMAN	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	AEDNADTLALVFEAPNQEK	1	4.256	4.256		3	2.5255	2.5255	1.0265	1.0265	1.0265	9.3155
		DLSHIGDAVVVSCAK	1	3.242	3.242								
		NLAMGVNLTSMSK	1	0.0784	0.0784								
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2	ATSGTEHQFCGGR	1	2.0387	2.0387		8	0.7275	0.7633	0.4314	0.4478	0.4441	3.2045
		EPGEGLAVTVSLIGAYK	1	0.2956	0.2956								
		FDLEPDTYCR	1	0.0905	0.0905								
		GESGYVASEGFPNLYPPNK	2	0.1248	0.1214	1.3919							
		GFLLWYSGR	1	0.751	0.751								
		TEESPSAFDAPTCPK	2	0.1901	0.1857	1.3601							
		YDALEVFAGSGTSGQR	3	1.5123	1.5121	1.0192							
		YDSVSVFNGAVSDDSR	1	0.817	0.817								
PDC6I_HUMAN	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	LANQAADYFGDAFK	1	2.7071	2.7071		2	4.0161	4.0161	3.7968	3.7968	3.7968	1.6135
		SVIEQGGIQTVDQLIK	1	5.3251	5.3251								
PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	AGVNFSEFTGVWK	1	22.2424	22.2424		1	22.2424	22.2424	22.2424	22.2424	22.2424	
PDE8B_HUMAN	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B OS=Homo sapiens GN=PDE8B PE=1 SV=2	TLDDLK	1	0.649	0.649		1	0.649	0.649	0.649	0.649	0.649	
PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	EADDVNVKLK	1	10.247	10.247		2	6.652	5.4537	5.5969	4.5751	4.5687	2.352
		ENLLDFIK	2	3.0571	3.0506	1.0961							
PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	DASIVGFFDDSFSEAHSEFLK	1	2.6303	2.6303		2	3.0183	3.0183	2.9933	2.9933	2.9933	1.2006
		GFPTIYFSPANK	1	3.4063	3.4063								
PDLI5_HUMAN	PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=4	DFNMPLTISSLK	1	4.0144	4.0144		3	2.4538	2.4538	2.1141	2.1141	2.1141	2.0098
		IGDVVLSIDGINAQGMTHLEAQNK	1	2.3419	2.3419								
		NTMAYIGFVEEK	1	1.0051	1.0051								
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	APVAGTCYQAEWDDYVPK	1	8.1261	8.1261		3	4.5206	4.5206	3.1048	3.1048	3.1048	3.3679
		LYEQLSGK	1	4.6424	4.6424								
		NRPTSISWDGLDSGK	1	0.7934	0.7934								
PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=3	ALYYDLISSPDIHGTYK	1	0.1245	0.1245		9	0.3129	0.3004	0.2661	0.2527	0.2339	1.843
		DTDTGALLFIGK	2	0.268	0.2676	1.0725							
		EIPDEISILLLGVAHFK	1	0.4551	0.4551								
		ELLDTVTAPQK	1	0.1233	0.1233								
		LAAVSNFGYDLYR	2	0.6593	0.4216	4.2043							
		LDLQEINNWVQAQMK	1	0.4989	0.4989								
		LQSLFDSPDFSK	4	0.1543	0.1472	1.4335							
		TSLEDFYLDEER	1	0.2395	0.2395								
		YSLDSDLSCK	1	0.2942	0.2942								
PERI_HUMAN	Periherin OS=Homo sapiens GN=PRPH PE=1 SV=2	KLLEGEESR	1	11.2815	11.2815		4	11.1382	10.1184	9.8431	8.776	7.5424	1.8718
		LEEETRK	1	17.0976	17.0976								
		LLEGEESR	2	12.1651	12.1517	1.0685							
		MALDIEIATYR	2	4.0006	2.5424	4.2641							
PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	ALPFWNEEIVPQIK	2	9.8121	9.8115	1.0155	2	9.3541	9.3541	9.3429	9.3429	8.9447	1.0717
		YADLTEDQLPSCESLK	2	8.8962	8.1545	1.8197							
PGAM2_HUMAN	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	ALPYWNEEIVPQIK	2	9.8121	9.8115	1.0155	1	9.8121	9.8121	9.812	9.812	9.8115	
PGAM4_HUMAN	Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=1 SV=1	ALPFWNEEIVPQIK	1	9.7051	9.7051		1	9.7051	9.7051	9.7051	9.7051	9.7051	
PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3	AAGVPSATITWR	1	5.295	5.295		27	5.9441	5.726	4.1726	4.4281	4.3099	2.3488
		AGFFGDAMK	1	3.5438	3.5438								
		AMDFNGLTIR	1	0.4763	0.4763								
		CSATGSPAPTIHWSK	1	2.3973	2.3973								
		ESDQGAYTCEAMNAR	1	6.1165	6.1165								
		EVSEAVVDTLESEYLK	4	5.1765	4.635	1.7354							
		FDQPDDFK	3	4.3325	4.2157	1.3359							
		FSSGITGCVK	2	6.3525	6.3253	1.14							
		GCVGEVSVNGIK	1	3.6726	3.6726								
		GPSCQDCDTGYTR	1	7.5061	7.5061								
		LDVEFKPLAPDGVLLFSGGK	2	6.212	6.1882	1.132							
		LEGDTLIPR	3	5.2567	4.4781	2.145							
		LHHVSPADSGEYVCR	1	5.0425	5.0425								
		LHQMSVADSGEYVCR	1	4.7419	4.7419								
		LLSGPYFWSLPSR	1	2.451	2.451								
		LYQASPADSGEYVCR	1	5.0728	5.0728								
		QPQAIITWYK	1	6.1304	6.1304								
		SGPVEDFVSLAMVGGHLEFR	1	3.13	3.13								
		SIGASVEFHCAVPSDR	1	6.6775	6.6775								
		SIVPQGGSHSLR	1	4.6547	4.6547								
		SPAYTLVWTR	2	6.1943	6.1836	1.0868							
		SPVSIDPPSSTVQQGDASFK	2	3.6314	3.6255	1.084							
		SQSVRPGADVTFICTAK	1	4.9605	4.9605								
		TDEANCPTK	1	3.1376	3.1376								
		TSTASGLLLWQGVEVGEAGQGK	1	3.477	3.477								
		VAEGQTLDLK	1	0.3492	0.3492								
		VTSYGGELR	1	44.5025	44.5025								
PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	ALMDEVVK	3	1.0073	0.2668	7.8011	8	5.5247	4.6212	4.4553	3.3093	2.2215	2.1514
		DCVGPEVEK	1	2.7464	2.7464								
		FHVEEEGK	1	6.1528	6.1528								
		GCITIGSGDTATCCAK	1	12.664	12.664								
		ITLPVDFVTADK	1	5.959	5.959								
		ITLPVDFVTADKFDENAK	1	3.1109	3.1109								
		TGQATVASGIPAGWMGLDCGPESSKK	1	5.5216	5.5216								
		VLNNMEIGTSLFDEEGAK	1	7.0355	7.0355								
PGK2_HUMAN	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3	FHVEEEGK	1	6.1528	6.1528		1	6.1528	6.1528	6.1528	6.1528	6.1528	
PGS1_HUMAN	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	EISPDTTLLDLQNNDISELRK	1	1.4493	1.4493		4	1.8151	1.8845	1.0678	1.2296	1.2293	4.5526
		ELHLDNNK	1	0.1175	0.1175								
		IQAIELEDLLR	2	2.1622	2.1606	1.0556							
		VGVNDFCPMGFGVK	1	3.5313	3.5313								
PGS2_HUMAN	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	AHENEITK	1	0.245	0.245		12	1.3676	1.4045	0.2815	0.2362	0.1988	5.1871
		ASYSGVSLFSNPVQYWEIQPSTFR	1	2.6836	2.6836								
		DFEPSLGPVCPFR	2	10.928	7.1432	4.0478							
		DLPPDTTLLDLQNNK	2	0.0981	0.0938	1.5314							
		ELHLDNNK	1	0.1175	0.1175								
		GLNNLAK	3	0.1101	0.0888	2.4458							
		NLHALILVNNK	1	1.2404	1.2404								
		SSGIENGAFQGMK	3	0.095	0.0739	2.3941							
		VSPGAFTPLVK	2	0.0535	0.0528	1.268							
		VTFNGLNQMIVIELGTNPLK	1	0.2767	0.2767								
		VVQCSDLGLDK	2	0.1887	0.1098	4.9939							
		VVQCSDLGLDKVPK	1	0.0743	0.0743								
PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	AKYPDYEVTWANDGY	1	6.3566	6.3566		1	6.3566	6.3566	6.3566	6.3566	6.3566	
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=3	VIGIDHIK	1	1.7446	1.7446		1	1.7446	1.7446	1.7446	1.7446	1.7446	
PIN_HUMAN	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1	NLDPFLLFDEFK	1	6.3879	6.3879		1	6.3879	6.3879	6.3879	6.3879	6.3879	
PLBL2_HUMAN	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	VLTSLDPQMVVVADK	1	0.3298	0.3298		1	0.3298	0.3298	0.3298	0.3298	0.3298	
PLEC1_HUMAN	Plectin-1 OS=Homo sapiens GN=PLEC1 PE=1 SV=3	DYELQLVTYK	1	38.6621	38.6621		2	20.0313	20.0313	7.3584	7.3584	7.3584	10.4458
		TLLQGSGCLAGIYLEDTK	1	1.4005	1.4005								
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	IFQNLDGALDEVVLK	1	0.8735	0.8735		1	0.8735	0.8735	0.8735	0.8735	0.8735	
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	IFQNLNGALDEVVLK	1	0.7748	0.7748		1	0.7748	0.7748	0.7748	0.7748	0.7748	
PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5	LNNAKYAISMAR	2	1.3168	1.2942	1.3017	1	1.3168	1.3168	1.3168	1.3168	1.2942	
PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	AESMLQQADK	1	7.1228	7.1228		8	7.1819	6.8863	5.5408	5.573	5.445	2.3386
		DCIETLEELMK	1	9.9356	9.9356								
		EGICALGGTSELSSEGTQHSYSEEEK	1	4.9875	4.9875								
		IDINMSGFNETDDLKR	1	4.9178	4.9178								
		LNLAFVANLFNK	1	18.8024	18.8024								
		VVALPEDLVEVKPK	1	5.038	5.038								
		YPALTKPENQDIDWTTLEGETR	1	0.9472	0.9472								
		YTLNVLEDLGDGQK	3	5.7038	5.2787	1.6664							
PLTP_HUMAN	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	ATYFGSYLLSPWVDSPLK	1	0.3279	0.3279		7	0.4536	0.5413	0.388	0.4447	0.3994	1.7605
		GAFFPLTER	1	0.2828	0.2828								
		GLREVIEK	1	0.18	0.18								
		SSVDELVGIDYSLMK	1	0.3992	0.3992								
		TGLELSR	1	0.4127	0.4127								
		TMLQIGVMPMLNER	1	0.4167	0.4167								
		VYDFLSTFITSGMR	2	1.1557	0.7521	4.0815							
PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens GN=NP PE=1 SV=2	HRPQVAWCGSCLGGLTDK	1	1.2182	1.2182		2	2.1665	2.1665	1.9465	1.9465	1.9465	1.9469
		VFGFSLITNK	1	3.1178	3.1178								
POSTN_HUMAN	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	AAAITSDILEALGR	1	0.1851	0.1851		13	1.7587	1.472	0.5722	0.4779	0.4707	4.4679
		DIVTNIGVIHLIDQVLIPDSAK	1	0.2856	0.2856								
		EGETITEVIHGEPIIK	1	0.3052	0.3052								
		ELLTQPGDWTLFVPTNDAFK	1	0.1054	0.1054								
		FSTFLSLLEAADLK	1	0.2449	0.2449								
		GFEPGVTNILK	1	2.7714	2.7714								
		GSFTYFAPSNEAWDNLDSDIR	1	3.0428	3.0428								
		LLYPADTPVGNDQLLEILNK	3	0.1768	0.1743	1.2284							
		NALQNILYHLTPGVFIGK	1	3.5793	3.5793								
		QVIELAGK	1	11.0674	11.0674								
		TTVLYECCPGYMR	1	0.6273	0.6273								
		VGLNELYNGQILETIGGK	1	0.1359	0.1359								
		VLTQIGTSIQDFIEAEDDLSSFR	2	0.3359	0.3039	1.9029							
POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	AGFAGDDAPR	3	13.8928	13.843	1.1086	5	9.5457	10.5035	8.6253	9.4468	8.6092	1.6784
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691							
		GILTLK	5	14.6377	14.2916	1.292							
		LCYVALDFEQEMATAASSSSLEK	3	4.2888	3.2457	2.8462							
		QEYDESGPSIVHR	2	6.5412	6.506	1.1582							
POTEF_HUMAN	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	AGFAGDDAPR	3	13.8928	13.843	1.1086	4	10.86	12.0571	10.2716	11.5087	10.9869	1.4808
		AVFPSIVGRPR	2	8.3682	6.7981	2.5691							
		GILTLK	5	14.6377	14.2916	1.292							
		QEYDESGPSIVHR	2	6.5412	6.506	1.1582							
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	5.0546	5.0546		1	5.0546	5.0546	5.0546	5.0546	5.0546	
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	TFTDCFNCLPIAAIVDEK	1	5.0546	5.0546		1	5.0546	5.0546	5.0546	5.0546	5.0546	
PP1G_HUMAN	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	5.0546	5.0546		1	5.0546	5.0546	5.0546	5.0546	5.0546	
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	EGMNIVEAMER	4	5.0115	2.49	3.584	11	10.8715	11.4232	8.101	9.171	7.7546	2.48
		FEDENFILK	3	17.1022	16.9434	1.1811							
		HTGPGILSMANAGPNTNGSQFFICTAK	1	3.9399	3.9399								
		IIPGFMCQGGDFTR	1	19.2145	19.2145								
		KITIADCGQLE	2	16.9957	16.7247	1.2895							
		SIYGEK	1	17.7785	17.7785								
		SIYGEKFEDENFILK	1	1.7653	1.7653								
		TEWLDGK	1	7.0656	7.0656								
		VKEGMNIVEAMER	1	1.9498	1.9498								
		VNPTVFFDIAVDGEPLGR	1	14.5499	14.5499								

		VSFELFADK	4	14.2138	12.552	1.9132							
PPM1F_HUMAN	Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=1 SV=3	AIGDVFQKPYVSGEADAASR	1	0.3009	0.3009		1	0.3009	0.3009	0.3009	0.3009	0.3009	
PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GLFIIDDK	4	10.9172	10.8507	1.1337	3	10.0647	9.8819	9.8283	9.646	8.9957	1.3152
		LVQAFQFTDK	3	12.0757	11.7008	1.3678							
		TIAQDYGVLK	4	7.2013	6.1231	1.9399							
PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	KEGGLGPLNIPLLADVTR	1	7.9093	7.9093		1	7.9093	7.9093	7.9093	7.9093	7.9093	
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	GLFIIDPNGVIK	2	3.5093	3.5054	1.0681	1	3.5093	3.5093	3.5092	3.5092	3.5054	
PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	GLFIIDDK	4	10.9172	10.8507	1.1337	1	10.9172	10.9172	10.9172	10.9172	10.8507	
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=3	GVLFGVPGAFTPGCSK	1	5.1145	5.1145		2	3.6991	3.6991	3.4176	3.4176	3.4176	1.7685
		VNLAELFK	1	2.2837	2.2837								
PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	DINAYNCEEPTEK	1	7.3218	7.3218		5	2.9412	2.9412	1.7893	1.7893	1.7893	3.79
		ELAILLGMLDPAEKDEK	1	2.6756	2.6756								
		LIALSIDSVEDHLAWSK	1	0.2062	0.2062								
		VVFVFGPDKK	1	1.525	1.525								
		VVISLQLTAEK	1	2.9773	2.9773								
PRELP_HUMAN	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	NLMQLNLAHNILR	1	1.2936	1.2936		1	1.2936	1.2936	1.2936	1.2936	1.2936	
PREP_HUMAN	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=2	LLPDHTYSVVSGGDPLCIPELTWEQLK	1	1.1599	1.1599		1	1.1599	1.1599	1.1599	1.1599	1.1599	
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	DSLLGDGEFSMDLR	1	6.5665	6.5665		7	9.2436	9.1365	8.89	8.8732	8.3933	1.3273
		DSPSVWAAVPGK	2	16.2383	16.165	1.1441							
		EGVHGGLINK	1	8.1405	8.1405								
		SSFYVNGLTLGGQK	3	8.3154	7.729	1.6417							
		STGGAPTFNVTVTK	2	8.6846	8.4956	1.3468							
		TFVNITPAEVGVLVGK	5	7.9184	7.1225	1.79							
		TLVLLMGK	4	8.8414	8.4125	1.4723							
PRS10_HUMAN	26S protease regulatory subunit S10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	ALQSVGQIVGEVLK	1	4.5198	4.5198		1	4.5198	4.5198	4.5198	4.5198	4.5198	
PRS23_HUMAN	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1	DFLLNYPFSTSVK	1	0.1186	0.1186		2	2.0411	2.0411	0.6856	0.6856	0.6856	11.9571
		FCDVKDETYDLLYQQCDAQPGASGSGVYVR	1	3.9635	3.9635								
PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	ATFDSLVVPK	1	0.0121	0.0121		2	0.8622	0.8622	0.1439	0.1439	0.1439	33.176
		TIQQCCENILLNAAWLK	1	1.7122	1.7122								
PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GYSFSLTTFSPSGK	1	6.8371	6.8371		2	4.9682	4.9682	4.6033	4.6033	4.6033	1.7497
		YNEDLELEDAIHTAILTLK	1	3.0993	3.0993								
PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	ESLKEEDESDDDNM	1	18.4286	18.4286		1	18.4286	18.4286	18.4286	18.4286	18.4286	
PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	LLDEVFFSEK	1	8.1668	8.1668		1	8.1668	8.1668	8.1668	8.1668	8.1668	
PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	LFQVEYAIEAIK	1	2.8489	2.8489		2	5.1653	5.1653	4.6167	4.6167	4.6167	1.9793
		SSLILK	1	7.4816	7.4816								
PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	CDPAGYYCGFK	1	0.3414	0.3414		3	1.579	1.579	0.4622	0.4622	0.4622	8.1832
		LLDSSTVTHLFK	1	0.0668	0.0668								
		YGYEIPVDMLCK	1	4.3287	4.3287								
PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	LYQTDPSGTYHAWK	1	1.9735	1.9735		1	1.9735	1.9735	1.9735	1.9735	1.9735	
PSA7L_HUMAN	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	LYQTDPSGTYHAWK	1	1.9735	1.9735		1	1.9735	1.9735	1.9735	1.9735	1.9735	
PSAL_HUMAN	Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens GN=NPEPPSL1 PE=2 SV=3	ATFDSLVVPK	1	0.0121	0.0121		1	0.0121	0.0121	0.0121	0.0121	0.0121	
PSB3_HUMAN	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	DAVSGMGVIVHIIEK	1	7.5724	7.5724		2	8.3711	8.3711	8.3329	8.3329	8.3329	1.1449
		LNLYELK	1	9.1697	9.1697								
PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	ATEGMVVADK	1	3.4777	3.4777		2	3.475	3.475	3.475	3.475	3.475	1.0011
		GTTAVLTEK	1	3.4723	3.4723								
PSG4_HUMAN	Pregnancy-specific beta-1-glycoprotein 4 OS=Homo sapiens GN=PSG4 PE=2 SV=2	SGENLYLSCFAESNPR	1	0.1043	0.1043		1	0.1043	0.1043	0.1043	0.1043	0.1043	
PSME1_HUMAN	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	IEDGNNFGVAVQEK	1	0.2234	0.2234		3	2.6324	2.6324	1.4698	1.4698	1.4698	5.1672
		ISELDAFLK	1	3.1231	3.1231								
		TENLLGSYFPK	1	4.5508	4.5508								
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	NNQFQALLQYADPVSAQHAK	1	3.2759	3.2759		2	4.2992	4.2992	4.1756	4.1756	4.1756	1.4094
		VTNLLMLK	1	5.3225	5.3225								
PTBP2_HUMAN	Polypyrimidine tract-binding protein 2 OS=Homo sapiens GN=PTBP2 PE=1 SV=1	VTNLMLK	1	5.3225	5.3225		1	5.3225	5.3225	5.3225	5.3225	5.3225	
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1	TMLLQPAGSLGSYSYR	2	0.6603	0.5341	2.5955	1	0.6603	0.6603	0.6603	0.6603	0.5341	
PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2	EVVEEAENGR	1	3.32	3.32		1	3.32	3.32	3.32	3.32	3.32	
PTRF_HUMAN	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	SDQVNGVLVLSLLDK	3	4.5894	4.3515	1.4747	1	4.5894	4.5894	4.5894	4.5894	4.3515	
PTX3_HUMAN	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=2	ALAAVLEELR	1	3.134	3.134		4	2.075	2.075	0.8766	0.8766	0.8766	7.3176
		LTGFNIWDSVLSNEEIR	1	4.3095	4.3095								
		MLLQATDDVLR	1	0.8021	0.8021								
		TILFSYSTK	1	0.0545	0.0545								
PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	GYGFIEYEK	1	0.2808	0.2808		1	0.2808	0.2808	0.2808	0.2808	0.2808	
PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	ITSCIFQLLQEAGIK	1	2.1452	2.1452		1	2.1452	2.1452	2.1452	2.1452	2.1452	
PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	LDILDMFTEIK	1	3.9956	3.9956		1	3.9956	3.9956	3.9956	3.9958	3.9956	
PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	DAC7ICECCK	1	1.415	1.436		6	1.091	1.091	0.9636	0.9636	0.9636	1.8303
		LGPTLMCLLSTQFK	1	0.3205	0.3205								
		LNPHWDGDTIYYETR	1	0.8626	0.8626								
		LWYENPGVFSPAQLTQIK	1	0.8748	0.8748								
		SPNDLLALFR	1	1.3866	1.3866								
		VAEFPHGYGSCDEIPR	1	1.6867	1.6867								
QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	EVNYIDK	1	1.6692	1.6692		1	1.6692	1.6692	1.6692	1.6692	1.6692	
QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	AWRPALYLAALDCAEETNSAVCR	1	0.2522	0.2522		14	0.4492	0.4513	0.2997	0.2701	0.2623	2.2905
		DVQNVAAAPELAMGALELESR	1	0.3631	0.3631								
		ELCSACHNER	1	0.8791	0.8791								
		EVALDLSQHK	1	0.169	0.169								
		FGVTDFPSCYLLFR	1	0.4074	0.4074								
		GGSYLGR	1	0.2714	0.2714								
		LAGAPSEDPQFPK	1	0.4396	0.4396								
		LDVPVWDVEATLNFLK	3	0.3673	0.3624	1.2198							
		LEEIDGFFAR	1	0.1154	0.1154								
		NGSGAVFPVAGADVQTLR	1	0.2511	0.2511								
		NNEEYLALIFEK	4	0.1212	0.12	1.1784							
		SALYSPSDPLTLLQADTVR	3	0.1088	0.1085	1.1066							
		SFYTAYLQR	2	2.3246	1.7576	3.0263							
		VGSPNAVLWLWSSHNR	1	0.2185	0.2185								
RAL2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like protein 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	DYFEQYGK	3	5.4526	5.035	1.6296	1	5.4526	5.4526	5.4526	5.4526	5.035	
RA1L3_HUMAN	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3 OS=Homo sapiens GN=HNRPA1L3 PE=5 SV=1	DYFEQYGK	1	8.3825	8.3825		1	8.3825	8.3825	8.3825	8.3825	8.3825	
RAB28_HUMAN	Ras-related protein Rab-28 OS=Homo sapiens GN=RAB28 PE=1 SV=2	IVVLGDGASGK	1	3.2996	3.2996		1	3.2996	3.2996	3.2996	3.2996	3.2996	
RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	LVFLGEQSVGK	1	0.0295	0.0295		1	0.0295	0.0295	0.0295	0.0295	0.0295	
RAB6B_HUMAN	Ras-related protein Rab-6B OS=Homo sapiens GN=RAB6B PE=1 SV=1	LVFLGEQSVGK	1	0.0295	0.0295		1	0.0295	0.0295	0.0295	0.0295	0.0295	
RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	ATIGADFLTK	1	0.729	0.729		3	1.5324	1.5324	1.3655	1.3655	1.3655	1.8294
		DPENFPFVVLGNK	1	2.4322	2.4322								
		GADCVLVFDVTAPNTFK	1	1.436	1.436								
RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1	EDSMMEYLK	1	27.3342	27.3342		4	12.0846	11.459	5.9742	6.4782	6.4756	5.9937
		LFFLQVK	1	11.5991	11.5991								
		QLFDQVVK	2	8.9565	8.9477	1.0649							
		VLEQHK	1	0.4486	0.4486								
RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	HLTGEFEK	1	1.752	1.752		3	2.9135	3.1074	2.7731	2.9782	2.9779	1.4942
		LVLVGDGGTGK	1	3.2996	3.2996								
		NLQYYDISAK	2	3.6889	3.6882	1.0275							
RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	TLEEDEEELFK	1	7.0271	7.0271		1	7.0271	7.0271	7.0271	7.0271	7.0271	
RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	GAVGALLVVDIAK	1	6.1429	6.1429		1	6.1429	6.1429	6.1429	6.1429	6.1429	
RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	TPSSDVLVFDYTK	1	6.1364	6.1364		1	6.1364	6.1364	6.1364	6.1364	6.1364	
RBBP7_HUMAN	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	TPSSDVLVFDYTK	1	6.1364	6.1364		1	6.1364	6.1364	6.1364	6.1364	6.1364	
RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	TCLLIVFSK	1	6.3409	6.3409		1	6.3409	6.3409	6.3409	6.3409	6.3409	
RHOB_HUMAN	Rho-related GTP-binding protein RhoB OS=Homo sapiens GN=RHOB PE=1 SV=1	TCLLIVFSK	1	6.3409	6.3409		1	6.3409	6.3409	6.3409	6.3409	6.3409	
RHOC_HUMAN	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	TCLLIVFSK	1	6.3409	6.3409		1	6.3409	6.3409	6.3409	6.3409	6.3409	
RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	AVDIPHMDIEALK	1	4.4861	4.4861		2	5.4343	5.9084	5.3509	5.844	3.1513	1.2831
		FSVCVLGDQQHCDEAK	3	6.3825	2.8013	5.1241							
RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	CTGGEVGATSALAPK	1	6.3129	6.3129		2	3.225	3.225	0.9303	0.9303	0.9303	14.9987
		IGPLGLSPK	1	0.1371	0.1371								
RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	AVVLMGK	1	0.7038	0.7038		5	4.252	3.3942	2.9473	2.3456	1.2401	2.9636
		GHLENNPALEK	1	7.2409	7.2409								
		GTIEILSDVQLIK	1	6.4097	6.4097								
		IIQLLDDYPK	4	1.1915	0.8769	2.7861							
		TSFFQALGITTK	2	5.714	0.5992	64.4325							
RLA0L_HUMAN	60S acidic ribosomal protein P0-like OS=Homo sapiens PE=2 SV=1	GHLENNPALEK	1	7.2409	7.2409		4	5.139	3.7306	4.2161	2.7265	1.3311	2.335
		GTIEILSDVQLIK	1	6.4097	6.4097								
		IIQLLDDYPK	4	1.1915	0.8769	2.7861							
		TSFFQALGITTK	2	5.714	0.5992	64.4325							
RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	AAGVNVEPFWPGLFAK	2	12.0628	11.9979	1.1584	2	13.5183	13.0331	13.4397	12.9641	12.9176	1.1652
		KEESEESDDDMGFGLFD	1	14.9738	14.9738								
RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	KEESEESDDDMGFGLFD	2	14.4846	14.4866	1.0479	3	13.6699	17.4811	8.6743	13.3916	13.386	3.9613
		NIEDVIAQGIGK	3	24.6913	24.6795	1.0385							
		YVASYLLAALGGNSSPSAK	1	1.8237	1.8237								
RMP_HUMAN	Unconventional prefoldin RPB5 interactor OS=Homo sapiens GN=RMP PE=1 SV=3	TIDDLK	1	0.649	0.649		1	0.649	0.649	0.649	0.649	0.649	
RMXL3_HUMAN	RNA-binding motif protein, X-linked-like-3 OS=Homo sapiens GN=RBMXL3 PE=2 SV=2	GFAFVITFSPADAK	1	3.6019	3.6019		1	3.6019	3.6019	3.6019	3.6019	3.6019	
RNBP6_HUMAN	Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2	FMQDASNVMQLLLK	1	1.2574	1.2574		1	1.2574	1.2574	1.2574	1.2574	1.2574	
RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2	MTANSVLEPGNSEVSLVCEK	1	2.736	2.736		1	2.736	2.736	2.736	2.736	2.736	
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=4	DYFEQYGK	2	5.7746	5.1522	1.9904	3	4.8975	5.1168	4.7224	4.9659	4.6907	1.4098
		GFAFVTFDDHDSVDK	1	3.1764	3.1764								
		LFIGGLSFETTDESLR	1	5.7415	5.7415								
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	DYFEEYGK	1	7.2217	7.2217		3	4.9708	4.9708	4.7399	4.7399	4.7399	1.4454
		GFGFVTFDDHDPVDK	1	3.645	3.645								
		IDTIEIITDR	1	4.0456	4.0456								
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2	GFGFILFK	1	7.4459	7.4459		1	7.4459	7.4459	7.4459	7.4459	7.4459	
ROD1_HUMAN	Regulator of differentiation 1 OS=Homo sapiens GN=ROD1 PE=1 SV=2	VTNLLMLK	1	5.3225	5.3225		1	5.3225	5.3225	5.3225	5.3225	5.3225	
RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	DVEEEYFK	1	18.2989	18.2989		3	10.2737	10.2737	8.5298	8.5298	8.5298	2.1492
		KVVGCSCVVVK	1	3.9617	3.9617								
		LVEALCAEHQINLIK	1	8.5606	8.5606								
RS20_HUMAN	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	LIDLHSPSEIVK	1	0.135	0.135		1	0.135	0.135	0.135	0.135	0.135	
RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	DHASQMNVAEVDK	1	6.9733	6.9733		1	6.9733	6.9733	6.9733	6.9733	6.9733	
RS25_HUMAN	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	AALQELLSK	1	0.7817	0.7817		1	0.7817	0.7817	0.7817	0.7817	0.7817	
RSU1_HUMAN	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3	DNDLISLPK	1	1.7729	1.7729		1	1.7729	1.7729	1.7729	1.7729	1.7729	
S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	CIESLIAVFQK	3	6.3113	3.4405	4.5263	3	5.3177	5.0653	5.2201	4.9454	3.9019	1.2721
		DGYNYTLSK	1	5.6597	5.6597								
		TEFLSFMNTELAAFTK	4	3.9821	3.9074	1.2606							
S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1	DVGSLDEK	1	5.5987	5.5987		1	5.5987	5.5987	5.5987	5.5987	5.5987	
SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1	EALEVDWSSEK	1	0.1716	0.1716		1	0.1716	0.1716	0.1716	0.1716	0.1716	
SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	GISEETTTGVHNLYK	1	6.5432	6.5432		2	3.3501	3.3501	1.0132	1.0132	1.0132	13.984
		VAVVAGYGDVGK	1	0.1569	0.1569								
SAP_HUMAN	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	DGGFCEVCK	2	4.731	4.7096	1.1444	9	9.6012	11.5618	8.0115	9.8796	7.4566	1.8672
		DVVTAAGDMLK	1	4.0024	4.0024								
		EILDAFDK	3	21.6799	21.5019	1.1734							
		EIVDSYLPVILDIIK	6	14.4539	13.5671	1.5104							
		GCSFLPDPYQK	2	4.2769	2.0103	7.1164							
		LGPGMADICK	3	7.5605	2.0075	17.4374							
		QEILAALEK	2	16.6285	16.57	1.126							
		SDVYCEVCEFLVK	1	6.1675	6.1675								
		SLPCDICK	1	6.9102	6.9102								
SENP7_HUMAN	Sentrin-specific protease 7 OS=Homo sapiens GN=SENP7 PE=1 SV=3	TIDNDLR	1	0.189	0.189		1	0.189	0.189	0.189	0.189	0.189	
SEPT11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3	STLMDTLFNTK	1	0.686	0.686		1	0.686	0.686	0.686	0.686	0.686	
SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	LYPWGVVEVENPEHNDFLK	1	0.2495	0.2495		1	0.2495	0.2495	0.2495	0.2495	0.2495	
SEPT6_HUMAN	Septin-6 OS=Homo sapiens GN=SEPT6 PE=1 SV=4	STLMDTLFNTK	1	0.686	0.686		1	0.686	0.686	0.686	0.686	0.686	
SET_HUMAN	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	EFHLNESGDPSSK	1	3.726	3.726		2	3.5857	3.5857	3.583	3.583	3.583	1.0569
		IDFYFDENPYFENK	1	3.4454	3.4454								
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1 OS=Homo sapiens GN=SFRS1 PE=1 SV=2	DIEDVFYK	1	7.228	7.228		1	7.228	7.228	7.228	7.228	7.228	
SH3BG_HUMAN		QGEVVGFLEANK	1	2.8675	2.8675		1	2.8675	2.8675	2.8675	2.8675	2.8675	
SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	QGDVLGFLEANK	1	2.8675	2.8675		1	2.8675	2.8675	2.8675	2.8675	2.8675	
SKP1_HUMAN	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	RTDDIPVWDQEFLK	1	0.3927	0.3927		1	0.3927	0.3927	0.3927	0.3927	0.3927	

SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	LSHETVTIELK	1	0.252	0.252		1	0.252	0.252	0.252	0.252	0.252	
SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	GDGPVQGIINFEQK	3	5.5885	5.5169	1.2187	1	5.5885	5.5885	5.5885	5.5885	5.5169	
SOX30_HUMAN	Transcription factor SOX-30 OS=Homo sapiens GN=SOX30 PE=1 SV=1	LCAVETGPR	2	1.4707	1.1678	2.7118	1	1.4707	1.4707	1.4707	1.4707	1.1678	
SPB6_HUMAN	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	ADFSGMSQTDLSLSK	1	1.894	1.894		2	3.4807	3.4807	3.098	3.098	3.098	2.0055
		NLGMTDAFELGK	1	5.0673	5.0673								
SPB8_HUMAN	Serpin B8 OS=Homo sapiens GN=SERPINB8 PE=1 SV=2	LVLVNAIYFK	1	5.9377	5.9377		1	5.9377	5.9377	5.9377	5.9377	5.9377	
SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1	AFQSLTEVNK	1	6.9443	6.9443		3	4.3497	4.3497	1.9025	1.9026	1.9025	8.2353
		LVLVNAIYFK	1	5.9377	5.9377								
		STEVEVLLPK	1	0.167	0.167								
SPI2_HUMAN	Serpin I2 OS=Homo sapiens GN=SERPINI2 PE=2 SV=1	LVLVNAIYFK	1	5.9377	5.9377		1	5.9377	5.9377	5.9377	5.9377	5.9377	
SPON2_HUMAN	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=2	AFPPAPVLPSR	1	0.2731	0.2731		3	1.0796	1.7097	0.4037	0.7485	0.415	6.0628
		GEAWALMK	2	0.0836	0.0798	1.5411							
		IVPSPDWFVGVDSLDLCDGDR	4	2.882	1.0506	6.7243							
SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	DEDNNLLTEK	1	3.3075	3.3075		9	2.7371	2.8009	2.7116	2.7802	2.7473	1.1574
		DIDKDLVI	2	3.0271	2.993	1.2377							
		FFETCDLDNDK	3	3.1616	3.1568	1.0696							
		FFETCDLDNDKYIALDEWAGCFGIK	1	2.1438	2.1438								
		LEAGDHPVELLAR	1	2.5743	2.5743								
		LHLDYIGPCK	1	2.2922	2.2922								
		TFDSSCHFFATK	2	2.5039	2.3663	1.6161							
		YIALDEWAGCFGIK	3	2.7628	2.7275	1.213							
		YIPPCLDSELTEFPLR	1	2.8612	2.8612								
SPSY_HUMAN	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	DVLILGGGDGGILCEIVK	1	2.0715	2.0715		1	2.0715	2.0715	2.0715	2.0715	2.0715	
SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	DLAALEDK	1	5.9184	5.9184		10	3.9554	3.7496	1.9233	1.8799	1.7599	5.4767
		DLTSWVTEMK	1	9.0435	9.0435								
		DTEQVDNWMSK	1	0.2142	0.2142								
		DVDEIEAWISEK	1	5.8961	5.8961								
		DVDETSWIK	1	6.5512	6.5512								
		LDENSAFLQFNWK	2	0.5785	0.4647	2.6389							
		LIQEQHPEEELIK	1	2.0532	2.0532								
		MNEVISLWK	1	4.3745	4.3745								
		QWELLLEK	2	4.8627	4.0753	2.3762							
		VNEVNQFAAK	1	0.0019	0.0019								
SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	ENEVLEAWK	1	3.9014	3.9014		6	2.1457	2.147	1.3946	1.484	1.2311	3.0942
		MFSEADACELWIDEK	1	1.3743	1.3743								
		NDSFTTCIELGK	1	0.2874	0.2874								
		QAEAFLNNGEYVLAHTEMPTTLEGAEAAIK	1	4.6835	4.6835								
		TAASGIPYHSEVPVSLK	2	2.1547	1.1204	6.0378							
		VDTVNHLADELINSGHSDAATIAEWK	1	0.473	0.473								
SRGN_HUMAN	Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=2	GPMFELLPGESNK	2	5.1696	5.1556	1.1098	2	2.8	2.8	1.4916	1.4916	1.4773	5.7994
		TDLFPK	2	0.4304	0.4233	1.2945							
SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	VTDDLVCLVYK	2	6.2745	6.2577	1.109	1	6.2745	6.2745	6.2745	6.2745	6.2577	
SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1	LLGMGDIEGLIDK	1	0.0577	0.0577		1	0.0577	0.0577	0.0577	0.0577	0.0577	
SRPX_HUMAN	Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1	DTADGILTDVILK	1	0.9633	0.9633		1	0.9633	0.9633	0.9633	0.9633	0.9633	
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	SEISQVFEALK	1	0.303	0.303		1	0.303	0.303	0.303	0.303	0.303	
STC2_HUMAN	Stanniocalcin-2 OS=Homo sapiens GN=STC2 PE=1 SV=1	VIVEMIHFK	1	0.1377	0.1377		1	0.1377	0.1377	0.1377	0.1377	0.1377	
STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	ALSVGNIDDALQCYSEAIK	1	5.0671	5.0671		7	4.4289	4.9258	3.3119	3.7207	3.5736	2.2825
		DCEECIQLEPTFIK	1	2.3981	2.3981								
		DPQALSEHLK	1	1.3923	1.3923								
		ELDPTNMTYITNQAAVYFEK	2	8.4036	7.1512	2.2824							
		FMNPFNMPNLYQK	1	1.411	1.411								
		LAYINPDLALEEPK	1	2.1375	2.1375								
		LLEFQLALK	1	10.1928	10.1928								
STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	AIEENNNFSK	1	3.2872	3.2872		4	4.6371	4.6371	2.6957	2.6957	2.6957	4.3508
		DLSLEEIQK	1	10.2239	10.2239								
		ESVPEFPLSPPK	1	0.3341	0.3341								
		KLEAAEER	1	4.7031	4.7031								
STMN2_HUMAN	Stathmin-2 OS=Homo sapiens GN=STMN2 PE=1 SV=3	ALEENNNFSK	1	3.2872	3.2872		3	6.0714	6.0714	5.4068	5.4068	5.4068	1.7861
		DLSLEEIQK	1	10.2239	10.2239								
		KLEAAEER	1	4.7031	4.7031								
STMN4_HUMAN	Stathmin-4 OS=Homo sapiens GN=STMN4 PE=2 SV=1	KLEAAEER	1	4.7031	4.7031		1	4.7031	4.7031	4.7031	4.7031	4.7031	
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	YDYNSGEELESYK	1	4.845	4.845		1	4.845	4.845	4.845	4.845	4.845	
STRBP_HUMAN	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	GWPLELICEK	1	2.1615	2.1615		1	2.1615	2.1615	2.1615	2.1615	2.1615	
SUMO2_HUMAN	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=1	TENNDHINLK	1	2.4404	2.4404		2	1.3348	0.9663	0.748	0.5043	0.4446	5.3248
		VAGQDGSVVQFK	2	0.2293	0.1898	2.451							
SUMO3_HUMAN	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	VAGQDGSVVQFK	2	0.2293	0.1898	2.451	1	0.2293	0.2293	0.2292	0.2292	0.1898	
SUMO4_HUMAN	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2	VAGQDGSVVQFK	1	0.1007	0.1007		1	0.1007	0.1007	0.1007	0.1007	0.1007	
SVEP1_HUMAN	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=2	AFCLACPFYGTTPFAGSR	1	1.2807	1.2807		2	1.7368	1.7368	1.6758	1.6758	1.6758	1.4627
		TTGPNVVYSCNR	1	2.1928	2.1928								
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=4	LGVENCYFPMFVSQSALEK	1	1.9869	1.9869		1	1.9869	1.9869	1.9869	1.9869	1.9869	
SYG_HUMAN	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=2	TFSSFWVAPFK	1	1.8824	1.8824		1	1.8824	1.8824	1.8824	1.8824	1.8824	
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	IFDSEEILAGYK	1	3.7154	3.7154		1	3.7154	3.7154	3.7154	3.7154	3.7154	
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	FLGDIEVWDQAEK	1	2.0446	2.0446		1	2.0446	2.0446	2.0446	2.0446	2.0446	
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	DIIACGFDINK	1	0.3146	0.3146		2	3.0814	3.0814	1.3564	1.3564	1.3564	7.8977
		DMNQVLDAYENIK	1	5.8481	5.8481								
TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	AAEDYGVIK	1	0.407	0.407		6	0.4321	0.4321	0.323	0.323	0.323	2.2352
		DMAAVQR	1	0.1967	0.1967								
		GDPNWFMK	1	0.4807	0.4807								
		LVNSLYPDGSKPVK	1	1.1897	1.1897								
		TDMFQTVDLFEGK	1	0.1354	0.1354								
		TLMALGSLAVTK	1	0.1832	0.1832								
TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	DDGLFSGDPNWFPK	2	8.1318	8.0628	1.2031	7	5.8815	5.3176	4.9588	4.4193	3.9334	2.0011
		DGTVLCELINALYPEGQAPVKK	2	4.9818	4.6606	1.6855							
		ENFQNWLK	2	1.9122	1.7686	1.7615							
		IQASTMAFK	1	9.6058	9.6058								
		NFSDNQLQEGK	2	7.7066	7.6644	1.1599							
		TLMNLGGLAVAR	4	1.8383	1.2344	2.6153							
		YGINTTDIFQTVDLWEGK	4	6.9939	6.8732	1.2486							
TAGL3_HUMAN	Transgelin-3 OS=Homo sapiens GN=TAGLN3 PE=1 SV=2	DMAAVQR	1	0.1967	0.1967		1	0.1967	0.1967	0.1967	0.1967	0.1967	
TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	AAQASDLEK	1	7.5981	7.5981		5	5.5016	5.0845	4.9686	4.5905	3.0525	1.6564
		ALAGCDFLTISPK	2	9.1783	9.1167	1.1784							
		LLGELLQDNAK	2	4.5481	1.7903	9.3977							
		LSSTWEGIQAGK	4	3.2035	1.8472	4.8802							
		WLHNEDQMAVEK	1	2.9803	2.9803								
TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	DVNAAIATIK	1	8.4984	8.4984		4	4.8403	4.8403	1.4987	1.4987	1.4987	17.7953
		EDMAALEK	1	5.4319	5.4319								
		TIGGGDDSFNTFFSETGAGK	1	5.4106	5.4106								
		TIQFVDWCPTGFK	1	0.0202	0.0202								
TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	LISQIVSSITASLR	1	4.0786	4.0786		4	3.9735	3.8157	3.3421	3.0422	3.0169	2.1675
		QLFHPEQLITGK	1	4.8148	4.8148								
		SIQFVDWCPTGFK	2	1.0716	1.0492	1.3384							
		TIGGGDDSFNTFFSETGAGK	2	5.9288	5.9061	1.1319							
TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	DVNAAIATIK	1	8.4984	8.4984		6	4.7955	4.9574	2.1842	2.5191	2.5163	10.0486
		EDMAALEK	1	5.4319	5.4319								
		LISQIVSSITASLR	1	4.0786	4.0786								
		QLFHPEQLITGK	1	4.8148	4.8148								
		TIGGGDDSFNTFFSETGAGK	2	5.9288	5.9061	1.1319							
		TIQFVDWCPTGFK	1	0.0202	0.0202								
TBA3C_HUMAN	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3	DVNAAIATIK	1	8.4984	8.4984		4	4.8156	5.0382	1.4878	1.9617	1.9587	17.7407
		QLFHPEQLITGK	1	4.8148	4.8148								
		TIGGGDDSFNTFFSETGAGK	2	5.9288	5.9061	1.1319							
		TIQFVDWCPTGFK	1	0.0202	0.0202								
TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	EDMAALEK	1	5.4319	5.4319		2	3.2518	2.525	2.4126	1.8408	1.8151	3.151
		SIQFVDWCPTGFK	2	1.0716	1.0492	1.3384							
TBA4B_HUMAN	Putative tubulin-like protein alpha-4B OS=Homo sapiens GN=TUBA4B PE=5 SV=2	LISQIVSSITASLR	1	4.0786	4.0786		2	4.4467	4.4467	4.4314	4.4314	4.4314	1.1245
		QIFHPEQLITGK	1	4.8148	4.8148								
TBA8_HUMAN	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	LISQIVSSITASLR	1	4.0786	4.0786		3	2.9712	2.9712	0.7348	0.7348	0.7348	22.4993
		QLFHPEQLITGK	1	4.8148	4.8148								
		TIQFVDWCPTGFK	1	0.0202	0.0202								
TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	EIVHIQAGQCGNQIGAK	1	8.3639	8.3639		3	5.49	4.7519	5.1426	4.4811	4.3856	1.5421
		MSATFIGNSTAIQELFK	3	3.6449	3.5164	1.38							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	4.4612	4.4612								
TBB2C_HUMAN	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	3.3544	3.3352	1.1635	5	4.0551	3.865	2.902	3.1283	3.0821	3.005
		EIVHLQAGQCGNQIGAK	1	8.3639	8.3639								
		IMNTFSVVPSPK	1	0.4512	0.4512								
		MSATFIGNSTAIQELFK	3	3.6449	3.5164	1.38							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	4.4612	4.4612								
TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	EIVHIQAGQCGNQIGAK	1	8.3639	8.3639		3	4.3062	4.2555	2.4925	2.8234	2.7849	4.5831
		IMNTFSVVPSPK	1	0.4512	0.4512								
		MSSTFIGNSTAIQELFK	2	4.1034	3.9924	1.3948							
TBB4_HUMAN	Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	3.3544	3.3352	1.1635	5	3.8717	3.7855	2.7386	2.8328	2.8274	2.9829
		EIVHLQAGQCGNQIGAK	1	8.3639	8.3639								
		IMNTFSVVPSPK	1	0.4512	0.4512								
		MSATFIGNSTAIQELFK	1	2.7278	2.7278								
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	4.4612	4.4612								
TBB4Q_HUMAN	Putative tubulin beta-4q chain OS=Homo sapiens GN=TUBB4Q PE=5 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	3.3544	3.3352	1.1635	1	3.3544	3.3544	3.3543	3.3543	3.3352	
TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	ALTVPELTQQVFDAK	1	3.1123	3.1123		7	4.2735	3.9949	3.2128	3.1645	3.1534	2.6338
		EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	3.3544	3.3352	1.1635							
		EIVHIQAGQCGNQIGAK	1	8.3639	8.3639								
		IMNTFSVVPSPK	1	0.4512	0.4512								
		ISVYYNEATGGK	1	7.4865	7.4865								
		MAVTFIGNSTAIQELFK	2	2.6852	2.6581	1.2235							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	4.4612	4.4612								
TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	MASTFIGNSTAIQELFK	3	3.6449	3.5164	1.38	1	3.6449	3.6449	3.6449	3.6449	3.5164	
TBB8_HUMAN	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	2	3.3544	3.3352	1.1635	1	3.3544	3.3544	3.3543	3.3543	3.3352	
TBB8B_HUMAN	Tubulin beta-8 chain B OS=Homo sapiens PE=1 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	3.3544	3.3352	1.1635	1	3.3544	3.3544	3.3543	3.3543	3.3352	
TBC8B_HUMAN	TBC1 domain family member 8B OS=Homo sapiens GN=TBC1D8B PE=2 SV=2	SVIISIK	1	3.4654	3.4654		1	3.4654	3.4654	3.4654	3.4654	3.4654	
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	DDNMFQIGK	1	4.8909	4.8909		2	3.2988	3.2988	2.8891	2.8891	2.8891	2.1054
		GISLNPEQWSQLK	1	1.7066	1.7066								
TCPA_HUMAN	T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1	ICDDELILIK	1	4.6819	4.6819		2	4.0132	3.7903	3.9571	3.7414	2.964	1.2685
		SLLVIPNTLAVNAAQDSTDLVAK	2	3.3446	2.3583	3.4975							
TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	DALSDLALHFLNK	1	3.1578	3.1578		2	1.6346	1.6346	0.5928	0.5928	0.5928	10.65
		KLGGTIDDCELVEGLVLTQK	1	0.1113	0.1113								
TCPG_HUMAN	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	IVLLDSSLEYK	2	0.1572	0.1553	1.2403	1	0.1572	0.1572	0.1572	0.1572	0.1553	
TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	QQLLIGAVAK	1	14.5169	14.5169		1	14.5169	14.5169	14.5169	14.5169	14.5169	
TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	DMLEAGILDTYLGK	2	3.6418	3.6024	1.2321	2	4.0225	3.8956	4.0044	3.8797	3.8517	1.1437
		LVPGGGATEIELAK	1	4.4032	4.4032								
TCTP_HUMAN	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	DLISHDEMFSDIYK	3	2.6831	2.0266	2.79	3	6.1206	4.7456	5.246	4.012	3.3902	1.9892
		EIADGLCLEVEGK	1	10.6044	10.6044								
		VKPFMTGAAEQIK	1	5.0742	5.0742								
TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1	LNWLSVDFNNWK	1	4.9283	4.9283		1	4.9283	4.9283	4.9283	4.9283	4.9283	
TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	AIANECQANFISIK	1	9.3933	9.3933		9	6.217	6.7068	4.5587	5.2738	4.7848	2.7445
		DVDLEFLAK	1	2.455	2.455								
		ETVVEVPQVTWEDIGGLEDVKR	1	4.0092	4.0092								
		GDDLSTAILK	1	9.7291	9.7291								
		IVSQLLTLMDGLK	1	10.6414	10.6414								
		LDQLIYRLPDEK	1	2.5651	2.5651								
		NAPAIIFIDELDAIAPK	3	7.8686	6.2485	2.5573							
		QAAPCVLFFDELDSIAK	2	8.7908	6.9289	2.7589							
		QLAQIK	1	0.5007	0.5007								
TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2	LDTLAQEVALLK	1	0.3363	0.3363		1	0.3363	0.3363	0.3363	0.3363	0.3363	

TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	NEFGEIQGDK	1	0.043	0.043		2	1.8668	1.8668	0.3984	0.3984	0.3984	23.2956
		YLLNELNLEPFSEK	1	3.6905	3.6905								
THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	TAFQEALDAAGDK	2	7.3911	7.3895	1.03	1	7.3911	7.3911	7.3911	7.3911	7.3895	
THIOM_HUMAN	Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2	VVNSETPVVVDFHAQWCGPCK	1	0.1832	0.1832		1	0.1832	0.1832	0.1832	0.1832	0.1832	
TICN1_HUMAN	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	DSLGWMFNK	2	3.7237	3.4166	1.8134	5	1.7307	1.819	1.3526	1.2917	1.2076	2.3479
		FDTSILPICK	2	0.358	0.3065	2.2108							
		LSNNEWCYCFQKPGGLPCQNEMNR	1	1.3063	1.3063								
		SLATLCDGPCPCLPEPEPPK	1	1.3997	1.3997								
		VCVTGDYQTALCVSR	1	1.8678	1.8678								
TICN3_HUMAN	Testican-3 OS=Homo sapiens GN=SPOCK3 PE=1 SV=2	DSLGWMFNR	1	0.3206	0.3206		2	0.3383	0.3442	0.3378	0.3438	0.3111	1.0769
		FDTSILPICK	2	0.356	0.3065	2.2108							
TIMP1_HUMAN	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	EPGLCTWQSLR	2	1.435	0.8654	4.6864	8	4.7386	4.3066	0.6602	0.7386	0.4249	12.6841
		FVYTPAMESVCGYYHR	3	3.3505	0.8889	7.8101							
		GFQALGDAADIR	5	11.9789	3.1406	15.1229							
		HLACLPR	1	0.0225	0.0225								
		LQDGLLHITTCSFVAPWNSLSLAQR	1	20.7589	20.7589								
		LQSGTHCLWTDQLLQGSEK	3	0.133	0.1216	1.6525							
		SEEFLIAGK	4	0.059	0.0561	1.4488							
		TVTVCGEECTVFPCLSIPCK	3	0.1711	0.1706	1.1016							
TIMP2_HUMAN	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	DIEFIYTSAVCQVSLDVGGK	1	0.4101	0.4101		5	0.3405	0.3418	0.3361	0.3398	0.3367	1.2024
		EVDSGNDIYGNPIK	1	0.2497	0.2497								
		EVDSGNDIYGNPIKR	5	0.3306	0.3288	1.122							
		EYLIAGK	2	0.3478	0.3391	1.3747							
		SDGSCAWYR	3	0.3646	0.3608	1.1921							
TKT_HUMAN	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	AVELAANTK	1	0.6046	0.6046		7	3.9315	3.9098	3.0123	3.1769	2.9556	2.4384
		IIALDGDTK	1	5.3891	5.3891								
		LGQSDPAPLQHQIMDIYQK	1	3.9189	3.9189								
		NMAEQIIQEIYSQIQSK	2	4.0604	4.0584	1.0449							
		NSTFSEIFK	1	8.5296	8.5296								
		QAFTDVATGSLGGGLGAACGMAYTGK	1	1.4107	1.4107								
		TSRPENAIIYNNNEDFQVGQAK	2	3.6075	2.6079	3.3259							
TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	AQEACGPLEMDSALSVQNLEK	1	2.0475	2.0475		10	3.5048	2.9591	2.3447	1.4885	1.4169	3.4666
		EADESLNFEEQILEAAK	1	6.9334	6.9334								
		GVGAAATAVTQALNELLQHVK	1	3.014	3.014								
		ILAQATSDLVNAIK	1	4.2805	4.2805								
		SIAATSALVK	3	0.1045	0.0889	2.1497							
		TEDSGLQTQVMAATQCALSTSQLVACTK	1	2.1384	2.1384								
		TLAESALQLLYTAK	1	1.0459	1.0459								
		TYGVSFFLVK	1	5.0795	5.0795								
		VAGSVTELQAAEAMK	2	3.2113	2.9708	1.7599							
		VSQMAGYFEPLTLAAVGAASK	1	7.1929	7.1929								
TLN2_HUMAN	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	SIAATSALVK	3	0.1045	0.0889	2.1497	2	2.592	1.3483	0.7286	0.2759	0.2444	15.584
		TYGVSFFLVK	1	5.0795	5.0795								
TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2	VEEEIQTLSQVLAAK	1	0.8281	0.8281		1	0.8281	0.8281	0.8281	0.8281	0.8281	
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	EAGITEK	1	1.538	1.538		10	10.0147	8.5256	7.0028	6.8332	6.2365	2.3421
		ELASQPDVDGFLVGGASLKPEFVDIINAK	2	10.6666	10.0027	1.6694							
		HVFGESDELIGQK	1	40.7285	40.7285								
		IAVAAQNCYK	1	8.9745	8.9745								
		IIYGGSVTGATCK	1	9.3899	9.3899								
		QSLGELIGTLNAAK	3	7.6556	6.3251	2.2868							
		TATPQQAQEVHEK	3	4.973	3.7442	2.8634							
		VTNGAFTGEISPGMIK	3	5.2821	5.0209	1.4611							
		VVFEQTK	1	3.2632	3.2632								
		VVLAYEPVWAIGTGK	3	7.6759	7.5963	1.1957							
TPISL_HUMAN	Putative triosephosphate isomerase-like protein LOC286016 OS=Homo sapiens PE=1 SV=2	EAGITEK	1	1.538	1.538		2	2.4006	2.4006	2.2403	2.2403	2.2403	1.7022
		VVFEQTK	1	3.2632	3.2632								
TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	IQLVEEELDR	1	11.6397	11.6397		3	8.0746	8.4343	6.9799	7.5417	7.4485	2.0506
		LATALQK	1	3.071	3.071								
		MEIQEIQLK	2	9.5132	9.2795	1.3726							
TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	IQLVEEELDR	1	11.6397	11.6397		3	6.0454	6.0454	4.9658	4.9658	4.9658	2.0954
		LATALQK	1	3.071	3.071								
		MELQEMQLK	1	3.4256	3.4256								
TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	IQLVEEELDR	1	11.6397	11.6397		3	8.0746	8.4343	6.9799	7.5417	7.4485	2.0506
		LATALQK	1	3.071	3.071								
		MELQEIQLK	2	9.5132	9.2795	1.3726							
TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like protein OS=Homo sapiens PE=5 SV=2	MELQEIQLK	2	9.5132	9.2795	1.3726	1	9.5132	9.5132	9.5132	9.5132	9.2795	
TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	AEVSELK	2	2.2934	2.2411	1.3563	8	6.6199	6.1391	2.8458	2.7783	2.7641	8.2657
		EENVGLHQTLDQTLNELNCI	1	5.8183	5.8183								
		EKAEGDVAALNR	1	6.1249	6.1249								
		IQLVEEELDR	1	11.6397	11.6397								
		KIQALQQQADEAEDR	1	20.5651	20.5651								
		LATALQK	1	3.071	3.071								
		MEIQEMQLK	1	3.4256	3.4256								
		TIDDLEEK	1	0.0209	0.0209								
TPT1L_HUMAN	TPT1-like protein OS=Homo sapiens PE=1 SV=1	VKPFMTGAAEQIK	1	5.0742	5.0742		1	5.0742	5.0742	5.0742	5.0742	5.0742	
TR150_HUMAN	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	GSFSDTGLGDGK	1	0.2245	0.2245		1	0.2245	0.2245	0.2245	0.2245	0.2245	
TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=2	GDVAFVK	2	1.5476	1.3625	2.0727	1	1.5476	1.5476	1.5475	1.5475	1.3625	
TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	CGLVPVLAENYK	1	0.6019	0.6019		1	0.6019	0.6019	0.6019	0.6019	0.6019	
TRI14_HUMAN		LLLDEEALAK	1	7.1996	7.1996		1	7.1996	7.1996	7.1996	7.1996	7.1996	
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	SYDYDLIIIGGGSGGLAAAK	1	3.8551	3.8551		1	3.8551	3.8551	3.8551	3.8551	3.8551	
TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	AGTLDLSLTVQGK	3	33.8041	29.9431	1.8228	24	13.791	14.6824	7.8557	10.2297	9.19	5.0334
		AQGYSGLSVK	2	16.5804	13.3354	2.6316							
		AQLYIDCEK	2	9.8545	9.1587	1.7295							
		CTSYPDGSWK	2	20.9883	20.9852	1.0248							
		DCVGDVTENQICNK	2	15.872	14.4191	1.8769							
		DHSGQVFSVVSNGK	1	9.2613	9.2613								
		FQMIPLDPK	1	27.0198	27.0198								
		FTGSQPFGQGVEHATANK	5	13.7338	10.6905	2.3555							
		GDACKDDFDHDSVPDIDDICPENVDISETDFR	1	0.5684	0.5684								
		GTLLALER	1	14.2407	14.2407								
		GTSQNDPNWVVR	2	31.1048	30.9716	1.1401							
		IEDANLIPPVPDDKFQDLVDAVR	1	19.8628	19.8628								
		IMADSGPIYDK	3	9.936	7.119	3.1824							
		KDHSGQVFSVVSNGK	1	5.8227	5.8227								
		LCNNPTPGFGGK	5	11.0466	8.6312	2.2428							
		LCNSPSPQMNGKPCEGEAR	1	3.1297	3.1297								
		MENAELDVPIQSVFTR	1	0.7629	0.7629								
		NPCTDGTHDCNK	1	15.014	15.014								
		QVTQSYWDTNPTR	1	20.5769	20.5769								
		SITLFVQEDR	1	21.3954	21.3954								
		TIVTTLQDSIR	2	21.1362	21.1362	1.0005							
		TKDLQAICGSCDELSSMVLELR	1	2.7944	2.7944								
		VTEENKELANELR	3	6.4525	6.277	1.3396							
		VVMYEGKK	1	0.0251	0.0251								
TXD15_HUMAN		TLETLK	1	0.6492	0.6492		1	0.6492	0.6492	0.6492	0.6492	0.6492	
TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	ALAPTWEQLALGLEHSETVK	2	4.7783	4.589	1.499	3	6.0118	5.0502	5.0134	4.2985	4.2081	2.1094
		EFPGLAGVK	2	2.4374	2.4065	1.254							
		TLAPTWEELSK	1	10.8196	10.8196								
TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	SEPTQALELTEDDIKEDGIVPLR	1	2.2684	2.2684		1	2.2684	2.2684	2.2684	2.2684	2.2684	
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	ELLTSFGPLK	1	0.2004	0.2004		2	1.1772	1.1772	0.657	0.657	0.657	5.3613
		LFIGGLPNYLNDDQVK	1	2.154	2.154								
UAP56_HUMAN	Spliceosome RNA helicase BAT1 OS=Homo sapiens GN=BAT1 PE=1 SV=1	GLAITFVSDENDAK	1	2.298	2.298		1	2.298	2.298	2.298	2.298	2.298	
UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	GQVCLPVISAENWKPATK	1	1.0372	1.0372		2	1.9502	1.9502	1.7233	1.7233	1.7233	2.0503
		IEINFPAEYPFKPPK	1	2.8632	2.8632								
UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1	NPDGTMNLMNWECAIPGK	1	2.8342	2.8342		2	1.5479	1.5479	0.8609	0.8609	0.8609	5.3929
		NPDGTMNLMNWECAIPGKK	1	0.2615	0.2615								
UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	LELPLPEEYPMAAPK	1	7.2231	7.2231		1	7.2231	7.2231	7.2231	7.2231	7.2231	
UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	LGFEDGSVLK	1	4.7473	4.7473		5	4.8571	4.8571	4.5185	4.5185	4.5185	1.5227
		MPFPVNHGASSEDTLLK	1	3.4869	3.4869								
		MQLKPMEINPEMLNK	1	2.7154	2.7154								
		QFLSETEK	1	8.2678	8.2678								
		QTIGNSCGTIGLIHAVANNQDK	1	5.0683	5.0683								
UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	TLDGGLNVQLETAVGAAIK	1	2.3101	2.3101		2	2.5671	2.5671	2.5542	2.5542	2.5542	1.1526
		TYNTDVPLVLMNSFNTDEDTKK	1	2.824	2.824								
ULK4_HUMAN	Serine/threonine-protein kinase ULK4 OS=Homo sapiens GN=ULK4 PE=2 SV=2	EQKLLLR	1	11.8494	11.8494		1	11.8494	11.8494	11.8494	11.8494	11.8494	
UVRAG_HUMAN		ALGREVALLHK	1	0.1028	0.1028		1	0.1028	0.1028	0.1028	0.1028	0.1028	
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1	LAGLGLQQLDEGLFSR	1	0.9379	0.9379		1	0.9379	0.9379	0.9379	0.9379	0.9379	
VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	DNLAEDIMR	3	10.953	10.835	1.1943	23	8.7108	9.5566	7.1193	8.2237	8.0177	2.1702
		EEAENTLQSFR	1	14.2633	14.2633								
		EKLQEEMLQR	3	8.7804	7.7275	1.9479							
		EYQDLLNVK	4	12.6181	12.3633	1.264							
		FADLSEAANR	2	1.0476	1.0464	1.0689							
		FANYIDK	4	9.938	9.5717	1.3879							
		FLEQQNK	3	9.9734	9.9349	1.1139							
		GTNESLER	3	9.8554	9.7679	1.1803							
		ILLAELEQLK	5	10.5451	9.8962	1.5476							
		ILLAELEQLKQQK	1	2.9208	2.9208								
		ISLPLPNFSSLNLR	1	1.6398	1.6398								
		KLLEGEESR	1	11.2815	11.2815								
		KVESLQEEIAFLK	3	13.3818	12.9644	1.3519							
		LLEGEESR	2	12.1651	12.1517	1.0685							
		LQDEIQNMK	4	9.4633	9.2053	1.3214							
		LQEEMLQR	1	7.7841	7.7841								
		MALDIEIATYR	1	7.0893	7.0893								
		QDVDNASLAR	1	11.7973	11.7973								
		QQYESVAAK	2	1.3652	1.3651	1.0189							
		QVDQLTNDK	3	14.1664	13.7935	1.3231							
		RQVDQLTNDK	1	3.6675	3.6675								
		TNEKVELQELNDR	1	5.5858	5.5858								
		VELQELNDR	1	10.0673	10.0673								
VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	AAVHLEGK	1	6.5083	6.5083		5	3.5366	3.5366	3.0125	3.0125	3.0125	1.9049
		AVAGNISDPGLQK	1	2.8558	2.8558								
		ELLPVLISAMIK	1	1.3802	1.3802								
		SLGEISALTSK	1	1.9315	1.9315								
		TNISDEESEQATEMLVHNAQNLMQSVK	1	5.007	5.007								
VTA1_HUMAN	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	QLGDNEAITQEIVQCAHLENYALK	1	0.7399	0.7399		1	0.7399	0.7399	0.7399	0.7399	0.7399	
VWF_HUMAN	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=2	GLRPSCPNSQSPVK	1	2.6421	2.6421		7	4.3495	4.3495	3.185	3.185	3.185	2.2197
		GLWEQCQLLK	1	4.4916	4.4916								
		IEDLPTMVTLGNSFLHK	1	1.2322	1.2322								
		ILTSDVFQDCNK	1	3.4963	3.4963								
		LSEAEFEVLK	1	1.5077	1.5077								
		NSQWICSNEECPGECLVTGQSHFK	1	13.9942	13.9942								
		VEDFGNAWK	1	3.0823	3.0823								
WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	DYSQGGVVK	1	8.7341	8.7341		5	5.4714	6.0868	3.9872	4.5804	4.5251	2.8152
		FATASADGQIIYIYDGK	1	2.6984	2.6984								
		LYSILGTTLKDEGK	1	0.7802	0.7802								
		YAPSGFYASGDVSGK	1	5.9803	5.9803								
		YEYQPFAGK	2	9.164	8.8362	1.4682							
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	SVGDGETVEFDVVEGEK	1	1.8794	1.8794		1	1.8794	1.8794	1.8794	1.8794	1.8794	
		SVGDGETVEFDVVEGEK	1	1.8794	1.8794								
		MLLSQNSK	1	0.0674	0.0674								

HUVEC:LA Fibroblasts

Accession	Description	Sequence	# Indiv oeos	Pep SM ratio	Pep GM ratio	Pep ratio SDoeo	# pep soecies	Prot SM of pep SMs	Prot weighted SM of pep SMs	Prot GM of pep SMs	Prot weighted GM of pep SMs	Prot GM of pep GMs	Prot weighted GM of pep GMs	Protein SDoeo
1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	DSTLIMQLLR	2	7.0837	0.4206	144.3775	7	4.9472	4.4767	1.9014	1.7926		0.8116	6.5935
		IEAELQDICNDVLELLDK	0											
		NLLSVAYK	1	14.9084	14.9084									
		QTTVSNSQQAYQEAFEISK	2	3.353	3.2835	1.337								
		TAFDEAIAELDTLNEESYK	1	3.9702	3.9702									
		YDDMAAAMK	2	0.1703	0.0828	6.7355								
		YLSEVASGDNK	1	0.1974	0.1974									
1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	AAFDDAIAELDTLSEESYK	3	4.255	1.691	7.313	7	8.3592	7.6395	7.5799	6.9205		1.3935	1.6198
		DSTLIMQLLR	2	7.0837	0.4206	144.3775								
		EAAENSLVAYK	2	9.0606	7.5362	2.423								
		HLIPAANTGESK	1	7.0626	7.0626									
		LICCDILDVLDK	2	11.9664	11.9426	1.0932								
		NLLSVAYK	1	14.9084	14.9084									
		QMVETELK	2	4.1779	2.2193	5.8272								
1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	DSTLIMQLLR	2	7.0837	0.4206	144.3775	6	6.569	6.6702	3.7686	4.5437		2.3828	4.8112
		ELETVCNDVLSLLDK	2	9.0306	8.9334	1.2317								
		NLLSVAYK	1	14.9084	14.9084									
		NSVVEASEAAYK	2	4.5036	4.2	1.7066								
		QAFDEAIAELDTLNEDSYK	1	3.7078	3.7078									
		YLAEVASGEK	1	0.1799	0.1799									
1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	DSTLIMQLLR	1	14.1548	14.1548		4	3.8767	2.1263	0.7831	0.4441		0.3191	8.3304
		TAFDDAIAELDTLNEDSYK	3	0.1514	0.1195	2.4092								
		YDDMAAAMK	2	0.1703	0.0828	6.7355								
		YLAEVATGEK	2	1.0304	0.806	2.8071								
1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	DSTLIMQLLR	2	7.0837	0.4206	144.3775	2	10.996	9.6919	10.2765	9.0778		1.3816	1.6925
		NLLSVAYK	1	14.9084	14.9084									
1433T_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	DSTLIMQLLR	2	7.0837	0.4206	144.3775	7	8.2592	7.8118	7.364	7.0998		2.7837	1.6755
		NLLSVAYK	1	14.9084	14.9084									
		QTIDNSQAAYQEAFDISK	1	5.4836	5.4836									
		SICTTVLELLDK	2	8.7494	8.2472	1.634								
		TAFDEAIAELDTLNEDSYK	2	4.4713	0.7402	33.578								
		YDDMATQMK	1	13.1871	13.1871									
		YLIANATNPESK	1	3.9307	3.9307									
1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	DICNDVLSLLEK	5	12.6032	11.8722	1.5314	10	8.3587	8.4026	7.6182	7.7713		5.7595	1.5845
		DSTLIMQLLR	2	7.0837	0.4206	144.3775								
		EKIETELR	1	10.8501	10.8501									
		FLIPNASQAESK	1	4.2878	4.2878									
		GIVDQSQQAYQEAFEISK	2	9.5286	9.144	1.5049								
		NLLSVAYK	1	14.9084	14.9084									
		TAFDEAIAELDTLNEESYK	6	5.5868	5.1199	1.6034								
		VVSSIEQK	2	9.4766	9.1453	1.4616								
		YDDMAACMK	2	5.2375	4.584	2.1095								
		YLAEVAAGDDK	1	4.0245	4.0245									
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	QLSQSLLPAIVELAEDAK	2	5.4525	5.4524	1.0079	1	5.4525	5.4525	5.4525	5.4525		5.4524	
2AAB_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	QLSQSLLPAIVELAEDAK	2	5.4525	5.4524	1.0079	1	5.4525	5.4525	5.4525	5.4525		5.4524	
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	AGQAVDDFIEK	1	4.3062	4.3062		3	4.3206	4.9926	3.6766	4.3202		4.3031	2.0897
		NPELQNLLLDDFFK	2	7.0088	6.9535	1.1952								
		VGTGEPCCDWVGDEGAGHFVK	1	1.6467	1.6467									
AATM_HUMAN	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=2	ASAELALGENSEVLK	1	5.1365	5.1365		4	3.0482	2.8476	2.8207	2.6679		2.0242	1.5553
		EFSIYMTK	1	2.1636	2.1636									
		NLDKEYLPIGGLAEFCK	2	1.909	0.844	7.8438								
		TCGFDFTGAVEDISK	2	2.9839	2.9478	1.2474								
ACBP_HUMAN	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2	QATVGDITERPQMLDFTGK	1	3.0895	3.0895		1	3.0895	3.0895	3.0895	3.0895		3.0895	
ACOC_HUMAN	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	YQQAGLPLIVLAGK	1	7.3345	7.3345		1	7.3345	7.3345	7.3345	7.3345		7.3345	
ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	AGFAGDDAPR	2	7.7658	7.7594	1.0589	6	5.9208	5.7633	5.618	5.4885		5.3296	1.4477
		DLTDYLMK	4	6.2071	6.1868	1.098								
		DSYVGDEAQSK	2	7.4039	7.3152	1.246								
		EITALAPSTMK	4	3.7131	3.3676	1.7063								
		GILTLK	3	7.0868	6.9762	1.2479								
		LCYVALDFENEMATAASSSSLEK	2	3.3481	3.3103	1.238								
ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	AGFAGDDAPR	3	7.7571	7.7529	1.0413	12	5.0254	5.3852	4.5323	5.0657		4.6378	1.682
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572								
		DLTDYLMK	5	6.2628	6.2454	1.0872								
		DSYVGDEAQSK	2	7.4039	7.3152	1.246								
		EITALAPSTMK	5	3.849	3.5514	1.6125								
		GILTLK	5	6.7833	6.6869	1.2097								
		GYSFTTTAER	4	6.5826	6.5592	1.1011								
		HQGVMVGMGQK	1	1.3378	1.3378									
		IIAPPERK	1	2.5084	2.5084									
		LCYVALDFEQEMATAASSSSLEK	2	3.5452	3.5451	1.0019								
		QEYDESGPSIVHR	2	4.9003	4.8987	1.0365								
		VAPEEHPVLLTEAPLNPK	5	3.6275	2.2201	4.6117								
ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	DLTDYLMK	6	6.2628	6.2454	1.0872	4	3.7975	5.0358	3.2146	4.5493		4.5423	2.0207
		HQGVMVGMGQK	1	1.3378	1.3378									
		IIAPPERK	1	2.5084	2.5084									
		VAPDEPILLTEAPLNPK	2	5.0811	5.081	1.0021								
ACTBM_HUMAN	Beta-actin-like protein 3 OS=Homo sapiens GN=ACTBL3 PE=1 SV=1	QEYDESGPSIVHR	2	4.9003	4.8987	1.0365	1	4.9003	4.9003	4.9002	4.9002		4.8987	
ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	AGFAGDDAPR	1	7.7397	7.7397		8	4.836	5.2633	4.2539	4.7522		4.6205	1.8116
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572								
		DLTDYLMK	1	6.4855	6.4855									
		EITALAPSTMK	1	4.3925	4.3925									
		GILTLK	3	6.7306	6.6702	1.1818								
		HQGVMVGMGQK	1	1.3378	1.3378									
		IIAPPERK	1	2.5084	2.5084									
		LCYVALDFENEMATAASSSSLEK	1	3.7465	3.7465									
ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	AGFAGDDAPR	3	7.7571	7.7529	1.0413	12	5.0254	5.3852	4.5323	5.0657		4.6378	1.682
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572								
		DLTDYLMK	5	6.2628	6.2454	1.0872								
		DSYVGDEAQSK	2	7.4039	7.3152	1.246								
		EITALAPSTMK	5	3.849	3.5514	1.6125								
		GILTLK	5	6.7833	6.6869	1.2097								
		GYSFTTTAER	4	6.5826	6.5592	1.1011								
		HQGVMVGMGQK	1	1.3378	1.3378									
		IIAPPERK	1	2.5084	2.5084									
		LCYVALDFEQEMATAASSSSLEK	2	3.5452	3.5451	1.0019								
		QEYDESGPSIVHR	2	4.9003	4.8987	1.0365								
		VAPEEHPVLLTEAPLNPK	5	3.6275	2.2201	4.6117								
ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	AGFAGDDAPR	1	8.08	8.08		5	5.3826	5.0435	4.6012	4.3637		4.3473	1.9688
		DLTDYLMK	1	5.5332	5.5332									
		EITALAPSTMK	1	1.662	1.662									
		GILTLK	1	8.2898	8.2898									
		LCYVALDFENEMATAASSSSLEK	2	3.3481	3.3103	1.238								
ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	3.8878	3.0319	2.8266	15	5.3561	5.3225	4.9906	4.997		4.82	1.5075
		ASIHEAWTDGK	1	6.0725	6.0725									
		CQLEINFNTLQTK	1	7.392	7.392									
		DLLLDPAWEK	3	7.1141	7.0612	1.1599								
		FAIQDISVEETSAK	3	5.3681	5.279	1.2556								
		GYEEWLLNEIR	1	7.5351	7.5351									
		ICDQWDNLGALTQK	2	5.0949	4.8513	1.5625								
		IDQLEGDHQLIQEALIFDNK	1	5.4902	5.4902									
		IVQTYHVNMAGTNPYTTITPQEINGK	1	2.5793	2.5793									
		LAILGIHNEVSK	1	2.859	2.859									
		LLETDQLYLEYAK	2	6.0491	6.0257	1.1328								
		QKDYETATLSEIK	2	2.162	2.0782	1.4922								
		TINEVENQILTR	1	4.813	4.813									
		VGWEQLLTTIAR	1	8.683	8.683									
		VLAVNQENEQLMEDYEK	2	5.2408	4.9584	1.6081								
ACTN2_HUMAN	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	CQLEINFNTLQTK	1	7.392	7.392		5	5.6405	5.9074	4.4201	5.13		5.0888	2.6381
		DLLLDPAWEK	3	7.1141	7.0612	1.1599								
		FAIQDISVEETSAK	3	5.3681	5.279	1.2556								
		GYEEWLLNEIR	1	7.5351	7.5351									
		LEQAEKGYEEWLLNEIR	1	0.7932	0.7932									
ACTN3_HUMAN	Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	CQLEINFNTLQTK	1	7.392	7.392		3	6.6247	6.4055	6.56	6.3399		6.2745	1.1909
		DLLLDPAWEK	3	7.1141	7.0612	1.1599								
		FAIQDISVEETSAK	3	5.3681	5.279	1.2556								
ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	AIMTYVSSFYHAFSGAQK	2	3.8878	3.0319	2.8266	14	4.9113	5.0846	3.9309	4.3089		3.7596	2.4547
		ASIHEAWTDGK	1	6.0725	6.0725									
		CQLEINFNTLQTK	1	7.392	7.392									
		DLLLDPAWEK	3	7.1141	7.0612	1.1599								
		EAILAHK	2	4.0822	1.388	11.7416								
		ETTDTDTADQVIASFK	1	2.2989	2.2989									
		FAIQDISVEETSAK	3	5.3681	5.279	1.2556								
		GYEEWLLNEIR	1	7.5351	7.5351									
		ISIEMNGTLEDQLSHLK	1	0.2507	0.2507									
		KDDPVTNLNNAFEVAEK	1	3.6066	3.6066									
		LSGSNPYTTVTPQIINSK	1	5.5108	5.5108									
		QFASQANVVGPWIQTK	1	2.1432	2.1432									
		TINEVENQILTR	1	4.813	4.813									
		VGWEQLLTTIAR	1	8.683	8.683									
ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	AGFAGDDAPR	3	7.7571	7.7529	1.0413	9	5.0145	5.494	4.4096	5.1179		4.9644	1.8034
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572								
		DLTDYLMK	5	6.2628	6.2454	1.0872								
		DSYVGDEAQSK	2	7.4039	7.3152	1.246								
		EITALAPSTMK	5	3.849	3.5514	1.6125								
		GILTLK	5	6.7833	6.6869	1.2097								
		HQGVMVGMGQK	1	1.3378	1.3378									
		IIAPPERK	1	2.5084	2.5084									
		LCYVALDFENEMATAASSSSLEK	3	3.4809	3.4497	1.1818								
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1	DLLPEDFVVYTYNK	1	1.0626	1.0626		2	0.9504	0.9504	0.9438	0.9438		0.9438	1.1826
		QVSYVIQAEGK	1	0.8382	0.8382									
ADK_HUMAN	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2	ELFDELVK	1	0.7746	0.7746		1	0.7746	0.7746	0.7746	0.7746		0.7746	
AEBP1_HUMAN	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1	GEDEDEVSEAQETPDHAIFR	1	4.6305	4.6305		2	3.0258	3.0258	2.5652	2.5652		2.5652	2.3054
		YLSPDATVSTEVR	1	1.4211	1.4211									
AGRIN_HUMAN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4	SIESTLDDLFR	1	1.7021	1.7021		1	1.7021	1.7021	1.7021	1.7021		1.7021	
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	ADIDVSGPK	1	0.31	0.31		6	1.9432	2.1627	1.5727	1.7616		1.7614	2.3266
		AEGPEVDVNLPK	1	1.8759	1.8759									
		ISMPDIDLNLK	2	3.4798	3.4785	1.0379								
		ISMPDVDLHLK	1	1.6774	1.6774									
		VDINAPDVDVGGPDWHLK	1	2.6053	2.6053									
		VDVSAPDVEAHGPEWNLK	1	1.7108	1.7108									
AIBP_HUMAN	Apolipoprotein A-I-binding protein OS=Homo sapiens GN=APOA1BP PE=1 SV=2	GNAGGIQPDLLISLTAPK	1	5.1262	5.1262		1	5.1262	5.1262	5.1262	5.1262		5.1262	
AIMP1_HUMAN	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	GAEADQIIEYLK	1	2.8486	2.8486		1	2.8486	2.8486	2.8486	2.8486		2.8486	
AINX_HUMAN	Alpha-internexin OS=Homo sapiens GN=INA PE=1 SV=2	EYQDLLNVK	4	8.7829	8.7662	1.0732	1	8.7829	8.7829	8.7829	8.7829		8.7662	
AK1A1_HUMAN	Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	VFDTFSPEEMK	2	6.6125	6.5171	1.2734	1	6.6125	6.6125	6.6125	6.6125		6.5171	
AKAP2_HUMAN	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=3	VELPSEEQVSQSQGPSEEKPAPLATEVFDEK	2	6.2494	5.3358	2.2619	1	6.2494	6.2494	6.2494	6.2494		5.3358	
AL1A1_HUMAN	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	1	0.1597	0.1597		6	6.2708	6.36	2.361	2.7516		2.7009	6.0879
		IFINNEWHDSVSGK	1	0.9089	0.9089									

		LYSNAYLNDLAGCIK	2	6.8953	6.4606	1.6752						
		SLDDVIK	1	8.6794	8.6794							
		VAFTGSTEVGK	1	0.9978	0.9978							
		YILGNPLTPGVTQGPQIDKEQYDK	1	19.9837	19.9837							
ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	KVPQVSTPTLVEVSR	3	1.1561	1.1516	1.1145	2	1.1238	1.1192	1.1233	1.1187	1.1154	1.0415
		LVTDLTK	4	1.0915	1.089	1.0803						
ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	AAQEEYVK	1	7.1965	7.1965		8	4.9451	5.0454	4.7399	4.8535	4.7768	1.3709
		ADDGRPFPQVIK	1	3.6922	3.6922								
		ALANSLACQGIK	3	5.4176	5.2195	1.3972							
		GGVVGIK	1	2.9391	2.9391								
		GILAADESTGSIAK	3	6.6107	6.5619	1.1636							
		VLAAVYK	1	4.9311	4.9311								
		VNPCIGGVILFHETLYQK	1	5.2638	5.2638								
		YASICQQNGIVPIVEPEILPDGDHDLK	3	3.5093	3.407	1.3479							
ALDOB_HUMAN	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2	VLAAVYK	1	4.9311	4.9311		1	4.9311	4.9311	4.9311	4.9311	4.9311	
ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	VLAAVYK	1	4.9311	4.9311		2	4.2202	3.8648	4.1599	3.8208	3.7369	1.2719
		YASICQQNGIVPIVEPEILPDGDHDLK	3	3.5093	3.407	1.3479							
AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	GLVLGIYSK	1	0.7778	0.7778		1	0.7778	0.7778	0.7778	0.7778	0.7778	
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	IKDLSTIEPLK	1	0.4225	0.4225		3	1.4366	1.4366	0.4336	0.4336	0.4336	8.7351
		SLDLFNCEVTNLNDYR	1	0.0503	0.0503								
		VSGGLEVLAEK	1	3.8371	3.8371								
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	IFGGLDMLAEK	1	11.692	11.692		2	6.0573	6.0573	2.2226	2.2226	2.2226	10.4639
		LKDISTLEPLK	1	0.4225	0.4225								
AN32C_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Homo sapiens GN=ANP32C PE=2 SV=1	IKDLSTIEPLK	1	0.4225	0.4225		2	2.1298	2.1298	1.2733	1.2733	1.2733	4.7592
		VSGGLEVLAEK	1	3.8371	3.8371								
AN32D_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member D OS=Homo sapiens GN=ANP32D PE=1 SV=2	IKDLSTIEPLK	1	0.4225	0.4225		1	0.4225	0.4225	0.4225	0.4225	0.4225	
ANM1_HUMAN	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	IVKANK	1	39.1624	39.1624		3	14.5134	14.5134	5.6659	5.6659	5.6659	5.3848
		VEDLTFTSPYCLQVK	1	1.8055	1.8055								
		VVLDVGSGTGILCMFAAK	1	2.5724	2.5724								
ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	GLGTDEDTLIEILASR	1	4.907	4.907		2	4.2927	4.2927	4.2485	4.2485	4.2485	1.226
		GVDEATIDILTK	1	3.6784	3.6784								
ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	DALNIETAIK	1	2.3245	2.3245		2	2.348	2.348	2.3478	2.3478	2.3478	1.0142
		SALSGHLETVILGLLK	1	2.3714	2.3714								
ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	ETSGNLEQLLLAVVK	3	2.5636	2.5622	1.0407	2	2.9216	2.7426	2.8996	2.7264	2.7253	1.1903
		LVDAYELK	1	3.2797	3.2797								
AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	TSVQFQNFSPTVVHPGDLQTQLAVQTK	1	2.7934	2.7934		1	2.7934	2.7934	2.7934	2.7934	2.7934	
API5_HUMAN	Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=2	DAYQVILDGVK	1	9.4547	9.4547		1	9.4547	9.4547	9.4547	9.4547	9.4547	
APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	EQLGPVTQEFWDNLEK	2	1.1104	1.1091	1.071	1	1.1104	1.1104	1.1104	1.1104	1.1091	
ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	DAVLLVFANK	1	3.1228	3.1228		1	3.1228	3.1228	3.1228	3.1228	3.1228	
ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	DAVLLVFANK	2	7.4264	6.7133	1.9083	2	6.4117	6.7499	6.3308	6.6768	6.2422	1.2532
		NISFTVWDVGGQDK	1	5.3969	5.3969								
ARF5_HUMAN	ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	DAVLLVFANK	3	5.9919	5.2016	1.8882	1	5.9919	5.9919	5.9919	5.9919	5.2016	
ARPP1_HUMAN		KYENILK	1	3.5219	3.5219		1	3.5219	3.5219	3.5219	3.5219	3.5219	
ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	FMEQVIFK	1	2.2046	2.2046		4	3.2471	3.9339	2.2065	2.9564	2.9117	3.3523
		GVDDLDFFIGDEAIEKPTYATK	3	5.3076	5.148	1.3678							
		TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1	0.399	0.399								
		YSYVCPDLVK	1	5.0772	5.0772								
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	DTDIVDEAIVYFK	1	4.3621	4.3621		1	4.3621	4.3621	4.3621	4.3621	4.3621	
ATX10_HUMAN		MEEQGLADASLLKK	1	1.0918	1.0918		1	1.0918	1.0918	1.0918	1.0918	1.0918	
ATX2L_HUMAN	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	GINGGPSR	1	5.2166	5.2166		1	5.2166	5.2166	5.2166	5.2166	5.2166	
AXA2L_HUMAN	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2	DALNIETAIK	1	2.3245	2.3245		2	2.348	2.348	2.3478	2.3478	2.3478	1.0142
		SALSGHLETVILGLLK	1	2.3714	2.3714								
B2MG_HUMAN	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	SNFLNCYVSGFHPSDIEVDLLK	1	2.6172	2.6172		3	2.5818	2.5747	2.5805	2.5733	2.5633	1.0389
		VEHSDLSFSK	2	2.6569	2.6568	1.0008							
		VNHVTLSQPK	2	2.4713	2.4474	1.2182							
BAF_HUMAN	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	AYVVLGQFLVLK	1	5.6175	5.6175		1	5.6175	5.6175	5.6175	5.6175	5.6175	
BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	ITDSEDK	1	1.039	1.039		1	1.039	1.039	1.039	1.039	1.039	
BCAT1_HUMAN	Branched-chain-amino-acid aminotransferase, cytosolic OS=Homo sapiens GN=BCAT1 PE=1 SV=3	ATLPVFDKEELEQIQQLVK	1	0.1508	0.1508		1	0.1508	0.1508	0.1508	0.1508	0.1508	
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	DLLNHHLK	1	0.1595	0.1595		9	0.6574	0.6787	0.5409	0.581	0.5129	1.9997
		EGVYTVFAPTNEAFR	1	0.2611	0.2611								
		ELANILK	1	1.0978	1.0978								
		GDELADSALEIFK	3	0.8825	0.5941	2.7838							
		LTLLAPLNSVFK	2	0.5023	0.4155	2.4574							
		QAGLGNHLSGISER	1	0.6642	0.6642								
		SPYQLVLQHSR	1	1.4577	1.4577								
		VLTPPMGTVMDVLK	1	0.489	0.489								
		YLYHGQTLETLGGK	1	0.4225	0.4225								
BIG1_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	KGLECLVSILK	1	1.6407	1.6407		1	1.6407	1.6407	1.6407	1.6407	1.6407	
BIG2_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	KGLECLVSILK	1	1.6407	1.6407		1	1.6407	1.6407	1.6407	1.6407	1.6407	
BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	LNSDPQFVLAQNVGTHTHDLLDICLK	1	0.2174	0.2174		1	0.2174	0.2174	0.2174	0.2174	0.2174	
BPNT1_HUMAN	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	LTDIHGNVLQYHK	1	1.0551	1.0551		1	1.0551	1.0551	1.0551	1.0551	1.0551	
BRE1A_HUMAN	E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	LMSERIK	1	1.5766	1.5766		1	1.5766	1.5766	1.5766	1.5766	1.5766	
BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=3	LMSERIK	1	1.5766	1.5766		1	1.5766	1.5766	1.5766	1.5766	1.5766	
C1R_HUMAN	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	ESEQGVYTCTAQGIWK	2	1.0784	1.0477	1.4069	7	0.7465	0.7156	0.5454	0.5045	0.4954	2.6273
		GGGALLGDR	1	0.1535	0.1535								
		LPVANPQACENWLR	1	0.4981	0.4981								
		QDACQGDSGGVFAVR	1	0.8135	0.8135								
		QRPPDLDTSSNAVDLLFFTDESGDSR	1	1.5097	1.5097								
		TLDEFTIQNLQPQYQFR	2	0.1369	0.1298	1.5946							
		VTTTMGVNTYK	1	1.0354	1.0354								
C1RL_HUMAN	Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	GGGALLGDR	1	0.1535	0.1535		1	0.1535	0.1535	0.1535	0.1535	0.1535	
C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	GFQVVVTLR	2	0.6966	0.5495	2.7535	8	5.0281	4.1971	1.1297	1.0685	1.0157	4.3498
		IIGGSDADIK	1	34.8878	34.8878								
		NYVDWIMK	2	1.0495	1.033	1.2872							
		QFGPYCGHGFPGPLNIETK	1	0.2328	0.2328								
		SNALDIIFQTDLTGQK	1	0.6483	0.6483								
		SSNNPHSPVEEFQVPYNK	1	1.1203	1.1203								
		TMQENSTPRED	1	0.6656	0.6656								
		TNFDNDIALVR	1	0.9241	0.9241								
C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	VRLSVLER	1	0.6302	0.6302		1	0.6302	0.6302	0.6302	0.6302	0.6302	
CAD13_HUMAN	Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1	DIQGSLQDIFK	1	2.5944	2.5944		1	2.5944	2.5944	2.5944	2.5944	2.5944	
CAD24_HUMAN		TLAELYGAK	1	3.0018	3.0018		1	3.0018	3.0018	3.0018	3.0018	3.0018	
CADH5_HUMAN	Cadherin-5 OS=Homo sapiens GN=CDH5 PE=1 SV=4	ELDSTGTPTGK	1	8.0816	8.0816		1	8.0816	8.0816	8.0816	8.0816	8.0816	
CALL3_HUMAN	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	EAFSLFDK	2	5.7089	5.6449	1.2369	1	5.7089	5.7089	5.7088	5.7088	5.6449	
CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	EAFSLFDK	2	5.7089	5.6449	1.2369	1	5.7089	5.7089	5.7088	5.7088	5.6449	
CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	IDNSQVESGSLEDDWDFLPPKK	2	1.3597	1.3596	1.004	1	1.3597	1.3597	1.3597	1.3597	1.3596	
CALU_HUMAN	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	EEFTAFLHPEEYDYMK	1	1.1805	1.1805		2	0.8844	0.8844	0.8334	0.8334	0.8334	1.6364
		EQFVEFR	1	0.5883	0.5883								
CAN2_HUMAN	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5	EFYILWTK	1	2.934	2.934		2	2.7981	2.7981	2.7948	2.7948	2.7948	1.0712
		SDGFSIETCK	1	2.6622	2.6622								
CAP1_HUMAN	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4	LSDLLAPISEQIK	2	7.1695	6.8545	1.5328	2	3.843	4.9518	1.9245	2.9834	2.8954	6.4232
		VENQENVSNLVIEDTELK	1	0.5166	0.5166								
CAPZB_HUMAN	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	LVEDMENK	1	6.1179	6.1179		2	6.5194	6.5194	6.507	6.507	6.507	1.0911
		STLNEIYFGK	1	6.9209	6.9209								
CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	DIMAEIYK	4	2.8578	2.8285	1.1856	6	1.8435	2.2829	1.2988	1.8444	1.8259	3.1214
		DQGSCGSCWAFGAVEAISDR	1	0.9218	0.9218								
		EQWPQCPTIK	1	2.9209	2.9209								
		ICEPGYSPTYK	3	2.7387	2.676	1.3115							
		NGPVEGAFSVYSDFLLYK	1	1.4665	1.4665								
		TDQYWEK	1	0.1553	0.1553								
CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	ISVNNVLPVFDNLMQQK	2	2.9354	2.8281	1.4745	2	5.5269	4.663	4.8816	4.1203	4.0193	2.053
		VSTLPAITLK	1	8.1183	8.1183								
CAZA2_HUMAN	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	KIDGQQTIACESHQFQAK	1	0.7201	0.7201		1	0.7201	0.7201	0.7201	0.7201	0.7201	
CB039_HUMAN		NKLISELQQELK	2	1.1859	1.1486	1.4325	1	1.1859	1.1859	1.1859	1.1859	1.1486	
CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	SETITEEELVGLMNK	1	1.4555	1.4555		2	2.9779	2.9779	2.5593	2.5593	2.5593	2.2215
		SPEEGAETPVYLALLPPDAEGPHGQFVSEK	1	4.5003	4.5003								
CCD57_HUMAN	Coiled-coil domain-containing protein 57 OS=Homo sapiens GN=CCDC57 PE=2 SV=1	AEVSEIK	1	2.704	2.704		1	2.704	2.704	2.704	2.704	2.704	
CCD58_HUMAN	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	NLDDLTLLK	1	3.7535	3.7535		1	3.7535	3.7535	3.7535	3.7535	3.7535	
CCL2_HUMAN	C-C motif chemokine 2 OS=Homo sapiens GN=CCL2 PE=1 SV=1	WVQDSMDHLDK	1	2.6303	2.6303		1	2.6303	2.6303	2.6303	2.6303	2.6303	
CD109_HUMAN	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	SNLIQQWLSQQSDLGVISK	1	6.8506	6.8506		1	6.8506	6.8506	6.8506	6.8506	6.8506	
CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2	YGFIEGHVVIPR	1	0.7547	0.7547		1	0.7547	0.7547	0.7547	0.7547	0.7547	
CDC37_HUMAN	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	CIDSGLWVPNSK	1	1.7625	1.7625		2	1.757	1.757	1.7569	1.7569	1.7569	1.0045
		QYMEGFNDELEAFK	1	1.7514	1.7514								
CFAH_HUMAN	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	SIDVACHPGYALPK	1	0.1576	0.1576		1	0.1576	0.1576	0.1576	0.1576	0.1576	
CH10_HUMAN	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	DGDILGK	1	0.0399	0.0399		3	2.4689	2.4689	0.8111	0.8111	0.8111	13.616
		VLLPEYGGTK	1	3.2421	3.2421								
		VVLDDKDYFLFR	1	4.1248	4.1248								
CH3L1_HUMAN	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2	EAGTLAYYEICDFLR	1	0.8588	0.8588		1	0.8588	0.8588	0.8588	0.8588	0.8588	
CING_HUMAN	Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	KVSLVLEK	1	1.1731	1.1731		1	1.1731	1.1731	1.1731	1.1731	1.1731	
CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	DLADLIPK	2	5.8164	5.6507	1.4072	1	5.8164	5.8164	5.8163	5.8163	5.6507	
CLC11_HUMAN	C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1	AALAPYNWPVWLGVHDR	1	0.8132	0.8132		3	0.9544	0.919	0.9351	0.9029	0.8928	1.2744
		DAVQALQEAQGR	2	0.8128	0.7947	1.3505							
		QQMEALTR	1	1.2373	1.2373								
CLCA_HUMAN		SVLISLK	1	5.2523	5.2523		1	5.2523	5.2523	5.2523	5.2523	5.2523	
CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	EAIDSYIK	2	5.2075	4.6784	1.9499	4	2.5762	3.1025	1.9561	2.3793	2.2791	2.539
		EDKLECSEELGDLVK	1	1.8904	1.8904								
		LPVVIGGLLDVDCSEDVIK	1	2.6446	2.6446								
		TLQIFNIEMK	1	0.5624	0.5624								
CLH2_HUMAN	Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2	EDKLECSEELGDLVK	1	1.8904	1.8904		2	1.2264	1.2264	1.0311	1.0311	1.0311	2.3567
		TLQIFNIEMK	1	0.5624	0.5624								
CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	EEFASTCPDDEIELAYEQVAK	1	0.0962	0.0962		5	2.9699	3.4478	1.7607	2.4359	2.1408	5.1169
		LAALNPESNTAGLDIFAK	2	3.2787	2.899	2.0466							
		LCPGGQLPFLLYGTEVHTDTNK	1	3.1914	3.1914								
		LHIVGVVCK	1	3.5564	3.5564								
		NSNPALNDNLEK	3	4.727	3.6364	2.6438							
CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	DEFTNTCPSDKEVEIAYSDVAK	1	0.3229	0.3229		3	1.9521	1.9521	0.4157	0.4157	0.4157	11.7596
		IEEFLEEVLCPPK	1	0.0405	0.0405								
		TDVNKIEEFLEEVLCPPK	1	5.4928	5.4928								
CLIC5_HUMAN	Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3	FLDGDELTLADCNLLPK	1	0.2009	0.2009		1	0.2009	0.2009	0.2009	0.2009	0.2009	
CLIC6_HUMAN	Chloride intracellular channel protein 6 OS=Homo sapiens GN=CLIC6 PE=2 SV=3	FLDGDELTLADCNLLPK	1	0.2009	0.2009		1	0.2009	0.2009	0.2009	0.2009	0.2009	
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	ALQEYR	1	1.9393	1.9393		16	4.0906	3.7572	2.8068	3.0388	2.6889	2.688
		ASSIIDELFQDR	4	5.5631	4.8956	1.8418							
		EILSVDCSTNNPSQAK	4	3.0405	2.6187	1.9541							
		EIQNAVNGVK	1	2.8282	2.8282								
		ELDESLQVAER	2	3.4956	3.1608	1.9065							
		FMETVAEK	4	3.8807	3.6409	1.5619							
		IDSLLENDR	3	3.7609	3.0903	2.3116							
		KTLLSNLEEAK	1	2.1206	2.1206								
		KYNELLK	1	3.5219	3.5219								
		LFDSDPITVTVPVEVSR	3	4.3697	3.8916	1.8797							
		QQTHMLDVMQDHFSR	1	2.9252	2.9252								
		RELDESLQVAER	1	0.1446	0.1446								
		SGSGLVGR	3	1.8157	1.7892	1.2396							
		TLLSNLEEAK	4	1.4777	0.905	4.2632							
		TLLSNLEEAKK	1	20.4187	20.4187								
		VTTVASHTSDSDVPSGVTEVVVK	3	4.1468	4.1199	1.1493							
CMBL_HUMAN	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	EVQVEHK	1	0.083	0.083		1	0.083	0.083	0.083	0.083	0.083	
CN153_HUMAN	UPF0671 protein C14orf153 OS=Homo sapiens GN=C14orf153 PE=2 SV=1	MVVLRAGK	1	0.7487	0.7487		1	0.7487	0.7487	0.7487	0.7487	0.7487	
CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	CYSCGEFGHIQK	1	1.6822	1.6822		1	1.6822	1.6822	1.6822	1.6822	1.6822	

CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	GNILIPGINEAVAAVTEEEHK	1	0.3197	0.3197		2	0.3955	0.3955	0.3882	0.3882	0.3882	1.3158
		MMEVAAADVK	1	0.4713	0.4713								
CNN2_HUMAN	Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	DGTILCTLMNK	2	0.9849	0.9504	1.4614	2	2.7143	2.1378	2.092	1.6274	1.5892	2.9021
		TWIEGLTGLSIGPDFQK	1	4.4437	4.4437								
CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4	ALLLQGSNEIEIR	3	12.8745	1.3997	17.5342	20	1.6867	2.2498	0.7408	0.8581	0.6491	3.2586
		DLEVDTTLK	1	0.3158	0.3158								
		FTYSVTVDGCTSHTGAWGK	2	0.5673	0.5197	1.8224							
		GDAGPAGPK	1	0.1371	0.1371								
		GESGPSGPAGPTGAR	1	0.4054	0.4054								
		GPFGADGVAGPK	1	1.8718	1.8718								
		GFSGLDGAK	1	2.1592	2.1592								
		GLTGSPGSPGPDGK	1	0.5312	0.5312								
		GNSGEPGAPGSK	1	0.5514	0.5514								
		GPAGPQGPR	2	1.0836	1.073	1.2202							
		GSEGPQGVR	3	3.1869	2.7384	2.0556							
		GVPGPPGAVGPAGK	1	0.8076	0.8076								
		GVQGPPGPAGPR	2	6.2306	2.3921	9.7651							
		NSVAYMDQQTGNLK	1	0.3582	0.3582								
		NSVAYMDQQTGNLKK	2	0.4507	0.4438	1.2834							
		SGDRGETGPAGPAGPVGPVGAR	2	1.0657	1.0581	1.184							
		SGEYWIDPNQGCNLDAIK	1	0.3427	0.3427								
		SLSQQIENIR	3	0.1597	0.1594	1.066							
		STGGISVPGPMGPSGPR	3	0.2819	0.2655	1.5395							
		VLCDDVICDETK	2	0.3537	0.3474	1.3099							
CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6	DGNPGNDGPPGR	1	0.4277	0.4277		25	0.9593	0.9404	0.5757	0.5799	0.5121	2.6796
		DYEVDATLK	1	0.1938	0.1938								
		EMATQLAFMR	1	0.4346	0.4346								
		FTYTVLVDGCSK	1	0.2794	0.2794								
		GAAGIPGGK	3	1.5759	1.4966	1.4817							
		GAPGAVGAPGPAGATGDR	1	0.5399	0.5399								
		GASGPAGVR	1	0.5704	0.5704								
		GDGGPPGMTGFPGAAGR	1	0.4597	0.4597								
		GDQGPVGR	1	4.8774	4.8774								
		GEAGAAGPAGPAGPR	1	0.382	0.382								
		GETGPSGPVGPAGAVGPR	1	0.4477	0.4477								
		GFPGTPGLPGFK	1	0.711	0.711								
		GHAGLAGAR	2	0.8803	0.88	1.035							
		GIPGPVGAAGATGAR	1	0.3222	0.3222								
		GPAGPSGPAGK	2	1.0479	1.045	1.1102							
		GPNGDAGRPGEPGLMGPR	1	4.2866	4.2866								
		GPSGPPGPDGNK	1	2.3116	2.3116								
		GPSGPQGIR	2	0.6438	0.6243	1.4229							
		GVGLGPGPMGLMGPR	4	1.5031	0.5522	4.4864							
		GVVGPQGAR	2	0.2443	0.2418	1.227							
		KTNEWGK	1	0.7499	0.7499								
		NSIAYMDEETGNLKK	2	0.1153	0.0989	2.23							
		SAPSLRPK	1	0.162	0.162								
		TGHPGTVGPAGIR	1	0.7047	0.7047								
		TIIEYK	3	0.1107	0.109	1.2478							
CO2A1_HUMAN	Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	FTYTALKDGCTK	1	0.8305	0.8305		1	0.8305	0.8305	0.8305	0.8305	0.8305	
CO3A1_HUMAN	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	DGNPGSDGLPGR	1	0.223	0.223		11	0.892	0.7805	0.6509	0.6211	0.5401	2.2718
		FTYTVLEDGCTK	3	0.6178	0.5841	1.5285							
		GAPGPQGPR	2	1.0644	1.0482	1.2811							
		GESGPAGPAGAPGAGSR	1	1.3594	1.3594								
		GPVGPSGPPGK	1	3.2707	3.2707								
		GRPGLPGAAGAR	1	0.4667	0.4667								
		INTDEIMTSLK	2	0.6158	0.6151	1.0649							
		SGEYWVDPNQGCK	2	0.5152	0.5016	1.3894							
		SVNGQIESLISPDGSR	4	0.736	0.3916	3.7773							
		TVFEYR	1	0.7838	0.7838								
		VFCNMETGETCISANPLNVPR	2	0.1597	0.1583	1.2009							
CO5A2_HUMAN	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	GSQFAYGDHQSPNTAITQMTFLR	2	0.6181	0.1744	15.5031	5	1.8073	1.6091	1.2344	1.1	0.7215	2.484
		NSVGYMDDQAK	1	0.6481	0.6481								
		QSGEYWIDPNQGSVEDAIK	1	1.74	1.74								
		SGLGSQVGLMPGSVGPVGPR	1	5.2466	5.2466								
		TVFEYR	1	0.7838	0.7838								
CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	DTTPLNVLCSPGIQVVSVGIK	4	0.396	0.3373	1.8673	9	0.4504	0.4829	0.3836	0.4105	0.3304	1.8471
		ENYKLLEDAFLK	2	0.2886	0.2793	1.4389							
		GLEQLLVGGSHLK	1	0.1382	0.1382								
		GTYTDCAIK	1	0.326	0.326								
		IALVITDGR	3	0.9964	0.397	5.2701							
		LLLFSDGNSQGATPAAIEK	2	0.2037	0.2028	1.1387							
		NNVEQVCCSFECQPAR	1	0.6082	0.6082								
		SLQWMAGGTFTGEALQYTR	1	0.6817	0.6817								
		YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1	0.415	0.415								
CO6A2_HUMAN	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	DDDLNLR	1	0.1741	0.1741		3	0.353	0.3895	0.3224	0.3596	0.3579	1.7314
		DVTVTAIGIDMFHEK	2	0.499	0.4943	1.2161							
		HESENLYSIACDKPQQVR	1	0.3858	0.3858								
CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=4	AAPLQGMLPGLLAPLR	1	0.4865	0.4865		23	2.548	2.5404	0.8613	0.9059	0.8623	3.5455
		ALILVGLER	1	0.2989	0.2989								
		DQNVFVAQK	1	11.1116	11.1116								
		EVITAVR	1	0.6855	0.6855								
		FWYGGCGGNENK	2	6.1395	3.3322	5.6207							
		IEEGVPQFLVLISSGK	1	0.4984	0.4984								
		ISLSPEYVFSVSTFTR	1	0.2826	0.2826								
		ITEGVPQLLIVLTADR	1	0.3749	0.3749								
		LLVLITGGK	1	23.6295	23.6295								
		NIDSEEVGK	1	0.4018	0.4018								
		NILVSSAGSR	1	5.6821	5.6821								
		NLQVALTSK	1	0.2792	0.2792								
		NNLFTSSAGYR	1	0.7513	0.7513								
		QINVGNALEYVSR	2	0.4515	0.4464	1.2361							
		QLQLQGGSGLNTGSALSYVYANHFTEAGGSR	1	0.5734	0.5734								
		QQSLETAMSFVAR	1	0.5162	0.5162								
		SQAPVLDAIR	1	0.5008	0.5008								
		SSGIVSLGVGDR	1	0.6226	0.6226								
		VAVGFSIDIPK	1	3.2072	3.2072								
		VEFSLTDYGSK	2	0.8567	0.8402	1.3228							
		VGVVQFSDEPR	1	0.3299	0.3299								
		VGVVQFSNDVFPEPYLK	1	0.4071	0.4071								
		YVELSLDYVGQDR	1	0.5162	0.5162								
CO7_HUMAN	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	SFFRSSSSSSR	3	0.8787	0.8769	1.08	1	0.8787	0.8787	0.8787	0.8787	0.8769	
COCA1_HUMAN	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	ALALGALQNIR	1	1.0506	1.0506		23	1.7504	1.5829	1.272	1.1689	1.1537	2.1571
		DLSFSEVTSYGFK	1	3.6834	3.6834								
		GEVQTVTFDTEEVK	1	3.4577	3.4577								
		GGNTLTGMALNFIR	1	0.9656	0.9656								
		GGNTMTGDAIDYLVK	1	1.0049	1.0049								
		GSETSHCFTGLSPDTDYGVTVFVQTPNLEGPGVSVK	2	0.5889	0.5574	1.6049							
		GSPQDLVTK	1	4.001	4.001								
		IVDDLTINLCNSVK	1	3.1917	3.1917								
		LGELVVGPYDNTVVLEELR	1	0.9017	0.9017								
		NFASVGGVSLESGSFPSYSAYR	1	1.1579	1.1579								
		NLPEDAIHTMIENLQPETK	1	1.1881	1.1881								
		NSDVEIFAVGVK	1	1.1184	1.1184								
		NTFTESAGAR	1	8.2907	8.2907								
		NVGVEVFSLGIK	2	0.9559	0.949	1.1863							
		QVCEQLISGQMNNR	1	0.7116	0.7116								
		SELEAIASPPAETHVFTVEDFDAFQR	1	0.7569	0.7569								
		SLYDDVDTGEK	1	1.2145	1.2145								
		TEFNLNQYYQR	2	0.812	0.5592	1.8402							
		TNWSPAGENVFSYHITYK	1	1.3592	1.3592								
		TVGLLPPQNIHISDEWYTR	1	1.0866	1.0866								
		TYQIGWDTFCWK	1	1.7746	1.7746								
		VEDIEAINTFPYR	3	0.9525	0.9325	1.2952							
		VMILITDGK	1	0.2359	0.2359								
COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	AVLFCLSEDKK	1	11.8534	11.8534		10	11.2236	11.6357	10.6009	10.9153	10.6778	1.4595
		EILVGDVGQTVDDPYATFVK	2	13.1374	12.7215	1.4343							
		HELQANCYEEVK	1	6.4693	6.4693								
		HELQANCYEEVKDR	2	4.9685	4.8299	1.4022							
		LGSSAVSLEGKPL	3	14.1043	13.1928	1.5988							
		MIYASSK	1	11.2436	11.2436								
		MLPDKDCR	1	11.5743	11.5743								
		NILEEGK	1	14.4616	14.4616								
		NILEEGKEILVGDVGQTVDDPYATFVK	1	8.4393	8.4393								
		YALYDATYETK	2	15.9847	15.9154	1.141							
COF2_HUMAN	Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1	MIYASSK	1	11.2436	11.2436		3	10.1908	8.1075	7.1458	5.1024	5.0734	3.2786
		QILVGDIGDTVEDPYTSFVK	2	1.8575	1.8365	1.2382							
		YALYDATYETK	1	17.4712	17.4712								
COIA1_HUMAN	Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	GLELEPGAGLFVAQAGGADPDKFGGVIAELK	1	4.3657	4.3657		1	4.3657	4.3657	4.3657	4.3657	4.3657	
COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	TALNLFFK	1	5.9269	5.9269		1	5.9269	5.9269	5.9269	5.9269	5.9269	
COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	NTLEWCLFYIDAK	1	3.1117	3.1117		1	3.1117	3.1117	3.1117	3.1117	3.1117	
COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	GMGYMPK	1	0.5883	0.5883		4	1.9952	2.1477	1.2408	1.4557	1.419	3.362
		KSDLFQDDLYPDTAGPEAALEAEEWFEGK	1	4.2946	4.2946								
		NADPLISLK	2	2.7578	2.5872	1.6665							
		YFEITDESPYVHYLNTFSSK	1	0.3402	0.3402								
COTL1_HUMAN	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	EFVISDR	1	4.5481	4.5481		3	2.7789	2.7789	2.3436	2.3436	2.3436	2.1368
		ELEEDFIK	1	1.0236	1.0236								
		YDGSTIVPGEQGAEYQHFIQQCTDDVR	1	2.7651	2.7651								
CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	SMVAVMDSDTTGK	1	0.407	0.407		1	0.407	0.407	0.407	0.407	0.407	
CPPED_HUMAN	Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=2	LTEQAVQAINK	1	0.7313	0.7313		1	0.7313	0.7313	0.7313	0.7313	0.7313	
CRIP2_HUMAN	Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR	2	2.8434	1.2496	7.918	2	4.731	4.1018	4.3381	3.7683	2.1782	1.8175
		GVNTGAVGSYIYGRDPEGK	1	6.6187	6.6187								
CSN5_HUMAN	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	GYKPPDEGPSEYQTIPLNK	1	1.9053	1.9053		1	1.9053	1.9053	1.9053	1.9053	1.9053	
CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	GFGFGQGAGALVHSE	1	5.4746	5.4746		4	4.1091	3.8205	3.9712	3.69	3.1926	1.3618
		GLESTTLAGKDGEIYCK	2	2.6367	1.7623	3.8812							
		SCFLCMVCK	1	4.4753	4.4753								
		TVYFAEEVQCEGNSFHK	2	3.8499	3.7305	1.4287							
CTCFL_HUMAN		LEEEQEK	1	30.7355	30.7355		1	30.7355	30.7355	30.7355	30.7355	30.7355	
CTGF_HUMAN	Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2	ANCLVQTTEWSACSK	1	9.0585	9.0585		4	8.1821	9.5503	7.0981	8.2465	8.0931	1.842
		CCEEWVCDEPK	1	4.5191	4.5191								
		SGESFGSSCK	1	4.1277	4.1277								
		TTTLPVEFK	2	15.0232	14.3345	1.5475							
CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	SQGMASLNLPAVSWK	1	1.1032	1.1032		1	1.1032	1.1032	1.1032	1.1032	1.1032	
CUTA_HUMAN	Protein CutA OS=Homo sapiens GN=CSTB PE=1 SV=2	LAACVNLIPQITSIYEWK	1	2.9092	2.9092		2	2.8254	2.8254	2.8242	2.8242	2.8242	1.0428
		SVHPYEVAEVIALPVEQGNFPYLQWVR	1	2.7416	2.7416								
CV028_HUMAN	UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1	GGQVGGFLPMIK	1	0.4366	0.4366		1	0.4366	0.4366	0.4366	0.4366	0.4366	
CYBP_HUMAN	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	ISNYGWDQSDK	1	2.7449	2.7449		1	2.7449	2.7449	2.7449	2.7449	2.7449	
CYC_HUMAN	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	ADLIAYLK	1	9.6802	9.6802		2	4.8786	4.8786	0.8628	0.8628	0.8628	30.5418
		TGQAPGYSYTAANK	1	0.0769	0.0769								
CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	GLECNFGASSTALK	2	7.1027	7.0893	1.0938	2	3.6728	3.6728	1.3134	1.3134	1.2951	10.8813
		VTGQCCEEWVCDEDSIKDPMEDQDGLLGK	2	0.2429	0.2366	1.3849							
CYTB_HUMAN	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	AKHDELTYF	1	7.4199	7.4199		2	5.2408	4.5144	4.7663	4.1125	4.0635	1.87
		SQVVAGTNYFIK	2	3.0617	3.0071	1.3089							
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	ALDFAVGEYNK	4	1.3987	1.3879	1.1564	4	1.8035	1.7141	1.7274	1.6543	1.6204	1.4096
		ALQVVR	1	2.3224	2.3224								

		LVGGPMDASVEEEGVR	2	2.3029	2.1526	1.691							
		TQPNLDNCPFHDQPHLK	1	1.1902	1.1902								
DBPA_HUMAN	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4	SVGDGETVEFDVVEGEK	1	2.847	2.847		1	2.847	2.847	2.847	2.847	2.847	
DCUP_HUMAN	Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2	EAGLAPVPMIIFAK	1	3.4702	3.4702		1	3.4702	3.4702	3.4702	3.4702	3.4702	
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	ELAQQVQGVADDYGK	1	2.7761	2.7761		1	2.7761	2.7761	2.7761	2.7761	2.7761	
DDX39_HUMAN	ATP-dependent RNA helicase DDX39 OS=Homo sapiens GN=DDX39 PE=1 SV=2	GLAITFVSDENDAK	1	2.8021	2.8021		1	2.8021	2.8021	2.8021	2.8021	2.8021	
DEOC_HUMAN	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	DSLAWLSLVK	1	2.7667	2.7667		1	2.7667	2.7667	2.7667	2.7667	2.7667	
DESM_HUMAN	Desmin OS=Homo sapiens GN=DES PE=1 SV=3	EYQDLLNVK	4	8.7829	8.7662	1.0732	5	8.0263	7.7287	7.8398	7.504	7.3978	1.2933
		KLLEGEESR	1	9.0346	9.0346								
		LLEGEESR	2	8.6285	8.5173	1.2564							
		TNEKVELQELNDR	3	4.9536	4.7542	1.4416							
		VELQELNDR	1	8.7321	8.7321								
DEST_HUMAN	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	MIYASSK	1	11.2436	11.2436		1	11.2436	11.2436	11.2436	11.2436	11.2436	
DKK3_HUMAN	Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1	DQDGELLPR	2	0.6387	0.501	2.789	6	0.8739	0.8256	0.8582	0.8109	0.7683	1.2356
		DSECCGDQLCVWGHCTK	1	0.9888	0.9888								
		EVEELMEDTQHK	1	1.0982	1.0982								
		LLDLITWELEPDGALDR	2	0.7016	0.7016	1.0154							
		QELEDLER	2	0.847	0.8469	1.0174							
		SAVEEMEAEEAAAK	1	0.9693	0.9693								
DLRB1_HUMAN	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3	STMDNPTTTQYASLMHSFILK	1	0.363	0.363		1	0.363	0.363	0.363	0.363	0.363	
DNJB4_HUMAN	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1	EIYDQFGEEGLK	1	0.3469	0.3469		1	0.3469	0.3469	0.3469	0.3469	0.3469	
DNJC9_HUMAN	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	ISLEDIQAFEK	1	1.3638	1.3638		1	1.3638	1.3638	1.3638	1.3638	1.3638	
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	GLYDGPVCEVSVTPK	1	3.9131	3.9131		2	1.9792	1.9792	0.421	0.421	0.421	23.4023
		GSPLVVISQGK	1	0.0453	0.0453								
DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	GMTTVDDFFQGTK	1	3.0207	3.0207		1	3.0207	3.0207	3.0207	3.0207	3.0207	
DYH2_HUMAN	Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=1 SV=3	QELLAQANK	1	14.6207	14.6207		1	14.6207	14.6207	14.6207	14.6207	14.6207	
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	QLQNISLAAASGGAK	1	0.6258	0.6258		1	0.6258	0.6258	0.6258	0.6258	0.6258	
DYSF_HUMAN	Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1	DLAAMDK	1	3.8285	3.8285		1	3.8285	3.8285	3.8285	3.8285	3.8285	
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	ALNALCDGLIDELNQALK	1	0.3317	0.3317		1	0.3317	0.3317	0.3317	0.3317	0.3317	
ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	DILTEDGR	2	0.3302	0.3189	1.4537	4	0.7604	0.664	0.6863	0.596	0.5865	1.7365
		LVWEEAMSR	1	0.9857	0.9857								
		NVALVSGDTENAK	2	0.6123	0.6038	1.2668							
		VTPNLMGHLCGNQR	1	1.1134	1.1134								
EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	EALMTELSTVK	1	4.8035	4.8035		1	4.8035	4.8035	4.8035	4.8035	4.8035	
EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	MDSTEPPYSQKR	1	1.5464	1.5464		4	3.8554	4.3118	3.3251	3.7588	3.7458	1.8839
		SGDAAIVDMVPGKPMCVESFSDYPPLGR	2	3.1693	3.1665	1.0614							
		STTTGHLIYK	2	7.2797	7.2108	1.2156							
		THINIVVIGHVDSGK	1	3.4264	3.4264								
EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	STTTGHLIYK	2	7.2797	7.2108	1.2156	2	5.353	5.9952	4.9943	5.6626	5.6269	1.7038
		THINIVVIGHVDSGK	1	3.4264	3.4264								
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1	EVSTYIK	1	9.695	9.695		2	7.4838	7.4838	7.1496	7.1496	7.1496	1.5383
		QTVAVGVIK	1	5.2725	5.2725								
EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	SPAGLQVLNDYLADK	2	12.7719	12.6769	1.1889	1	12.7719	12.7719	12.7718	12.7718	12.6769	
EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	GVVGELQQAISK	1	9.5371	9.5371		2	8.9294	8.7268	8.9086	8.7085	7.9445	1.1012
		SIQLDGLVVGASK	2	8.3216	7.2509	2.137							
EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	AVLGEVK	2	0.0442	0.044	1.148	3	4.6272	4.1007	1.2827	0.907	0.9042	18.4898
		ILGLLDAYLK	2	6.5779	6.5569	1.1196							
		YSNEDTLSVALPYFWEHFDK	1	7.2596	7.2596								
EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EGIPALDNFLDKL	3	8.733	8.3584	1.4508	9	8.7323	8.9149	7.8102	8.1825	8.0752	1.6529
		ETVSEESNVLCLSK	1	5.4165	5.4165								
		GPLMMYISK	1	6.3063	6.3063								
		GVQYLNEIK	1	9.3412	9.3412								
		IWCFGPDGTGPNILTDITK	2	10.9227	10.7771	1.2613							
		STLTDSLVCK	1	3.1293	3.1293								
		TFCQLILDPIFK	1	19.2739	19.2739								
		VFDAIMNFK	1	8.6844	8.6844								
		VFSGLVSTGLK	1	6.7831	6.7831								
EFHD1_HUMAN	EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1	DGFIDLMELK	1	0.2106	0.2106		1	0.2106	0.2106	0.2106	0.2106	0.2106	
EFHD2_HUMAN	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	DGFIDLMELK	1	0.2106	0.2106		1	0.2106	0.2106	0.2106	0.2106	0.2106	
EGLN_HUMAN	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2	GEVTYTTSQVSK	1	2.2311	2.2311		1	2.2311	2.2311	2.2311	2.2311	2.2311	
EHD2_HUMAN	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	DGMLDDEEFALASHLIEAK	2	2.7313	2.7308	1.0256	1	2.7313	2.7313	2.7313	2.7313	2.7308	
ELOB_HUMAN	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	LYKDDQLLDDGK	1	2.2472	2.2472		1	2.2472	2.2472	2.2472	2.2472	2.2472	
EMIL1_HUMAN	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	GLEEGQAQAGQCPSLEGR	1	1.758	1.758		3	2.3859	2.3859	2.3324	2.3324	2.3324	1.3025
		LVGSGLHTVEAAGEAR	1	2.4321	2.4321								
		QATLEGLQEVVGR	1	2.9675	2.9675								
ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	AVEHNK	1	0.4114	0.4114		17	12.9226	13.933	8.998	10.4284	8.5311	3.0175
		DATNVGDEGGFAPNILENK	1	22.4692	22.4692								
		DYPVVSIEDPFDQDDWGAWQK	1	10.4426	10.4426								
		EGLELLK	3	11.949	10.2236	1.9864							
		FGANAILGVSLAVCK	2	3.7593	3.7135	1.2483							
		FTASAGIQVVGDDLTVTNPK	1	13.1885	13.1885								
		GNPTVEVDLFTSK	3	23.8846	22.126	1.6547							
		HIADLAGNSEVILPVPAFNVINGGSHAGNK	1	6.1181	6.1181								
		IDKLMIEMDGTENK	1	5.7296	5.7296								
		IEEELGSK	2	22.352	21.2023	1.5898							
		IGAEVYHNLK	1	20.5447	20.5447								
		KLNVTEQEK	1	21.7022	21.7022								
		LMIEMDGTENK	3	12.769	4.486	12.214							
		SFIKDYPVVSIEDPFDQDDWGAWQK	1	5.6054	5.6054								
		TIAPALVSK	4	12.9525	11.7238	1.6833							
		VNQIGSVTESLQACK	2	1.5483	0.6865	7.8085							
		YSPDQLADLIYK	3	24.2577	22.4347	1.6677							
ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=4	FGANAILGVSLAVCK	2	3.7593	3.7135	1.2483	5	4.2827	3.9734	3.0625	3.2811	2.1172	2.7765
		HIADLAGNPDLILPVPAFNVINGGSHAGNK	2	3.1297	1.6274	6.0376							
		LAQSNGWGVMVSHR	1	0.6024	0.6024								
		SGETEDTFIADLVVGLCTGQIK	1	10.1936	10.1936								
		VNQIGSVTESIQACK	3	3.7287	1.5621	7.6505							
ENOG_HUMAN	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	FGNAILGVSLAVCK	2	3.7593	3.7135	1.2483	3	12.6125	14.8943	9.7092	11.1896	10.7259	2.523
		GNPTVEVDLVTAK	3	23.8846	22.126	1.6547							
		SGETEDTFIADLVVGLCTGQIK	1	10.1936	10.1936								
ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ELISNASDALDK	3	9.0731	8.3975	1.6392	1	9.0731	9.0731	9.0731	9.0731	8.3975	
EPCR_HUMAN	Endothelial protein C receptor OS=Homo sapiens GN=PROCR PE=1 SV=1	EFLEDTCVQYVQK	2	8.4092	6.5871	2.7983	1	8.4092	8.4092	8.4092	8.4092	6.5871	
ERF1_HUMAN	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	VNVAGLVLAGSADFK	1	0.826	0.826		2	0.4279	0.4279	0.1566	0.1566	0.1566	10.5007
		YFDEISQDTGK	1	0.0297	0.0297								
ERH_HUMAN	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	ADTQTYQPYNK	1	7.178	7.178		1	7.178	7.178	7.178	7.178	7.178	
ESYT3_HUMAN	Extended synaptotagmin-3 OS=Homo sapiens GN=ESYT3 PE=2 SV=1	VATNGGPK	2	0.0423	0.0342	2.5971	1	0.0423	0.0423	0.0422	0.0422	0.0342	
EVI5_HUMAN	Ecotropic viral integration site 5 protein homolog OS=Homo sapiens GN=EVI5 PE=1 SV=2	QIHAELTDK	2	9.2227	9.0813	1.283	1	9.2227	9.2227	9.2227	9.2227	9.0813	
EWS_HUMAN	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	AAVEWFDGK	1	0.1433	0.1433		1	0.1433	0.1433	0.1433	0.1433	0.1433	
EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	DNAMLEYLK	1	3.1187	3.1187		3	6.4034	6.0437	5.5643	5.4078	5.3195	1.9033
		LFFLQVK	1	11.127	11.127								
		QLFDQVVK	2	4.9645	4.8036	1.4404							
F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	AIDLFTDAIK	2	2.0656	2.011	1.3891	4	4.6488	4.1322	2.1963	2.1695	2.1464	5.5563
		EWVESMGGK	1	0.2117	0.2117								
		LDYDEDASAMLK	1	11.8138	11.8138								
		VAAIEALNDGELQK	1	4.5042	4.5042								
F10A4_HUMAN	Protein FAM10A4 OS=Homo sapiens GN=FAM10A4 PE=1 SV=1	AIDLFTDAIK	2	2.0656	2.011	1.3891	2	3.2849	2.8784	3.0502	2.6785	2.6312	1.7355
		VAAIEALNDGELQK	1	4.5042	4.5042								
F10A5_HUMAN	Protein FAM10A5 OS=Homo sapiens GN=FAM10A5 PE=1 SV=1	AIDLFTDAIK	1	1.594	1.594		3	4.5398	4.5398	1.5856	1.5856	1.5856	7.4703
		EWVESMGGK	1	0.2117	0.2117								
		LDYDEDASAMLK	1	11.8138	11.8138								
FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	TQTVCNFTDGALVQHQEWDGK	2	14.8125	1.2613	86.603	2	10.4557	11.9079	9.5047	11.0197	2.1329	1.8728
		TTQFSCTLGEK	1	6.0989	6.0989								
FAKD2_HUMAN	FAST kinase domain-containing protein 2 OS=Homo sapiens GN=FASTKD2 PE=1 SV=1	MQSTDIIR	1	0.0338	0.0338		1	0.0338	0.0338	0.0338	0.0338	0.0338	
FBSL3_HUMAN	Putative fatty acid-binding protein 5-like protein 3 OS=Homo sapiens GN=FABP5L3 PE=1 SV=1	TQTVCNFTDGALVQHQEWDGK	2	14.8125	1.2613	86.603	1	14.8125	14.8125	14.8125	14.8125	1.2613	
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	CCHCCLLGR	1	2.0803	2.0803		10	1.1795	1.1795	0.7338	0.7338	0.7338	2.4152
		DCSLPYATESK	1	0.4327	0.4327								
		DSSCGTGYELTEDNSCK	1	0.4461	0.4461								
		GYHLNEEGTR	1	0.7223	0.7223								
		IIEVEEQEDPYLNDR	1	0.4939	0.4939								
		LEMNYVVGGVVSHR	1	5.532	5.532								
		SAATLQQEK	1	0.8644	0.8644								
		SQETGDLDVGGLQETDK	1	0.4216	0.4216								
		SQETGDLDVGGLQETDKIIEVEEEQEDPYLNDR	1	0.4649	0.4649								
		YMDGMTVGVVR	1	0.337	0.337								
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	ADGVCNLR	2	14.5447	14.5387	1.0413	10	12.1287	12.0545	11.7905	11.6973	10.9598	1.2832
		CVCPVSNAMCR	2	10.7965	9.3657	2.1643							
		CVNHYGGYLCLPK	1	11.4865	11.4865								
		EHIVDLEMLTVSSIGTFR	1	8.5592	8.5592								
		ELPQSIVYK	3	9.4323	8.5279	1.8038							
		GSFACQCPPGYQK	4	12.9828	11.6768	1.7259							
		LNCEDIDECR	3	17.73	16.4652	1.6313							
		QTSPVSAMLVLVK	4	8.6462	8.141	1.5134							
		SGNENGEFYLR	2	11.4133	11.2809	1.2417							
		TCQDINECETTNECR	1	15.6955	15.6955								
FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3	AGNSQGDFYIR	1	0.4563	0.4563		2	0.7702	0.7702	0.7033	0.7033	0.7033	1.8439
		CVEPYIQVSENR	1	1.0841	1.0841								
FBLN5_HUMAN	Fibulin-5 OS=Homo sapiens GN=FBLN5 PE=1 SV=1	DMDVVSGR	2	0.4172	0.3798	1.8641	3	1.5744	1.1189	0.9005	0.6734	0.6385	3.5229
		DQFFTILYR	2	0.4545	0.4371	1.4875							
		SVPADIFQMQATTR	1	3.8514	3.8514								
FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=2	GFMTNGADIDECK	1	0.3216	0.3216		9	0.6196	0.6196	0.5997	0.5997	0.5997	1.3322
		GFQLDLR	1	0.5881	0.5881								
		GTCWQTVDDGR	1	0.701	0.701								
		GWGPHCEICPFGQTVAFK	1	0.5499	0.5499								
		GYILQEDGR	1	0.4669	0.4669								
		ILELLPALTTLTNHNR	1	0.7105	0.7105								
		TGCTDINECEIGAHNCGK	1	0.727	0.727								
		TGYTPDITGTSCVDLNECNQAPKPCNFICK	1	0.7271	0.7271								
		YLIESGNEDDFFK	1	0.7843	0.7843								
FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	GTCWLNIQDSR	1	0.7245	0.7245		1	0.7245	0.7245	0.7245	0.7245	0.7245	
FBN3_HUMAN	Fibrillin-3 OS=Homo sapiens GN=FBN3 PE=2 SV=2	ASCCCSLGR	1	0.4938	0.4938		1	0.4938	0.4938	0.4938	0.4938	0.4938	
FES_HUMAN	Proto-oncogene tyrosine-protein kinase Fes/Fps OS=Homo sapiens GN=FES PE=1 SV=3	QEMVTQLQQELR	2	9.1218	8.7704	1.4903	1	9.1218	9.1218	9.1218	9.1218	8.7704	
FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	CDSSPDSAEDVR	1	1.2245	1.2245		3	1.2832	1.293	1.2823	1.2925	1.2853	1.045
		CDSSPDSAEDVRK	4	1.2883	1.2763	1.1747							
		CNLLAEK	2	1.3367	1.3356	1.0577							
FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3	AQITGYR	3	0.897	0.895	1.0857	31	1.0104	0.9887	0.9872	0.9701	0.9648	1.2501
		ATITGYR	4	0.841	0.8364	1.1311							
		DAPIVNK	1	0.5236	0.5236								
		DLQFVEVTDVK	1	0.9203	0.9203								
		ESKPLTAQQQTTK	1	0.6937	0.6937								
		FTNIGPDTMR	2	0.9326	0.9268	1.1704							
		GATYNIIVEALK	2	0.8855	0.8481	1.5195							
		GDSPASSKPISINYR	1	1.5174	1.5174								
		GEWTCKPAEK	1	0.9238	0.9238								
		GLAFTDVDVDSIK	1	1.1369	1.1369								
		HTSVQTTSSGSGPFTDVR	1	1.3572	1.3572								
		HYQINQQWER	1	0.9745	0.9745								
		IGDQWDK	1	0.9646	0.9646								
		IGDTWR	1	1.138	1.138								
		IGDTWSK	3	0.9781	0.9764	1.0759							
		ISCTIANR	2	0.9584	0.9452	1.2666							
		ITGYIIK	1	0.8697	0.8697								

		IYLYTLNDNAR	1	1.3523	1.3523								
		LGVRPSQGGEAPR	1	1.0318	1.0318								
		QYNVGPSVSK	3	0.9148	0.9068	1.1735							
		SDTVPSPR	2	0.6492	0.644	1.1973							
		SERLIGR	3	1.0228	1.0208	1.0797							
		STTPDITGYR	4	0.8604	0.8539	1.1571							
		SYTITGLQPGTDYK	1	1.1466	1.1466								
		TFYSCTTEGR	2	1.2365	1.2296	1.1612							
		TYHVGEQWQK	1	1.2062	1.2062								
		VDVIPVNLPGEHGQR	1	1.3004	1.3004								
		VFAVSHGR	2	0.8899	0.8899	1.0011							
		YEKPGSPPR	1	0.9853	0.9853								
		YEVSVYALK	4	1.2626	1.2469	1.2001							
		YTGNTYR	1	0.95	0.95								
FKBP3_HUMAN	FK506-binding protein 3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1	FLQEHGSDSFLAEHK	1	3.3157	3.3157		2	3.3039	3.2999	3.3038	3.2999	3.2524	1.0051
		LEIEPEWAYGK	2	3.292	3.2212	1.3444							
FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	AGNNMLLVGVHGPR	1	1.3788	1.3788		21	3.3816	3.5	2.4735	2.6339	2.5616	2.5298
		AHVVPCFDASK	1	0.1824	0.1824								
		AWGPGLEGGVVGK	1	1.9495	1.9495								
		AYGPGIEPTGNMVK	1	0.9995	0.9995								
		DGSCGVAYVVQEPGDYEVSVK	1	1.5003	1.5003								
		DLAEDAPWK	2	1.7257	1.2316	3.4138							
		DVDIIDHHDNTYTVK	1	6.0663	6.0663								
		EATTEFSVDAR	1	6.4714	6.4714								
		FVPAEMGTHTVSVK	1	0.8186	0.8186								
		GKLDVQFSGLTK	1	6.5789	6.5789								
		LDVQFSGLTK	1	1.822	1.822								
		LIALLEVLSGK	2	7.8455	7.845	1.0155							
		LTVSSLQESGLK	1	3.2896	3.2896								
		LVSIDSK	2	3.2896	3.2843	1.0835							
		LYSVSYLLK	1	5.5256	5.5256								
		NDNDTFTVK	1	6.1431	6.1431								
		SAGQGEVLVYVEDPAGHQEEAK	2	4.9938	4.8985	1.3211							
		SPFEVYVDK	1	3.0786	3.0786								
		SPFSVAVSPSLDLSK	2	2.1324	2.1249	1.126							
		VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR	1	0.9143	0.9143								
		VTAGQPGLEPSGNIANK	1	4.3074	4.3074								
FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=1	AEITFDDHK	2	1.6538	1.6537	1.0098	20	5.5745	5.2589	4.1031	3.9949	3.8163	2.5612
		ALGALVDSCAPGLCPDWESWDPQKPVDNAR	1	3.7527	3.7527								
		DAGYGGISLAVEGPSK	1	5.8511	5.8511								
		DLAEDAPWK	2	1.7257	1.2316	3.4138							
		DLDIIDNYDYSHTVK	1	14.1455	14.1455								
		EAGAGGLSIAVEGPSK	2	3.2395	3.0324	1.6815							
		GAGTGGLGLTVEGPCEAK	1	6.2301	6.2301								
		GDYVLAVK	2	7.2255	7.2244	1.0247							
		GIEPTGNMVK	1	4.873	4.873								
		IEYNDQNDGSCDVK	1	4.6849	4.6849								
		LIALLEVLSGK	2	7.8455	7.845	1.0155							
		LTVMSLQESGLK	2	5.5201	4.4645	2.5967							
		LVSIDSK	2	3.2896	3.2843	1.0835							
		MDGTYACSYTPVK	1	8.1619	8.1619								
		TFEMSDFIVDTR	1	0.3217	0.3217								
		VKVEPAVDTSR	1	12.358	12.358								
		VLQSFTVDSSK	1	3.9312	3.9312								
		VLSEDEEDVDFDIIHNANDTFTVK	1	4.0579	4.0579								
		VTEAEIVPMGK	1	11.9178	11.9178								
		YMIGVTVGGDDIPLSPYR	1	0.7054	0.7054								
FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	AFGPGLEPTGCIVDKPAEFTIDAR	1	1.52	1.52		11	3.2836	3.4813	2.6095	2.8146	2.8666	2.023
		AWGPGLETGQVGK	1	1.0833	1.0833								
		DAGEGLLTVQILDPEGKPK	1	2.3912	2.3912								
		DFEIDNHDYSYTVK	1	1.302	1.302								
		DLAEDAPWK	2	1.7257	1.2316	3.4138							
		EAGAGGLSIAVEGPSK	2	3.2395	3.0324	1.6815							
		GAGTGGLGLTVEGPCEAK	1	6.2301	6.2301								
		LIALLEVLSGK	2	7.8455	7.845	1.0155							
		LVSIDSK	2	3.2896	3.2843	1.0835							
		LYAQDADGCPIDIK	1	1.3495	1.3495								
		NDNDTFTVK	1	6.1431	6.1431								
FRPD1_HUMAN	FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1	DIILTVK	2	8.4414	1.2871	37.7796	1	8.4414	8.4414	8.4413	8.4413	1.2871	
FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	LSCFAQTVSPAEK	1	3.7852	3.7852		4	4.5007	4.7034	4.342	4.5482	4.5067	1.348
		SSYDVFQLEFNDGAYNIK	2	6.6937	6.4831	1.4326							
		YLAADKDGNVTCER	1	3.4101	3.4101								
		YLTAEAFGFK	3	4.1136	4.1134	1.0123							
FST_HUMAN	Follistatin OS=Homo sapiens GN=FST PE=1 SV=2	EAACSSGVLLEVK	1	0.3597	0.3597		1	0.3597	0.3597	0.3597	0.3597	0.3597	
FSTL1_HUMAN	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1	CLNPSFNPPEKK	1	5.0951	5.0951		9	1.5326	1.3841	1.2593	1.2211	1.2156	1.7779
		GAQTQTEEEMTR	3	1.3959	1.3877	1.1442							
		GEPTCLCIEQCKPHK	1	1.0994	1.0994								
		GLCVDALIELSENADWK	1	0.7245	0.7245								
		ICANVFCGAGR	2	1.5203	1.5134	1.1449							
		IIQWLEAEIPDGWFSK	1	0.7937	0.7937								
		IQVDYDGHCK	1	1.1444	1.1444								
		LDSSEFLK	3	1.0575	1.0439	1.2147							
		LSFQEFLK	3	0.9624	0.9604	1.0836							
FTHFD_HUMAN	10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2	IGFTGSTEVGK	1	0.9978	0.9978		1	0.9978	0.9978	0.9978	0.9978	0.9978	
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	SELKDFFQSYGNVVELR	1	3.327	3.327		1	3.327	3.327	3.327	3.327	3.327	
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	AGAHLQGGAK	1	2.1297	2.1297		10	8.1122	9.4987	5.6736	7.3514	5.6346	2.6127
		GALQNIIPASTGAAK	4	15.8795	12.452	2.5996							
		IISNASCTTNCLAPLAK	3	10.2083	8.9707	1.9571							
		LISWYDNEFGYSNR	1	15.8596	15.8596								
		QASEGPLK	1	1.4424	1.4424								
		TVDGPSGK	1	2.2665	2.2665								
		VIHDNFGIVEGLMTTVHAITATQK	2	2.4756	1.6829	3.7575							
		VIISAPSADAPMFVMGVNHEK	2	13.9001	13.6124	1.3368							
		VVDLMAHMASK	3	12.4555	9.1914	2.5736							
		WGDAGAEYVVESTGVFTTMEK	3	4.5047	1.9581	8.1582							
G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	FAAYFQQGDMESNGK	2	3.6029	3.6026	1.0169	4	6.3158	5.7732	6.0236	5.4352	5.435	1.4496
		HFVALSTNTTK	1	8.0435	8.0435								
		TFTTQETITNAETAK	1	7.7708	7.7708								
		VWYVSNIDGTHIAK	1	5.8461	5.8461								
GALT5_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1	WKEGNFNVYLSDLIPVDR	1	9.3989	9.3989		1	9.3989	9.3989	9.3989	9.3989	9.3989	
GALT6_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	NLGTNQCLDVGENNR	1	3.7026	3.7026		1	3.7026	3.7026	3.7026	3.7026	3.7026	
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	FSPNSSNPIVVSCSWDK	1	9.0287	9.0287		2	7.0451	6.3839	6.7601	6.1385	6.0204	1.5057
		YWLCAATGPSIK	2	5.0615	4.9162	1.4092							
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	DWNVDLIPK	2	5.2141	5.1675	1.2091	3	2.7585	3.3724	1.7334	2.2828	2.2726	3.9543
		KFDLGQDVIDFTGHALALYR	1	0.3713	0.3713								
		MAGTAFDFENMK	3	2.6901	2.6901								
GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	DWNVDLIPK	2	5.2141	5.1675	1.2091	8	6.1459	6.5359	3.2232	3.8565	3.3178	4.7141
		FVSIDSLLVPK	2	14.2773	14.2496	1.0922							
		KFDLGQDVIDFTGHALALYR	1	0.3713	0.3713								
		MTGSEFDFEEMK	2	3.2363	1.43	7.8502							
		NPYYGGESASITPLEDLYK	1	12.2458	12.2458								
		TYDATTHFETTCDDIK	1	7.9514	7.9514								
		VICILSHPIK	1	5.634	5.634								
		VPSTEAEALASSLMGLFEK	1	0.2374	0.2374								
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	AEEYEFLTPVEEAPK	1	10.8851	10.8851		2	8.4189	8.4189	8.0496	8.0496	8.0496	1.5323
		IDKTDYMVGSYGPR	1	5.9527	5.9527								
GDIR2_HUMAN	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3	ATFMVGSYGPRPEEYEFLTPVEEAPK	1	4.191	4.191		2	7.5478	7.5478	6.7602	6.7602	6.7602	1.9663
		ELQEMDKDDESLIK	1	10.9045	10.9045								
GDN_HUMAN	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1	TIDSWMSMVPK	2	0.3937	0.3775	1.5113	1	0.3937	0.3937	0.3937	0.3937	0.3775	
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	EVQGFESATFLGYFK	1	3.824	3.824		2	2.3822	2.3822	1.8962	1.8962	1.8962	2.6965
		SEDCFILDHGK	1	0.9403	0.9403								
GFAP_HUMAN	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	FLEQQNK	3	8.3512	8.3483	1.033	3	5.4725	5.0088	3.6946	3.1841	3.1778	3.6321
		GTNESLER	3	7.2311	7.2165	1.0817							
		LALDIEIATYR	4	0.8352	0.8325	1.0964							
GLBD3_HUMAN	Glycosyltransferase 8 domain-containing protein 3 OS=Homo sapiens GN=GLT8D3 PE=1 SV=1	LFLPLILK	3	12.2089	11.8595	1.3429	1	12.2089	12.2089	12.2089	12.2089	11.8595	
GLCD4_HUMAN	Glycolase domain-containing protein 4 OS=Homo sapiens GN=GLCD4 PE=1 SV=1	ALLGYADNGCK	1	1.2161	1.2161		1	1.2161	1.2161	1.2161	1.2161	1.2161	
GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	WQTLLSVDDLVEK	1	3.131	3.131		1	3.131	3.131	3.131	3.131	3.131	
GPC1_HUMAN	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=1	GANLHLEETLAEFWAR	1	1.0241	1.0241		4	0.8416	0.8416	0.811	0.811	0.811	1.3872
		QLHPQLLLPDDYLDCLGK	1	1.025	1.025								
		SFVQGLGVASDVVR	1	0.5117	0.5117								
		VLQAMLATQLR	1	0.8054	0.8054								
GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	LYSPSQIGAFVLMK	1	1.1841	1.1841		1	1.1841	1.1841	1.1841	1.1841	1.1841	
GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	IINEPTAAAIAYGLDK	3	4.113	3.9515	1.434	5	4.2692	3.995	3.2755	3.3331	3.2697	2.175
		NELESYAYSLK	1	2.5617	2.5617								
		TFAPEESAMVLTK	1	1.3734	1.3734								
		TWNDPSVQQDIK	2	2.3882	2.3487	1.2955							
		VEIANDQGNR	1	10.9097	10.9097								
GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	EDPTVSALLTSEK	2	1.8185	1.7671	1.4049	1	1.8185	1.8185	1.8184	1.8184	1.7671	
GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	ALPQGLKPFETLLSQNQGGK	1	10.2844	10.2844		4	8.7645	8.7645	8.1186	8.1186	8.1186	1.6179
		EEVVTVETWQEGSLK	1	4.1081	4.1081								
		TLGLYGK	1	12.3175	12.3175								
		TLGLYGKDQQEAALVDMVNDGVEDLR	1	8.3479	8.3479								
H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	DNIQGITKPAIR	1	4.6872	4.6872		2	5.4608	5.8476	5.4057	5.8053	5.6498	1.2235
		TVTAMDVVYALK	3	6.2344	6.0127	1.3984							
H90B2_HUMAN	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2	ADLINNLGTIAK	1	16.269	16.269		5	11.8937	12.019	11.6016	11.7963	11.5202	1.2818
		SIYYITGESK	1	8.5901	8.5901								
		SLVSVTK	1	9.9455	9.9455								
		YESLTDPSK	2	11.406	10.6444	1.702							
		YIDQEELNK	2	13.2581	13.0765	1.2654							
H90B3_HUMAN	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	EGLELPEDEEEK	1	6.6564	6.6564		5	7.1684	7.6971	5.7006	6.4319	6.3061	2.4665
		EGLELPEDEEEKK	1	1.2022	1.2022								
		EMLGQSK	2	6.6317	6.6317	1.0034							
		SLVSVTK	1	9.9455	9.9455								
		YESLTDPSK	2	11.406	10.6444	1.702							
H90B4_HUMAN	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1	EGLELPEDEEEK	1	6.6564	6.6564		4	4.8963	6.1982	2.3256	3.1964	3.1093	5.1179
		EGLELPEDEEEKK	1	1.2022	1.2022								
		GFEVIYMSEPIDEYCVQQLK	1	0.3205	0.3205								
		YESLTDPSK	2	11.406	10.6444	1.702							
HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	MFLSFPTTK	3	1.1981	1.1709	1.2947	1	1.1981	1.1981	1.1981	1.1981	1.1709	
HDGF_HUMAN	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	GPPQEEEEEEEDEEEEATKEDAEAPGIR	2	2.676	1.2144	7.5268	2	2.5226	2.5737	2.5179	2.5696	1.5174	1.0899
		YQVFFFGTHETAFLGPK	1	2.3692	2.3692								
HEXA_HUMAN	Beta-hexosaminidase subunit alpha OS=Homo sapiens GN=HEXA PE=1 SV=1	GLETFSQLVWK	1	2.3824	2.3824		1	2.3824	2.3824	2.3824	2.3824	2.3824	
HEXB_HUMAN	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	GSIVWQEVFDDK	1	2.4436	8.2436		3	5.535	5.9101	4.2526	4.823	4.674	2.7519
		LAPGTIVEVWK	2	7.0354	6.6075	1.659							
		VLDIAITNK	1	1.3261	1.3261								
HGB1A_HUMAN	Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1L1 PE=5 SV=1	IKGEHPGLSIGDVAK	1	6.4301	6.4301		1	6.4301	6.4301	6.4301	6.4301	6.4301	
HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	IKGEHPGLSIGDVAK	1	6.4301	6.4301		3	5.3785	4.9413	5.2147	4.7632	4.6682	1.3703
		KHPDASVNFSEFSK	2	3.6299	3.4866	1.4978							
		LGEMWNNTAADDKQPYEK	1	6.0755	6.0755								
HMGL1_HUMAN	High mobility group protein 1-like 10 OS=Homo sapiens GN=HMG1L10 PE=1 SV=1	IKGEHPGLSIGDVAK	1	6.4301	6.4301		2	6.2528	6.2528	6.2503	6.2503	6.2503	1.0409
		LGEMWNNTAADDKQPYEK	1	6.0755	6.0755								
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3	GFGFVLFK	1	48.675	48.675		1	48.675	48.675	48.675	48.675	48.675	
HNRGT_HUMAN	RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens GN=RBMXL2 PE=1 SV=3	GFAFVTFESPADAK	1	4.7641	4.7641		2	2.4518	2.4518	0.8152	0.8152	0.8152	12.1418

		IVEVLLMK	1	0.1395	0.1395							
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	EYFGGFGEVESIELPMDNK	2	12.382	12.1058	1.3519	5	14.8686	11.4957	7.764	6.1447	4.4631	3.635
		GFCFITFK	1	8.0454	8.0454								
		GFGFVLFK	1	48.675	48.675								
		IFVGGLSPDTPEEK	2	3.6442	3.4186	1.667							
		MFIGGLSWDTTK	2	1.5965	0.4845	13.913							
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	TEMDWVLK	1	3.5424	3.5424		1	3.5424	3.5424	3.5424	3.5424	3.5424	
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=RBMX PE=1 SV=3	GFAFVTFESPADAK	1	4.7641	4.7641		3	2.4514	2.4514	1.1765	1.1765	1.1765	6.5292
		IVEVLLMK	1	0.1395	0.1395								
		VEQATKPSFESGR	1	2.4506	2.4506								
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	IILDLISESPIK	3	4.9563	4.8943	1.219	2	4.8136	4.8422	4.8115	4.8401	4.5663	1.0428
		ILSISADIETIGEILK	2	4.671	4.115	2.069							
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	EFNEQGALAVLQQFK	1	1.721	1.721		1	1.721	1.721	1.721	1.721	1.721	
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	EFNEEGALSVLQQFK	1	0.551	0.551		1	0.551	0.551	0.551	0.551	0.551	
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	NVLIVEDIIDTGK	1	3.5958	3.5958		2	2.4764	2.4764	2.209	2.209	2.209	1.9919
		VIGGDDLSTLTGK	1	1.357	1.357								
HPS6_HUMAN	Hermansky-Pudlak syndrome 6 protein OS=Homo sapiens GN=HPS6 PE=2 SV=1	LLLAEFAQHR	1	12.6855	12.6855		1	12.6855	12.6855	12.6855	12.6855	12.6855	
HS71L_HUMAN	Heat shock 70 kDa protein 1L OS=Homo sapiens GN=HSPA1L PE=1 SV=2	IINEPTAAAIAYGLDK	3	4.113	3.9515	1.434	4	4.0253	4.0546	1.4499	2.0524	2.0117	7.6554
		NALESYAFNMK	1	0.1007	0.1007								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.9779	0.9779								
		VEIIANDQGNR	1	10.9097	10.9097								
HS902_HUMAN	Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2	ADLINNLGTIAK	1	16.269	16.269		4	9.3326	10.1177	6.9378	7.8972	7.8538	2.7226
		ELHINLIPNK	1	6.0187	6.0187								
		ELISNSSDALDK	1	1.7846	1.7846								
		YDQEELNK	2	13.2581	13.0765	1.2654							
HS904_HUMAN	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1	TLTIVDTGIGMTK	5	8.1064	4.8488	4.0158	1	8.1064	8.1064	8.1064	8.1064	4.8488	
HS905_HUMAN	Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1	EGLELPEDEEEK	1	6.6564	6.6564		3	5.6716	5.6716	4.1845	4.1845	4.1845	2.9798
		EGLELPEDEEEKK	1	1.2022	1.2022								
		HSQFIGYPITLFVEK	1	9.1563	9.1563								
HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	ADLINNLGTIAK	1	16.269	16.269		12	8.2983	8.7546	6.7507	7.6386	6.6583	2.1836
		EGLELPEDEEEK	1	6.6564	6.6564								
		EGLELPEDEEEKK	1	1.2022	1.2022								
		ELHINLIPNK	1	6.0187	6.0187								
		ELISNSSDALDK	1	1.7846	1.7846								
		EMLQQSK	2	6.6317	6.6317	1.0034							
		HSQFIGYPITLFVEK	1	9.1563	9.1563								
		NPDDITNEEYGEFYK	2	11.7912	11.7216	1.1665							
		SLTNDWEDHLAVK	1	7.299	7.299								
		TLTIVDTGIGMTK	5	8.1064	4.8488	4.0158							
		YESLTDPSK	2	11.406	10.6444	1.702							
		YDQEELNK	2	13.2581	13.0765	1.2654							
HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	ADLINNLGTIAK	1	16.269	16.269		14	8.4072	8.6769	6.3221	7.2328	6.3573	2.8594
		CLELFSELAEDKENYK	1	7.279	7.279								
		EGLELPEDEEEK	1	6.6564	6.6564								
		EGLELPEDEEEKK	1	1.2022	1.2022								
		ELISNASDALDK	3	9.0731	8.3975	1.6392							
		EMLQQSK	2	6.6317	6.6317	1.0034							
		GFEVVYMTEPIDEYCVQQLK	1	0.3205	0.3205								
		NPDDITQEEYGEFYK	1	11.6643	11.6643								
		SIYYITGESK	1	8.5901	8.5901								
		SLTNDWEDHLAVK	1	7.299	7.299								
		SLVSVTK	1	9.9455	9.9455								
		TLTLVDTGIGMTK	5	8.1064	4.8488	4.0158							
		YESLTDPSK	2	11.406	10.6444	1.702							
		YDQEELNK	2	13.2581	13.0765	1.2654							
HSP71_HUMAN	Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5	AAAIGIDLGTTYSCVGVFQHGK	1	6.369	6.369		4	4.5893	4.5893	1.6173	1.6173	1.6173	8.3317
		NALESYAFNMK	1	0.1007	0.1007								
		QTQIFTTYSDNQPGVLIQVYEGER	1	0.9779	0.9779								
		VEIIANDQGNR	1	10.9097	10.9097								
HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	DNNLLGK	2	8.2624	7.7677	1.6521	5	8.4498	7.3422	7.8848	6.7402	6.538	1.5428
		FEELNADLFR	1	12.2578	12.2578								
		IINEPTAAAIAYGLDK	3	4.113	3.9515	1.434							
		IINEPTAAAIAYGLDKK	1	6.7061	6.7061								
		VEIIANDQGNR	1	10.9097	10.9097								
HSP74_HUMAN	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	LFEELGK	1	0.8231	0.8231		2	2.4765	2.4765	1.8437	1.8437	1.8437	3.1283
		SNLAYDIVQLPTGLTGIK	1	4.1298	4.1298								
HSP76_HUMAN	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	VEIIANDQGNR	1	10.9097	10.9097		1	10.9097	10.9097	10.9097	10.9097	10.9097	
HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	CNEIINWLDK	2	13.385	13.3834	1.0223	15	6.9618	6.8805	4.6143	5.0538	4.4897	3.5723
		DNNLLGK	2	8.2624	7.7677	1.6521							
		EIAEAYLGK	1	8.1842	8.1842								
		FDDAVVQSDMK	1	2.2868	2.2868								
		FEELNADLFR	1	12.2578	12.2578								
		GPAVGIDLGTTYSCVGVFQHGK	2	4.369	1.4713	11.9116							
		GTLDPVEK	1	0.2577	0.2577								
		IINEPTAAAIAYGLDK	3	4.113	3.9515	1.434							
		IINEPTAAAIAYGLDKK	1	6.7061	6.7061								
		MVNHFIAEFK	1	9.316	9.316								
		NQVAMNPTNTVFDAK	1	10.9599	10.9599								
		RFDDAVVQSDMK	1	6.8289	6.8289								
		SFYPEEVSSMVLTK	3	6.3504	5.974	1.5531							
		SINPDEAVAYGAAVQAAILSGDK	1	0.2405	0.2405								
		VEIIANDQGNR	1	10.9097	10.9097								
HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	AQLGGPEAAK	1	0.4377	0.4377		3	2.7206	2.7151	1.8106	2.0005	1.9594	3.555
		KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	2	2.6984	2.5887	1.5072							
		TKDGVVEITGK	1	5.0257	5.0257								
HTRA1_HUMAN	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	GACGQQEDPNSLR	1	1.855	1.855		3	4.5597	4.5597	3.4839	3.4839	3.4839	2.3866
		SSELRPGEFVVAIGSPFSLQNTVTTGIVSTTQR	1	2.4253	2.4253								
		VTAGISFAIPSDK	1	9.3988	9.3988								
IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2	EDARPVPQGSCQSELHR	1	0.3443	0.3443		2	0.5394	0.5394	0.5029	0.5029	0.5029	1.7087
		THEDLYIIPIPNCDR	1	0.7345	0.7345								
IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1	ALSMCPPSPLGCELVK	2	3.8838	1.8154	7.18	5	1.1522	1.4689	0.6396	0.8272	0.6652	3.2081
		EHEEPTTSEMEETYSPK	1	0.4126	0.4126								
		GICWCVDK	1	0.6707	0.6707								
		GVCLNEK	2	0.6377	0.636	1.1065							
		HMEASLQELK	1	0.1562	0.1562								
IBP6_HUMAN	Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1	APAVAEENPK	1	0.3889	0.3889		4	0.3763	0.3825	0.3328	0.3464	0.3433	1.8722
		EGQECGVYTPNCAPGLQCHPPKDDEAPLR	1	0.5746	0.5746								
		GAQTLVYVPNCDHR	2	0.407	0.3978	1.3545							
		HLDSVLQQLQTEVYR	1	0.1348	0.1348								
IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	AGAAAGGPGVSGVCVCK	1	1.8096	1.8096		8	2.5591	2.5222	2.3299	2.3665	2.3427	1.5303
		DACGCCPMCAR	1	2.8823	2.8823								
		EDACYECHASNSGQQASASAK	4	2.5508	2.4837	1.2958							
		GTCEQGPSIVTPPK	1	1.9371	1.9371								
		GYCAPGMECVK	1	5.8779	5.8779								
		HEVTGWLVSPLSK	1	1.6918	1.6918								
		ITVVDALHEIPVK	2	2.1414	2.1256	1.1879							
		SRYPVCGSDGTTYPSGCQLR	1	1.582	1.582								
IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	LVLLNAIYLSAK	1	0.336	0.336		2	0.5381	0.5381	0.4987	0.4987	0.4987	1.748
		TNLESLSYPK	1	0.7402	0.7402								
ICAM2_HUMAN	Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2	GGNIFHK	1	5.5452	5.5452		3	9.4807	9.4807	7.5725	7.5725	7.5725	2.2166
		ILLDEQAQWK	1	4.1848	4.1848								
		QVILTLQPTLVAVGK	1	18.7122	18.7122								
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	GWPLYLSTK	1	2.498	2.498		1	2.498	2.498	2.498	2.498	2.498	
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	TAWVFDDK	1	1.0413	1.0413		2	1.3281	1.3281	1.2968	1.2968	1.2968	1.3638
		TEGLSVLSQAMAVIK	1	1.6149	1.6149								
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	EVEPEPTEDKDLEADEEDTR	1	0.1895	0.1895		1	0.1895	0.1895	0.1895	0.1895	0.1895	
IF2BL_HUMAN	Eukaryotic translation initiation factor 2 subunit 2-like protein OS=Homo sapiens PE=2 SV=1	EVEPEPTEDKDLEADEEDTR	1	0.1895	0.1895		1	0.1895	0.1895	0.1895	0.1895	0.1895	
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GYDVIAQAQSGTGK	1	5.6595	5.6595		1	5.6595	5.6595	5.6595	5.6595	5.6595	
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	GYDVIAQAQSGTGK	1	5.6595	5.6595		1	5.6595	5.6595	5.6595	5.6595	5.6595	
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	EDLRLPEGDLGK	1	4.7527	4.7527		4	5.1489	5.1489	4.9045	4.9045	4.9045	1.4247
		IVEMSTSK	1	7.8747	7.8747								
		KYEDICPSTHNMDVPNIK	1	3.3414	3.3414								
		YEDICPSTHNMDVPNIK	1	4.6266	4.6266								
IF5A2_HUMAN	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3	IVEMSTSK	1	7.8747	7.8747		2	6.2507	6.2507	6.036	6.036	6.036	1.4565
		YEDICPSTHNMDVPNIK	1	4.6266	4.6266								
IF5AL_HUMAN	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5AL1 PE=1 SV=2	KYEDICPSTHNMDVPNIK	1	3.3414	3.3414		1	3.3414	3.3414	3.3414	3.3414	3.3414	
IF6_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	QTVADQVLVGSYCVFSNQGGLVHPK	1	2.5391	2.5391		1	2.5391	2.5391	2.5391	2.5391	2.5391	
IFNG_HUMAN	Interferon gamma OS=Homo sapiens GN=IFNG PE=1 SV=1	SVETIK	1	2.7709	2.7709		1	2.7709	2.7709	2.7709	2.7709	2.7709	
ILEU_HUMAN	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	LVLVNAIYFK	1	6.31	6.31		1	6.31	6.31	6.31	6.31	6.31	
ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	GTMTTGHNVADLVVILK	1	2.0199	2.0199		2	2.8366	2.8366	2.7164	2.7164	2.7164	1.5204
		ILPTLEAVAALGNK	1	3.6532	3.6532								
ILF3_HUMAN	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	AVSDWDEQEK	1	4.3962	4.3962		3	4.6552	4.6552	3.9287	3.9287	3.9287	2.1139
		GDLDLELVLLCK	1	1.7681	1.7681								
		GWPLELLCEK	1	7.8012	7.8012								
IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	LAATNALLNSLEFTK	2	3.3043	2.2245	3.8282	2	3.225	3.2092	3.224	3.2082	2.6235	1.0354
		SSAYESLMEIVK	3	3.1458	2.9286	1.588							
IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	HFADLLPGFLQAVNDSCYQNDDSVLK	1	3.045	3.045		3	4.1065	4.1065	3.8689	3.8689	3.8689	1.5073
		HIVENAVQK	1	6.2138	6.2138								
		QWGLCIFDDVIEHCSPASFK	1	3.0606	3.0606								
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	EQLSDMMMINK	1	0.0901	0.0901		5	2.061	2.061	1.1258	1.1258	1.1258	4.8103
		ILAIGLINEALDEGDAQK	1	3.7386	3.7386								
		LPYDVTPEQALAWEEVK	1	0.6806	0.6806								
		QSGQTDPLQKEELQSGVDAANSAAQQYQR	1	3.6114	3.6114								
		SWVNQMESQTGEASK	1	2.1844	2.1844								
ISLR_HUMAN	Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=1 SV=1	EVPLLQSLWLAHNEIR	1	0.4169	0.4169		1	0.4169	0.4169	0.4169	0.4169	0.4169	
ITGB1_HUMAN	Integrin beta-like protein 1 OS=Homo sapiens GN=ITGBL1 PE=2 SV=1	NLCESADGILCSGK	1	0.3675	0.3675		1	0.3675	0.3675	0.3675	0.3675	0.3675	
K0020_HUMAN	Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3	QMWEILR	1	0.391	0.391		1	0.391	0.391	0.391	0.391	0.391	
K0825_HUMAN	Uncharacterized protein KIAA0825 OS=Homo sapiens GN=KIAA0825 PE=2 SV=2	HIVPDCLLESMPK	1	0.2192	0.2192		1	0.2192	0.2192	0.2192	0.2192	0.2192	
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=5	AETECQNTEYQQLLDIK	3	0.7713	0.7698	1.0809	23	0.8147	0.836	0.7915	0.8196	0.8152	1.2992
		ALEESNYELEGK	3	0.8701	0.8693	1.0557							
		DAEAWFNEK	2	0.8086	0.8085	1.016							
		ELTTEIDNNIEQISSYK	1	0.7634	0.7634								
		GSSGGGCFGSGSGGYGGLGGFGGGSFR	2	0.7622	0.7608	1.088							
		ISSSKGSLGGGFSSGGFSGGSFSR	1	0.3197	0.3197								
		LAADDFR	2	0.8827	0.8814	1.0773							
		LASYLDK	2	0.7837	0.7832	1.0495							
		LENEIQTYR	1	1.2487	1.2487								
		LKYENEVALR	2	0.9474	0.9437	1.1315							
		NQILNLTTDNANILLQIDNAR	1	0.9143	0.9143								
		NVQALEIELQSLQALK	1	0.6883	0.6883								
		NVSTGDVNEVMNAAPGVDLTQLLNNMR	3	1.0146	0.9718	1.4199							
		QSLEASLAETEGR	1	0.7143	0.7143								
		QSVEADINGLR	1	0.858	0.858								
		QSVEADINGLRR	2	1.0029	0.9903	1.2532							
		RVLDELTLTK	1	0.5955	0.5955								
		SQYEQLAEQNR	3	0.8269	0.8206	1.1644							
		SQYEQLAEQNRK	1	0.7643	0.7643								
		TIDDLK	1	0.7175	0.7175								
		VLDELTLTK	1	0.5947	0.5947								
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
		YCVQLSQIQAQISALEEQLQQIR	1	1.0097	1.0097								
K1C12_HUMAN	Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	LASYLDK	2	0.7837	0.7832	1.0495	2	1.2963	1.1254	1.1906	1.0357	1.0353	1.8067
		VLDELTLTR	1	1.8089	1.8089								

K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=3	QSVEADINGLR	1	0.858	0.858		2	0.9305	0.9546	0.9276	0.9521	0.9441	1.1167
		QSVEADINGLRR	2	1.0029	0.9903	1.2532							
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	ADLEMQIESLKEELAYLK	1	1.5409	1.5409		7	0.7505	0.7798	0.5291	0.6093	0.6089	2.9016
		ASLENSLEETK	1	0.1095	0.1095								
		ISSVLAGGSCR	1	0.1207	0.1207								
		LAADDFR	2	0.8827	0.8814	1.0773							
		LASYLDK	2	0.7837	0.7832	1.0495							
		VLDELTLAR	1	0.9378	0.9378								
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C15_HUMAN	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=2	LAADDFR	2	0.8827	0.8814	1.0773	3	0.868	0.8541	0.8656	0.8519	0.8512	1.0957
		LASYLDK	2	0.7837	0.7832	1.0495							
		VLDELTLAR	1	0.9378	0.9378								
K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	ASLENSLEETK	1	0.1095	0.1095		6	0.6188	0.6953	0.4427	0.5496	0.5492	2.8476
		ISSVLAGGSCR	1	0.1207	0.1207								
		LAADDFR	2	0.8827	0.8814	1.0773							
		LASYLDK	2	0.7837	0.7832	1.0495							
		VLDELTLAR	1	0.9378	0.9378								
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	LAADDFR	2	0.8827	0.8814	1.0773	3	0.868	0.8541	0.8656	0.8519	0.8512	1.0957
		LASYLDK	2	0.7837	0.7832	1.0495							
		VLDELTLAR	1	0.9378	0.9378								
K1C18_HUMAN	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	LAADDFR	2	0.8827	0.8814	1.0773	2	5.648	4.0595	3.0317	2.0093	2.0075	5.7263
		LASYLDR	1	10.4133	10.4133								
K1C19_HUMAN	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=3	LAADDFR	2	0.8827	0.8814	1.0773	3	0.868	0.8541	0.8656	0.8519	0.8512	1.0957
		LASYLDK	2	0.7837	0.7832	1.0495							
		VLDELTLAR	1	0.9378	0.9378								
K1C20_HUMAN	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1	MAMQNLNDR	1	0.9297	0.9297		1	0.9297	0.9297	0.9297	0.9297	0.9297	
K1C24_HUMAN	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1	LAADDFR	2	0.8827	0.8814	1.0773	3	0.7958	0.8175	0.7883	0.8109	0.8103	1.1876
		QSVEADINGLR	1	0.858	0.858								
		QSVEADINGLRK	1	0.6468	0.6468								
K1C25_HUMAN	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1	DAEAWFNEK	2	0.8086	0.8085	1.016	2	0.8435	0.8435	0.8428	0.8428	0.8421	1.0603
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C26_HUMAN	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2	DAEAWFNER	1	17.0711	17.0711		2	8.9747	6.2759	3.8723	2.3616	2.3593	8.1503
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C27_HUMAN	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=1	DAEAWFNEK	2	0.8086	0.8085	1.016	2	0.8435	0.8435	0.8428	0.8428	0.8421	1.0603
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C28_HUMAN	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=1	DAEAWFNEK	2	0.8086	0.8085	1.016	3	0.8565	0.8565	0.8558	0.8558	0.855	1.0505
		LAADDFR	2	0.8827	0.8814	1.0773							
		VTMQNLNDR	2	0.8784	0.8771	1.0793							
K1C40_HUMAN	Keratin, type I cytoskeletal 40 OS=Homo sapiens GN=KRT40 PE=1 SV=2	ETMQFLNDR	1	3.8488	3.8488		1	3.8488	3.8488	3.8488	3.8488	3.8488	
K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	DIENQYETQITQIEHEVSSSGQEVQSSAK	3	0.6985	0.6952	1.1273	17	0.9511	1.1091	0.8619	0.9408	0.8532	1.4838
		EIETYHNLLEGQEDFESSGAGK	1	0.7204	0.7204								
		FSSSGGGGGGGR	1	0.6647	0.6647								
		FSSSSGYGGGSSR	3	0.8758	0.873	1.104							
		GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR	2	1.0883	1.069	1.3073							
		GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK	1	1.1093	1.1093								
		GGSGGSYGGGSGGGYGGGSGSR	2	0.8548	0.8504	1.1545							
		IKFEMEQNLR	1	0.7527	0.7527								
		LASYLDK	2	0.7837	0.7832	1.0495							
		MTLDDFR	1	0.5322	0.5322								
		NYSPYYNTIDDLKDQIVDLTVGNNK	1	0.8076	0.8076								
		QEIECQNQEYSLLLSIK	2	0.8831	0.8448	1.528							
		QVLDNLTMEK	1	1.0048	1.0048								
		SGGSGGGGLGSGGSIR	1	0.9511	0.9511								
		STMQELNSR	4	3.1973	1.5782	3.518							
		TLLDIDNTR	3	0.6184	0.6173	1.0783							
		VQALEEANNDLENK	2	0.6257	0.6136	1.3224							
K1H1_HUMAN	Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	ETMQFLNDR	1	3.8488	3.8488		4	8.0006	6.577	2.4069	1.9694	1.9682	6.5452
		LAADDFR	2	0.8827	0.8814	1.0773							
		LNVEVDAAPTVDLNR	1	0.3672	0.3672								
		SDLEAQVESLKEELLCLK	1	26.9037	26.9037								
K1H2_HUMAN	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=2	ETMQFLNDR	1	3.8488	3.8488		2	2.3657	1.8714	1.8431	1.442	1.4406	2.8328
		LAADDFR	2	0.8827	0.8814	1.0773							
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	AQYEEIAQR	2	1.0985	1.0984	1.0234	14	1.2893	1.0754	0.9952	0.9147	0.9006	1.8341
		DVDNAYMIK	1	0.7018	0.7018								
		DYQELMNVK	2	0.984	0.922	1.675							
		FASFIDK	1	1.2546	1.2546								
		FGGFGGPGGVGGLGGPCGFGPGGYPGGIHEVSVNQSLLQPLNVK	1	1.1166	1.1166								
		FLEQQNQVLQTK	5	0.8335	0.8014	1.3452							
		IEISELNR	2	0.58	0.5515	1.5717							
		LNDLEEALQQAK	2	0.9731	0.9731	1.0114							
		NLDLDSIIAEVK	4	0.9601	0.9597	1.0341							
		STSSFSQLSR	1	6.4408	6.4408								
		TSQNSELNNMQDLVEDYKK	1	0.9034	0.9034								
		VDLLNQEIEFLK	3	0.8955	0.8945	1.0605							
		YEELQVTVGR	2	0.4216	0.421	1.0777							
		YLDGLTAER	1	0.8863	0.8863								
K22O_HUMAN	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=1	DYQELMNVK	2	0.984	0.922	1.675	3	3.5299	4.7127	2.1765	2.9851	2.9205	3.2248
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	3	8.3512	8.3483	1.033							
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	AEAESLYQSK	2	15.5169	5.5701	10.8161	23	1.4287	1.4125	0.8754	0.8489	0.7639	1.9421
		AQYEDIAQK	3	0.7655	0.7615	1.1319							
		DVDGAYMTK	3	0.7529	0.7282	1.3846							
		DYQELMNTK	3	0.7388	0.7339	1.1493							
		FLEQQNQVLQTK	3	0.9063	0.8589	1.4777							
		FLEQQNQVLQTKWELLQQVDTSTR	1	1.056	1.056								
		FSSCGGGGCGSFGAGGGFGSR	1	0.7155	0.7155								
		GSGGGSSSGGSGGSIGGR	1	0.881	0.881								
		GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSSGGYR	1	0.7876	0.7876								
		IEISELNR	2	0.58	0.5515	1.5717							
		LALDIEIATYR	4	0.8352	0.8325	1.0964							
		LNDLEDALQQAK	1	0.9551	0.9551								
		NKLNDLEDALQQAK	1	0.7492	0.7492								
		NMQDMVEDYR	4	0.5521	0.3127	5.3864							
		SKAEAESLYQSK	1	0.5547	0.5547								
		SLDLDSIIAEVK	2	0.7415	0.7411	1.0465							
		SLNNQFASFIDK	2	0.6752	0.6752	1.0038							
		SLVNLGGSK	1	0.8411	0.8411								
		SLVNLGGSKSISISVAR	1	1.5024	1.5024								
		TLLEGEESR	2	0.7055	0.7047	1.0695							
		TNAENEFVTIK	3	0.6197	0.6177	1.1011							
		WELLQQVDTSTR	1	0.6729	0.6729								
		YEELQITAGR	2	0.7547	0.7547	1.0026							
K2C1B_HUMAN		YQELQITAGR	1	0.7387	0.7387		1	0.7387	0.7387	0.7387	0.7387	0.7387	
K2C3_HUMAN	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=2	AQYEDIAQR	1	5.7161	5.7161		5	15.6552	17.5481	5.1583	6.2954	5.6901	5.3166
		DYQELMNVK	2	0.984	0.922	1.675							
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	3	8.3512	8.3483	1.033							
		SLDLDSIIAEVR	2	61.9702	41.9876	3.7816							
K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	AQYEEIAQR	2	1.0985	1.0984	1.0234	4	1.2554	1.2841	1.2053	1.2124	1.165	1.3867
		FASFIDK	1	1.2546	1.2546								
		LALDIEIATYR	4	0.8352	0.8325	1.0964							
		NLDLDSIIAEVR	4	1.8333	1.6483	1.736							
K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	AQYEEIANR	1	1.6686	1.6686		6	2.1943	2.9771	1.0794	1.5166	1.5162	3.9643
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	3	8.3512	8.3483	1.033							
		NLDLDSIIAEVK	4	0.9601	0.9597	1.0341							
		QLDSIVGER	1	0.8158	0.8158								
		WTLLQEQGTK	1	0.1155	0.1155								
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	AQYEEIAQR	2	1.0985	1.0984	1.0234	7	1.85	2.2215	0.8131	1.0634	1.0633	3.9367
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	2	8.4939	8.4932	1.0185							
		ISIGGGSCAISGGYGSR	1	0.2249	0.2249								
		NLDLDSIIAEVK	3	0.9471	0.9469	1.025							
		QLDSIVGER	1	0.8158	0.8158								
		WTLLQEQGTK	1	0.1155	0.1155								
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	AQYEEIAQR	1	1.1165	1.1165		5	2.4897	3.1848	1.5369	1.832	1.8316	2.6247
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	3	8.3512	8.3483	1.033							
		NLDLDSIIAEVK	3	0.9713	0.971	1.03							
		YEELQITAGR	2	0.7547	0.7547	1.0026							
K2C8C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	AQYEEIAQR	1	1.1165	1.1165		6	2.4807	2.8134	1.6616	1.7678	1.7676	2.3858
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	2	8.4939	8.4932	1.0185							
		NLDLDSIIAEVK	3	0.9713	0.971	1.03							
		QLDSIVGER	1	0.8158	0.8158								
		YEELQVTAGR	1	2.2324	2.2324								
K2C7_HUMAN	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=3	FASFIDK	1	1.2546	1.2546		5	5.6208	5.0855	3.6878	3.0829	3.0718	3.2517
		FLEQQNK	3	8.3512	8.3483	1.033							
		KLLEGEESR	1	9.0346	9.0346								
		LALDIEIATYR	4	0.8352	0.8325	1.0964							
		LLEGEESR	2	8.6285	8.5173	1.2564							
K2C71_HUMAN	Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=2	FLEQQNQVLETK	1	0.6884	0.6884		1	0.6884	0.6884	0.6884	0.6884	0.6884	
K2C72_HUMAN	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	DLDLDSIIAEVR	4	1.9689	1.7872	1.6892	3	1.304	1.6365	1.1936	1.533	1.4372	1.6942
		FASFIDK	1	1.2546	1.2546								
		FLEQQNQVLETK	1	0.6884	0.6884								
K2C73_HUMAN	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	FASFIDK	1	1.2546	1.2546		3	1.2588	1.5461	1.1655	1.4618	1.3617	1.6387
		FLEQQNQVLETK	1	0.6884	0.6884								
		NLDLDSIIAEVR	4	1.8333	1.6483	1.736							
K2C74_HUMAN	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2	DLDLDSIIAEVR	4	1.9689	1.7872	1.6892	3	1.304	1.6365	1.1936	1.533	1.4372	1.6942
		FASFIDK	1	1.2546	1.2546								
		FLEQQNQVLETK	1	0.6884	0.6884								
K2C75_HUMAN	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2	FASFIDK	1	1.2546	1.2546		4	3.1996	3.5979	2.1769	2.234	2.2334	2.6195
		FLEQQNK	3	8.3512	8.3483	1.033							
		NLDLDSIIAEVK	4	0.9601	0.9597	1.0341							
		YEELQVTAGR	1	2.2324	2.2324								
K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	FLEQQNK	2	8.3349	8.3306	1.0467	1	8.3349	8.3349	8.3349	8.3349	8.3306	
K2C79_HUMAN	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=1	DYQELMNVK	2	0.984	0.922	1.675	5	2.4107	2.9655	1.379	1.681	1.6608	2.8924
		FASFIDK	1	1.2546	1.2546								
		FLEQQNK	3	8.3512	8.3483	1.033							
		NLDLDSIIAEVK	4	0.9601	0.9597	1.0341							
		YEELQVTAGK	1	0.5037	0.5037								
K2C8_HUMAN	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	FASFIDK	1	1.2546	1.2546		5	5.6208	5.0855	3.6878	3.0829	3.0718	3.2517
		FLEQQNK	3	8.3512	8.3483	1.033							
		KLLEGEESR	1	9.0346	9.0346								
		LALDIEIATYR	4	0.8352	0.8325	1.0964							
		LLEGEESR	2	8.6285	8.5173	1.2564							
K2C80_HUMAN	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	LALDIEIATYR	4	0.8352	0.8325	1.0964	1	0.8352	0.8352	0.8352	0.8352	0.8325	
KCC2D_HUMAN	Calcium/calmodulin-dependent protein kinase type II delta chain OS=Homo sapiens GN=CAMK2D PE=1 SV=3	FTDEYQLFEELGK	1	0.4652	0.4652		1	0.4652	0.4652	0.4652	0.4652	0.4652	
KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1	FNFLEQAFDK	1	1.0863	1.0863		1	1.0863	1.0863	1.0863	1.0863	1.0863	
KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	EMDQTMAANAQK	1	0.6796	0.6796		2	0.8554	0.8554	0.8371	0.8371	0.8371	1.3428
		IVPVEITISLLK	1	1.0311	1.0311								
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	DSLDPSFTHMKQLITAEIEK	1	2.8263	2.8263		2	2.7862	2.7862	2.7859	2.7859	2.7859	1.0206
		KDDEENYLDLFSHK	1	2.7461	2.7461								

KIF14_HUMAN	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1	NFGGTVSIIPVGEAKTYVNGK	1	1.4549	1.4549		1	1.4549	1.4549	1.4549	1.4549	1.4549	
KIF7_HUMAN	Kinesin-like protein KIF7 OS=Homo sapiens GN=KIF7 PE=1 SV=2	ELAINIR	1	2.3795	2.3795		1	2.3795	2.3795	2.3795	2.3795	2.3795	
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	AEGSDVANAVLDGADCIMLSGETAK	1	3.18	3.18		13	4.5404	4.7092	3.6102	3.9588	3.9089	2.4238
		AGKPVICATQMLESMIK	2	6.7253	6.508	1.4397							
		CDENILWLDYK	1	0.2845	0.2845								
		GADFLVTEVENGGSLGSK	2	3.5804	3.4994	1.3549							
		GDLGIEIPAEK	1	7.6489	7.6489								
		GDVVIVLTGWRPGSGFTNTMR	1	1.8508	1.8508								
		GIFPVLCK	1	8.6049	8.6049								
		GSGTAEVELK	1	4.1226	4.1226								
		ITLDNAYMEK	1	5.323	5.323								
		IVVDDGLISLQVK	2	5.3613	5.2997	1.2404							
		LAPITSDPTEATAVGAVEASFK	2	5.671	5.6677	1.0491							
		SVETLK	1	2.2709	2.2709								
		TATESFASDPILYRPVAVALDTK	2	4.4023	4.2028	1.5434							
KPYR_HUMAN	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2	GDLGIEIPAEK	1	7.6489	7.6489		1	7.6489	7.6489	7.6489	7.6489	7.6489	
KRT34_HUMAN	Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 PE=1 SV=2	ETMQFLNDR	1	3.8488	3.8488		1	3.8488	3.8488	3.8488	3.8488	3.8488	
KRT35_HUMAN	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=4	LAADDFR	2	0.8827	0.8814	1.0773	2	13.8932	9.5563	4.873	2.7572	2.7546	11.2037
		SDLEAQVESLKEELLCLK	1	26.9037	26.9037								
KRT36_HUMAN	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1	ETMQFLNDR	1	3.8488	3.8488		2	2.3657	1.8714	1.8431	1.442	1.4406	2.8328
		LAADDFR	2	0.8827	0.8814	1.0773							
KRT37_HUMAN	Keratin, type I cuticular Ha7 OS=Homo sapiens GN=KRT37 PE=2 SV=3	LAADDFR	2	0.8827	0.8814	1.0773	1	0.8827	0.8827	0.8827	0.8827	0.8814	
KRT38_HUMAN	Keratin, type I cuticular Ha8 OS=Homo sapiens GN=KRT38 PE=2 SV=3	ETMQFLNDR	1	3.8488	3.8488		2	2.389	2.389	1.891	1.891	1.891	2.7319
		LAADDFR	1	0.9291	0.9291								
KRT81_HUMAN	Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=2	FLEQQNK	3	8.3512	8.3483	1.033	1	8.3512	8.3512	8.3512	8.3512	8.3483	
KRT82_HUMAN	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3	LAGLEEALQK	1	1.1525	1.1525		1	1.1525	1.1525	1.1525	1.1525	1.1525	
KRT83_HUMAN	Keratin, type II cuticular Hb3 OS=Homo sapiens GN=KRT83 PE=1 SV=2	FLEQQNK	2	8.3349	8.3306	1.0467	1	8.3349	8.3349	8.3349	8.3349	8.3306	
KRT84_HUMAN	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=1 SV=1	FASFEIK	1	1.2546	1.2546		3	6.0781	7.2609	4.4881	6.1556	6.128	3.0161
		FLEQQNK	3	8.3512	8.3483	1.033							
		LLEGEESR	2	8.6285	8.5173	1.2564							
KRT85_HUMAN	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	FLEQQNK	3	8.3512	8.3483	1.033	1	8.3512	8.3512	8.3512	8.3512	8.3483	
KRT86_HUMAN	Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	FLEQQNK	2	8.3349	8.3306	1.0467	1	8.3349	8.3349	8.3349	8.3349	8.3306	
KT33A_HUMAN	Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT33A PE=1 SV=2	ETMQFLNDR	1	3.8488	3.8488		2	15.3763	15.3763	10.1758	10.1758	10.1758	3.955
		SDLEAQVESLKEELLCLK	1	26.9037	26.9037								
KT33B_HUMAN	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=1 SV=3	ETMQFLNDR	1	3.8488	3.8488		2	2.3657	1.8714	1.8431	1.442	1.4406	2.8328
		LAADDFR	2	0.8827	0.8814	1.0773							
LA_HUMAN	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	EVTWEVLEGEVEK	3	7.524	7.3642	1.2934	3	3.2655	4.9689	1.0915	2.3627	2.3324	10.5724
		GSIFVVFDSIESAK	1	0.0788	0.0788								
		LTTDFNWIVEALSK	1	2.1936	2.1936								
LAMA4_HUMAN	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=3	AHLPLDINFR	1	1.0346	1.0346		9	1.0657	1.0721	0.9237	0.9591	0.9517	1.945
		DAPSWDPVALK	1	1.169	1.169								
		DESENLLNQAR	1	1.7512	1.7512								
		ESMDTINHASQLVEQAHDMR	1	1.2715	1.2715								
		IPFTDIYIGGAPPEILQSR	1	1.2075	1.2075								
		LAALSIEEGK	2	0.4972	0.4849	1.3737							
		LSDLQEALDQALNHVR	1	0.2	0.2								
		SLLSDVEELVEK	3	1.2302	1.2171	1.1932							
		TLFPVVLEQLDDYNAK	3	1.2302	1.2193	1.1794							
LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1	AAQNSQEAEYEIDK	1	1.2134	1.2134		13	3.6304	3.1723	1.8398	1.6908	1.6881	2.4604
		ELAEQLEFIK	2	0.9633	0.9631	1.0293							
		ELDSLQTEAESLDNTVK	1	1.4329	1.4329								
		IEDPYSPR	1	27.873	27.873								
		KVDDIICDSR	1	4.5405	4.5405								
		LNVEGEHCDVCK	1	1.4592	1.4592								
		NFLTQDSADLDSIEAVANEVLK	2	1.182	1.1814	1.0457							
		NIGNLFEEAEK	1	1.3292	1.3292								
		SCACNPLGTIPGGNPCDSETGHCYCK	2	1.4156	1.3984	1.2477							
		TLDGELDEK	1	1.0856	1.0856								
		VESLSQVEVELQHSAQADIAR	1	1.8136	1.8136								
		YFAYDCEASFPGISTGPMIK	1	1.2426	1.2426								
		YSDIEPSTEGEVIFR	1	1.6446	1.6446								
LAMB2_HUMAN	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	GQVEGANGELQELIQSVK	1	0.3889	0.3889		1	0.3889	0.3889	0.3889	0.3889	0.3889	
LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	DIEEIMK	1	0.8411	0.8411		16	1.3663	1.2957	1.242	1.2086	1.1996	1.47
		DNVEGFNCER	1	4.5031	4.5031								
		EVMDLLR	2	0.972	0.9708	1.0733							
		KQEAAIMDYNR	1	0.989	0.989								
		LCQCSDNIDPNAVGNCNR	1	0.9857	0.9857								
		LGNNEACSSCHCSPVGSLSTQCDSYGR	1	1.4918	1.4918								
		MEAENLEQLDDQK	2	1.3512	1.3438	1.16							
		NTIEETGNLAEQAR	2	1.0173	1.0172	1.0005							
		QDIAVISDSYFPR	1	0.9871	0.9871								
		SQECYFDPELYR	2	0.9577	0.9427	1.2865							
		SWPGCQECPACYR	3	1.3135	1.2916	1.2548							
		SYYYAISDFAVGGR	2	1.1435	1.0967	1.5089							
		TAAEEALR	1	1.3832	1.3832								
		TFAEVTDLDNEVNNMLK	2	1.1675	1.1674	1.0154							
		TGQCECQPGITGQHCER	1	1.3324	1.3324								
		TLPSGCPNTPSIEKP	1	1.4253	1.4253								
LDH6A_HUMAN	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1	VGSGCNLDSAR	2	10.6327	10.5809	1.1501	1	10.6327	10.6327	10.6327	10.6327	10.5809	
LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	DLADELALVDVIEDK	6	4.6385	4.1053	1.8984	9	4.6761	5.0027	4.0517	4.5703	4.1207	1.7639
		DQLIYNLLKEEQTPQNK	3	5.9634	5.7035	1.465							
		DVNVTANSK	1	1.7445	1.7445								
		GLYGIKDDVFLSVPCILGQNGISDLVK	1	3.4468	3.4468								
		QVVESAYEVIK	1	2.4405	2.4405								
		SADTLWGIQK	2	2.3958	1.314	5.5224							
		VIGSGCNLDSAR	4	4.5027	4.3658	1.3312							
		VTLTSEEEAR	2	10.6327	10.5809	1.1501							
LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GEMIDLQHGSLFLQTPK	2	6.3198	6.0794	1.4865							
		GLTSVINQK	1	0.3593	0.3593		9	7.2834	8.2521	5.1264	6.2426	6.1708	3.1195
		ITVVGVGQVGMACAISILGK	2	5.5652	5.5537	1.0953							
		IVADKDYSVTANSK	2	2.6096	2.4405	1.6879							
		LIAPVAEEEATVPNNK	1	8.6728	8.6728								
		LKDDEVAQLK	1	3.7424	3.7424								
		SADTLWDIQK	1	8.2346	8.2346								
		SLADELALVDVLEDK	2	12.0449	12.0381	1.0486							
		VIGSGCNLDSAR	3	13.6891	13.5768	1.1682							
LDHC_HUMAN	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=2 SV=4	VIGSGCNLDSAR	2	10.6327	10.5809	1.1501	1	10.6327	10.6327	10.6327	10.6327	10.5809	
LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	DSGAWGTEQR	3	9.1414	9.1286	1.0673	6	6.9335	6.5442	6.4082	6.2585	5.1987	1.598
		DSNNLCLHFNPR	1	10.1678	10.1678								
		FNAHGDANTIVCNSK	4	6.7632	6.6027	1.298							
		GEVAPDAK	2	2.7272	0.8437	13.5212							
		LNLEAINYMAADGDFK	8	5.6665	4.7037	2.0769							
		SFVLNLGK	4	7.1352	6.8803	1.3857							
LEG3_HUMAN	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	MLTILGTVKPNANR	1	0.6372	0.6372		1	0.6372	0.6372	0.6372	0.6372	0.6372	
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	ELSEALQGFDSQGR	1	1.1092	1.1092		7	2.2314	2.0298	0.7536	0.7352	0.7062	4.2412
		GQWGTVCDNLWDLTDASVVCR	1	0.1641	0.1641								
		LASAYGAR	1	0.7577	0.7577								
		SLGWLK	1	0.8313	0.8313								
		STSSFPCPAGHFNGFR	1	11.9764	11.9764								
		TLQALEFHTVPFQLLAR	1	0.1625	0.1625								
		YSSDYFQAPSDYR	2	0.6184	0.5264	2.281							
LGMN_HUMAN	Legumain OS=Homo sapiens GN=LGMN PE=1 SV=1	ESSYACYYDEK	1	3.4787	3.4787		1	3.4787	3.4787	3.4787	3.4787	3.4787	
LGUL_HUMAN	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	GLAFIQDPDGYWIELNPNK	1	5.2725	5.2725		1	5.2725	5.2725	5.2725	5.2725	5.2725	
LIMC1_HUMAN	LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=3	SDSLSPPR	1	0.7314	0.7314		1	0.7314	0.7314	0.7314	0.7314	0.7314	
LKHA4_HUMAN	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	DLAAFDK	1	3.8664	3.8664		2	2.9322	2.9322	2.7793	2.7793	2.7793	1.595
		LTYTAEVSVPK	1	1.9979	1.9979								
LMNA_HUMAN	Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	AAYEAELGDAR	1	2.4341	2.4341		7	5.0087	4.1155	3.057	1.8644	1.7803	4.4469
		AGQVVTIWAAGAGATHSPPTDLVWK	1	4.7368	4.7368								
		AGNTWGCGNSLR	1	10.2158	10.2158								
		EDLQELNDR	3	0.1236	0.1057	2.1168							
		IDSLSAQLSQLQK	3	4.9811	4.9187	1.2196							
		MQQQLDEYQELLDIK	1	4.0269	4.0269								
		TLEGELHDLR	1	8.5423	8.5423								
LOXL2_HUMAN	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	LGQGIGPIHLNEIQCTGNEK	1	1.7128	1.7128		1	1.7128	1.7128	1.7128	1.7128	1.7128	
LRC57_HUMAN		TIDLSNNK	1	9.7102	9.7102		1	9.7102	9.7102	9.7102	9.7102	9.7102	
LRC59_HUMAN	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	LVNLDHLDLLNNK	1	5.6127	5.6127		2	7.9255	7.9255	7.5805	7.5805	7.5805	1.5297
		LVTLPVSFAQLK	1	10.2383	10.2383								
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=3	ASGLGDHCEDINECLEDK	2	0.6535	0.6534	1.0232	11	0.58	0.5799	0.5191	0.5264	0.4974	1.6473
		CEYCDSGYR	1	1.2713	1.2713								
		CVDIDECTQVQHLCSQGR	2	0.7574	0.7564	1.0746							
		DQCEDIDECQHR	2	0.595	0.3992	3.853							
		EAQPGQSQVSYQGLPVQK	1	0.622	0.622								
		EEPVEALTFSR	1	0.2796	0.2796								
		GFVPAGESSSEAGGENYKDADECLLFGQEICK	1	0.4046	0.4046								
		HPPEASVQIHQVSR	1	0.6212	0.6212								
		MTCVDVNECDELNNR	2	0.2481	0.239	1.4754							
		QEDCCGTVGTSWGFNK	2	0.6449	0.6352	1.2802							
		YTCICYEGYR	1	0.282	0.282								
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2 OS=Homo sapiens GN=LTBP2 PE=1 SV=2	AISMLQGLCYR	1	0.9847	0.9847		13	2.0947	2.183	1.8198	1.9424	1.8849	1.8196
		ALLEAPLK	3	2.7886	2.6168	1.5286							
		AQPGWGSPR	1	2.3891	2.3891								
		CEEVIPDEEFDPQNSR	1	3.0573	3.0573								
		DCDGGYRPSPLGDSCEDVDECEDPQSSCLGGECK	1	2.153	2.153								
		EQDAPVAGLQPVER	1	3.5552	3.5552								
		GAGGQSMSEAPTGDHAPAPTR	1	1.2244	1.2244								
		GQSGSCVDVNECLTPGVCAHGK	1	1.4969	1.4969								
		SGAAPPTPPR	1	0.4754	0.4754								
		SSAAGEGTLAR	2	1.0514	1.0401	1.2307							
		SSEVYAQLCNVAR	2	3.5722	3.5165	1.2858							
		STPLGQQQPAPR	3	1.7459	1.5838	1.7825							
		VTNDVCSEPLR	2	2.7365	2.6479	1.4404							
LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2	AGPDLASCLDVDECR	1	1.3344	1.3344		3	6.023	6.023	3.1554	3.1554	3.1554	3.9068
		DVDECQLFR	1	1.5505	1.5505								
		GCQLCPPFGSEGFR	1	15.184	15.184								
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	FNALQYLR	1	0.1048	0.1048		6	0.6592	0.6281	0.4457	0.4692	0.4158	2.8636
		ISNIPDEYFK	1	1.2569	1.2569								
		LKEDAVSAAFK	2	0.5144	0.4989	1.4208							
		LPSGLPVSLLTLYLDNNK	4	0.4941	0.4085	2.1603							
		NIPTVNENLENYYLEVNQLEK	2	1.4201	1.309	1.7834							
		SLEYLDLSFNQIAR	2	0.1648	0.1302	2.743							
LYAR_HUMAN	Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2	SEEELLVIFNK	1	0.1329	0.1329		1	0.1329	0.1329	0.1329	0.1329	0.1329	
LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	STDYGIFQINSR	1	1.3372	1.3372		1	1.3372	1.3372	1.3372	1.3372	1.3372	
MA1A1_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens GN=MAN1A1 PE=1 SV=3	SSSGLTYIAEWK	1	0.4487	0.4487		1	0.4487	0.4487	0.4487	0.4487	0.4487	
MAP1A_HUMAN	Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=5	AVLDALLEGK	1	0.9138	0.9138		1	0.9138	0.9138	0.9138	0.9138	0.9138	
MAP1B_HUMAN	Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=1	AVLDALLEGK	1	0.9138	0.9138		1	0.9138	0.9138	0.9138	0.9138	0.9138	
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	EELQANGSAPAADKEEPAAAGSGAASPSAAEK	1	6.5917	6.5917		2	6.3179	6.3179	6.312	6.312	6.312	1.0632
		VNGDASPAAAESGAK	1	6.0441	6.0441								
MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	VECSDNLTQR	2	2.2585	1.4532	4.1682	1	2.2585	2.2585	2.2585	2.2585	1.4532	
MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	IGPYQPNVPVGIDYVIPK	2	4.1069	3.9585	1.4711	1	4.1069	4.1069	4.1069	4.1069	3.9585	
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	NVIIWGNHSSTQYPDVNHAK	1	4.4273	4.4273		2	3.3054	3.3054	3.1092	3.1092	3.1092	1.6484
		VIVVGNPANTNCLTASK	1	2.1835	2.1835								
MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	ANTPVAELK	2	3.1027	3.0995	1.0654	7	4.5563	4.9935	4.1828	4.6182	4.1255	1.569

		FVFSLVDAMNGK	1	3.6076	3.6076								
		GYLGPEQLPDCLK	2	6.721	4.0133	4.769							
		LTLYDIAHTPGVAADLSHIETK	1	2.3618	2.3618								
		SQETECTYFSTPLLLGK	2	6.5515	6.0925	1.7256							
		TIPLISQCTPK	1	2.8894	2.8894								
		VAVLGASGGIGQPLSLLLK	2	6.66	6.4554	1.4263							
MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	EVTGIITQGAR	1	0.4844	0.4844		2	0.4177	0.4177	0.4123	0.4123	0.4123	1.2561
		NLFETPILAR	1	0.3509	0.3509								
MGN_HUMAN	Protein mago nashi homolog OS=Homo sapiens GN=MAGOH PE=1 SV=1	VFYYLVQDLK	1	2.085	2.085		1	2.085	2.085	2.085	2.085	2.085	
MINP1_HUMAN	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1	SSCTLFQDIFQHLDK	1	1.1299	1.1299		1	1.1299	1.1299	1.1299	1.1299	1.1299	
MK09_HUMAN	Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 PE=1 SV=2	EVMDWEER	1	3.9039	3.9039		1	3.9039	3.9039	3.9039	3.9039	3.9039	
ML12B_HUMAN	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	ATSNVFAMFDQSQIQEFK	1	2.1211	2.1211		2	1.8847	1.8847	1.8698	1.8698	1.8698	1.1952
		GNFNYIEFTR	1	1.6483	1.6483								
MLL3_HUMAN	Histone-lysine N-methyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	LEEQNGSK	1	15.5521	15.5521		1	15.5521	15.5521	15.5521	15.5521	15.5521	
MMP1_HUMAN	Interstitial collagenase OS=Homo sapiens GN=MMP1 PE=1 SV=3	ADVDHAIEK	1	0.7693	0.7693		2	1.6314	1.6314	1.385	1.385	1.385	2.2968
		IENYTPDLPR	1	2.4935	2.4935								
MMP2_HUMAN	72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2	AFQVWSDVTPLR	2	2.929	2.8978	1.23	19	2.0435	2.2555	1.5858	1.8895	1.8113	2.7723
		DKPMGPLLVATFWPELPEK	1	1.8284	1.8284								
		ESCNLFVLK	4	4.2107	3.414	2.0128							
		EYNSCTDTGR	1	1.5124	1.5124								
		FFGLPQTGDLDQNTIETMR	4	1.8371	1.789	1.3065							
		FQGTSYDSCTTEGR	3	2.1789	2.0546	1.5116							
		GAYYLK	1	0.0336	0.0336								
		IDAVYEAPQEEK	2	1.5736	1.5609	1.1979							
		IHDGEADIMINFGR	1	1.1293	1.1293								
		IIGYTPDLDPETVDDAFAR	1	5.0598	5.0598								
		LIADAWNAIPDNLDAVIDLQGGGHSYFFK	1	1.3443	1.3443								
		MWCATTANYDDDRK	1	1.5943	1.5943								
		QDIVFDGIAQIR	1	1.4064	1.4064								
		TDKELAVQYLNTFYGCPK	2	1.5958	1.5284	1.5196							
		TYIFAGDK	3	2.0362	1.9496	1.4568							
		WCGTTEDYDR	3	3.1791	3.1377	1.2183							
		WEHGDGYPFDGK	1	2.3264	2.3264								
		YGFCPHEALFTMGGNAEGQPCK	1	1.9636	1.9636								
		YGNADGEYCK	2	1.0876	1.0533	1.4328							
MMP3_HUMAN	Stromelysin-1 OS=Homo sapiens GN=MMP3 PE=1 SV=2	GEDTSMNLVQK	1	1.0915	1.0915		1	1.0915	1.0915	1.0915	1.0915	1.0915	
MMRN1_HUMAN	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	EFQSLLK	1	5.1539	5.1539		7	6.3286	6.3286	3.3187	3.3187	3.3187	4.4686
		GLTEFVEPIIQIK	1	10.0762	10.0762								
		IFGNDMQETVAQLFK	1	18.1455	18.1455								
		LSPTVILDNQVTVVPGGK	1	0.7621	0.7621								
		LVEENALAPDFSK	1	5.1905	5.1905								
		MTDQVNYQAMK	1	4.7198	4.7198								
		YNFVLQVAK	1	0.252	0.252								
MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	ALELEGER	2	10.8594	10.7535	1.2193	10	5.6704	6.2661	3.638	4.7127	4.5094	3.731
		AQMVQEDLEK	1	1.9766	1.9766								
		EDAVLEYLK	2	5.7464	5.5179	1.5001							
		ESEAVEWQQK	2	4.4399	4.2385	1.5438							
		EVWFFGLQYQDTK	2	8.2137	8.1648	1.1672							
		GFSTWLK	3	7.798	6.6486	1.984							
		LFFLQVK	1	11.127	11.127								
		QLFDQVVK	2	4.9645	4.8036	1.4404							
		SGYLAGDK	1	0.1463	0.1463								
		VLEQHK	1	1.4326	1.4326								
MP3B2_HUMAN	Microtubule-associated proteins 1A/1B light chain 3 beta 2 OS=Homo sapiens GN=MAP1LC3B2 PE=2 SV=1	FLVPDHVNMSELIK	1	2.2142	2.2142		1	2.2142	2.2142	2.2142	2.2142	2.2142	
MT1A_HUMAN	Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=1	CAQGCICK	2	8.0959	8.0959	1.0015	1	8.0959	8.0959	8.0959	8.0959	8.0959	
MT1E_HUMAN	Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1	SCCSCCPVGCAK	2	7.3272	7.0904	1.4398	1	7.3272	7.3272	7.3272	7.3272	7.0904	
MT1G_HUMAN	Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2	CAQGCICK	1	8.0872	8.0872		2	7.1915	6.893	7.1355	6.8439	6.3291	1.1937
		SCDSCCPVGCAK	2	6.2959	5.599	2.0106							
MT1H_HUMAN	Metallothionein-1H OS=Homo sapiens GN=MT1H PE=1 SV=1	CAQGCICK	2	8.0959	8.0959	1.0015	1	8.0959	8.0959	8.0959	8.0959	8.0959	
MT1M_HUMAN	Metallothionein-1M OS=Homo sapiens GN=MT1M PE=2 SV=2	SCCSCCPVGCAK	2	7.3272	7.0904	1.4398	1	7.3272	7.3272	7.3272	7.3272	7.0904	
MT1X_HUMAN	Metallothionein-1X OS=Homo sapiens GN=MT1X PE=1 SV=1	CAQGCICK	1	8.1046	8.1046		2	6.7921	6.7921	6.664	6.664	6.664	1.3189
		SCCSCCPVGCAK	1	5.4795	5.4795								
MT2_HUMAN	Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1	CAQGCICK	2	8.0959	8.0959	1.0015	2	7.7116	7.7116	7.702	7.702	7.5765	1.0731
		SCCSCCPVGCAK	2	7.3272	7.0904	1.4398							
MUC18_HUMAN	Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2	CLAQGNPPPHFSISK	1	0.308	0.308		4	6.6191	6.6191	3.6509	3.6509	3.6509	5.3606
		EDKDAQFYCELNYR	1	10.7339	10.7339								
		EVTVPVFYPTEK	1	5.3053	5.3053								
		GPVLQLHDLK	1	10.1291	10.1291								
MVP_HUMAN	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	DITPLQVVLPNTALHLK	1	37.4533	37.4533		1	37.4533	37.4533	37.4533	37.4533	37.4533	
MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	TQLEELEDELQATEDAK	1	6.0551	6.0551		1	6.0551	6.0551	6.0551	6.0551	6.0551	
MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	DLGEELEALK	1	4.4979	4.4979		4	5.1765	5.1765	5.0817	5.0817	5.0817	1.2508
		KEEELQAALAR	1	6.2104	6.2104								
		QLLQANPLEAFGNAK	1	3.9427	3.9427								
		TQLEELEDELQATEDAK	1	6.0551	6.0551								
MYH14_HUMAN	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=1	EQADFALEALAK	2	0.1811	0.1524	2.3501	3	3.4447	2.6288	1.6429	0.9466	0.8684	6.8428
		KEEELQAALAR	1	6.2104	6.2104								
		QLLQANPLEAFGNAK	1	3.9427	3.9427								
MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	DLGEELEALK	1	4.4979	4.4979		14	3.6712	3.8802	2.7502	2.6117	2.525	2.6979
		EQADFAIEALAK	2	0.1811	0.1524	2.3501							
		EQEVNILK	1	2.1727	2.1727								
		EQLEEEEEAK	1	1.0337	1.0337								
		IAEFTTNLTEEEEK	3	7.0888	6.6418	1.572							
		KEEELQAALAR	1	6.2104	6.2104								
		KLEEEQIILEDQNCK	1	2.9466	2.9466								
		KLEGSDTDLSDQIAELQAQIAELK	1	5.0622	5.0622								
		LQVELDNVTGLLSQSDSK	1	2.1206	2.1206								
		QIATLHAQVADMK	1	1.8592	1.8592								
		QLLQANPLEAFGNAK	1	3.9427	3.9427								
		TDLLLEPYNK	0										
		TQLEELEDELQATEDAK	1	6.0551	6.0551								
		VISGVLQLGNIVFK	1	4.5542	4.5542								
MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	HVLVTLGEK	1	3.7743	3.7743		2	4.3501	4.3501	4.3118	4.3118	4.3118	1.2072
		VLDFEHFLPMLQTVAK	1	4.9259	4.9259								
MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	ILVDNLCDMEMVNK	1	0.7194	0.7194		1	0.7194	0.7194	0.7194	0.7194	0.7194	
NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	DPVPGYSVPAAEHSTITAWGK	1	3.2027	3.2027		6	2.2167	2.7506	1.3488	1.8077	0.9261	4.4392
		GWNVILEK	1	1.1923	1.1923								
		MWSIENIAFGSGGGLLQK	1	2.577	2.577								
		STQAPLIIRPDSGNPLDTVLK	1	0.0739	0.0739								
		VIQGDGVDINTLQEIVEGMK	3	4.3523	0.7314	27.3486							
		YLLETSGNLDGLEYK	1	1.9021	1.9021								
NBL1_HUMAN	Neuroblastoma suppressor of tumorigenicity 1 OS=Homo sapiens GN=NBL1 PE=1 SV=1	ILHCSCQACGK	1	0.7387	0.7387		1	0.7387	0.7387	0.7387	0.7387	0.7387	
NDK8_HUMAN	Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1	DRPFFPGLVK	1	7.051	7.051		3	4.6626	4.0538	4.3807	3.8347	3.7942	1.5265
		VMLGETNPADSKPGTIR	1	3.7963	3.7963								
		YMNSGPVVAMVWEGLNVVK	3	3.1406	3.0855	1.2659							
NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	GLVGEIIK	2	4.5287	4.2487	1.6664	5	3.7993	3.8922	3.7488	3.8471	3.7671	1.2062
		GLVGEIIKR	1	4.1858	4.1858								
		NIIHGSDSVESAEK	2	3.7201	3.684	1.2186							
		VMLGETNPADSKPGTIR	1	3.7963	3.7963								
		YMHSGPVVAMVWEGLNVVK	1	2.7655	2.7655								
NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	DRPFFPGLVK	1	7.051	7.051		5	4.5405	4.189	4.3699	4.0415	3.9513	1.3504
		GLVGEIIK	2	4.5287	4.2487	1.6664							
		GLVGEIIKR	1	4.1858	4.1858								
		VMLGETNPADSKPGTIR	1	3.7963	3.7963								
		YMNSGPVVAMVWEGLNVVK	3	3.1406	3.0855	1.2659							
NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2	DIEEIIDELK	1	0.7395	0.7395		1	0.7395	0.7395	0.7395	0.7395	0.7395	
NEDD8_HUMAN	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1	EIEIDIEPTDKVER	1	0.2704	0.2704		1	0.2704	0.2704	0.2704	0.2704	0.2704	
NELL1_HUMAN	Protein kinase C-binding protein NELL1 OS=Homo sapiens GN=NELL1 PE=2 SV=3	GIIQDGK	1	0.6039	0.6039		1	0.6039	0.6039	0.6039	0.6039	0.6039	
NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	AELGALPDDFDSLEK	1	5.8565	5.8565		1	5.8565	5.8565	5.8565	5.8565	5.8565	
NFH_HUMAN	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	EYQDLLNVK	4	8.7829	8.7662	1.0732	1	8.7829	8.7829	8.7829	8.7829	8.7662	
NFL_HUMAN	Neurofilament light polypeptide OS=Homo sapiens GN=NEFL PE=1 SV=3	EYQDLLNVK	4	8.7829	8.7662	1.0732	1	8.7829	8.7829	8.7829	8.7829	8.7662	
NFM_HUMAN	Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=2	EYQDLLNVK	4	8.7829	8.7662	1.0732	1	8.7829	8.7829	8.7829	8.7829	8.7662	
NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	EVTDMNLNVINEGGIDK	1	3.0596	3.0596		2	1.6626	1.6626	0.9013	0.9013	0.9013	5.632
		QWIQISDAVYHMVYEQAK	1	0.2655	0.2655								
NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	EDLSPSITQR	1	1.1628	1.1628		5	7.0462	7.0462	2.7239	2.7239	2.7239	4.5571
		GNLYWTDWNR	1	0.6369	0.6369								
		MNSVALDLAISK	1	6.2175	6.2175								
		NIFWTDSNLDR	1	25.9595	25.9595								
		VLFETDLVNPR	1	1.2545	1.2545								
NID2_HUMAN	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=2	EDTSPWLGLAAR	1	0.3952	0.3952		4	0.7907	0.7907	0.7259	0.7259	0.7259	1.6306
		ELYHYSDSTVTSTSSR	1	0.8863	0.8863								
		ETQYVDYDFPTDFPAIAPFLADIDTSHGR	1	1.2444	1.2444								
		GNLYWTDWNR	1	0.6369	0.6369								
NNMT_HUMAN	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	IFCLDGVK	1	1.062	1.062		1	1.062	1.062	1.062	1.062	1.062	
NOTC3_HUMAN	Neurogenic locus notch homolog protein 3 OS=Homo sapiens GN=NOTCH3 PE=1 SV=1	AGLGPQGPR	1	0.8229	0.8229		1	0.8229	0.8229	0.8229	0.8229	0.8229	
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	GIPEFWLTVFK	1	8.2867	8.2867		1	8.2867	8.2867	8.2867	8.2867	8.2867	
NP1L4_HUMAN	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	NVDMLSELVQEYDEPILK	1	4.9211	4.9211		1	4.9211	4.9211	4.9211	4.9211	4.9211	
NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	GPSSVEDIK	1	16.4139	16.4139		2	12.9662	12.9662	12.4994	12.4994	12.4994	1.4701
		MTDQEAIQDLWQWR	1	9.5184	9.5184								
NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	ADEDPIMGFHQMFLLK	1	4.0044	4.0044		1	4.0044	4.0044	4.0044	4.0044	4.0044	
NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	DLELLIQTATR	1	0.2037	0.2037		5	1.5528	1.5528	1.1695	1.1695	1.1695	2.7697
		EFGDTGEGWETVEMHPAYTEEELR	1	1.726	1.726								
		LSQETEALGR	1	1.2639	1.2639								
		LVTLEEFLASTQR	1	1.7384	1.7384								
		MDAEQDPNVQVDHLNLLK	1	2.8322	2.8322								
NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	ALELTGLK	2	11.8473	11.5893	1.347	8	7.0332	6.8574	2.4875	2.4568	2.4168	5.8606
		EVEEDSEDEEMSEDEEDDSSGEEVVIPQKK	1	0.2965	0.2965								
		FGYVDFESAEDLEK	1	3.4396	3.4396								
		GFGFVDFNSEEDAK	1	2.0952	2.0952								
		GIAYIEFK	2	0.4613	0.4344	1.6412							
		GYAFIEFASFEDAK	1	21.1735	21.1735								
		KEDSDEEEDDDSEEDEDEDEDEDEDEDEIEPAAMK	1	0.3573	0.3573								
		TGISDVFAK	1	16.5949	16.5949								
NUDC_HUMAN	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	VEESSWLIEDGK	1	5.158	5.158		1	5.158	5.158	5.158	5.158	5.158	
OLA1_HUMAN	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	IPAFLNVVDIAGLVK	1	3.086	3.086		2	2.2078	2.2078	2.0255	2.0255	2.0255	1.8138
		NYIVEDGDIIFFK	1	1.3295	1.3295								
OSTF1_HUMAN	Osteoclast-stimulating factor 1 OS=Homo sapiens GN=OSTF1 PE=1 SV=2	TGLIPSNYVAEQAESIDNFLHEAAK	1	1.6292	1.6292		1	1.6292	1.6292	1.6292	1.6292	1.6292	
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2	AFGFSHLEALLDDSK	1	4.6947	4.6947		3	4.0272	4.0272	2.3113	2.3113	2.3113	4.8915
		EYAEDDNIYQQK	1	0.3751	0.3751								
		LELSVLYK	1	7.0118	7.0118								
P2RY4_HUMAN	P2Y purinoceptor 4 OS=Homo sapiens GN=P2RY4 PE=1 SV=1	ASTESSLLR	2	0.1514	0.1155	2.9681	1	0.1514	0.1514	0.1514	0.1514	0.1155	
PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	HELLQPFNVLYEK	1	0.9204	0.9204		2	4.5835	5.8045	2.755	3.9705	3.825	4.7139
		SLVEASSQVSVLSLCEK	2	8.2466	7.7975	1.6124							
PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	ALYDTFSAFGNILSCK	2	4.7716	4.702	1.2752	1	4.7716	4.7716	4.7716	4.7716	4.702	
PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	ALYDTFSAFGNILSCK	2	4.7716	4.702	1.2752	1	4.7716	4.7716	4.7716	4.7716	4.702	
PAI1_HUMAN	Plasminogen activator inhibitor 1 OS=Homo sapiens GN=SERPINE1 PE=1 SV=1	DEISTTDAIFVQR	2	2.7863	2.7838	1.0609	17	3.6209	3.6357	3.5483	3.5706	3.4603	1.2397
		ELMGPWNKDEISTTDAIFVQR	2	3.9252	3.9135	1.1151							
		EVPLSALTNILSAQLISHWK	1	3.4565	3.4565								
		FIINDWVK	4	3.2496	2.4786	2.7971							
		FSLETEVDLR	4	4.2429	4.2318	1.087							
		GAVDQLTR	2	3.8431	3.8408	1.0506							
		GMAPALR	1	4.4857	4.4857								

		GMISNLLGK	3	4.4212	4.4081	1.098							
		IEVNESGTVASSSTAVIVSAR	2	2.0046	1.9993	1.108							
		KPLENLGMTDMFR	1	3.1419	3.1419								
		LLVLPK	1	3.695	3.695								
		LVLVNALYFNGQIVK	2	3.0457	2.9706	1.3735							
		LVQGFMPHFFR	1	4.6821	4.6821								
		QFQADFTSLSDQEPLHVAQALQK	3	2.8791	2.8735	1.0799							
		QVDFSEVER	5	4.0787	4.0678	1.0849							
		SDGSTVSVPMMAQTNK	2	3.99	3.971	1.1483							
		VFQQVAQASK	4	3.6279	3.5743	1.2227							
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	EMTLDEWK	1	7.2479	7.2479		1	7.2479	7.2479	7.2479	7.2479	7.2479	
PAL4B_HUMAN	Peptidylprolyl cis-trans isomerase A-like 4B OS=Homo sapiens GN=PPIAL4B PE=1 SV=1	IIPGPMCQGGDFTR	1	17.0747	17.0747		2	21.7914	21.7914	21.2748	21.2748	21.2748	1.3648
		SIYGEK	1	26.5081	26.5081								
PARK7_HUMAN	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	ALVILAK	2	2.6552	2.5331	1.5486	2	3.1709	2.999	3.1287	2.9621	2.8706	1.2612
		GLIAAICAGPTALLAHEIGFGSK	1	3.6866	3.6866								
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	SDAYYCTGDVTAWTK	1	2.0109	2.0109		1	2.0109	2.0109	2.0109	2.0109	2.0109	
PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	IITLTGPTNAIFK	2	0.7018	0.5876	2.3826	1	0.7018	0.7018	0.7018	0.7018	0.5876	
PCD12_HUMAN	Protocadherin-12 OS=Homo sapiens GN=PCDH12 PE=2 SV=1	YTLTLLAQDGGLQPLSAK	1	1.0385	1.0385		1	1.0385	1.0385	1.0385	1.0385	1.0385	
PCNA_HUMAN	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	AEDNADTLALVFEAPNQEK	1	4.5439	4.5439		3	3.2172	3.2172	2.9224	2.9224	2.9224	1.7651
		DLSHIGDAVVVSCAK	1	3.5683	3.5683								
		NLAMGVNLTSMSK	1	1.5393	1.5393								
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 OS=Homo sapiens GN=PCOLCE PE=1 SV=2	ATSGTEHQFCGGR	1	0.4493	0.4493		8	0.6129	0.6192	0.4002	0.3977	0.3886	3.0275
		EPGEGLAVTVSLIGAYK	1	0.7788	0.7788								
		FDLEPDTYCR	1	1.0848	1.0848								
		GESGYVASEGFPNLYPPNK	2	1.2027	1.1944	1.1817							
		GFLLWYSGR	1	0.0945	0.0945								
		TEESPSAPDAPTCPK	2	1.0501	1.0476	1.1036							
		YDALEVFAGSGTSGQR	3	0.1372	0.1258	1.6671							
		YDSVSVFNGAVSDDSR	1	0.1059	0.1059								
PDC6I_HUMAN	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	LANQAADYFGDAFK	1	1.7181	1.7181		2	2.5038	2.5038	2.3773	2.3773	2.3773	1.5829
		SVIEQGGIQTVDQLIK	1	3.2895	3.2895								
PDCD6_HUMAN	Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	AGVNFSEFTGVWK	1	12.143	12.143		1	12.143	12.143	12.143	12.143	12.143	
PDE8B_HUMAN	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B OS=Homo sapiens GN=PDE8B PE=1 SV=2	TLDDLK	1	0.7175	0.7175		1	0.7175	0.7175	0.7175	0.7175	0.7175	
PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	EADDVVNLK	1	5.7232	5.7232		2	3.7561	3.1003	3.1997	2.6359	2.6327	2.2758
		ENLLDFIK	2	1.7889	1.7856	1.0903							
PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	DASIVGFFDDSFSEAHSEFLK	1	2.1358	2.1358		2	2.4728	2.4728	2.4497	2.4497	2.4497	1.214
		GFPTIYFSPANK	1	2.8097	2.8097								
PDLI5_HUMAN	PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=4	DFNMPLTISSLK	1	3.782	3.782		3	2.1432	2.1432	1.3769	1.3769	1.3769	3.8975
		IGDVVLSIDGINAQGMTHLEAQNK	1	2.3543	2.3543								
		NTMAYIGFVEEK	1	0.2932	0.2932								
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	APVAGTCYQAEWDDYVPK	1	6.2802	6.2802		3	4.5866	4.5866	3.5876	3.5876	3.5876	2.6503
		LYEQLSGK	1	6.3155	6.3155								
		NRPTSISWDGLDSGK	1	1.1642	1.1642								
PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=3	ALYYDLISSPDIHGTYK	1	0.5052	0.5052		9	0.7342	0.7431	0.6813	0.6913	0.6564	1.5151
		DTDTGALLFIGK	2	1.2456	1.2007	1.4702							
		EIPDEISILLLGVAHFK	1	0.6794	0.6794								
		ELLDTVTAPQK	1	0.3906	0.3906								
		LAAVSNFGYDLYR	2	0.3841	0.3082	2.646							
		LDLQEINNWVQAQMK	1	1.0837	1.0837								
		LQSLFDSPDFSK	4	0.7222	0.6848	1.4476							
		TSLEDFYLDEER	1	0.7112	0.7112								
		YGLDSLSCK	1	0.8855	0.8855								
PERI_HUMAN	Periherin OS=Homo sapiens GN=PRPH PE=1 SV=2	KLLEGEESR	1	9.0346	9.0346		4	12.4628	10.188	8.8371	7.2004	3.6866	2.6772
		LEEETRK	1	29.5398	29.5398								
		LLEGEESR	2	8.6285	8.5173	1.2564							
		MALDIEIATYR	2	2.6484	0.3601	44.4945							
PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	ALPFWNEEIVPQIK	2	11.0539	11.0488	1.0439	2	10.5362	10.5362	10.5234	10.5234	10.0471	1.072
		YADLTEDQLPSCESLK	2	10.0184	9.1362	1.8526							
PGAM2_HUMAN	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	ALPFWNEEIVPQIK	2	11.0539	11.0488	1.0439	1	11.0539	11.0539	11.0539	11.0539	11.0488	
PGAM4_HUMAN	Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=1 SV=1	ALPFWNEEIVPQIK	1	11.3897	11.3897		1	11.3897	11.3897	11.3897	11.3897	11.3897	
PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3	AAGVPSATITWR	1	2.2873	2.2873		27	7.8571	8.7173	5.7873	6.8294	5.8807	2.6419
		AGFFGDAMK	1	3.5853	3.5853								
		AMDFNGILTIR	1	1.8824	1.8824								
		CSATGSPAPTIHWSK	1	4.4329	4.4329								
		ESDQGAYTCEAMNAR	1	17.7146	17.7146								
		EVSEAVVDTLESEYLK	4	10.4583	8.7145	2.0779							
		FDQPDDFK	3	13.0035	9.299	2.8072							
		FSSGITGCVK	2	8.3831	8.3819	1.0238							
		GCVGEVSVNGIK	1	4.3609	4.3609								
		GPSCQDCDTGYTR	1	12.6469	12.6469								
		LDVEFKPLAPDGVLLFSGGK	2	17.1538	15.7643	1.8031							
		LEGDTLIPR	3	12.6392	3.6208	17.4503							
		LHHVSPADSGEYVCR	1	6.7624	6.7624								
		LHQMSVADSGEYVCR	1	8.8448	8.8448								
		LLSGPYFWSLPSR	1	0.1973	0.1973								
		LYQASPADSGEYVCR	1	11.9022	11.9022								
		QPQAIITWYK	1	6.1361	6.1361								
		SGPVEDPVSLAMVGGHLEFR	1	5.199	5.199								
		SIGASVEFHCAVPSDR	1	17.7677	17.7677								
		SIVPQGGSHSLR	1	8.28	8.28								
		SPAYTLVWTR	2	5.0738	5.0133	1.245							
		SPVSIDPPSSTVQQGDASFK	2	5.8433	5.8316	1.0934							
		SQSVRPGADVTFICTAK	1	12.8316	12.8316								
		TDEANCPTK	1	4.6902	4.6902								
		TSTASGLLLWQGVEVGEAGQGK	1	6.3872	6.3872								
		VAEGQTLDLK	1	1.3181	1.3181								
		VTSYGGELR	1	2.36	2.36								
PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	ALMDEVVK	3	3.8884	2.5844	2.9154	8	5.1711	4.9145	4.7828	4.5888	4.0595	1.5239
		DCVGPEVEK	1	2.5384	2.5384								
		FHVEEEGK	1	3.9521	3.9521								
		GCITIIGGGDTATCCAK	1	9.5894	9.5894								
		ITLPVDFVTADK	1	5.8651	5.8651								
		ITLPVDFVTADKFDENAK	1	3.3771	3.3771								
		TGQATVASGIPAGWMGLDCGPESSKK	1	6.0923	6.0923								
		VLNNMEIGTSLFDEEGAK	1	0.6658	0.6658								
PGK2_HUMAN	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3	FHVEEEGK	1	3.9521	3.9521		1	3.9521	3.9521	3.9521	3.9521	3.9521	
PGS1_HUMAN	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	EISPDTTLLDLQNNDISELRK	1	3.9221	3.9221		4	4.9344	5.6072	3.4712	4.1322	4.0478	3.1956
		ELHLDNNK	1	0.6495	0.6495								
		IQAIELEDLLR	2	8.2982	7.8809	1.5812							
		VGVNDFCPMGFGVK	1	6.8679	6.8679								
PGS2_HUMAN	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	AHENEITK	1	0.7286	0.7286		12	0.6995	0.6293	0.5114	0.4774	0.4396	2.398
		ASYSGVSLFSNPVQYWEIQPSTFR	1	0.1117	0.1117								
		DFEPSLGPVCPFR	2	0.1091	0.1088	1.0945							
		DLPPDTTLLDLQNNK	2	0.6237	0.6147	1.2725							
		ELHLDNNK	1	0.6495	0.6495								
		GLNNLAK	3	0.5064	0.4029	2.5205							
		NLHALILVNNK	1	2.298	2.298								
		SSGIENGAFQGMK	3	0.3654	0.3605	1.2274							
		VSPGAFTPLVK	2	0.3791	0.3784	1.0834							
		VTFNGLNQMIVIELGTNPLK	1	0.6667	0.6667								
		VVQCSDLGLDK	2	1.3363	0.8583	4.1815							
		VVQCSDLGLDKVPK	1	0.6203	0.6203								
PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	AKYPDYEVTWANDGY	1	12.9724	12.9724		1	12.9724	12.9724	12.9724	12.9724	12.9724	
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=3	VIGIDHIK	1	2.3878	2.3878		1	2.3878	2.3878	2.3878	2.3878	2.3878	
PIN_HUMAN	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1	NLDPFLLFDEFK	1	6.981	6.981		1	6.981	6.981	6.981	6.981	6.981	
PLBL2_HUMAN	Putative phospholipase B-like 2 OS=Homo sapiens GN=PLBD2 PE=1 SV=2	VLTHLEQPGMVVVADK	1	0.9514	0.9514		1	0.9514	0.9514	0.9514	0.9514	0.9514	
PLEC1_HUMAN	Plectin-1 OS=Homo sapiens GN=PLEC1 PE=1 SV=3	DYELQLVTYK	1	23.7055	23.7055		2	12.0892	12.0892	3.3482	3.3482	3.3482	15.9271
		TLLQGSGCLAGIYLEDTK	1	0.4729	0.4729								
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	IFQNLDGALDEVVLK	1	1.3135	1.3135		1	1.3135	1.3135	1.3135	1.3135	1.3135	
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	IFQNLNGALDEVVLK	1	1.1235	1.1235		1	1.1235	1.1235	1.1235	1.1235	1.1235	
PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5	LNNAKYAISMAR	2	2.0249	1.7977	2.0214	1	2.0249	2.0249	2.0249	2.0249	1.7977	
PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	AESMLQQADK	1	6.519	6.519		8	7.3626	7.3238	5.0494	5.416	5.0738	3.6374
		DGETLEELMK	1	7.2126	7.2126								
		EGICALGGTSELSSEGTQHSYSEEEK	1	5.1447	5.1447								
		IDINMSGFNETDDLKR	1	6.402	6.402								
		LNLAFVANLFNK	1	15.9795	15.9795								
		VVALPEDLVEVKPK	1	10.2419	10.2419								
		YPALTKPENQDIDWTTLEGETR	1	0.2326	0.2326								
		YTLNVLEDLGDGGK	3	7.1686	5.7668	2.4679							
PLTP_HUMAN	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	ATYFGSVLLSPWVDSPLK	1	1.3304	1.3304		7	1.1383	1.072	0.9635	0.9096	0.8439	1.9524
		GAFFPLTER	1	1.0413	1.0413								
		GLREVIEK	1	0.994	0.994								
		SSVDELVGIDYSLMK	1	1.3579	1.3579								
		TGLELSR	1	0.2888	0.2888								
		TMLQIGVMPMLNER	1	2.3477	2.3477								
		VYDFLSTFITSGMR	2	0.6079	0.4505	3.1579							
PNPH_HUMAN	Purine nucleoside phosphorylase OS=Homo sapiens GN=NP PE=1 SV=2	HRPQVAWCSSCLGGLTDK	2	0.4231	0.4231		2	1.7872	1.7872	1.1547	1.1547	1.1547	4.1365
		VFGFSLITNK	1	3.1513	3.1513								
POSTN_HUMAN	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	AAAITSDILEALGR	1	2.2972	2.2972		13	1.9913	1.7551	1.1017	1.0201	0.9415	3.2061
		DIVTNNGVIHLIDQVLIPDSAK	1	1.052	1.052								
		EGETITEVIHGEPIIK	1	1.2367	1.2367								
		ELLTQPGDWTLFVPTNDAFK	1	0.5932	0.5932								
		FSTFLSLLEAADLK	1	1.1365	1.1365								
		GFEPGVTNILK	1	7.1877	7.1877								
		GSFTYFAPSNEAWDNLDSDIR	1	0.1231	0.1231								
		LLYPADTPVGNDQLLEILNK	3	0.7114	0.6714	1.5332							
		NALQNILYHLTPGVFIGK	1	3.2369	3.2369								
		QVIELAGK	1	6.6502	6.6502								
		TTVLYECCPGYMR	1	0.2688	0.2688								
		VGLNELYNGQILETIGGK	1	0.6226	0.6226								
		VLTQIGTSIQDFIEAEDDLSSFR	2	0.771	0.4429	5.1025							
POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	AGFAGDDAPR	3	7.7571	7.7529	1.0413	5	5.5406	5.7353	5.1795	5.3518	4.8825	1.5514
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572							
		GILTLK	5	6.7833	6.6869	1.2097							
		LCYVALDFEQEMATAASSSSLEK	3	2.5155	1.7899	3.2664							
		QEYDESGPSIVHR	2	4.9003	4.8987	1.0365							
POTEF_HUMAN	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	AGFAGDDAPR	3	7.7571	7.7529	1.0413	4	6.2969	6.5402	6.2044	6.4635	6.2747	1.2208
		AVFPSIVGRPR	2	5.7471	4.9912	2.1572							
		GILTLK	5	6.7833	6.6869	1.2097							
		QEYDESGPSIVHR	2	4.9003	4.8987	1.0365							
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	3.8849	3.8849		1	3.8849	3.8849	3.8849	3.8849	3.8849	
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	TFTDCFNCLPIAAIVDEK	1	3.8849	3.8849		1	3.8849	3.8849	3.8849	3.8849	3.8849	
PP1G_HUMAN	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1	TFTDCFNCLPIAAIVDEK	1	3.8849	3.8849		1	3.8849	3.8849	3.8849	3.8849	3.8849	
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	EGMNIVEAMER	4	4.2026	0.4979	11.4237	11	12.7141	12.8035	10.14	10.411	6.7794	2.1349
		FEDENFILK	3	18.3682	18.2716	1.1353							
		HTGPGILSMANAGPNTNGSQFFICTAK	1	4.7811	4.7811								
		IIPGPMCQGGDFTR	1	17.0747	17.0747								
		KITADCGQLE	2	19.5871	19.5844	1.0236							
		SIYGEK	1	26.5081	26.5081								
		SIYGEKFEDENFILK	1	5.2985	5.2985								
		TEWLDGK	1	8.9487	8.9487								
		VKEGMNIVEAMER	1	2.9019	2.9019								
		VNPTVFFDIAVDGEPLGR	1	16.4223	16.4223								

		VSFELFADK	4	15.7614	15.6394	1.1576							
PPM1F_HUMAN	Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=1 SV=3	AIGDVFQKPYVSGEADAASR	1	0.6968	0.6968		1	0.6968	0.6968	0.6968	0.6968	0.6968	
PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GLFIIDDK	4	7.7939	7.6596	1.2375	3	8.1601	7.9834	8.033	7.8673	7.4364	1.2409
		LVQAFQFTDK	3	10.1038	9.6915	1.4441							
		TIAQDYGVLK	4	6.5825	5.919	1.7239							
PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	KEGGLGPLNIPLLADVTR	1	8.5599	8.5599		1	8.5599	8.5599	8.5599	8.5599	8.5599	
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	GLFIIDPNGVIK	2	5.2759	5.2006	1.2718	1	5.2759	5.2759	5.2759	5.2759	5.2006	
PRDX4_HUMAN	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	GLFIIDDK	4	7.7939	7.6596	1.2375	1	7.7939	7.7939	7.7939	7.7939	7.6596	
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=3	GVLFGVPGAFTPGCSK	1	3.797	3.797		2	7.3689	7.3689	6.4453	6.4453	6.4453	2.1135
		VNLAELFPK	1	10.9408	10.9408								
PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	DINAYNCEEPTEK	1	3.2562	3.2562		5	1.6214	1.6214	0.8862	0.8862	0.8862	5.2371
		ELAILLGMLDPAEKDEK	1	0.0524	0.0524								
		LIALSIDSVEDHLAWSK	1	0.8984	0.8984								
		VVFVFGPDKK	1	2.4362	2.4362								
		VVISLQLTAEK	1	1.464	1.464								
PRELP_HUMAN	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	NLMQLNLAHNILR	1	3.2161	3.2161		1	3.2161	3.2161	3.2161	3.2161	3.2161	
PREP_HUMAN	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=2	LLPDHTYSVVSGGDPLCIPELTWEQLK	1	0.3999	0.3999		1	0.3999	0.3999	0.3999	0.3999	0.3999	
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	DSLLGDGEFSMDLR	1	6.5164	6.5164		7	8.8259	9.0532	8.5872	8.8882	8.5126	1.2761
		DSPSVWAAVPGK	2	13.8069	13.806	1.0166							
		EGVHGGLINK	1	7.1973	7.1973								
		SSFYVNGLTLGGQK	3	7.952	7.6084	1.4577							
		STGGAPTFNVTVTK	2	8.0398	7.8325	1.3835							
		TFVNITPAEVGVLVGK	5	8.6184	8.1972	1.4387							
		TLVLLMGK	4	9.6504	8.8604	1.679							
PRS10_HUMAN	26S protease regulatory subunit S10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	ALQSVGQIVGEVLK	1	3.0539	3.0539		1	3.0539	3.0539	3.0539	3.0539	3.0539	
PRS23_HUMAN	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1	DFLLNYPFSTSVK	1	0.0835	0.0835		2	2.4485	2.4485	0.634	0.634	0.634	17.5815
		FCDVKDETYDLLYQGCDAQPGASGSGVYVR	1	4.8135	4.8135								
PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	ATFDSLVVPK	1	0.9455	0.9455		2	0.6251	0.6251	0.5367	0.5367	0.5367	2.2277
		TIQQCCENILLNAAWLK	1	0.3046	0.3046								
PSA2_HUMAN	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GYSFSLTTFSPSGK	1	5.4847	5.4847		2	5.2308	5.2308	5.2246	5.2246	5.2246	1.0711
		YNEDLELEDAIHTAILTLK	1	4.9768	4.9768								
PSA3_HUMAN	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	ESLKEEDESDDDNM	1	19.5273	19.5273		1	19.5273	19.5273	19.5273	19.5273	19.5273	
PSA4_HUMAN	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	LLDEVFFSEK	1	11.6321	11.6321		1	11.6321	11.6321	11.6321	11.6321	11.6321	
PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	LFQVEYAIEAIK	1	4.2397	4.2397		2	4.4272	4.4272	4.4232	4.4232	4.4232	1.0618
		SSLIILK	1	4.6147	4.6147								
PSA6_HUMAN	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	CDPAGYYCGFK	1	2.2021	2.2021		3	4.3939	4.3939	3.3548	3.3548	3.3548	2.38
		LLDSSTVTHLFK	1	1.8854	1.8854								
		YGYEIPVDMLCK	1	9.0942	9.0942								
PSA7_HUMAN	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	LYQTDPSGTYHAWK	1	3.0212	3.0212		1	3.0212	3.0212	3.0212	3.0212	3.0212	
PSA7L_HUMAN	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	LYQTDPSGTYHAWK	1	3.0212	3.0212		1	3.0212	3.0212	3.0212	3.0212	3.0212	
PSAL_HUMAN	Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens GN=NPEPPSL1 PE=2 SV=3	ATFDSLVVPK	1	0.9455	0.9455		1	0.9455	0.9455	0.9455	0.9455	0.9455	
PSB3_HUMAN	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	DAVSGMGVIVHIIEK	1	5.6072	5.6072		2	3.1991	3.1991	2.106	2.106	2.106	3.9943
		LNLYELK	1	0.791	0.791								
PSB7_HUMAN	Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	ATEGMVVADK	1	3.7969	3.7969		2	4.9932	4.9932	4.8478	4.8478	4.8478	1.4128
		GTTAVLTEK	1	6.1895	6.1895								
PSG4_HUMAN	Pregnancy-specific beta-1-glycoprotein 4 OS=Homo sapiens GN=PSG4 PE=2 SV=2	SGENLYLSCFAESNPR	1	0.0062	0.0062		1	0.0062	0.0062	0.0062	0.0062	0.0062	
PSME1_HUMAN	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	IEDGNNFGVAVQEK	1	0.6404	0.6404		3	2.0657	2.0657	1.7014	1.7014	1.7014	2.3359
		ISELDAFLK	1	2.6084	2.6084								
		TENLLGSYFPK	1	2.9483	2.9483								
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	NNQFQALLQYADPVSAQHAK	1	3.727	3.727		2	4.0117	4.0117	4.0015	4.0015	4.0015	1.1057
		VTNLLMLK	1	4.2963	4.2963								
PTBP2_HUMAN	Polypyrimidine tract-binding protein 2 OS=Homo sapiens GN=PTBP2 PE=1 SV=1	VTNLMLK	1	4.2963	4.2963		1	4.2963	4.2963	4.2963	4.2963	4.2963	
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1	TMLLQPAGSLGSYSYR	2	0.7362	0.5671	2.905	1	0.7362	0.7362	0.7362	0.7362	0.5671	
PTMA_HUMAN	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2	EVVEEAENGR	1	6.7531	6.7531		1	6.7531	6.7531	6.7531	6.7531	6.7531	
PTRF_HUMAN	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	SDQVNGVLVLSLLDK	3	5.3205	5.3021	1.1062	1	5.3205	5.3205	5.3205	5.3205	5.3021	
PTX3_HUMAN	Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=2	ALAAVLEELR	1	6.7246	6.7246		4	3.5189	3.5189	1.9361	1.9361	1.9361	4.2209
		LTGFNIWDSVLSNEEIR	1	5.9982	5.9982								
		MLLQATDDVLR	1	0.3461	0.3461								
		TILFSYGTK	1	1.0065	1.0065								
PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	GYGFIEYEK	1	1.1457	1.1457		1	1.1457	1.1457	1.1457	1.1457	1.1457	
PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	ITSCIFQLLQEAGIK	1	3.0354	3.0354		1	3.0354	3.0354	3.0354	3.0354	3.0354	
PURA2_HUMAN	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	LDILDMFTEIK	1	5.5056	5.5056		1	5.5056	5.5056	5.5056	5.5056	5.5056	
PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	DAC7ICECK	1	1.4446	1.4446		6	1.3826	1.3826	1.3463	1.3463	1.3463	1.2834
		LGPTLMCLLSTQFK	1	1.0008	1.0008								
		LNPHWDGDTIYYETR	1	1.2259	1.2259								
		LWYENPGVFSPAQLTQIK	1	1.1061	1.1061								
		SPNDLLALFR	1	1.9993	1.9993								
		VAEFPHGYGSCDEIPR	1	1.5191	1.5191								
QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	EVNYIDK	1	0.1454	0.1454		1	0.1454	0.1454	0.1454	0.1454	0.1454	
QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	AWRPALVLAALDCAEETNSAVCR	1	0.8835	0.8835		14	0.6247	0.6126	0.5027	0.489	0.468	1.9632
		DVQNVAAAPELAMGALELESR	1	0.8366	0.8366								
		ELCSACHNER	1	0.41	0.41								
		EVALDLSQHK	1	0.401	0.401								
		FGVTDFPSCVLLFR	1	1.031	1.031								
		GGSYLGR	1	0.2286	0.2286								
		LAGAPSEDPQFPK	1	0.156	0.156								
		LDVSWDVEATLNFLK	3	0.5819	0.5737	1.2266							
		LEEIDGFFAR	1	0.3132	0.3132								
		NGSGAVFPVAGADVQTLR	1	0.4569	0.4569								
		NNEEYLALIFEK	4	0.2815	0.2786	1.1804							
		SALYSPSDPLTLLQADTVR	3	0.3889	0.3868	1.1373							
		SFYTAYLQR	2	1.945	1.2617	4.1053							
		VGSPNAAVLWLWSSHNR	1	0.831	0.831								
RAL2_HUMAN	Heterogeneous nuclear ribonucleoprotein A1-like protein 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	DYFEQYGK	3	20.1589	14.0508	2.9801	1	20.1589	20.1589	20.1589	20.1589	14.0508	
RA1L3_HUMAN	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3 OS=Homo sapiens GN=HNRPA1L3 PE=5 SV=1	DYFEQYGK	1	41.5036	41.5036		1	41.5036	41.5036	41.5036	41.5036	41.5036	
RAB28_HUMAN	Ras-related protein Rab-28 OS=Homo sapiens GN=RAB28 PE=1 SV=2	IVVLGDGASGK	1	4.6187	4.6187		1	4.6187	4.6187	4.6187	4.6187	4.6187	
RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	LVFLGEQSVGK	1	1.2956	1.2956		1	1.2956	1.2956	1.2956	1.2956	1.2956	
RAB6B_HUMAN	Ras-related protein Rab-6B OS=Homo sapiens GN=RAB6B PE=1 SV=1	LVFLGEQSVGK	1	2.2956	1.2956		1	1.2956	1.2956	1.2956	1.2956	1.2956	
RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	ATIGADFLTK	1	2.7477	2.7477		3	3.0798	3.0798	3.0691	3.0691	3.0691	1.1082
		DPENFPFVVLGNK	1	3.3663	3.3663								
		GADCVLVFDVTAPNTFK	1	3.1253	3.1253								
RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1	EDSMMEYLK	1	12.8302	12.8302		4	7.5886	7.0637	5.6448	5.5017	5.4297	2.7326
		LFFLQVK	1	11.127	11.127								
		QLFDQVVK	2	4.9645	4.8036	1.4404							
		VLEQHK	1	1.4326	1.4326								
RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	HLTGEFEK	1	3.1353	3.1353		3	4.9532	5.4913	4.686	5.2	5.1339	1.5057
		LVLVGDGGTGK	1	4.6187	4.6187								
		NLQYYDISAK	2	7.1056	6.9263	1.3786							
RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	TLEEDEEELFK	1	9.8891	9.8891		1	9.8891	9.8891	9.8891	9.8891	9.8891	
RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	GAVGALLVYDIAK	1	6.3381	6.3381		1	6.3381	6.3381	6.3381	6.3381	6.3381	
RBBP4_HUMAN	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	TPSSDVLVFDYTK	1	7.5171	7.5171		1	7.5171	7.5171	7.5171	7.5171	7.5171	
RBBP7_HUMAN	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	TPSSDVLVFDYTK	1	7.5171	7.5171		1	7.5171	7.5171	7.5171	7.5171	7.5171	
RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	TCLLIVFSK	1	5.3207	5.3207		1	5.3207	5.3207	5.3207	5.3207	5.3207	
RHOB_HUMAN	Rho-related GTP-binding protein RhoB OS=Homo sapiens GN=RHOB PE=1 SV=1	TCLLIVFSK	1	5.3207	5.3207		1	5.3207	5.3207	5.3207	5.3207	5.3207	
RHOC_HUMAN	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	TCLLIVFSK	1	5.3207	5.3207		1	5.3207	5.3207	5.3207	5.3207	5.3207	
RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	AVDIPHMDIEALK	1	6.9564	6.9564		2	5.161	4.2633	4.8386	4.0354	1.4127	1.671
		FSVCVLGDQQHCDEAK	3	3.3655	0.8304	8.5687							
RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	CTGGEVGATSALAPK	1	8.3687	8.3687		2	4.675	4.675	2.8655	2.8655	2.8655	4.5525
		IGPLGLSPK	1	0.9812	0.9812								
RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	AVVLMGK	1	0.0264	0.0264		5	6.126	6.0224	2.3416	3.5203	1.9713	12.5561
		GHLENNPALEK	1	12.6062	12.6062								
		GTIEILSDVQLIK	1	5.4652	5.4652								
		IIQLLDDYPK	4	5.5195	4.5267	2.0591							
		TSFFQALGITTK	2	7.0129	0.7673	60.6536							
RLA0L_HUMAN	60S acidic ribosomal protein P0-like OS=Homo sapiens GN=RPLP0 PE=2 SV=1	GHLENNPALEK	1	12.6062	12.6062		4	7.651	6.7719	7.1862	6.4893	3.3799	1.48
		GTIEILSDVQLIK	1	5.4652	5.4652								
		IIQLLDDYPK	4	5.5195	4.5267	2.0591							
		TSFFQALGITTK	2	7.0129	0.7673	60.6536							
RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	AAGVNVEPFWPGLFAK	2	18.9845	18.944	1.0969	2	22.3141	21.2042	22.0643	20.9858	20.956	1.2369
		KEESEESDDDMGFGLFD	1	25.6438	25.6438								
RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	KEESEESDDDMGFGLFD	2	26.9751	26.9422	1.0723	3	16.2027	19.0706	10.5046	15.087	14.9964	3.8919
		NIEDVIAQGIGK	3	19.4202	19.2033	1.2053							
		YVASYLLAALGGNSSPSAK	1	2.2127	2.2127								
RMP_HUMAN	Unconventional prefoldin RPB5 interactor OS=Homo sapiens GN=RMP PE=1 SV=3	TIDDLK	1	0.7175	0.7175		1	0.7175	0.7175	0.7175	0.7175	0.7175	
RMXL3_HUMAN	RNA-binding motif protein, X-linked-like-3 OS=Homo sapiens GN=RBMXL3 PE=2 SV=2	GFAFVTFESPADAK	1	4.7641	4.7641		1	4.7641	4.7641	4.7641	4.7641	4.7641	
RNBP6_HUMAN	Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2	FMQDASNVMQLLLK	1	0.0919	0.0919		1	0.0919	0.0919	0.0919	0.0919	0.0919	
RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2	MTANSVLEPGNSEVSLVCEK	1	3.3785	3.3785		1	3.3785	3.3785	3.3785	3.3785	3.3785	
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=4	DYFEQYGK	2	23.089	13.9285	4.6837	3	13.0754	15.5788	11.1445	13.3705	10.3848	2.0016
		GFAFVTFDDHDSVDK	1	5.7986	5.7986								
		LFIGGLSFETTDESLR	1	10.3385	10.3385								
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	DYFEEYGK	1	15.8603	15.8603		3	9.1182	9.1182	7.9371	7.9371	7.9371	1.8917
		GFGFVTFDDHDPVDK	1	4.5213	4.5213								
		IDTIEIITDR	1	6.9729	6.9729								
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2	GFGFILFK	1	8.6403	8.6403		1	8.6403	8.6403	8.6403	8.6403	8.6403	
ROD1_HUMAN	Regulator of differentiation 1 OS=Homo sapiens GN=ROD1 PE=1 SV=2	VTNLLMLK	1	4.2963	4.2963		1	4.2963	4.2963	4.2963	4.2963	4.2963	
RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	DVIEEYFK	1	23.4548	23.4548		3	13.1267	13.1267	11.4131	11.4131	11.4131	1.8665
		KVVGCSCVVVK	1	7.8189	7.8189								
		LVEALCAEHQINLIK	1	8.1064	8.1064								
RS20_HUMAN	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	LIDLHSPSEIVK	1	0.9087	0.9087		1	0.9087	0.9087	0.9087	0.9087	0.9087	
RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	DIASIQMMVAEVDK	1	6.3692	6.3692		1	6.3692	6.3692	6.3692	6.3692	6.3692	
RS25_HUMAN	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	AALQELLSK	1	0.1761	0.1761		1	0.1761	0.1761	0.1761	0.1761	0.1761	
RSU1_HUMAN	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3	DNDLISLPK	1	2.8805	2.8805		1	2.8805	2.8805	2.8805	2.8805	2.8805	
S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	CIESLIAVFQK	3	3.8294	2.9436	2.7583	3	3.6302	3.4651	3.6056	3.4407	3.0871	1.1556
		DGYNYTLSK	1	4.004	4.004								
		TEFLSFMNTELAAFTK	4	3.0571	2.998	1.2667							
S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1	DVGSLDEK	1	8.4785	8.4785		1	8.4785	8.4785	8.4785	8.4785	8.4785	
SAE1_HUMAN	SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1	EALEVDWSSEK	1	0.872	0.872		1	0.872	0.872	0.872	0.872	0.872	
SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	GISEETTTGVHNLYK	1	3.7966	3.7966		2	2.5522	2.5522	2.2282	2.2282	2.2282	2.1248
		VAVVAGYGDVGK	1	1.3077	1.3077								
SAP_HUMAN	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	DGGFCEVCK	2	7.3513	6.9674	1.5958	9	11.1141	13.1456	9.3621	11.5673	10.4515	1.9634
		DVVTAAGDMLK	1	2.309	2.309								
		EILDAFDK	3	21.1059	21.0705	1.0732							
		EIVDSYLPVILDIIK	6	17.0417	15.5673	1.6518							
		GCSFLPDPYQK	2	9.5627	9.4062	1.2937							
		LGPGMADICK	3	6.9222	4.2877	3.9373							
		QEILAALEK	2	17.8528	17.8083	1.1051							
		SDVYCVCEFLVK	1	10.7709	10.7709								
		SLPCDICK	1	7.1102	7.1102								
SENP7_HUMAN	Sentrin-specific protease 7 OS=Homo sapiens GN=SENP7 PE=1 SV=3	TIDNDLR	1	2.1282	2.1282		1	2.1282	2.1282	2.1282	2.1282	2.1282	
SEPT11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3	STLMDTLFNTK	1	2.8012	2.8012		1	2.8012	2.8012	2.8012	2.8012	2.8012	
SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	LYPWGVVEVENPEHNDFLK	1	1.4173	1.4173		1	1.4173	1.4173	1.4173	1.4173	1.4173	
SEPT6_HUMAN	Septin-6 OS=Homo sapiens GN=SEPT6 PE=1 SV=4	STLMDTLFNTK	1	2.8012	2.8012		1	2.8012	2.8012	2.8012	2.8012	2.8012	
SET_HUMAN	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	EFHLNESGDPSSK	1	6.0149	6.0149		2	6.8699	6.8699	6.8164	6.8164	6.8164	1.1935
		IDFYFDENPYFENK	1	7.7248	7.7248								
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1 OS=Homo sapiens GN=SFRS1 PE=1 SV=2	DIEDVFYK	1	4.0015	4.0015		1	4.0015	4.0015	4.0015	4.0015	4.0015	
SH3BG_HUMAN		QQEVVGFLEANK	1	6.3357	6.3357		1	6.3357	6.3357	6.3357	6.3357	6.3357	
SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL PE=1 SV=1	QQDVLGFLEANK	1	6.3357	6.3357		1	6.3357	6.3357	6.3357	6.3357	6.3357	
SKP1_HUMAN	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	RTDDIPVWDQEFLK	1	1.7445	1.7445		1	1.7445	1.7445	1.7445	1.7445	1.7445	

SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	LSHETVTIELK	1	1.3507	1.3507		1	1.3507	1.3507	1.3507	1.3507	1.3507	
SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	GDGPVQGIINFEQK	3	6.6142	6.6063	1.0619	1	6.6142	6.6142	6.6142	6.6142	6.6063	
SOX30_HUMAN	Transcription factor SOX-30 OS=Homo sapiens GN=SOX30 PE=1 SV=1	TLAAVETGPR	2	23.1982	18.1964	2.7897	1	23.1982	23.1982	23.1982	23.1982	18.1964	
SPB6_HUMAN	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	ADFSGMSQTDLSLSK	1	0.7562	0.7562		2	2.4755	2.4755	1.781	1.781	1.781	3.3584
		NLGMTDAFELGK	1	4.1947	4.1947								
SPB8_HUMAN	Serpin B8 OS=Homo sapiens GN=SERPINB8 PE=1 SV=2	LVLVNAIYFK	1	6.31	6.31		1	6.31	6.31	6.31	6.31	6.31	
SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1	AFQSLTEVNK	1	6.8898	6.8898		3	4.4671	4.4671	2.0614	2.0614	2.0614	7.4955
		LVLVNAIYFK	1	6.31	6.31								
		STEVEVLLPK	1	0.2015	0.2015								
SPI2_HUMAN	Serpin I2 OS=Homo sapiens GN=SERPINI2 PE=2 SV=1	LVLVNAIYFK	1	6.31	6.31		1	6.31	6.31	6.31	6.31	6.31	
SPON2_HUMAN	Spondin-2 OS=Homo sapiens GN=SPON2 PE=1 SV=2	AFPPAPVLPSR	1	0.1982	0.1982		3	0.5227	0.5589	0.4401	0.5077	0.4779	2.1214
		GEAWALMK	2	0.8829	0.872	1.2494							
		IVPSPDWFVGVDSLDLCDGDR	4	0.4871	0.4409	1.7139							
SPRC_HUMAN	SPARC OS=Homo sapiens GN=SPARC PE=1 SV=1	DEDNNLLTEK	1	3.9885	3.9885		9	3.1987	3.1345	3.1577	3.1002	3.0922	1.1867
		DIDKDLVI	2	3.713	3.7071	1.083							
		FFETCDLDNDK	3	3.1485	3.1477	1.0276							
		FFETCDLDNDKYIALDEWAGCFGIK	1	2.402	2.402								
		LEAGDHPVELLAR	1	3.2999	3.2999								
		LHLDYIGPCK	1	2.8794	2.8794								
		TFDSSCHFFATK	2	2.9886	2.9432	1.2813							
		YIALDEWAGCFGIK	3	2.6154	2.6117	1.0665							
		YIPPCLDSELTEFPLR	1	3.7529	3.7529								
SPSY_HUMAN	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	DVLILGGGDGGILCEIVK	1	2.8055	2.8055		1	2.8055	2.8055	2.8055	2.8055	2.8055	
SPTA2_HUMAN	Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	DLAALEDK	1	4.8904	4.8904		10	3.1535	2.7921	2.2722	1.7784	1.5464	3.0037
		DLTSWVTEMK	1	3.7689	3.7689								
		DTEQVDNWMSK	1	1.2772	1.2772								
		DVDEIEAWISEK	1	4.3639	4.3639								
		DVDETSWIK	1	5.0137	5.0137								
		LDENSAFLQFNWK	2	0.1499	0.0775	6.0928							
		LIQEQHPEEELIK	1	4.1783	4.1783								
		MNEVISLWK	1	4.7601	4.7601								
		QWELLLEK	2	1.8208	1.5219	2.3925							
		VNEVNQFAAK	1	1.3118	1.3118								
SPTB2_HUMAN	Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	ENEVLEAWK	1	4.7493	4.7493		6	2.9384	2.9224	1.667	1.7976	1.702	5.0921
		MFSEADACELWIDEK	1	3.3908	3.3908								
		NDSFTTCIELGK	1	0.0716	0.0716								
		QAEAFLNKEYVLAHTEMPTTLEGAEAAIK	1	5.3651	5.3651								
		TAASGIPYHSEVPVSLK	2	2.8262	2.3342	2.4663							
		VDTVNHLADELINSGHSDAATIAEWK	1	1.2276	1.2276								
SRGN_HUMAN	Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=2	GPMFELLPGESNK	2	7.2814	7.2013	1.2345	2	3.7175	3.7175	1.0576	1.0576	1.0348	15.3103
		TDLFPK	2	0.1536	0.1487	1.4337							
SRP09_HUMAN	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	VTDDLVCLVYK	2	5.8253	5.7767	1.201	1	5.8253	5.8253	5.8253	5.8253	5.7767	
SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1	LLGMGDIEGLIDK	1	0.316	0.316		1	0.316	0.316	0.316	0.316	0.316	
SRPX_HUMAN	Sushi repeat-containing protein SRPX OS=Homo sapiens GN=SRPX PE=2 SV=1	DTADGILTDVILK	1	3.7183	3.7183		1	3.7183	3.7183	3.7183	3.7183	3.7183	
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	SEISQVFEALK	1	1.012	1.012		1	1.012	1.012	1.012	1.012	1.012	
STC2_HUMAN	Stanniocalcin-2 OS=Homo sapiens GN=STC2 PE=1 SV=1	VIVEMIHFK	1	0.289	0.289		1	0.289	0.289	0.289	0.289	0.289	
STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	ALSVGNIDDALQCYSEAIK	1	7.0532	7.0532		7	5.1534	5.1955	4.673	4.7681	4.5616	1.6405
		DCEECIQLEPTFIK	1	2.8756	2.8756								
		DPQALSEHLK	1	8.1105	8.1105								
		ELDPTNMTYITNQAAVYFEK	2	5.4899	4.599	2.3789							
		FMNPFNMPNLYQK	1	3.4359	3.4359								
		LAYINPDLALEEPK	1	2.305	2.305								
		LLEFQLALK	1	6.8037	6.8037								
STMN1_HUMAN	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	AIEENNNFSK	1	2.5856	2.5856		4	5.6201	5.6201	3.5144	3.5144	3.5144	2.9287
		DLSLEEIQK	1	15.534	15.534								
		ESVPEPPLSPPK	1	1.2027	1.2027								
		KLEAAEER	1	3.158	3.158								
STMN2_HUMAN	Stathmin-2 OS=Homo sapiens GN=STMN2 PE=1 SV=3	ALEENNNFSK	1	2.5856	2.5856		3	7.0925	7.0925	5.0244	5.0244	5.0244	2.6714
		DLSLEEIQK	1	15.534	15.534								
		KLEAAEER	1	3.158	3.158								
STMN4_HUMAN	Stathmin-4 OS=Homo sapiens GN=STMN4 PE=2 SV=1	KLEAAEER	1	3.158	3.158		1	3.158	3.158	3.158	3.158	3.158	
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	YDYNSGEELESYK	1	6.0871	6.0871		1	6.0871	6.0871	6.0871	6.0871	6.0871	
STRBP_HUMAN	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	GWPLELICEK	1	7.8012	7.8012		1	7.8012	7.8012	7.8012	7.8012	7.8012	
SUMO2_HUMAN	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=1	TENNDHINLK	1	4.4023	4.4023		2	3.067	2.6219	2.761	2.3634	2.1657	1.9343
		VAGQDGSVVQFK	2	1.7317	1.519	2.0957							
SUMO3_HUMAN	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	VAGQDGSVVQFK	2	1.7317	1.519	2.0957	1	1.7317	1.7317	1.7316	1.7316	1.519	
SUMO4_HUMAN	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2	VAGQDGSVVQFK	1	0.9002	0.9002		1	0.9002	0.9002	0.9002	0.9002	0.9002	
SVEP1_HUMAN	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=2	AFCLACPFYGTTPFAGSR	1	0.5167	0.5167		2	1.2659	1.2659	1.0204	1.0204	1.0204	2.6177
		TTGPNVVYSCNR	1	2.015	2.015								
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=4	LGVENCYFPMIFVSQSALEK	1	2.3089	2.3089		1	2.3089	2.3089	2.3089	2.3089	2.3089	
SYG_HUMAN	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=2	TFFSFWVAPFK	1	1.7217	1.7217		1	1.7217	1.7217	1.7217	1.7217	1.7217	
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	IFDSEEILAGYK	1	2.9484	2.9484		1	2.9484	2.9484	2.9484	2.9484	2.9484	
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	FLGDIEVWDQAEK	1	1.5262	1.5262		1	1.5262	1.5262	1.5262	1.5262	1.5262	
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	DIIACGFDINK	1	1.1229	1.1229		2	2.6646	2.6646	2.1733	2.1733	2.1733	2.5443
		DMNQVLDAYENIK	1	4.2062	4.2062								
TAGL_HUMAN	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	AAEDVGVIK	1	0.2877	0.2877		6	0.2944	0.2944	0.2258	0.2258	0.2258	2.1593
		DMAAVQR	1	0.1507	0.1507								
		GDPNWFMK	1	0.3437	0.3437								
		LVNSLYPDGSKPVK	1	0.7812	0.7812								
		TDMFQTVDLFEGK	1	0.0971	0.0971								
		TLMALGSLAVTK	1	0.1259	0.1259								
TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	DDGLFSGDPNWFPK	2	10.9705	10.9451	1.1012	7	6.4615	6.1096	4.9165	4.6334	2.9216	2.6016
		DGTVLCELINALYPEGQAPVKK	2	6.5788	5.8686	1.9915							
		ENFQNWLK	2	0.8039	0.7002	2.1396							
		IQASTMAFK	1	7.2708	7.2708								
		NFSDNQLQEGK	2	9.2703	9.2656	1.0457							
		TLMNLGGLAVAR	4	2.1758	0.3551	8.4915							
		YGINTTDIFQTVDLWEGK	4	8.1608	8.0023	1.2659							
TAGL3_HUMAN	Transgelin-3 OS=Homo sapiens GN=TAGLN3 PE=1 SV=2	DMAAVQR	1	0.1507	0.1507		1	0.1507	0.1507	0.1507	0.1507	0.1507	
TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	AAQASDLEK	1	7.0422	7.0422		5	4.9293	4.6911	4.7633	4.5723	3.7273	1.3378
		ALAGCDFLTSPK	2	3.3484	3.3086	1.245							
		LLGELLQDNAK	2	5.7363	5.3139	1.751							
		LSSTWEGIQAGK	4	4.3933	2.7551	4.2817							
		WLHNEDQMAVEK	1	4.1265	4.1265								
TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	DVNAAIATIK	1	3.8056	3.8056		4	4.2783	4.2783	3.8251	3.8251	3.8251	1.8022
		EDMAALEK	1	5.3012	5.3012								
		TIGGGDDSFNTFFSETGAGK	1	6.3298	6.3298								
		TIQFVDWCPTGFK	1	1.6764	1.6764								
TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	LISQIVSSITASLR	1	5.8835	5.8835		4	3.79	3.5268	1.9776	1.516	1.463	6.1054
		QLFHPEQLITGK	1	3.2755	3.2755								
		SIQFVDWCPTGFK	2	0.1353	0.122	1.9217							
		TIGGGDDSFNTFFSETGAGK	2	5.8657	5.8473	1.1187							
TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	DVNAAIATIK	1	3.8056	3.8056		6	4.3013	4.5248	3.9543	4.1834	4.1797	1.823
		EDMAALEK	1	5.3012	5.3012								
		LISQIVSSITASLR	1	5.8835	5.8835								
		QLFHPEQLITGK	1	3.2755	3.2755								
		TIGGGDDSFNTFFSETGAGK	2	5.8657	5.8473	1.1187							
		TIQFVDWCPTGFK	1	1.6764	1.6764								
TBA3C_HUMAN	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3	DVNAAIATIK	1	3.8056	3.8056		4	3.6558	4.0978	3.3274	3.7269	3.7222	1.6812
		QLFHPEQLITGK	1	3.2755	3.2755								
		TIGGGDDSFNTFFSETGAGK	2	5.8657	5.8473	1.1187							
		TIQFVDWCPTGFK	1	1.6764	1.6764								
TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	EDMAALEK	1	5.3012	5.3012		2	2.7183	1.8573	0.8469	0.4595	0.4289	13.3806
		SIQFVDWCPTGFK	2	0.1353	0.122	1.9217							
TBA4B_HUMAN	Putative tubulin-like protein alpha-4B OS=Homo sapiens GN=TUBA4B PE=5 SV=2	LISQIVSSITASLR	1	5.8835	5.8835		2	4.5795	4.5795	4.3899	4.3899	4.3899	1.5131
		QIFHPEQLITGK	1	3.2755	3.2755								
TBA8_HUMAN	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	LISQIVSSITASLR	1	5.8835	5.8835		3	3.6118	3.6118	3.1849	3.1849	3.1849	1.8743
		QLFHPEQLITGK	1	3.2755	3.2755								
		TIQFVDWCPTGFK	1	1.6764	1.6764								
TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	EIVHIQAGQCGNQIGAK	1	3.2811	3.2811		3	3.013	3.094	2.9935	3.0803	3.057	1.1523
		MSATFIGNSTAIQELFK	3	3.2154	3.1748	1.2192							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	2.5426	2.5426								
TBB2C_HUMAN	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	5.1092	4.8472	1.5887	5	3.1372	3.4032	2.9157	3.2049	3.148	1.5492
		EIVHLQAGQCGNQIGAK	1	3.2811	3.2811								
		IMNTFSVVPSPK	1	1.5376	1.5376								
		MSATFIGNSTAIQELFK	3	3.2154	3.1748	1.2192							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	2.5426	2.5426								
TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	EIVHIQAGQCGNQIGAK	1	3.2811	3.2811		3	2.5925	2.6841	2.4622	2.5779	2.5652	1.5084
		IMNTFSVVPSPK	1	1.5376	1.5376								
		MSSTFIGNSTAIQELFK	2	2.9588	2.9296	1.2208							
TBB4_HUMAN	Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	5.1092	4.8472	1.5887	5	3.2398	3.5514	3.0034	3.2814	3.2244	1.5696
		EIVHLQAGQCGNQIGAK	1	3.2811	3.2811								
		IMNTFSVVPSPK	1	1.5376	1.5376								
		MSATFIGNSTAIQELFK	1	3.7286	3.7286								
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	2.5426	2.5426								
TBB4Q_HUMAN	Putative tubulin beta-4q chain OS=Homo sapiens GN=TUBB4Q PE=5 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	5.1092	4.8472	1.5887	1	5.1092	5.1092	5.1091	5.1091	4.8472	
TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	ALTVPELTQQVFDAK	1	2.5483	2.5483		7	3.1861	3.3721	2.9891	3.1664	3.1031	1.4825
		EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	5.1092	4.8472	1.5887							
		EIVHIQAGQCGNQIGAK	1	3.2811	3.2811								
		IMNTFSVVPSPK	1	1.5376	1.5376								
		ISVYYNEATGGK	1	4.347	4.347								
		MAVTFIGNSTAIQELFK	2	2.9369	2.8267	1.4822							
		SGPFGQIFRPDNFVFGQSGAGNNWAK	1	2.5426	2.5426								
TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	MASTFIGNSTAIQELFK	3	3.2154	3.1748	1.2192	1	3.2154	3.2154	3.2154	3.2154	3.1748	
TBB8_HUMAN	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	2	5.1092	4.8472	1.5887	1	5.1092	5.1092	5.1091	5.1091	4.8472	
TBB8B_HUMAN	Tubulin beta-8 chain B OS=Homo sapiens PE=1 SV=1	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2	5.1092	4.8472	1.5887	1	5.1092	5.1092	5.1091	5.1091	4.8472	
TBC8B_HUMAN	TBC1 domain family member 8B OS=Homo sapiens GN=TBC1D8B PE=2 SV=2	SVIISIK	1	5.2523	5.2523		1	5.2523	5.2523	5.2523	5.2523	5.2523	
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	DDNMFQIGK	1	0.6899	0.6899		2	1.9778	1.9778	1.501	1.501	1.501	3.0021
		GISLNPEQWSQLK	1	3.2657	3.2657								
TCPA_HUMAN	T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1	ICDDELILIK	1	4.7459	4.7459		2	3.3456	2.8788	3.0384	2.6187	1.7095	1.8789
		SLLVIPNTLAVNAAQDSTDLVAK	2	1.9453	1.026	5.8964							
TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	DALSDLALHFLNK	1	6.5881	6.5881		2	3.8738	3.8738	2.7639	2.7639	2.7639	3.4159
		KLGGTIDDCELVEGLVLTQK	1	1.1595	1.1595								
TCPG_HUMAN	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	IVLLDSSLEYK	2	0.1342	0.1334	1.1695	1	0.1342	0.1342	0.1342	0.1342	0.1334	
TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	QQLLIGAVAK	1	9.2753	9.2753		1	9.2753	9.2753	9.2753	9.2753	9.2753	
TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	DMLEAGILDTYLGK	2	3.3322	3.15	1.614	2	4.1379	3.8693	4.0587	3.8005	3.6606	1.3217
		LVPGGGATEIELAK	1	4.9436	4.9436								
TCTP_HUMAN	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	DLISHDEMFSDIYK	3	3.903	1.5696	8.8307	3	4.9441	4.5277	4.8793	4.4625	2.5835	1.2236
		EIADGLCLEVEGK	1	5.7794	5.7794								
		VKPFMTGAAEQIK	1	5.1499	5.1499								
TEBP_HUMAN	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1	LNWLSVDFNNWK	1	4.1275	4.1275		1	4.1275	4.1275	4.1275	4.1275	4.1275	
TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	AIANECQANFISIK	1	4.6582	4.6582		9	6.3135	6.5715	4.9482	5.4411	5.1902	2.4339
		DVDLEFLAK	1	8.8386	8.8386								
		ETVVEVPQVTWEDIGGLEDVKR	1	8.8831	8.8831								
		GDDLSTAILK	1	8.1645	8.1645								
		IVSQLLTLMDGLK	1	8.3936	8.3936								
		LDQLIYIPLPDEK	1	0.8593	0.8593								
		NAPAIIFIDELDAIAPK	3	6.4095	5.7781	1.8199							
		QAAPCVLFFDELDSIAK	2	9.2172	8.1118	2.0754							
		QLAQIK	1	1.3977	1.3977								
TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=2	LDTLAQEVALLK	1	0.8263	0.8263		1	0.8263	0.8263	0.8263	0.8263	0.8263	

TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	NEFGEIQGDK	1	2.8584	2.8584		2	2.7146	2.7146	2.7108	2.7108	2.7108	1.0779
		YLLNELNLEPFSEK	1	2.5708	2.5708								
THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	TAFQEALDAAGDK	2	5.5429	5.508	1.1724	1	5.5429	5.5429	5.5429	5.5429	5.508	
THIOM_HUMAN	Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2	VVNSETPVVVDFHAQWCGPCK	1	1.2144	1.2144		1	1.2144	1.2144	1.2144	1.2144	1.2144	
TICN1_HUMAN	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	DSLGWMFNK	2	4.0696	4.0349	1.2036	5	2.6877	2.8982	2.5548	2.7635	2.7436	1.4418
		FDTSILPICK	2	2.5692	2.5356	1.2583							
		LSNNEWCYCFQKPGGLPCQNEMNR	1	2.4463	2.4463								
		SLATLCDGPCPCLPEPEPPK	0										
		VCVTGDYQTALCVSR	1	1.6657	1.6657								
TICN3_HUMAN	Testican-3 OS=Homo sapiens GN=SPOCK3 PE=1 SV=2	DSLGWMFNR	1	1.4998	1.4998		2	2.0345	2.2127	1.963	2.1472	2.1285	1.4632
		FDTSILPICK	2	2.5692	2.5356	1.2583							
TIMP1_HUMAN	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	EPGLCTWQSLR	2	0.5272	0.4368	2.4458	8	0.3997	0.4554	0.3094	0.3823	0.3102	2.3064
		FVYTPAMESVCGYFHR	3	0.8329	0.5743	3.0686							
		GFQALGDAADIR	5	0.6026	0.3511	2.8061							
		HLACLPR	1	0.0768	0.0768								
		LQDGLLHITTCSFVAPWNSLSLAQR	1	0.1366	0.1366								
		LQSGTHCLWTDQLLQGSEK	3	0.3441	0.3241	1.513							
		SEEFLIAGK	4	0.1751	0.1668	1.437							
		TVTVCGEECTVFPCLSIPCK	3	0.502	0.4975	1.1798							
TIMP2_HUMAN	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=1 SV=2	DIEFIYVSAVCGVSLDVGGK	1	0.9105	0.9105		5	0.8204	0.8417	0.8053	0.8283	0.8195	1.2386
		EVDSGNDIYGNPIK	1	0.6389	0.6389								
		EVDSGNDIYGNPIKR	5	0.7879	0.7803	1.1692							
		EYLVAGK	2	0.6833	0.6833	1.0058							
		SDGSCAWYR	3	1.0816	1.0531	1.3292							
TKT_HUMAN	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	AVELAANTK	1	0.075	0.075		7	4.0656	4.3231	1.9938	2.4697	1.8356	5.995
		IIALDGDTK	1	7.2289	7.2289								
		LGQSDPAPLQHQMDIYQK	1	6.5806	6.5806								
		NMAEQIIQEIYSQIQSK	2	5.1866	5.1821	1.0605							
		NSTFSEIFK	1	3.7861	3.7861								
		QAFTDVATGSLGGGLGAACGMAYTGK	1	0.3397	0.3397								
		TSRPENAIIYNNNEDFQVGQAK	2	5.2622	1.3856	17.1538							
TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	AQEACGPLEMDSALSVQNLEK	1	2.8337	2.8337		10	3.3756	2.7779	1.9614	1.4541	1.3135	4.0857
		EADESLNFEEQILEAAK	1	7.0877	7.0877								
		GVGAAATAVTQALNELLQHVK	1	2.8335	2.8335								
		ILAQATSDLVNAIK	1	5.9473	5.9473								
		SIAATSALVK	3	0.2956	0.2544	2.0837							
		TEDSGLQTQVAAATQCALSTSQLVACTK	1	1.3976	1.3976								
		TLAESALQLLYTAK	1	0.1034	0.1034								
		TYGVSFFLVK	1	5.8567	5.8567								
		VAGSVTELIQAAEAMK	2	1.7661	1.1415	4.1333							
		VSQMAGYFEPLTLAAVGAASK	1	5.6341	5.6341								
TLN2_HUMAN	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	SIAATSALVK	3	0.2956	0.2544	2.0837	2	3.0761	1.6859	1.3157	0.6236	0.5573	8.2626
		TYGVSFFLVK	1	5.8567	5.8567								
TPD52_HUMAN	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2	VEEEIQTLSQVLAAK	1	0.1243	0.1243		1	0.1243	0.1243	0.1243	0.1243	0.1243	
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	EAGITEK	1	1.0178	1.0178		10	7.6083	7.3258	6.3246	6.5523	5.5113	2.1206
		ELASQPDVDGFLVGGASLKPEFVDIINAK	2	8.6843	8.3623	1.4787							
		HVFGESDELIGQK	1	14.3983	14.3983								
		IAVAAQNCYK	1	9.3287	9.3287								
		IIYGGSVTGATCK	1	11.5259	11.5259								
		QSLGELIGTLNAAK	3	5.4617	4.6467	2.1408							
		TATPQQAQEVHEK	3	5.2123	2.3227	7.8017							
		VTNGAFTGEISPGMIK	3	7.1478	6.5871	1.6834							
		VVFEQTK	1	3.9174	3.9174								
		VVLAYEPVWAIGTGK	3	9.3893	9.2127	1.2759							
TPISL_HUMAN	Putative triosephosphate isomerase-like protein LOC286016 OS=Homo sapiens PE=1 SV=2	EAGITEK	1	1.0178	1.0178		2	2.4676	2.4676	1.9968	1.9968	1.9968	2.5936
		VVFEQTK	1	3.9174	3.9174								
TPM1_HUMAN	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	IQLVEEELDR	1	5.8269	5.8269		3	6.6012	7.4121	6.1886	6.9502	6.9489	1.5484
		LATALQK	1	4.1317	4.1317								
		MEIQEIQLK	2	9.8449	9.8413	1.039							
TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	IQLVEEELDR	1	5.8269	5.8269		3	4.5166	4.5166	4.4218	4.4218	4.4218	1.2828
		LATALQK	1	4.1317	4.1317								
		MELQEMQLK	1	3.5912	3.5912								
TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	IQLVEEELDR	1	5.8269	5.8269		3	6.6012	7.4121	6.1886	6.9502	6.9489	1.5484
		LATALQK	1	4.1317	4.1317								
		MELQEIQLK	2	9.8449	9.8413	1.039							
TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like protein OS=Homo sapiens PE=5 SV=2	MELQEIQLK	2	9.8449	9.8413	1.039	1	9.8449	9.8449	9.8448	9.8448	9.8413	
TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	AEVSELK	2	1.41	0.5601	9.2684	8	4.2095	3.8984	3.794	3.3989	2.7684	1.6772
		EENVGLHQTLDQTLNELNCI	1	4.138	4.138								
		EKAEGDVAALNR	1	4.5825	4.5825								
		IQLVEEELDR	1	5.8269	5.8269								
		KIQALQGQADEAEDR	1	7.5283	7.5283								
		LATALQK	1	4.1317	4.1317								
		MEIQEMQLK	1	3.5912	3.5912								
		TIDDLEEK	1	2.4671	2.4671								
TPT1L_HUMAN	TPT1-like protein OS=Homo sapiens PE=1 SV=1	VKPFMTGAAEQIK	1	5.1499	5.1499		1	5.1499	5.1499	5.1499	5.1499	5.1499	
TR150_HUMAN	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	GSFSDTGLGDGK	1	0.1734	0.1734		1	0.1734	0.1734	0.1734	0.1734	0.1734	
TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=2	GDVAFVK	2	2.2833	2.0441	1.9694	1	2.2833	2.2833	2.2833	2.2833	2.0441	
TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	CGLVPVLAENYK	1	0.8108	0.8108		1	0.8108	0.8108	0.8108	0.8108	0.8108	
TRI14_HUMAN		LLLDEEALAK	1	6.104	6.104		1	6.104	6.104	6.104	6.104	6.104	
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	SYDYDLIIIGGGSGGLAAAK	1	3.3619	3.3619		1	3.3619	3.3619	3.3619	3.3619	3.3619	
TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	AGTLDLSLTVQGK	3	15.8415	15.4807	1.2968	24	11.2703	12.1572	6.6433	8.9754	8.4132	5.063
		AQGYSGLSVK	2	13.4969	11.4446	2.3042							
		AQLYIDCEK	2	7.3808	7.0994	1.4871							
		CTSYPDGSWK	2	19.6098	19.5904	1.0648							
		DCVGDVTENQICNK	2	19.9882	19.782	1.2263							
		DHSGQVFSVVSNGK	1	6.9452	6.9452								
		FQMIPLDPK	1	22.0436	22.0436								
		FTGSQPFGQGVEHATANK	5	11.0277	9.2513	2.0464							
		GDACKDDFDHDSVPDIDDICPENVDISETDFR	1	0.0956	0.0956								
		GTLLALER	1	13.7624	13.7624								
		GTSQNDPNWVVR	2	17.0479	17.0349	1.0567							
		IEDANLIPPVPDDKFQDLVDAVR	1	14.0143	14.0143								
		IMADSGPIYDK	3	10.3953	8.9126	2.0705							
		KDHSGQVFSVVSNGK	1	7.4166	7.4166								
		LCNNPTPGFGGK	5	13.0708	10.9357	2.045							
		LCNSPSPQMNGKPCEGEAR	1	5.0398	5.0398								
		MENAELDVPIQSVFTR	1	0.1861	0.1861								
		NPCTDGTHDCNK	1	12.5212	12.5212								
		QVTQSYWDTNPTR	1	12.8774	12.8774								
		SITLFVQEDR	1	17.2532	17.2532								
		TIVTTLQDSIR	2	14.0925	13.9784	1.1979							
		TKDLQAICGISCDELSSMVLELR	1	4.32	4.32								
		VTEENKELANELR	3	11.9732	11.5921	1.3607							
		VVMYEGKK	1	0.0868	0.0868								
TXD15_HUMAN		TLETLK	1	0.7146	0.7146		1	0.7146	0.7146	0.7146	0.7146	0.7146	
TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	ALAPTWEQLALGLEHSETVK	2	4.626	4.5193	1.3589	3	4.3169	3.6499	2.877	2.3658	2.2805	3.6088
		EFPGLAGVK	2	0.6728	0.6282	1.6977							
		TLAPTWEELSK	1	7.652	7.652								
TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	SEPTQALELTEQDIKEDGIVPLR	1	3.1451	3.1451		1	3.1451	3.1451	3.1451	3.1451	3.1451	
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	ELLTSFGPLK	1	1.334	1.334		2	2.0587	2.0587	1.9269	1.9269	1.9269	1.6821
		LFIGGLPNYLNDDQVK	1	2.7834	2.7834								
UAP56_HUMAN	Spliceosome RNA helicase BAT1 OS=Homo sapiens GN=BAT1 PE=1 SV=1	GLAITFVSDENDAK	1	2.8021	2.8021		1	2.8021	2.8021	2.8021	2.8021	2.8021	
UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	GQVCLPVISAENWKPATK	1	2.2294	0.2294		2	1.7189	1.7189	0.8579	0.8579	0.8579	6.4585
		IEINFPAEYPFKPPK	1	3.2084	3.2084								
UBC9_HUMAN	SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1	NPDGTMNLMNWECAIPGK	1	2.344	2.344		2	1.6752	1.6752	1.5359	1.5359	1.5359	1.8182
		NPDGTMNLMNWECAIPGKK	1	1.0064	1.0064								
UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	LEILFLPEEYPMAAPK	1	7.8794	7.8794		1	7.8794	7.8794	7.8794	7.8794	7.8794	
UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	LGFEDGSVLK	1	6.9911	6.9911		5	5.0535	5.0535	4.4976	4.4976	4.4976	1.7897
		MPFPVNHGASSEDTLLK	1	5.3541	5.3541								
		MQLKPMEINPEMLNK	1	1.8183	1.8183								
		QFLSETEK	1	7.4978	7.4978								
		QTIGNSCGTIGLIHAVANNQDK	1	3.6062	3.6062								
UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	TLDGGLNVIQLETAVGAAIK	1	3.7587	3.7587		2	3.0182	3.0182	2.9259	2.9259	2.9259	1.4251
		TYNTDVPLVLMNSFNTDEDTKK	1	2.2776	2.2776								
ULK4_HUMAN	Serine/threonine-protein kinase ULK4 OS=Homo sapiens GN=ULK4 PE=2 SV=2	EQKLLLR	1	4.991	4.991		1	4.991	4.991	4.991	4.991	4.991	
UVRAG_HUMAN		ALGREVALLHK	1	1.3666	1.3666		1	1.3666	1.3666	1.3666	1.3666	1.3666	
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1	LAGLGLQQLDEGLFSR	1	0.4002	0.4002		1	0.4002	0.4002	0.4002	0.4002	0.4002	
VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	DNLAEDIMR	3	9.8144	9.7077	1.2015	23	7.1336	7.4708	5.9723	6.5205	6.2624	2.1158
		EEAENTLQSFR	1	10.792	10.792								
		EKLQEEMLQR	3	6.8337	3.9347	4.9799							
		EYQDLLNVK	4	8.7829	8.7662	1.0732							
		FADLSEAANR	2	0.7251	0.7208	1.1678							
		FANYIDK	4	7.3511	7.0488	1.4284							
		FLEQQNK	3	8.3512	8.3483	1.033							
		GTNESLER	3	7.2311	7.2165	1.0817							
		ILLAELEQLK	5	8.7807	8.5788	1.2908							
		ILLAELEQLKQQK	1	2.7795	2.7795								
		ISLPLPNFSSLNLR	1	1.598	1.598								
		KLLEGEESR	1	9.0346	9.0346								
		KVESLQEEIAFLK	3	8.2837	8.2758	1.0548							
		LLEGEESR	2	8.6285	8.5173	1.2564							
		LQDEIQNMK	4	7.5038	7.2959	1.3332							
		LQEEMLQR	1	9.2177	9.2177								
		MALDIEIATYR	1	5.2722	5.2722								
		QDVDNASLAR	1	11.4114	11.4114								
		QQYESVAAK	2	1.0541	1.0539	1.0201							
		QVDQLTNDK	3	9.7333	9.733	1.0092							
		RQVDQLTNDK	1	6.2164	6.2164								
		TNEKVELQELNDR	1	5.9459	5.9459								
		VELQELNDR	1	8.7321	8.7321								
VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	AAVHLEGK	1	6.1788	6.1788		5	3.4375	3.4375	3.0378	3.0378	3.0378	1.7308
		AVAGNISDPGLQK	1	1.748	1.748								
		ELLPVLISAMK	1	2.2485	2.2485								
		SLGEISALTSK	1	2.2255	2.2255								
		TNISDEESEQATEMLVHNAQNLMQSVK	1	4.7869	4.7869								
VTA1_HUMAN	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	QLGDNEAITQEIVGCAHLENYALK	1	1.0978	1.0978		1	1.0978	1.0978	1.0978	1.0978	1.0978	
VWF_HUMAN	von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=2	GLRPSCPNSCSPVK	1	4.4507	4.4507		7	4.132	4.132	2.0236	2.0236	2.0236	4.5506
		GLWEQCQLLK	1	7.303	7.303								
		IEDLPTMVTLGNSFLHK	1	0.148	0.148								
		ILTSDVFQDCNK	1	2.3556	2.3556								
		LSEAEFEVLK	1	0.6756	0.6756								
		NSQWICSNEECPGECLVTGQSHFK	1	12.5443	12.5443								
		VEDFGNAWK	1	1.4471	1.4471								
WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	DYSQGGVVK	1	4.1718	4.1718		5	6.2014	6.8509	4.5838	5.2288	5.2247	2.5332
		FATASADGQIIYIYDGK	1	3.0881	3.0881								
		LYSILGTTLKDEGK	1	1.2551	1.2551								
		YAPSGFYIASGDVSGK	1	12.3933	12.3933								
		YEYQPFAGK	2	10.0987	10.0748	1.1021							
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	SVGDGETVEFDVVEGEK	1	2.847	2.847		1	2.847	2.847	2.847	2.847	2.847	
		SVGDGETVEFDVVEGEK	1	2.847	2.847								
		MLLSQNSK	1	4.3909	4.3909								

Supplemental Table III

Extracellular Space	
1433S_HUMAN	14-3-3 protein sigma
MMP2_HUMAN	72 kDa type IV collagenase
AGRIN_HUMAN	Agrin
FETUA_HUMAN	Alpha-2-HS-glycoprotein
AIMP1_HUMAN	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1
CCL2_HUMAN	C-C motif chemokine 2
CAD13_HUMAN	Cadherin-13
CALR_HUMAN	Calreticulin
CD109_HUMAN	CD109 antigen
CH3L1_HUMAN	Chitinase-3-like protein 1
CLUS_HUMAN	Clusterin
COPA_HUMAN	Coatomer subunit alpha
CO2A1_HUMAN	Collagen alpha-1(II) chain
CO3A1_HUMAN	Collagen alpha-1(III) chain
CO1A2_HUMAN	Collagen alpha-2(I) chain
C1RL_HUMAN	Complement C1r subcomponent-like protein
CFAH_HUMAN	Complement factor H
CYTC_HUMAN	Cystatin-C
DKK3_HUMAN	Dickkopf-related protein 3
ADAM9_HUMAN	Disintegrin and metalloproteinase domain-containing protein 9
EGLN_HUMAN	Endoglin
FBN1_HUMAN	Fibrillin-1
FBLN1_HUMAN	Fibulin-1
FSTL1_HUMAN	Follistatin-related protein 1
LEG1_HUMAN	Galectin-1
LG3BP_HUMAN	Galectin-3-binding protein
G6PI_HUMAN	Glucose-6-phosphate isomerase
GPC1_HUMAN	Glypican-1
HDGF_HUMAN	Hepatoma-derived growth factor
HMGB1_HUMAN	High mobility group protein B1
IBP4_HUMAN	Insulin-like growth factor-binding protein 4
IFNG_HUMAN	Interferon gamma
MFGM_HUMAN	Lactadherin
LYSC_HUMAN	Lysozyme C
LOXL2_HUMAN	Lysyl oxidase homolog 2
TIMP2_HUMAN	Metalloproteinase inhibitor 2
NUCB1_HUMAN	Nucleobindin-1
PEDF_HUMAN	Pigment epithelium-derived factor
SAP_HUMAN	Proactivator polypeptide
HGB1A_HUMAN	Putative high mobility group protein B1-like 1
SRGN_HUMAN	Serglycin
HTRA1_HUMAN	Serine protease HTRA1
TRFE_HUMAN	Serotransferrin
ALBU_HUMAN	Serum albumin
MMP3_HUMAN	Stromelysin-1
QSOX1_HUMAN	Sulfhydryl oxidase 1
SODC_HUMAN	Superoxide dismutase [Cu-Zn]
TETN_HUMAN	Tetranectin
TPT1L_HUMAN	TPT1-like protein
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3
TCTP_HUMAN	Translationally-controlled tumor protein

Structural Constituent	
PGS1_HUMAN	Biglycan
CH3L1_HUMAN	Chitinase-3-like protein 1
CO1A1_HUMAN	Collagen alpha-1(I) chain
CO3A1_HUMAN	Collagen alpha-1(III) chain
COIA1_HUMAN	Collagen alpha-1(XVIII) chain
CO1A2_HUMAN	Collagen alpha-2(I) chain
CO5A2_HUMAN	Collagen alpha-2(V) chain
CO6A2_HUMAN	Collagen alpha-2(VI) chain
FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2
FBN1_HUMAN	Fibrillin-1
FBN2_HUMAN	Fibrillin-2
FBN3_HUMAN	Fibrillin-3
FINC_HUMAN	Fibronectin
FBLN1_HUMAN	Fibulin-1
LAMA4_HUMAN	Laminin subunit alpha-4
LAMB1_HUMAN	Laminin subunit beta-1
LAMB2_HUMAN	Laminin subunit beta-2
LAMC1_HUMAN	Laminin subunit gamma-1
LUM_HUMAN	Lumican
PRELP_HUMAN	Prolargin

Proteinaceous Extracellular Matrix	
MMP2_HUMAN	72 kDa type IV collagenase
PGS1_HUMAN	Biglycan
CALR_HUMAN	Calreticulin
CH3L1_HUMAN	Chitinase-3-like protein 1
CO6A2_HUMAN	Collagen alpha-2(VI) chain
CTGF_HUMAN	Connective tissue growth factor
PGS2_HUMAN	Decorin
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1
EMIL1_HUMAN	EMILIN-1
ECM1_HUMAN	Extracellular matrix protein 1
FBN3_HUMAN	Fibrillin-3
FBLN5_HUMAN	Fibulin-5
LEG3_HUMAN	Galectin-3
LG3BP_HUMAN	Galectin-3-binding protein
GPC1_HUMAN	Glypican-1
MMP1_HUMAN	Interstitial collagenase
LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1
LTBP2_HUMAN	Latent-transforming growth factor beta-binding protein 2
LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4
POSTN_HUMAN	Periostin
SAP_HUMAN	Proactivator polypeptide
PRELP_HUMAN	Prolargin
SPON2_HUMAN	Spondin-2
MMP3_HUMAN	Stromelysin-1
TICN1_HUMAN	Testican-1
TICN3_HUMAN	Testican-3
TETN_HUMAN	Tetranectin
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3
VWF_HUMAN	von Willebrand factor

Supplemental Table IV

Gene	Forward 5' - 3'	Reverse 5' - 3'
GAPDH	TCGACAGTCAGCCGCATCTTCTT	GCGCCCAATACGACCAAATCC
SPARC	CAGGGCTCTTCTCAGGGGCTCTA	CAACCGATTCACCAACTCCACTTT
Col1A1	CGATGGCTGCACGAGTCACAC	GGGCAGGCGGGAGGTCTT
PCOLCE	CCGGAGGCTGGGGAAGT	TTGGGCCGGTGGAGAAC
βig-h3	TGAACTGTGCCCGGCTGCTGAAAG	CCCCGTTGGTGGCTAGGATGTCT
Ang-1	GTCAATGGGGGAGGTTGGACTGTA	AGCCAATATTCACCGGAGGGATTT
VEGFC	GAACAAGACCTGCCCCACCAAT	CCAGCATCCGAGGAAAACATAAAA
SDF-1α	CTGGGTTTTGTGATTGCCTCTGAA	TTGGAACCTGAAACCCTGCTGTG
HGF	CAATGCCTCTGGTTCCCCTTCA	CTGTTCCCTTGTAGCTGCGTCCTT
SCF	TATGCCTTGGCAGAGGGGAGAC	GGTCAAGGGAAAAGGCGGACTT
MMP2	CGCAGTGACGGAAAGATGTGGT	AGAGCTCCTGAATGCCCTTGATGT
FN1	CGCCACGTGCCAGGATTACC	AGGGGCTCGCTCTTCTGATTATTC
alpha-SMA	CAAGGCCAACCCGGGAGAAAAT	ACCGCCTGGATAGCCACATAC