

Supplementary Table 1. Signal peptides and cleavage sites of 270 verified human proteins.

Accession	Signal peptide sequences	Length	15-aa seq after cleavage
AAF91396.1	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNSCLFISS	40	FNGTDLELRVLVNGDG
AAG24923.1	MLQPGSLLLLFLASHCCLGSARG	24	LFLFGQPDFSYKRSN
AAH11006	MAPHGPGSLTTLVFWAAALLLALGVERALA	30	LPEICTQCPGVSQNL
AAH33819	MGAPAAASLLLLLFFACCWAPGGA	24	NLSQDDSQPWTSDET
AAH41453.1	MRGPAVLLTVALATLLAPGAG	21	APVQSQGSQNKLLLV
AAH47013	MEPGPALAWLLLLSLLADCLKA	22	AQSRDFTVKDIIYLH
AAM20925	MALRRPRLRLCARLPDFLLLLFRGCLIGA	31	VNLKSSNRTPVVQEF
AAH52117	MFCPLKLIILPVLLDYSLG	19	LNLDLNVSPPELTVHV
AAQ03084	MGVPTALEAGSWRWGSLFALFLAASLGPVAA	32	FKVATPYSLYVCPFG
AAQ88874	MGLPGLFCLAVLAASSFSKA	20	REEEITPVVSYAYKV
AAQ88892	MRSTILLFCLLGSTRS	16	LPQLKPALGLPPTKL
AAQ88906	MTAEFLSLLCLGLCLG	16	YEDEKKNKPKPKPPL
AAQ89078	MKLSGMFLLLSALFCFLTGVS	23	QGGQVDCGEFQDPKV
AAQ89081	MAMGVPRVILLCLFGAALCLTGSQA	25	LQCYSFHEHTYFGPFD
AAQ89091	MKPVVWATLLWMLLVPRLGA	21	ARKGSPEEASFYYGT
AAQ89135	MWGARRSSVSSWNAASLLQLLLAALLAAGARA	33	SGEYCHGWLDQGVW
AAQ89182	MAAALALVAGVLSGAVLPLWS	21	ALPQYKKKITDRCFH
AAQ89294	MDSLRKMLISVAMLGAGAGVGYA	23	LLVIVTPGERKQEM
AAQ89372	MAPRGCIVAVFAIFCISRLLCSHG	24	APVAPMTPYMLCQP
AAQ89411	MRLSVCLLMVSLALCCYQAHA	21	LVCPAVASEITVFLF
AAQ89416	MGSGLPLVLLLTLLGSSHG	19	TGPGMTLQLKLESFV
AAQ89429	MLGAKPHWLPGLHSPGLPLVLLVLLALGAGWA	32	QEGSEPVLEGECLV
ANL3_HUMAN	MFTIKLFFFIVPLVIS	16	SRIDQDNSSFDLSLP
APM1_HUMAN	MLLLGAVLLLLALPGHDQ	18	ETTTQGGVLLPLPK
AXO1_HUMAN	MGTATRKRPHLLLVAVALVSSSAWSSALG	30	SQTTFGPVFEDQPLS
BAC03564.1	MASSPWGCVCGLLLLLLPLLGTGPAFG	27	RGFPRLENSEIPIMI
BP1L_HUMAN	MAWASRLGLLLALLPVVGA	20	STPGTVVRLNKAALS
C17_HUMAN	MRTPGPLPVLLLLLAGAPAARP	22	TPPTCYSRMRALSQE
C180_HUMAN	MAFDVSCFFWVWVLSAGCKVITS	23	WDQMCIEKEANKTYN
CAC17635	MRPGLSFLALLFFLGQAAG	20	DLGDVGGPIPSPGFS
CAC38526.1	MRPRCCILALVCWITVFLQCCKG	24	TTDAPVGSGLWLCQP
CAC39828.1	MAGPAIHTAPMLFLVLLLPLELSLA	25	GALAPGTPARNFPEN
CAD23758	MVPEVRVLSLLGLALLWFLDLSHA	25	RARPDMFCLFHGKRY
CAD59976	MARAAPLLAAALTAALAAAAAGG	22	DAPPGKIAVVGAGIG
CAH9_HUMAN	MAPLCPSPWPLLIIPAPAGLTVQLLSLLLLMPVHP	37	QRLPRMQEDSPLGGG
CALR_HUMAN	MRFTFTSRCLALFLLLNHPPIIP	24	AFSNQTYPTIEPKPF
CART_HUMAN	MESSRVLLPPLGAALLMLPLLGTRA	27	QEDAELQPRALDIYS
CATW_HUMAN	MALTAHPSCLLALLVAGLAQG	21	IRGPLRAQDLGPPQL
CD4_HUMAN	MNRGVPPFRHLLVLQALLPAATQG	25	KKVVLGKKGDVVELT
CD5L_HUMAN	MALLFSLILAICTRPGFLA	19	SPSGVRLVGGHRCRE
CD83_HUMAN	MSRGLQLLLSCAYSLAPA	19	TPEVKVACSEDDVLP
CDBA_HUMAN	MAVRELCFPRQRQVFLFLFWGVSLA	26	GGSGFRYSVTEETEK
CEA6_HUMAN	MGPPSAPPRLHVPKWEVLLTASLLTFWNPPTTA	34	KLTIESTPFNVAEKG
CEA7_HUMAN	MGSFSAACPYRVCIPWQGLLLTASLLTFWNLNSAQ	35	TNIDVVPFNVAEKGE
CERL_HUMAN	MGSGRRLSAPVAVLLVLTPLGPLVWA	27	QNDTEPIVLEKCLV
CGRH_HUMAN	MEKKCTLYFLVLLPFFMILVTA	22	ELEESPEDSIQLGVT
CK15_HUMAN	MATLWGGLLRLGSLLSLCLALSULLAQLSDA	33	AKNFEDVRCKKICPP
CN27_HUMAN	MRPAFALCLLWQALWPGPGGG	21	EHPTADRAGCSASGA
COLI_HUMAN	MPRSCCSRSRGAALLLALLQASMEVRG	26	WCLESSQCQLTTES
CQT5_HUMAN	MRPLLVLVLLGLAAG	15	SPPLDDNKIPSLCPG
CQT6_HUMAN	MQWLRVRESPEATGHRVTMGTAALGFPVWAAALLFLLMCEIPMVEL	46	TFDRAVASGCQRCCD
CRI1_HUMAN	MDCRKMARFYSYVWIMAIKVFELGLVAG	30	LGHQEFARPSRGYLA
CST9_HUMAN	MLGLPWKGLSWALLLLLSGSQILLIYA	28	WHFHEQRDCDEHNVN
CYTC_HUMAN	MAGPLRAPLLLLAIALAVALVSPAAG	26	SSPGKPPRLVGGPMD
CYTN_HUMAN	MAQHLSTLLLLLATLAVALA	20	WSPKEEDRIIPGGIY
CYTT_HUMAN	MAWFLCTLLLLLATQAVALA	20	WSPQEDRIIEGGIY
D127_HUMAN	MGLFMIIAILLFQKPTVTEQ	20	LKKCWNNYVQGHCRK
DCD_HUMAN	MRFMTLLFLTALAGALVCA	19	YDPEAASAPGSGNPC
DEF1_HUMAN	MRTLAILAAILLVALQAQA	19	EPLQARADEVAAAPE
DKK1_HUMAN	MMALGAAGATRVFVMAVAALGGHPLLGVSA	31	TLNSVLNSNAIKNPL
DKK3_HUMAN	MQRIGATLLCLLAAAVPTAP	21	APAPTATSAPVKPGP
DKK4_HUMAN	MVAAVLLGLSWLCSPLGA	18	LVLDNFNNIRSSADLH
DLK_HUMAN	MTATEALLRVLLLLLAFGHSTYG	23	AECFFACNPQNGFCE
DLL4_HUMAN	MAAASRSASGALLLLVALWQQRAGG	26	SGVFQLQLQEFINER
EDAR_HUMAN	MAHVGDCTQTPWLPVLLVSLMCSARA	26	EYSCNGCENEYNYQTT
EFA1_HUMAN	MEFLWAPLLGLCCSLAAA	18	DRHTVFWNSSNPKFR
EFA4_HUMAN	MRLPLLRVTVLWAAFLGSPLRGGSS	25	LRHVYVWNSNPRLL

EFB1_HUMAN	MARPGQRWLKWLVMVVALCRLATP	27	LAKNLEPVSWSSLNP
EFB3_HUMAN	MGPPHSGGGVVRGALLLGLVGLVSG	27	LSLEFPVYWSANKRF
EGFR_HUMAN	MRPSGTAGAALLALLAALCPASRA	24	LEEKVCQGTSNKLT
EPB1_HUMAN	MALDYLLLLLLASAVAA	17	MEETLMDTRTATAEL
EPB6_HUMAN	MVCSLWVLLLVSSVLA	16	LEEVLLDTTGETSEI
FCG1_HUMAN	MWFLTLLLLWVPVDG	15	QVDTTKAVISLQPPW
FCGN_HUMAN	MGVPRQPWALGLLLFLPGSLG	23	AESHLSLLYHLTAVS
FCN1_HUMAN	MELSGATMARGLAVLLVFLHIKNLPAQA	29	ADTCPEVKVVGLEGS
FCN3_HUMAN	MDLLWILPSSLWLLLGGPACLKT	23	QEHPSPCPGPRELEAS
FGFJ_HUMAN	MRSQCVVHVWVILAGLWLVAVAGRP	24	LAFSDAGPHVHYGWW
FGFL_HUMAN	MDSDETFEHSGLWVSVLAGLLGACQA	28	HPIDPSSPLLQFGGQ
FGFN_HUMAN	MLGARLRLWVCALCSVCSMSVLRA	24	YPNASPLLGSSWGG
FGR4_HUMAN	MRLLLALLGVLLSVPGPPVLS	21	LEASEVELEPCCLAP
FIG1_HUMAN	MAPLALHLLVLPILLSLIVAS	21	QDWKAERSQDPFEKC
FK14_HUMAN	MRLFLWNAVLTFLVTSLIG	19	ALIPPEVKIEVLQK
FLR2_HUMAN	MGLQTTKWPSHGAFLLKSWLIIISGLYSQVSKLLA	35	CPSVCRCDRNFVYCN
FRZB_HUMAN	MVCGSPGGMLLRRAGLLAALCLLRVPGARA	32	AACEFVRIPLCKSLP
FSA_HUMAN	MVRARHPGGCLLLLLLQCFMEDRSAQA	29	GNCWLQRQAKNGRCQV
FSL1_HUMAN	MWKRWLALALAVAVAVVRA	20	EEELRSKSKICANVF
FSL3_HUMAN	MRPGAPGLWPLPWGALAWAVGFVSS	26	MGSGNPAPGGVCWLQ
FZD3_HUMAN	MAMTWIVFSLWPLTVFMGHIGG	22	HSLFSCPEPITLRMQV
GDN_HUMAN	MNWHPLPLFLASVTLPSIC	19	SHFNPLSLEELGSNT
GFR3_HUMAN	MVRPLNRPRLPPVVLMLLLLLPPSPPLAAG	31	DPLPTESRLMNSCLQ
GHRL_HUMAN	MPSPGTVCSLLLLGMLWLDLAMA	23	GSSFLSPEHQVRVQR
GRAB_HUMAN	MQPILLLLAFLLPRADA	18	GEIIGGHEAKPHSRP
GRO_HUMAN	MARAALSAAPSNRLLRVALLLVAAGRRAAG	34	ASVATELRCQCLQTL
HGFA_HUMAN	MGRWAWVPSWPPEGLGPFLLLLLLLPRGFQP	35	QFGGNRTESPENAT
I10R_HUMAN	MLPCLVLLAALLSLRLGSDA	21	HGTELPSPVWFEEA
I10S_HUMAN	MAWSLGSWLGCLLVLSALG	19	MVPPENVRMNSVNF
I17E_HUMAN	MRERPRLGEDSSLSLFLQVVAFLAMVMGHT	32	YSHWFPSCCPKQDPT
I17F_HUMAN	MVKYLLLSILGLAFLSEAAA	20	RKIPKVGHTFFQKPE
I17R_HUMAN	MGAARSPPSAVPGPLGLLGLLVGLAPGGAS	32	LRLLDHRLVCSQPG
I17S_HUMAN	MSLVLLSLAALCRSAVP	17	REPTVQCGSETGPS
I18B_HUMAN	MRHNWTPDLSPLVWVLLCAHVVTLLVRA	28	TPVQTTTAAATASVR
I21R_HUMAN	MPRGWAAPLLLLLQGGWG	19	CPDLVICYTDYLTQVI
IBP3_HUMAN	MQRARPTLWAAALTLVLLRGPVVARA	27	GASSGGLGPVVRCEP
IBP7_HUMAN	MERPSLRALLGAAGLLLLLPLSSS	26	SSSDTCGPCEPASC
IL10_HUMAN	MHSSALLCCLVLLTGVARA	18	SPGQGTQSENCTHF
IL17_HUMAN	MTPGKTSLSVLLLLSLEAIVKA	23	GITIPRNPGPCNSED
IL19_HUMAN	MKLQCVSLWLLGTILLLCSVDNHG	24	LRRCLISTDMHHEE
IL20_HUMAN	MKASSLAFSLLSAFYLLWTPSTG	24	LKTLNLGSCVIATNL
IL22_HUMAN	MAALQKSVSSFLMGTLATSCLLLALLVQGGAA	33	APISSHCRDKSNFQ
IL24_HUMAN	MNFQQRLQSLWTLARPFCLLATASQMMVLPCLGFTLLLSQVSGAQQ	51	QEFHFGPCQVKGVPV
INA5_HUMAN	MALPFVLLMALVVLNCKSICS	21	LGCDLPQTHSLSNRR
INA6_HUMAN	MALPFALLMALVVLSCKSSC	20	SLDCDLPQTHSLGHR
INL3_HUMAN	MDPRLPAWALVLLGPAVFA	20	LGPAPTPEMREKLCG
INL4_HUMAN	MASLFRSYLPAIWLILLSQLLRESLA	25	AELRGCGRPFKHL
INL5_HUMAN	MKGSIFTLFLFSVLFATSEVRS	22	KESVRLCGLEYIRTV
INO1_HUMAN	MALLFPLLAALVMTSYSVPGS	21	LGCDLPQNHLGSLRN
IRL1_HUMAN	MGFWILAILTILMYSTAA	18	KFSKQSWGLENEALI
ITA7_HUMAN	MAGARSRDWPGASGICYLFGSLLVELLFSRAVA	33	FNLDVMGALRKEGEP
JAM1_HUMAN	MGTKAQVERKLLCLFILAILLCSLALG	27	SVTVHSSSEPEVRIPE
JAM2_HUMAN	MARRSRHRLLLLLRVLVVALGYHKAYG	28	FSAPKDQVVTAVEY
KLK3_HUMAN	MWVPPVFLTSLVTVIGA	17	APLILSRIVGWECE
LIA3_HUMAN	MTSILTVLICLGLSLDPRTHVQA	23	GFLPKPTLWAEPGSV
LITA_HUMAN	MAQTSSYFMLISCLMFLSQSQG	22	QEAQTELPQARISCP
LMP2_HUMAN	MVCFRLFVPVPGSLVCLVLAGAVRSYA	28	LELNLTDSENATCLY
LY6D_HUMAN	MRTALLLLAALAVATGPALT	20	LRCHVCTSSSNCKHS
LY86_HUMAN	MKGFTATLFLWTLIFPSCSG	20	GGGKAWPTHVVCSD
MDP1_HUMAN	MWSGWWLSLVAVCTA	16	DFFRDEAERIMRDS
MFA4_HUMAN	MKALLALPLLLLSTPPCAPQ	21	VSGIRGDALERFCLQ
M12B_HUMAN	MAHATLSAAPSNRLLRVALLLVAASRRRAAG	34	ASVVTTELRCQCLQTL
MIA_HUMAN	MARSLVCLGVIIILSAFSGPGVVRG	24	GPMPKLADRKLKADQ
MIME_HUMAN	MKTLQSTLLLLLVPLKPA	20	PPTQQDSRIIYDYG
MK_HUMAN	MQHRGFLLLTLLALLALTS	20	VAKKDKVKKGGPGS
MOTI_HUMAN	MVSRKAVAALLVHVVAAMLASQTEA	25	FVPIFTYGELQRMQE
MOXR_HUMAN	MLCPWRTANLGLLLILTIFLVAEAEAG	26	AAQPNNLMLQTSKE
NEL2_HUMAN	MESRVLLRTFCLIFGLGAVWG	21	LGVDPSLQIDVLTTEL
NLG4_HUMAN	MSRPQGLLWLPPLFTPVCVMLNSNVLLWLTALAIKFTLIDS	41	QAQYFVVNTNYGKIR
NMA_HUMAN	MDRHSSYIFLWQLELCAMA	20	VLLTKGEIRCYCDA
NOV_HUMAN	MQSVQSTSFCLRKQCLCTFLLHLLGQVAA	31	TQRCPPQCPGRCPAT

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NP_659441.1 MFRLWLLLAGLCLLLA
NP_660316.1 MRLLVLLWGCCLLPGYEA
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NP_689992.1 MALKNKFSCLWILGLCLVATTS
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OTOR_HUMAN MARILLFLPLGLVAVCA
PA2Z_HUMAN MKLASGFLVWLSLGGGLA
PGDR_HUMAN MRLPGAMPALAKGELLLLLLLEPQISQG
PRK1_HUMAN MRGATRVSIMLLLVTVSDC
PRK2_HUMAN MRSLLCAPLLLLLLPPLLLTPRAGDA

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37 AHTAVISQDPTLLI
17 TRHQDGRNQSSLSLSP
25 RGHREDFRFSQRNQ
20 RDTTVKPGAKKDTKD
29 QFSVLGPGSGPILAMV
19 RPILEVPEVSVTPGWK
28 FFQTEKISPNWESG
33 AGRHPPVVLPVGDGLG
23 QSPERPVTFCGGILT
24 KKKGSQGAIPPPDKA
23 VEVKVPTEPLSTPLG
29 VPCVSGGLPKPANIT
20 LPTSAPLSVSLPTNI
23 FKNDATEILYSHVVK
18 HLGVLGPKNVQSKDA
30 WNDPDRMLLRDVKAL
40 FPTSLSDCQPTGWN
32 ELQEADGQCPVDRSL
21 CQGSADHVVISIGVP
34 LVCLPCDESKCEEPR
35 SPLSTPTSAQAAGPS
28 QNEPRIVTSEVIR
18 AETKPHPAEQWRVAV
22 IAVAQKTQDQGNIGI
27 LDCNLLNVHLRRVTV
22 AQVLSKVGGSVLLVA
23 RQKESGSKWVFIDQ
21 LLCQFGTVQHVWVVS
26 QKLSKHKTPAQVQLK
22 SGPVKELVGSVGGAV
24 ARGPPKMAKVVPRQ
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24 AKKPTPCHRCRGLVD
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19 LFTVTVPKELYIIEH
28 LEVQVPEDPVVALVG
25 AKGGLSRESQVCSK
19 LTLVAPSSVFEQDSI
30 RPSGPDYLRGWMR
22 DIIMRPSCAPGWFYH
20 GFSPHLQQPEDLVV
27 ASFTLQCEGPVCTE
26 ELEPQIDQWAEARA
30 DLNEVPQTVVQPAST
21 SGGCFWDNGHLYRED
21 SLPLMLDSVQALAE
21 QSSLTPLMVNGILGE
26 HESAMAETLQHVPS
21 TQSTHESLKPQRVQF
20 NPTTAAADTYPATG
30 SEIPKQKQAKLQRQ
29 QLQLHLPANRLQAVE
19 ALPAKPENISCVYYY
19 TQITGPTTVNGLERG
22 LSVQGGPNLQVRQG
22 DEDENSPCAHEALLD
16 SRPGFQNSLLQIVIP
18 LEGPEISGFEGDTV
16 NAIQARSSSYSGEYG
22 SKIPSITDPHFIDNC
20 LERLVGPQDATHCSF
20 QEKPTGPRNTCLGS
28 HYDLCKTQIYTEEGK
33 GDATFPKAMDNVTVR
22 QDDGPPGSEDPERDD
17 VHGFMDRLASKKLC
19 QSDTSPDTEESYSDW
32 LVVTPPGPELVNVS
19 AVITGACERDVQCGA
27 AVITGACDKDSQCGG

PSCA_HUMAN	MKAVLLALMAGLALQPGTA	20	LLCYSCKAQVSNEDC
PTHY_HUMAN	MIPAKDMAKVMIVMLAICFLTKSDG	25	KSVKRSVSEIQLMH
Q6UXLO	MQFTFMVLEEIWTSLFMWFFYALIPCLLT	29	DEVALLPAPQNLVSL
Q8IZL7	MAAALFVLLGFALLGTHGASG	21	AAGFVQAPLSQQRWV
RISC_HUMAN	MELALRRSPVPRWLLLLPLLLGLNAG	26	AVIDWPTEEGKEVWD
RT4R_HUMAN	MKRASAGGSRLAWVWLQAWQVAAP	26	CPGACVCYNEPKVTT
SM4B_HUMAN	MGLRSWLAAPW GALPPRPPLLLLLLLLLLQPPPPTWA	38	LSPRISLPLGSEERP
SM6B_HUMAN	MQTPRASPPRPALLLLLLLLGGAHG	25	LFPEDEPPPLSVAPRD
SOST_HUMAN	MQLPLALCLVCLLVHTAFRVVEG	23	QGWQAFKNDATEIIP
SPT1_HUMAN	MAPARTMARARLAPAGIPAVALWLLCTLGLQGTQA	35	GPPPAPPGLPAGADC
SPT2_HUMAN	MAQLCGLRRSRAFLALLGSLLSGVLA	27	ADRERSIHDFCLVSK
SRG1_HUMAN	MKLMVLVFTIGLTLGLLVGVA	20	MPANRLSCYRKILKD
STC1_HUMAN	MLQNSAVLLVLVISASA	17	THEAEQNDVSVPKRS
SY01_HUMAN	MQIITTTALVCLLLAGMWPEDVDS	23	KSMQVPPFSRCCFSA
SY07_HUMAN	MKASAALLCLLLTAAAFSPQGLA	23	QPVGINTSTTCCYRF
SY15_HUMAN	MKVSVAALSCLMLVAVLGSQA	21	QFINDAETELMMSKL
SY24_HUMAN	MAGLMTIVTSLFLGVCAHHIIP TGS	26	VVIPSPPCMFFVSKR
SY3L_HUMAN	MQVSTAALAVLLCTMALCNQVLS	23	APLAADPTACCFSY
SYC2_HUMAN	MRLILLALLGICSLTAYIVEG	21	VGSEVSHRRTCVSLT
SZ07_HUMAN	MSLRDLTTPSCNSARPLHALQVLLLLSLLLTALA	34	SSTKGQTKRNLAKGK
T10C_HUMAN	MARIPKTLKFVVVIVAVLLPVLAYS	25	ATTARQEEVPPQTTVA
T10D_HUMAN	MGLWQGSVPTASSARAGRYPGARTASGTRPWLDPKILKFVVFIVAVLLPVRVDS	55	ATIPRQDEVPPQTTVA
T11B_HUMAN	MNKLLCCALVFLDISIKWTTQ	21	ETFFPKYLHYDEETS
TFF1_HUMAN	MATMENKVICALLVLSMALGTLA	24	EAQTETCTVAPRERQ
TFF3_HUMAN	MAARALCMLGLVLLSSSSA	21	EEYVGLSANQCAVPA
TFPI_HUMAN	MIYTMKKVHALWASVCLLLNLAPAPLNA	28	DSEEDDEHTIITDTE
TGR2_HUMAN	MGRGLRGLWPLHIVLWTRIAS	22	TIPPHVQKSVNNDMI
TIC2_HUMAN	MRAPGCGRLVPLLLLLAAAALA	22	EGDAKGLKEGETPGN
TIE1_HUMAN	MVWRVPFLLPIFLASHVGA	21	AVDLTLLANRLTDP
TIE2_HUMAN	MDSLASLVLCGVSLLSGTVG	22	AMDLLILNSLPLVSD
TIM1_HUMAN	MAPFEPLASGILLLLWLIAPSRA	23	CTCVPPHPQTAFCSN
TL19_HUMAN	METRPRLGATCLLGFSLLLVSSDG	26	HNGLGKGFGDHIHWR
TLR1_HUMAN	MTSIFHFIIIFMLILQIRIQLSEE	24	SEFLVDRSKNGLIHV
TLR3_HUMAN	MRQTLPCIYFWGGLLPFGMLCAS	23	STTKCTVSHEVADCS
TLR4_HUMAN	MMSASRLAGTLIPAMAFSLCVRP	23	ESWEPCVEVVPNITY
TLR5_HUMAN	MGDHLDLLLGVVLMAGPVFG	20	IPSCSFDGRIAFYRF
TNR5_HUMAN	MVRLPLQCVLWGCCLLTAVHP	20	EPPTACREKQYLINS
TNR7_HUMAN	MARPHPWVLCVGLTLVGLS	19	ATPAPKSCPERHYWA
TNR9_HUMAN	MGNSCYNIVATLLLVLNFERTRS	23	LQDPCSNCPAGTFCD
TR14_HUMAN	MEPPGDWGGPPWRSTPKTDVLRVLYLTFGLGAPCYAPA	38	LPSCKEDEYPPVGSEC
TR18_HUMAN	MAQHGMAGAFRALCGLALLCALSLG	25	QRPTGGPGCGPGRLL
TR19_HUMAN	MALKVLEQEKTFFTLLVLLGYLSCKVTC	29	ESGDCRQQEFRDRSG
TRLT_HUMAN	MKPSLLCRPLSCFLMLLPWPLATLT	25	STTLWQCPPGEEPDL
UGR2_HUMAN	MKLAALLGLCVALSCESSARA	20	FLVGSAPVAPQVAA
UR2_HUMAN	MYKLASCLLFIGFLNPLLS	20	LPLLDSREISFQLSA
VCA1_HUMAN	MPGKMVVILGASNILWIMFAASQA	24	FKIETTPESRYLAQI
VEGA_HUMAN	MNLLSWVHWSLALLLYLHHAKWSQA	26	APMAEGGQNHHEVV
VEGC_HUMAN	MHLGFFSVACSLLAALLPGPREAPAAAAA	31	FESGLDLSDAEPDAG
VGR3_HUMAN	MQRGAALCLRLWLCLGLLDGLVSG	24	YSMTPTPLNITEESH
WSP2_HUMAN	MRGTPKTHLLAFSLCLLSKVRT	23	QLCPTPCTCPWPPPR
XP_059401	MLPPMALPSVSWMLLSCLILLCQVQG	26	EETQKELPSPRISCP
XP_086156	MEAPGPRALRTALCGGCCCLLCAQLAVA	29	GKGARGFGRGALIRL
XP_113683	MQQRGAAGSRGALFLLGVLFQGVYIVFS	31	LEIRADAHVRGVVGE
XP_166510	MMLHSALGLCLLLVTSSNLA	21	IAIKKEKRPPTLSR
XP_166856	MLLISLLLAAGLMHSDA	17	GTSCFVLCTCRNQVV
XP_171078	MALGVPI SVYLLFNAMTALTEE	22	AAVTVTPPIAQQGN
XP_208606	MMVALRGASALLVFLAFLPPPQCTQD	28	PAMVHYIYQFRVLE
XP_208962	MERGAGAKLLPLLLLLRATGFTCA	24	QTDGRNGYTAVIEVT
XP_209141	MKVLISL LLLLPLMLMSMVSS	22	SLNPGVARGHRDRGQ
XP_291069	MARMSFVIAACQLVLLGMLTSLTES	25	SIQNSECQLCVCEI
ZA2G_HUMAN	MVPVLLSLLLLGPAVF	17	QENQDGRYSLTYIYT

The SwissProt accessions are preferentially used when multiple accessions from different data sources are available.