

Supplementary materials

Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners

Judith Weisz,¹ and Vladimir N. Uversky^{2,3,*}

¹ Departments of Gynecology and Pathology, Pennsylvania State University College of Medicine, Hershey, PA 17033, USA; E-Mail: jxw7@psu.edu

² Institute for Biological Instrumentation of the Russian Academy of Sciences, Federal Research Center “Pushchino Scientific Center for Biological Research of the Russian Academy of Sciences”, Pushchino, 142290 Moscow, Russia

³ Department of Molecular Medicine and USF Health Byrd Alzheimer’s Research Institute, Morsani College of Medicine, University of South Florida, Tampa, FL 33612, USA

* Correspondence: vuffersky@usf.edu; Tel.: +1-813-974-5816 (ext. 123); Fax: +1-813-974-7357.

Amino acid sequences of Human Annexins

>sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2
MAMVSEFLKQAWFIENEEQEYVQTVKSSKGGPGSAVSPYPTFNPSSDVAALHKAIMVKGV
DEATIIDILTKRNNARQQIKAAAYLQETGKPLDETLKKALTGHLEEVVLALLKTPAQFDA
DELRAAMKGLGTDEDTLIEILASRTNKEIRDINRVYREELKRDIAKDITSDTSGDFRNAL
LSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTILTTRSYPQLRRVFQKY
TKYSKHDMNKVLDLELKGDIKCLTAIVKCATSKPAFFAEKHLHQAMKGVGTRHKALIRIM
VSRSEIDMNDIKAFYQKMYGISLCQAILDDETKGDYEKILVALCGGN
PDB ID: 1AIN; 346 residues

>sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2
MSTVHEILCKLSLEGDHSTPPSAYGSVKAYTNFDAERDALNIETAIKTKGVDEVTIVNII
TNRSNAQRQDIAFAYQRRTKELASALKSALSGHLETVILGLLKTPAQYDASELKASMKG
LGTDEDSLIEIICSRTNQELQEIINRVYKEMYKTDLEKDIISDTSGDFRKLMLVALAKGRR
EDGSVIDYELIDQDARDLYDAGVKRKGTDVPKWISIMTERSVPHLQKVFDKYSPYDM
LESIRKEVKGDLNENAFNLVQCIQNKPLYFADRLYDSMKGKGTDRDKVLIRIMVSRSEVDM
LKIRSEFKRKYGKSLYYYIQQDTKGDYQKALLYLCGGDD
PDB ID: 1W7B; 339 residues

>sp|P12429|ANXA3_HUMAN Annexin A3 OS=Homo sapiens OX=9606 GN=ANXA3 PE=1 SV=3
MASIWVGHRTVRDYPDFSPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEY
QAAYGKELKDDLKGLDLSGHFEHLMVALVTPPAVFDKQLKSMKGAGTNEDALIEILTTR
TSRQMKDISQAYYTVYKKSIGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQ
ILYKAGENRWGTDEDKFTEILCLRSFPQLKLTDFEYRNISQKDIVDSIKGELSGHFEDLL
LAIVNVCVRNTPAFLAERLHRALKGIGTDEFTLNRIMVSRSEIDLLDIRTEFKKHGYSLY
SAIKSDTSGDYEITLLKICGGDD
PDB ID: 1AXN; 323 residues

>sp|P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens OX=9606 GN=ANXA4 PE=1 SV=4
MATKGGTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNATAQRQEIRTAYKSTI
GRDLIDDLKSELSGNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEE
IRRISQTYQQQYGRSLEDDIRSDTSFMFORVLVLSAGGRDEGNYLDDALVRQDAQDLYE
AGEKKWGTDEVKFLTVLCSRNRNHLHVFDEYKRISQKDIEQSIKSETSGSFEDALLAIV
KCMRNKSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSFIK
GDTSGDYRKVLLVLCGGDD
PDB ID: 2ZOC; 319 residues

>sp|P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2
MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
FGRDLLDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
ELRAIKQVYEEYGSSEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF
QAGELKWTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
KGTSGDYKKALLLLCGEDD
PDB ID: 1AVR; 320 residues

>sp|P08133|ANXA6_HUMAN Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3
MAKPAQGAQYRGSIHDFPGFDPNQDAEALYTAMKGFSGDKEAILDIITSRSNRQRQEVQ
SYKSLYGKDLIADLKYELTGKFERLIVGLMRPPAYCDAKEIKDAISGIGTDEKCLIEILA
SRTNEQMHQLVAAYKDAYERDLEADIIGDTSGHFQKMLVLLQGTREEDDVVSEDLVQQD
VQDLYEAGELKWTDEAQFIYILGNRSKQHLRLVDFEYLYKTTGKPIEASIRGELSGDFEK
LMLAVVKCIRSTPEYFAERLFAKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTKYEKS
LYSMIKNDTSGEYKKTLLKLSGGDDAAGQFFPEAAQVAYQMWELSAVARVELKGTVRPA
NDFNPDADAKALRKAMKGLGTDEDTIIDIIITHRSNVQRQIRQTFKSHFGRDLMTDLKSE
ISGDLARLILGLMPPAHYDAKQLKKAMEGAGTDEKALIEILATRTNAEIRAINAYKED

YHKSLEDALSSDTSGHFRILISLATGHREEGGENLDQAREDAQVAEILEIADTPSGDK
TSLETRFMTILCTRSYPHLRRVFQEFIKMTNYDVEHTIKKEMSGDVRDAFVAIVQSVKNK
PLFFADKLYKSMKGAGTDEKTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSGD
FLKALLALCGGED
PDB ID: 1M9I; 673 residues

>sp|P20073|ANXA7_HUMAN Annexin A7 OS=Homo sapiens OX=9606 GN=ANXA7 PE=1 SV=3
MSYPGYPPPTGYPPFGYPAGQESSFPSPGQYPYPSGFPPMGGGAYPQVPSSGYPGAGGY
PAPGGYPAPGGYPGAPQPGGAPSYPGVPPGQGFGVPPGGAGFSGYPQPPSQSYGGGPAQV
PLPGGFPGGQMP SQYPGQPTYP SQINTDSFSSYPVFSVSLDYSSEPATVTQVTQGTIR
PAANFDAIRDAEILRKAMKGFGTDEQAIVDVVANRSDNRQKIKAAFKTSYKDLIKDLK
SELSGNMEELILALFMPPTYDDAWSLRKAMQGAGTQERVLEILCTRTNQEIREIVRCYQ
SEFGRDLEKDIRSDTSGHFERLLVSMCQGNRDENQ SINHQMAQEDAQRLYQAGEGRLGTD
ESCFNMILATRSFPQLRATMEAYS RMANRDLLSVSREFSGYVESGLKTI LQCALNRPAF
FAERLYYAMKGAGTDDSTLVRIVVTRSEIDL VQIKQMFQMYQKTLGTMIAGDTSGDYRR
LLLAIVGQ
No structure; 488 residues

>sp|P13928|ANXA8_HUMAN Annexin A8 OS=Homo sapiens OX=9606 GN=ANXA8 PE=1 SV=3
MAWWKSWIEQEGVTVKSSSHFNPDPAETLYKAMKGIGTNEQAIIDVLTKRSNTQRQQIA
KSFKAQFGKDLTETLKSELSGKFERLIVALMYPPYRYEAKELHDAMKGLGTKEGVIIIEIL
ASRTKNQLREIMKAYEEDYGSSLEEDIQADTSGLERILVCLLQGSRDDVSSFVDPGLAL
QDAQDLYAAGEKIRGTDEMKFITILCTRSATHLLRVFEEYEKIANKSIEDSIKSETHGSL
EEAMLT VVKCTQNLHSYFAERLYYAMKGAGTRDGT LIRNIVSRSEIDLNLIKCHFCKMYG
KTLSSMIMEDTSGDYKNALLSLVGSDP
PDB ID: 1W3W; 327 residues

>sp|O76027|ANXA9_HUMAN Annexin A9 OS=Homo sapiens OX=9606 GN=ANXA9 PE=1 SV=3
MSVTGGKMAPSLTQEILSHLGLASKTAAWGTLGLTFLNFSVDKDAQRLRLRAITGQGV
RSAIVDVL TNRSREQRLISRNFQERTQQDLMKSLQAALSGNLERIVMALLQPTAQFDAQ
ELRTALKASDSAVDVAIEILATRTPPQLQECLAVYKHNQVEAVDDITSETSGILQDLLL
ALAKGGRDSYSGIIDYNLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
TGQEELEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQETEPNYQVLIRILISR
CETDLLSIRAEFRKKFGKSLYSSLQDAVKGDCQSALLALCRAEDM
No structure; 345 residues

>sp|Q9UJ72|ANX10_HUMAN Annexin A10 OS=Homo sapiens OX=9606 GN=ANXA10 PE=1
SV=3
MFCGDYVQGTIFPAPNFPNIMDAQMLGGALQGFDCDKMLINILTQRCNAQRMMIAEAYQ
SMYGRDLIGDMREQLSDHFKDVMAGLMYPPPLYDAHELWHAMKGVGTDENCLIEILASRT
NGEIFQMREAYCLQYSNNLQEDIYSETSGHFRDTLMNLVQGTREEGYTDPAMAAQDAMVL
WEACQQKTGEHKTMLQMILCNKSYQQRLRVFQEFQNISGQDMVD AINECYDGYFQELLVA
IVLCVRDKPAYFAYRLYSAIHDFGFHNKTVIRIL IARSEIDLLTIRKRYKERYGKSLFHD
IRNFASGHYKKALLAICAGDAEDY
No structure; 324 residues

>sp|P50995|ANX11_HUMAN Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1
SV=1
MSYPGYPPPPGGYPAPAGGGPWGGAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGMAAN
MSGTFGGANMPNLYPGAPGAGYPPVPPGGFGQPPSAQQPVPPYGMYPGGNPPSRMP
PPYPGAPVPQGPMPPPGQPPGAYPGQPPVTPYQPPVPLPGQQQPVPSYPGYPGSGTVT
PAVPPTQFGSRGTITDAPGFDPLRDAEVL RKAMKGFGTDEQAIIDCLGSRSNKQRQQIIL
SFKTAYGKDLIKDLKSELSGNFEKTILALMKTPVLFDIYEIKEAIKGVGTDEACLIEILA
SRSNEHIRELNRAYKA EFKKTL EEAIRSDTSGHFQRL LISLSQGNRDESTNVDMSLAQ
AQELYAAGENRLGTD ESKFNAVLCSRSRAHLVAVFNEYQRM TGRDIEKSICREMSGDLEE
GMLAVVKCLKNTPAFFAERLNKAMRGAGTKDR TLRIMVSRSETDLLDIRSEYKRMYGKS

LYHDISGDTSGDYRKILLKICGGND
No structure; 505 residues

>sp|P27216|ANX13_HUMAN Annexin A13 OS=Homo sapiens OX=9606 GN=ANXA13 PE=1
SV=3
MGNRHAKASSPQGFDVDRDAKKLNKACKGMGTNEAAIIEILSGRTSDERQQIKQKYKATY
GKELEEV LKSEL SGNFEKTALALLDRPSEYAARQLQKAMKGLGTDESVLIEVLCTR TNKE
IIAIKEAYQRLFDRLSDVKGDTSGNLKKILVSL LQANRNEGDDVDKDLAGQDAKDLYD
AGEGRWGTDELAFNEVLAKRSYKQLRATFQAYQILIGKDIEEAIEEETSGDLQKAYLTLV
RCAQDCEDYFAERLYKSMKGAGTDEETLIRIVVTRAEVDLQGIKAKFQEKYQKSLSDMVR
SDTSGD FRKLLVALLH
PDB ID: 6B3I 316 residues

Amino acid sequences of Human S100 proteins

>sp|P23297|S10A1_HUMAN Protein S100-A1 OS=Homo sapiens OX=9606 GN=S100A1 PE=1 SV=2
MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVAVDKVMK
ELDENGDGQVDFQYVVLVAALTVACNNFFWENS
PDB ID: 2LP3; 94 residues

>sp|P29034|S10A2_HUMAN Protein S100-A2 OS=Homo sapiens OX=9606 GN=S100A2 PE=1 SV=3
MMCSSLEQALAVLVTTTFHKYSCQEGDKFKLSKGEMKELLHKELPSFVGEKVDEEGLKKLM
GSLDENSQQVDFQYAVFLALITVMCNDFFQGCPCDRP
PDB ID: 4DUQ; 98 residues

>sp|P33764|S10A3_HUMAN Protein S100-A3 OS=Homo sapiens OX=9606 GN=S100A3 PE=1 SV=1
MARPLEQAVAAIVCTFQYAGRCGDKYKLCQAEKELLQKELATWTPTEFRECDYNKFMS
VLDTNKDCEVDFVEYVRSLACLCLYCHEYFKDCPSEPPCSQ
PDB ID: 3NSK; 101 residues

>sp|P26447|S10A4_HUMAN Protein S100-A4 OS=Homo sapiens OX=9606 GN=S100A4 PE=1 SV=1
MACPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMS
NLDSNRDNEVDFQYCVFLSCIAMMCNEFFEGFPDKQPRKK
PDB ID: 2MRD; 101 residues

>sp|P33763|S10A5_HUMAN Protein S100-A5 OS=Homo sapiens OX=9606 GN=S100A5 PE=1 SV=2
METPLEKALTMTVTTTFHKYSGREGSKLTLSRKELKELIKKELCLGEMKESSIDDLMKSLD
KNSDQEIDFKEYSVFLTMLCMAYNDFFLDNK
PDB ID: 2KAX; 92 residues

>sp|P06703|S10A6_HUMAN Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1
MACPLDQAIGLLVAIFHKYSGREGDKHTLSKKELKELIQKELTIGSKLQDAEIARLMEDL
DRNKDQEVNFQYVTFLLGALALIYNEALKG
PDB ID: 1K8U; 90 residues

>sp|P31151|S10A7_HUMAN Protein S100-A7 OS=Homo sapiens OX=9606 GN=S100A7 PE=1 SV=4
MSNTQAERSIIGMIDMFHKYTRRDDKIEKPSLLTMMKENFPNFLSACDKKGTNYLADVFE
KKDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ
PDB ID: 1PSR; 101 residues

>sp|Q86SG5|S1A7A_HUMAN Protein S100-A7A OS=Homo sapiens OX=9606 GN=S100A7A PE=1 SV=3
MSNTQAERSIIGMIDMFHKYTRDGDGKIEKPSLLTMMKENFPNFLSACDKKGIHYLATVFE
KKDKNEDKKIDFSEFLSLLGDIADYHKQSHGAAPCSGGSQ
PDB ID: 4AQI; 101 residues

>sp|Q5SY68|S1A7B_HUMAN Protein S100-A7-like 2 OS=Homo sapiens OX=9606
GN=S100A7L2 PE=1 SV=1
MNIPLGEKVMLDIVAMFRQYSGDDGRMDMPGLVNLMKENFPNFLSGCEKSDMDYLSNALE
KKDDNKDKKVNYSEFLSLLGDITIDHHKIMHGVAPCSGGSQ
No structure; 101 residues

>sp|P05109|S10A8_HUMAN Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1
SV=1
MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLLKKLLETCEPQYIRKKGADVWFKELDI
NTDGAVNFQEFLLILVIKMGVAAHKKSHKE
PDB ID: 1MR8; 93 residues

>sp|P06702|S10A9_HUMAN Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1
SV=1
MTCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIE
HIMEDLDTNADKQLSFEEFIMLMARLTWASHEKMHEGDEGPGHHHKPGLGEGTP
PDB ID: 5I8N; 114 residues

>sp|P60903|S10AA_HUMAN Protein S100-A10 OS=Homo sapiens OX=9606 GN=S100A10
PE=1 SV=2
MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLD
QCRDGKVGFSFFSLIAGLTACNDYFVVHMKQKGGK
PDB ID: 4FTG; 97 residues

>sp|P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens OX=9606 GN=S100A11
PE=1 SV=2
MAKISSPTETERCIESLIAVFQKYAGKDGNYTSLKTEFLSFMNTELAFTKNQKDPGVL
DRMMKKLDTNSDGQLDFSEFLNLIGGLAMACHDSFLKAVPSQKRT
PDB ID: 2LUC; 105 residues

>sp|P80511|S10AC_HUMAN Protein S100-A12 OS=Homo sapiens OX=9606 GN=S100A12
PE=1 SV=2
MTKLEEHLEGIVNIFHQYSVRKGFDTLSKGELKQLLTKEANTIKNIKDKAVIDEIFQG
LDANQDEQVDFQEFISLVAIALKAAHYHTHKE
PDB ID: 2M9G; 92 residues

>sp|Q99584|S10AD_HUMAN Protein S100-A13 OS=Homo sapiens OX=9606 GN=S100A13
PE=1 SV=1
MAAEPLTELEESIETVVTFTFFARQEGRKDSLVSNEFKELVTQQLPHLLKDVGSLDEKM
KSLDVNQDSELKFNEYWRLIGELAKEIRKKKDLKIRKK
PDB ID: 1YUS; 98 residues

>sp|Q9HCY8|S10AE_HUMAN Protein S100-A14 OS=Homo sapiens OX=9606 GN=S100A14
PE=1 SV=1
MGQCRSANAEDAQEFSDVERAIETLIKNFHQYSVEGGKETLTPSELRLDVTQQLPHLMPS
NCGLEEKIANLGSNDKLEFRSFWELIGEAAKSVKLERPVRGH
PDB ID: 2M0R; 104 residues

>sp|Q96FQ6|S10AG_HUMAN Protein S100-A16 OS=Homo sapiens OX=9606 GN=S100A16
PE=1 SV=1
MSDCYTELEKAVIVLVENFYKYVSKYSLVKNKISKSSFREMLQKELNHMLSDTGNRKAAD
KLIQNLDANHDGRISFDEYWTLLGGITGPIAKLIHEQEQQSSS
PDB ID: 2L50; 103 residues

>sp|P04271|S100B_HUMAN Protein S100-B OS=Homo sapiens OX=9606 GN=S100B PE=1 SV=2
MSELEKAMVALIDVFHQYSGREGDKHKLKSELKELINNELSHFLEEIKEQEVVDKVMET
LDNDGDGECDFQEEFMAFVAMVTTACHEFFEHE
PDB ID: 1UWO; 92 residues

>sp|P29377|S100G_HUMAN Protein S100-G OS=Homo sapiens OX=9606 GN=S100G PE=3 SV=2
MSTKKSPEELKRIFEKYAAKEGDPDQLSKDELKLLIQAEFPSLLKGPNTLDDLFQELDKN
GDGEVSFEEFQVLVKKISQ
No structure; 79 residues

>sp|P25815|S100P_HUMAN Protein S100-P OS=Homo sapiens OX=9606 GN=S100P PE=1 SV=2
MTELETAMGMIIDVFSRYSGSEGSTQTLTKGELKVLMEKELPGFLQSGKDKDAVDKLLKD
LDANGDAQVDFSEFIVFVAAITSACHKYFEKAGLK
PDB ID: 1OZO; 95 residues

>sp|Q8WXG8|S100Z_HUMAN Protein S100-Z OS=Homo sapiens OX=9606 GN=S100Z PE=1 SV=4
MPTQLEMAMDTMIRIFHRYSGKERKRFKLSKGELKLLQLRELTEFLSCQKETQLVDKIVQ
DLDANKDNEVDFNEFVVMVAALTVACNDYFVEQLKKKGK
PDB ID: 5HYD; 99 residues

>sp|Q5QJ38|TCHL1_HUMAN Trichohyalin-like protein 1 (Protein S100-A17) OS=Homo sapiens OX=9606 GN=TCHL1 PE=2 SV=1
MPQLLRNVLCVIEFTHKYASEDSNGATLTGRELKQLIQGEFGDFFQPCVLHAVEKNSNLL
NIDSNGLIISFDEFVLAIFNLLNLCYLDIKSLLSSELRQVTKPEKEKLDDVDVQATTGDGQ
WTVGTSPTQEKRLMPSGMASSSQLIPEESGAVGNRRVDPWREAKTHNFPGEASEHNDPKN
KHLEGDEQSQEVAQDIQTEDNEGQLKTNKPMAGSKKTSSPTERKQDKEISQEGDEPAR
EQSVSKIRDQFGEQEGNLATQSSPPKEATQRPCEDQEV RTEKEKHSNIQEPPLQREDEPS
SQHADLPEQAAARSPSQTKSTDSKDVCRMFDTQEPGKDADQTPAKTKNLGEPEDYGRTS
ETQEKECETKDLPVQYGSRNGETSDMRDERKERRGPEAHGTAGQKERDRKTRPLVLETQ
TQDGKYQELQGLSKSKDAEKGSETQYLSSEGGDQTHPELEGTAVSGEEAEHTKEGTAEAF
VNSKNAPAAERTLGARETQDLAPLEKQSVGENTRVTKTHDQPVVEEDGYQGDPESPFT
QSDEGSSETPNLASEEGNSSSETGELPVQGDSSQSGDQHGESVQGGHNNNPDTQRQGT
GEKNRALEAVVPAVRGEDVQLTEDQEQPARGEHKNQPGTKGPGA AVEPNGHPEAQESTA
GDENRKSLEIEITGALDEDFDQLSLMQLPGKGDNRNELKVQGPSSKEEKGRATEAQNTL
LESLEDNSASLKIQLTKPEVPTSEEEDESPQELAGEGGDQKSPAKKEHNSVWPSSLEK
QMQRDQEPCSV ERGAVYSSPLYQYLQEKILQQTNTVTQEEHQKQVQIAQASGPCLCSVSLT
SEISDCSVFFNYSQASQPYTRGLPLDESPAGAQETPAPQALEDKQGHQPQRRERLVLQREAS
TTKQ
No structure; 904 residues

>sp|Q86YZ3|HORN_HUMAN Hornerin (Protein S100-A18) OS=Homo sapiens OX=9606 GN=HRNR PE=1 SV=2
MPKLLQG VITVIDVFYQYATQHGEYDTLNKAELKELLENEFHQILKNPNPDPTVDIILQS
LDRDHNKKVDFTEYLLMIFKLQARNKIIGKDYCQVSGSKLRDDTHQHQQEEQEETEKEEN
KRQESSFSHSSWSAGENDSYSRNVGRSLKPGTESISRRLSFQRDFSGQHNSYSGQSSSYG
EQNSDSHQSSGRGQCGSGSGQSPNYGQHGSGSGQSSSNDTHGSGSGQSSGFSQHKSSSGQ
SSGYSQHSGSGHSSGYGQHGSRSGQSSRGERHRSSSGSSSYGQHGSGSRQSLGHGRQG
SGSRQSPSHVRHSGSGHSSSHGQHGSGSSYSYSRGHYESGSGQTSFGGQHESGSGQSSG
YSKHGSGSGHSSSQGHGSTSGQASSSGQHSGSSSRQSSSYGQHESASRHSSGRGQHSSGS
GQSPGHGQRGSGSGQSPSSQHGHTGFRSSSSGPPYVSGSGYSSGFGHHESSEHSSGYTQ
HGSGSGHSSGHGQHGSRSGQSSRGERQGSAGSSSSYGQHGSGSRQSLGHSRHSGSGSQS

PSPSRGRHESGSRQSSSYGPHGYGSGRSSSRGPYESGSGHSSGLGHQESRSGQSSSGYGQH
GSSSGHSSSTHGQHGSTSGQSSSCGQHGATSGQSSSHGQHSGSSQSSRYGQQGSGSGQSP
SRGRHGSDFGHSSSYGQHSGSGWSSSNPGHGSVSGQSSGFGHKSGSGQSSGYSQHSGGS
SHSSGYRKHGSRSGQSSRSEQHGSSSGLSSSYGQHSGSGHQSSGHGRQGSGSGHSPSRVR
HGSSSGHSSSHGQHSGTSCSSSCGHYESGSGQASGFGQHESGSGQGYSQHGSASGHFSS
QGRHGSTSGQSSSSGQHDSSSGQSSSYGQHEASASHASGRGRHGSGSGQSPGHGQRGSGS
GQSPSYGRHGSGSGRSSSSGRHGSGSGQSSGFGHKSSSGQSSGYTQHSGSGHSSSYEQH
GSRSGQSSRSEQHGSSSGSSSSSYGQHSGSGRQSLGHGQHSGSGQSPSPSRGRHGSGSGQ
SSSYGPYRSGSGWSSSRGPYESGSGHSSGLGHRESRSGQSSGYGQHSGSSGHSSSTHGQH
STSGQSSSCGQHGAASSGQSSSHGQHSGSSQSSGYGRQGSGSGQSPGHGQRGSGSRQSPS
YGRHGSGSGRSSSSGQHSGSLGESSGFGHHESSSGQSSSYSQHSGSGHSSGYGQHGSRS
GQSSRGERHGSSSGSSSHYQHGSGSRQSSGHGRQGSGSGHSPSRGRHGSLGHSSSHGQ
HGSGSGRSSSRGPYESRSGHSSVFGQHEGSGSGHSSAYSQHSGSGGHFCSQGQHGSTSGQS
STFDQEGSSTGQSSSYGHRGSGSSQSSGYGRHGAGSGQSPSRGRHGSGSGHSSSYGQHGS
GSGWSSSSGRHGSGSGQSSGFGHHESSWQSSGCTQHSGSGHSSSYEQHGSRSQGSSRG
ERHGSSSGSSSYGQHSGSGRQSLGHGQHSGSGQSPSPSRGRHGSGSGQSSSYSPYGS
SGWSSSRGPYESGSSSHSSGLGHRESRSGQSSGYGQHSGSSGHSSSTHGQHGSTSGQSSSC
QHGAASSGQSSSHGQHSGSSQSSGYGRQGSGSGQSPGHGQRGSGSRQSPSYGRHGSGSGR
SSSSGQHSGSLGESSGFGHHESSSGQSSSYQHSGSGHSSGYGQHGSRSQGQSSRGERHG
SSSRSSRYGQHSGSGRQSSSGHGRQGSGSGQSPSRGRHGSLGHSSSHGQHSGSGSRSS
RGPYESRSGHSSVFGQHEGSGSGHSSAYSQHSGSGGHFCSQGQHGSTSGQSSTFDQEGSST
GQSSSHGQHSGSSQSSSYGQQGSGSGQSPSRGRHGSGSGHSSSYGQHSGSGWSSSSGR
HGSGSGQSSGFGHHESSWQSSGYTQHSGSGHSSSYEQHGSRSQGQSSRGEQHSGSSGSS
SSYGQHSGSGRQSLGHGQHSGSGQSPSPSRGRHGSGSGQSSSYGPYGS SGWSSSRGPY
ESGSGHSSGLGHRESRSGQSSGYGQHSGSSGHSSSTHGQHGSASGQSSSCGQHGAASSGQSS
SHGQHSGSGSSQSSGYGRQGSGSGQSPGHGQRGSGSRQSPSYGRHGSGSGRSSSSGQHGP
LGESSGFGHHESSSGQSSSYSQHSGSGHSSGYGQHGSRSQGQSSRGERHGSSSGSSSYG
QHSGSGRQSSGHGRQGSGSGHSPSRGRHGSGSGHSSSHGQHSGSGRSSSRGPYESRSGH
SSVFGQHEGSGSGHSSAYSQHSGSGGHFCSQGQHGSTSGQSSTFDQEGSSTGQSSSHGQH
SGSSQSSSYGQQGSGSGQSPSRGRHGSGSGHSSSYGQHSGSGWSSSSGRHGSGSGQSSG
FGHHESSWQSSGYTQHSGSGHSSSYEQHGSRSQGQSSRGERHGSSSGSSSYGQHSGS
RQSLGHGQHSGSGQSPSPSRGRHGSGSGQSSSYSPYGS SGWSSSRGPYESGSGHSSGL
GHRESRSGQSSGYGQHSGSSGHSSSTHGQHGSTSGQSSSCGQHGAASSGQSSSHGQHSGSG
QSSGYGRQGSGSGQSPGHGQRGSGSRQSPSYGRHGSGSGRSSSSGQHSGSLGESSGFGHH
ESSSGQSSSYSQHSGSGHSSGYGQHGSRSQGQSSRGERHGSSSGSSSHYQHGSGSRQSS
GHGRQGSGSGQSPSRGRHGSLGHSSSHGQHSGSGRSSSRGPYESRLGHSSVFGQHESG
SGHSSAYSQHSGSGGHFCSQGQHGSTSGQSSTFDQEGSSTGQSSSYGHRGSGSSQSSGY
RHGAGSGQSLSHGRHGSGSGQSSSYGQHSGSGQSSGYSQHSGSGQDGYSYCKGGSNHD
GSSSGSYFLSPSSSTSPYEVVQEQRCYFYQ

No structure; 2850 residues

UniProt IDs of human annexins and S100 proteins

Annexins

P04083
P07355
P12429
P09525
P08758
P08133
P20073
P13928
O76027
Q9UJ72
P50995
P27216

S100 proteins

P23297
P29034
P33764
P26447
P33763
P06703
P31151
Q86SG5
Q5SY68
P05109
P06702
P60903
P31949
P80511
Q99584
Q9HCY8
Q96FQ6
P04271
P29377
P25815
Q8WVG8
Q5QJ38
Q86YZ3

CLUSTAL O(1.2.4) multiple sequence alignment

sp P04083 ANXA1_HUMAN	AMKGLGTDDEDTLIEILASRTNKEIRDIRNVYREELKKRLAKDITSDTSGDFRNALLSLAK	185
sp P07355 ANXA2_HUMAN	SMKGLGTDDEDSLIEILCSRTNQELQEIINRVYKEMKYKLTDEKDIISDTSGDFRKLMLVALAK	176
sp P12429 ANXA3_HUMAN	SMKAGTNEDALIELTTRTSRQMKDISQAYYTVYKSLGDDISSETSGDFRKKALLTLAD	161
sp P09525 ANXA4_HUMAN	AMKGAGTDEGCLIELLASRTPEEIRIRISQTYQQQYGRSLEDDIRSDTGFMFQRVLVSLSA	157
sp P08758 ANXA5_HUMAN	ALKGAGTNEKVLTEIIASRTPEELRAIKQYDEEYGGSSLEDDVVGDTSGYYQRMLVVLLQ	158
sp P08133 ANXA6_HUMAN	AISGIGTDEKCLIELIEILASRTNEQMHLQVLAAYKDAYERDLEADIGDTSGHFQKMLVVLLQ	163

sp P20073 ANXA7_HUMAN	AMQGAGTQERVLIEILCTRTRNQEI REIVRCYQSEFGRDLEKDIRSDTSGHFERLLVSMCQ	328
sp P13928 ANXA8_HUMAN	AMKGLGTKEGVIIEILASRTKNQLEIRIMKAYEEDYGSSELEDIQTADTSGYLERILVCLLQ	164
sp O76027 ANXA9_HUMAN	ALKASDSDAVDVIIEILAFTRTPPQLQCECLVYKHNFGVEAVDDITSETSGILQDLLALAK	184
sp Q9UJ72 ANX10_HUMAN	AMKGVGTDENCLIEILASRTNGEIFQMREAYCLQYSNNLQEDIYSETSGHFRTDLMNLVQ	160
sp P50995 ANX11_HUMAN	AIKGVGTDEACLIEILASRSNEHIRELNRAYKAEFKKTLLEAIRSDTSGHFQRLILSLSQ	343
sp P27216 ANX13_HUMAN	AMKGLGTDESVLIEVLCTRTRNKEIIAIEKAYQRLFDRLSDVKGDTSGNLKKILVSLQ	157
	:. . . . : * : : * : . : *	
	:. . . . : * : : * : . : *	

sp P09525 ANXA4_HUMAN	-----	319
sp P08758 ANXA5_HUMAN	-----	320
sp P08133 ANXA6_HUMAN	ATRTNAEIRAINAEYKEDYHKSLEDALSSDTSGHFRRLISLATGHREEGGENLDQARED	522
sp P20073 ANXA7_HUMAN	-----	488
sp P13928 ANXA8_HUMAN	-----	327
sp O76027 ANXA9_HUMAN	-----	345
sp Q9UJ72 ANX10_HUMAN	-----	324
sp P50995 ANX11_HUMAN	-----	505
sp P27216 ANX13_HUMAN	-----	316

sp P04083 ANXA1_HUMAN	-----	346
sp P07355 ANXA2_HUMAN	-----	339
sp P12429 ANXA3_HUMAN	-----	323
sp P09525 ANXA4_HUMAN	-----	319
sp P08758 ANXA5_HUMAN	-----	320
sp P08133 ANXA6_HUMAN	AQVAAEILEIADTPSGDKTSLETRFMTILCTRSYPHLRRVFQEFIKMTNYDVEHTIKKEM	582
sp P20073 ANXA7_HUMAN	-----	488
sp P13928 ANXA8_HUMAN	-----	327
sp O76027 ANXA9_HUMAN	-----	345
sp Q9UJ72 ANX10_HUMAN	-----	324
sp P50995 ANX11_HUMAN	-----	505
sp P27216 ANX13_HUMAN	-----	316

sp P04083 ANXA1_HUMAN	-----	346
sp P07355 ANXA2_HUMAN	-----	339
sp P12429 ANXA3_HUMAN	-----	323
sp P09525 ANXA4_HUMAN	-----	319
sp P08758 ANXA5_HUMAN	-----	320
sp P08133 ANXA6_HUMAN	SGDVRDAFVAIVQSVKNKPLFFADKLYKSMKGAGTDEKTLTRIMVSRSEIDLLNIRREFI	642
sp P20073 ANXA7_HUMAN	-----	488
sp P13928 ANXA8_HUMAN	-----	327
sp O76027 ANXA9_HUMAN	-----	345
sp Q9UJ72 ANX10_HUMAN	-----	324
sp P50995 ANX11_HUMAN	-----	505
sp P27216 ANX13_HUMAN	-----	316

sp P04083 ANXA1_HUMAN	-----	346
sp P07355 ANXA2_HUMAN	-----	339
sp P12429 ANXA3_HUMAN	-----	323
sp P09525 ANXA4_HUMAN	-----	319
sp P08758 ANXA5_HUMAN	-----	320
sp P08133 ANXA6_HUMAN	EKYDKSLHQAIEGDTSGDFLKALLALCGGED	673
sp P20073 ANXA7_HUMAN	-----	488
sp P13928 ANXA8_HUMAN	-----	327
sp O76027 ANXA9_HUMAN	-----	345
sp Q9UJ72 ANX10_HUMAN	-----	324
sp P50995 ANX11_HUMAN	-----	505
sp P27216 ANX13_HUMAN	-----	316

Percent Identity Matrix - created by Clustal2.1

#

1:	sp P04083 ANXA1_HUMAN	100.00	52.52	48.91	45.43	42.45	43.34	42.40	44.00	34.23	39.18	44.06	43.17
2:	sp P07355 ANXA2_HUMAN	52.52	100.00	47.37	48.90	45.31	46.46	41.32	44.65	39.64	37.38	44.97	42.09
3:	sp P12429 ANXA3_HUMAN	48.91	47.37	100.00	52.66	49.38	50.77	45.17	48.61	35.62	42.99	51.39	42.09
4:	sp P09525 ANXA4_HUMAN	45.43	48.90	52.66	100.00	57.68	53.92	48.90	55.49	35.76	43.71	56.74	46.52
5:	sp P08758 ANXA5_HUMAN	42.45	45.31	49.38	57.68	100.00	56.88	48.11	55.00	36.91	37.30	52.81	43.04
6:	sp P08133 ANXA6_HUMAN	43.34	46.46	50.77	53.92	56.88	100.00	43.96	51.08	33.44	41.98	56.62	43.99
7:	sp P20073 ANXA7_HUMAN	42.40	41.32	45.17	48.90	48.11	43.96	100.00	49.07	31.36	36.99	51.91	49.05
8:	sp P13928 ANXA8_HUMAN	44.00	44.65	48.61	55.49	55.00	51.08	49.07	100.00	34.47	37.07	51.84	48.10
9:	sp O76027 ANXA9_HUMAN	34.23	39.64	35.62	35.76	36.91	33.44	31.36	34.47	100.00	29.78	35.38	30.35
10:	sp Q9UJ72 ANX10_HUMAN	39.18	37.38	42.99	43.71	37.30	41.98	36.99	37.07	29.78	100.00	41.74	34.29
11:	sp P50995 ANX11_HUMAN	44.06	44.97	51.39	56.74	52.81	56.62	51.91	51.84	35.38	41.74	100.00	46.84
12:	sp P27216 ANX13_HUMAN	43.17	42.09	42.09	46.52	43.04	43.99	49.05	48.10	30.35	34.29	46.84	100.00

Multiple sequence alignment of human S100 proteins

CLUSTAL O(1.2.4) multiple sequence alignment

```

sp|P23297|S10A1_HUMAN      -----MGSELETAMETLINVFHAHSGKEG-DKYKLSKKELKELLQTELSGFL      46
sp|P29034|S10A2_HUMAN      -----MMCSSLEQALAVLVTFHKEYSCQEG-DKFKLSKGEMKELLHKELPSFV      47
sp|P33764|S10A3_HUMAN      -----MARPLEQAVAAIVCTFQEYAGRCG-DKYKLCQAEKELLQKELATWT      46
sp|P26447|S10A4_HUMAN      -----MACPLEKALDVMVSTFHKYSGKEG-DKFKLNKSELKELLTRELPSFL      46
sp|P33763|S10A5_HUMAN      -----METPLEKALTMTVTFHKEYSGREG-SKLTLSRKELKELIKKELC--L      44
sp|P06703|S10A6_HUMAN      -----MACPLDQAIGLLVAIFHKYSGREG-DKHTLSKKELKELIQKELT--I      44
sp|P31151|S10A7_HUMAN      -----MSNTQAERSIIIGMIDMFHKYTRRDD---KIEKPSLLTMMKENFPNFL      44
sp|Q86SG5|S1A7A_HUMAN      -----MSNTQAERSIIIGMIDMFHKYTRDGD---KIEKPSLLTMMKENFPNFL      44
sp|Q5SY68|S1A7B_HUMAN      -----MNIPLGEKVMLDIVAMFRQYSGDDG---RMDMPGLVNLMMKENFPNFL      44
sp|P05109|S10A8_HUMAN      -----MLTELEKALNSIIDVYHKYSLIKG-NFHAVYRDDLKLLLETECPQYI      46
sp|P06702|S10A9_HUMAN      -----MTCKMSQLEARNIETIIINTFHQYSVKLG-HPDTLNQGEFKELVKDLQNFL      49
sp|P60903|S10AA_HUMAN      -----MPSQMEHAMETMMFTFHKFAGDKG---YLTKEDLRVLMEKEFPGF      43
sp|P31949|S10AB_HUMAN      -----MAKISSPTETERCIESLIAVFQKYAGKDG-YNITLSKTEFLSFMNTELAFT      51
sp|P80511|S10AC_HUMAN      -----MTKLEEHLEGIVNIFHQYSVRKG-HFDTLKSGELKQLLTKELANTI      45
sp|Q99584|S10AD_HUMAN      -----MAAEPLTELEESIETVVTFTFFARQEG-RKDSLSVNEFKELVQQLPHLL      50
sp|Q9HCY8|S10AE_HUMAN      MGQCRSANAEDAQEFSDVERAIETLIKNFHQYSVE-G-GKETLTPSELRLDLVTQQLPHLM      58
sp|Q96FQ6|S10AG_HUMAN      -----MSDCYTELEKAVIVLVENFYKYVSKYSLVKNKISKSSFREMLQKELNHML      50
sp|P04271|S10OB_HUMAN      -----MSELEKAMVALIDVFHQYSGREG-DKHKLKSELKELINNELSHFL      45
sp|P29377|S10OG_HUMAN      -----MSTKKSPEELKRIFEKYAAKEG-DPDQLSKDELKLLIQAEFPPLL      44
sp|P25815|S10OP_HUMAN      -----MTELETAMGMIIDVFSRYSGSEG-STQTLTKGELKVLMEKELPGFL      45
sp|Q8WXG8|S10OZ_HUMAN      -----MPTQLEMAMDTMIRIFHRYSGKER-KRFKLSKGELKLLQLRELTEFL      46
sp|Q5QJ38|TCHL1_HUMAN      -----MPQLLRNVLCVIETFHKYASEDS-NGATLTGRELKQLIQGEFGDFF      45
sp|Q86YZ3|HORN_HUMAN       -----MPKLLQGVITVIDVFYQYATQHG-EYDTLNKAELKELLENEFHQIL      45
      :      :      .      :      :      ::      :

```

```

sp|P23297|S10A1_HUMAN      DAQ--KDVDKAVDKVMKELDENGDEVDQFQYVVLVAALTVACNNFFWENS-----      94
sp|P29034|S10A2_HUMAN      GEK--VDEEGLKKLMGSLDENSDDQVDFQEYAVFLALITVMCNDFQGCPCDRP-----      98
sp|P33764|S10A3_HUMAN      PTE--FRECDYNKFMVSLDTNKDCVDFVEYVRSACLCLYCHEYFKDCPSEPPCSQ---      101
sp|P26447|S10A4_HUMAN      GKR--TDEAAFQKLMSNLDNRDNEVDQFQYCVFLSCIAMMCNEFFEGFPDKQPRKK---      101
sp|P33763|S10A5_HUMAN      GE---MKESSIDDLMKSLDKNSDQEI DFKEYSVFLTMLCMAYNDFLEDNK-----      92
sp|P06703|S10A6_HUMAN      GSK--LQDAEIA RL MEDLDRNKDQEVNFQYVTF LGALALIYNEALKG-----      90
sp|P31151|S10A7_HUMAN      SACDKKGTNYLADVFEKKDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ---      101
sp|Q86SG5|S1A7A_HUMAN      SACDKKGIHYLATVFEKKDKNEDKKIDFSEFLSLLGDIADYHKQSHGAAPCSGGSQ---      101
sp|Q5SY68|S1A7B_HUMAN      SGCEKSDMDYLSNALEKKDKDNKDKVNYSEFLSLLGDIIDHKKIMHGVAAPCSGGSQ---      101
sp|P05109|S10A8_HUMAN      RKK-----GADVWFKELDINTDGA VNFQEFLLIVIKMGVAAHKKSHKE-----      93
sp|P06702|S10A9_HUMAN      KKEN-KNEKVIEHIMEDLDTNADKQLSFEEFIMLMARLTWASHEKMHEGDEGPGHHKP-      107
sp|P60903|S10AA_HUMAN      ENQ--KDPLAVDKIMKDLQCRDQGVGFQSFFSLIAGLTACNDYFVVMHKQKQKK---      97
sp|P31949|S10AB_HUMAN      KNQ--KDPGVLD RMMKKLDTNSDGQLDFSEFLNLIGGLAMACHDSFLKAVPSQKRT---      105
sp|P80511|S10AC_HUMAN      KNI--KDKAVIDEIFQGLDANQDEQVDFQEFISLVAIALKAAHYHTHKE-----      92
sp|Q99584|S10AD_HUMAN      KD----VGSLEDEKMSLDVNQDSELKFNEYWRLIGELAKEIRKKDLKIRKK-----      98
sp|Q9HCY8|S10AE_HUMAN      PS----NCGLEEKIANLGSCNDSKLEFRSFWE LIGEA AKSVKLER-----PVRGH---      104
sp|Q96FQ6|S10AG_HUMAN      SDT--GNRKAADKLIQNLDANHDGRISFDEYWT LIGGITGPIAKLIHQEQQSSS-----      103
sp|P04271|S10OB_HUMAN      EEI--KEQEVVDKVMETLNDGDGECDFQEFMAFVAMVTTACHEFFEHE-----      92
sp|P29377|S10OG_HUMAN      KG----PNTLDDL FQELDKNGDGEVSFE EFQVLVKKISQ-----      79
sp|P25815|S10OP_HUMAN      QSG--KDKDAVDKLLKDL DANGDAQVDFSEFIVFVAIT SACHKYFEKAGLK-----      95
sp|Q8WXG8|S10OZ_HUMAN      SCQ--KETQLVDKIVQDL DANKDNEVD FNEFVVMVAALTVACNDYFVEQLKKKKGK-----      99
sp|Q5QJ38|TCHL1_HUMAN      QPC---VLHAVEKNSNLLNIDSNGIISFDEFVLAIFNLLNLCYLDIKSLSSSEL RQVTKP      102
sp|Q86YZ3|HORN_HUMAN      KNP--NDPDTVDIILQSLDRDHNNKVDFTEYLLMIFKLVQARNKIIGKDYCQVSGSKLRD      103
      .      :      :      :      :

```

```

sp|P23297|S10A1_HUMAN      -----      94
sp|P29034|S10A2_HUMAN      -----      98
sp|P33764|S10A3_HUMAN      -----      101
sp|P26447|S10A4_HUMAN      -----      101
sp|P33763|S10A5_HUMAN      -----      92
sp|P06703|S10A6_HUMAN      -----      90
sp|P31151|S10A7_HUMAN      -----      101
sp|Q86SG5|S1A7A_HUMAN      -----      101
sp|Q5SY68|S1A7B_HUMAN      -----      101
sp|P05109|S10A8_HUMAN      -----      93
sp|P06702|S10A9_HUMAN      -----GLGEGTP-----      114

```

sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	E-----KEKLDDVDVQATTGDGQWTVGTSPQTQEKRML---PSGMASSSQLIPEES	149
sp Q86YZ3 HORN_HUMAN	DTHQHQQEEQEETEKEENKRQESSFSHSSWSAGENDSYSRNVRGSLKPGTESISRRLSFQR	163

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	GAVGNRRVDPWREAKTHNFPGEASEHNDPKNK-H-LEGDEQSQE-VA--QDIQTTEDNEG	204
sp Q86YZ3 HORN_HUMAN	DFS-----GQHNSYSGQSSSYGEQNSDSHQSSGRGQCGSGSGQSPNYGQHSGSGS	213

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	QLKTNKPM-AGSKKTS---SPTERKGQDKEISQEGDEFAREQSVSKIRDQFGEQEGNLAT	260
sp Q86YZ3 HORN_HUMAN	QSSSNDTHGSGSGQSSGFSQHKSSSGQSSGYSQHGSGSGH-----SSGYGQHG-SRSG	265

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101

sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	QSSPPKEATQRPC-----EDQEV RTEKEKHSNIQEPPLQREDEPSSQHADLP	307
sp Q86YZ3 HORN_HUMAN	QSSRG--ERHRSSSGSSSSYQGHGSGSRQSLGHGRQGSGSRQSPSHVRHGS-GSGHSSSH	322

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	EQAAARS-PSQTQKS-TDSKDVCRMFDTQEPGKDADQTPAKTKNLGEPEDYGR TSETQ--	363
sp Q86YZ3 HORN_HUMAN	GQHGSGSSSYSYSRGHYESGSGQTSGFGQHESGS-----GQSSGYSKHGSGSGH	370

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95

sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	----EKE-----CETKDLVPQYGSRNGSETSDMRDERKERRGPEAHGT----	402
sp Q86YZ3 HORN_HUMAN	SSSQGQHGSTSGQASSSGQHGSSSRQSSSYGQHESA----SR--HSSGRGQHSSGSGQSP	424

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-AGQKERDRKTRPL-----VLETQTQDGKYQELQGLSKSKDAEK--GSETQYLSSEGG	452
sp Q86YZ3 HORN_HUMAN	GHGQRGSGSGQSPSSGQHGTGFRSSSSGPYVSGSGYSSGFGHHESSEHSSGYTQHGSG	484

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----DQTHPELEGTAVSGEEAHTKEGTAEAFVNSKNAPAAERTLGARERTQDLAPLE	506
sp Q86YZ3 HORN_HUMAN	SGHSSGHGQHGSRSRGQSSRGERQ-GSSAGSSSSYGQ--HGSGSRQSLGHSRHGSGSGQSP	541

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97

sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	KQSVGENTRVTKTHDQPVEEEDGYQGE--DPESPFTQSDEG----SSETPNSLASEEGN	559
sp Q86YZ3 HORN_HUMAN	SPSRGRHES--GSRQSSSYGPHGYGSGRSSSRGPYESGSGHSSGLGHQESRSGQSSGYGQ	599

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	SSSETGELPVQGDSQSQGDQHGESVQGGHNNNPD--TQRQGTPEKKNRALEAVVPAVRGE	617
sp Q86YZ3 HORN_HUMAN	HGSSSGHSSTHGQH---GSTSGQSSSCGQHGATSGQSSSHGQHSGSGSSQ-----SSRYG-	650

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	DVQLTEDQEQPARGEHKNQ----GPGTKGPAAV---EPNGHPEAQESTAGDENRKSL	668
sp Q86YZ3 HORN_HUMAN	-QQGSGSGQSPSRGRHGSDFGHSSSYGQHSGSGSGWSSSNGPHGSVSGQSS-----	699

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101

sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	EIEITGALDEDFTDQLSLMQLPGKGDsrNELKVQGPSSKEEKGRATEAQNTLLESLED-	727
sp Q86YZ3 HORN_HUMAN	-----GFGH-----KSGSGQSSG-YSQHSGSGSSHSSGYRKHGSRSGQSSRSEQH	742

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-NSASLKIQLTKPEVPTSEEEDESPQELAGEGGDQKSPAKKEHNSSVPWSSLEKQMQRDQ	786
sp Q86YZ3 HORN_HUMAN	GSSSGLSSSYGQHGS---GSHQSSGHGRQG-SGSGHSPSRVRHGSSSGHSSSHGQ-HGSG	797

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99

sp Q5QJ38 TCHL1_HUMAN	EPCSVERGAVYSSPLYQYLQEKILQQTNVTQEEHQKQVQIAQASGPCLSVSLTSEISDC	846
sp Q86YZ3 HORN_HUMAN	TSCS-----SSC	804

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	SVFFNYSQASQPY-----TRGLPLDESPAGA-----QETPAPQA	880
sp Q86YZ3 HORN_HUMAN	GHYESGSGQASGFGQHESGSGQGYSQHGSASGHFSSQGRHGSTSGQSSSSGQHDSSSGQS	864

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	L-----EDKQGHPQRERL-----VLQREASTT-----KQ--	904
sp Q86YZ3 HORN_HUMAN	SSYGQHEASASHHASGRGRHGSGSGQSPGHGQRGSGSGQSPSYGRHGSGSGRSSSSGRHGS	924

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105

sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GSGQSSGFGHKSSSGQSSGYTQHSGSGHSSSYEQHGSRSGQSSRSEQHGSSSGSSSYG	984

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QHSGSRQSLGHGQHSGSGQSPSPSRGRHSGSGQSSSYGPYRSGSGWSSSRGPYESGS	1044

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GHSSGLGHRESRSGQSSGYGQHGSSSGHSSTHGQHGSTSGQSSSCGQHGASSGQSSSHGQ	1104

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92

sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	HGSGSSQSSGYGRQGSGSGQSPGHGQRGSGSRQSPSYGRHSGSGSRSSSSGQHGSGLGES	1164

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SGFGHHESSSGQSSSYSQHGSGSGHSSGYGQHGSRSRGQSSRGERHGSSSGSSSHYGQHGS	1224

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904

sp|Q86YZ3|HORN_HUMAN

GSRQSSGHGRQSGSGSHSPSRGRHGSGLGHSSSHGQHGSGSGRSSSRGPYESRSGHSSVF

1284

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GQHESGSGHSSAYSQHGSGSGHFCSQGQHGSTSGQSSTFDQEGSSTGQSSSYGHRGSGSS	1344

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QSSGYGRHGAGSGQSPSRGRHGSGSGHSSSYGQHGSGSGWSSSSGRHGSGSGQSSGFGHH	1404

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92

sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	ESSSWQSSGCTQHGGSGSGHSSSYEQHGSRSGQSSRGERHGSSSGSSSYGQHGGSGSRQSL	1464

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GHGQHGGSGSGQSPSPSRGRHGGSGSGQSSSYSPYGGSGGWSSSRGPYESGSSSHSSGLGHRE	1524

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SRSGQSSGYGQHGGSSSGHSSSTHGQHGSTSGQSSSCGQHGAASSGQSSSHGQHGGSGSSQSSG	1584

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90

sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	YGRQSGSGSQSPGHGQRGSGSRQSPSYGRHSGSGSRSSSSGQHSGSLGESSGFGHHESSS	1644

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GQSSSYSQHGSGSGHSSGYGQHGSRSQGSSRGERHGSSSRSSRYGQHSGSGSRQSSGHGR	1704

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QGGSGSQSPSRGRHGSGSLGHSSSHGQHSGSGSRSSSRGPYESRSGHSSVFGQHESGSGHS	1764

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SAYSQHSGSGSGHFCSQGQHGSTSGQSSTFDQEGSSTGQSSSHGQHGSGSSQSSSYGQQGS	1824

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GSGQSPSRGRHGSGSGHSSSYGQHSGSGSWSSSSGRHGSGSGQSSGFHHESSWQSSGY	1884

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98

sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	TQHSGSGHSSSYEQHGSRSGQSSRGEQHGSSSGSSSYGQHGSGSRQSLGHGQHGSGSG	1944

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QSPSPSRGRHSGSGSQSSSYGPGSGSGWSSSRGPYESGSGHSSGLGHRRESRSGQSSGYG	2004

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QHGSSSGHSSSTHGQHGASAGQSSSCGQHGASSGQSSSHGQHGSGSSQSSGYGRQGSGSGQ	2064

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101

sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SPGHGQRGSGSRQSPSYGRHGSGSGRSSSSGQHGPGLGESSGFGHHESSGQSSSYSQHG	2124

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SGSGHSSGYGQHGSRSQGSSRGERHGSSSGSSSSRYGQHGSRSRQSSGHGRQGSGSGHSPS	2184

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	RGRHGSGSGHSSSHGQHGSRGSGRSSSRGPYESRSGHSSVFGQHESGSGHSSAYSQHGSGS	2244

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GHFCSQGQHGSTSGQSSTFDQEGSSTGQSSSHGQHGS GSSQSSSYGQQGSGSGQSPSRGR	2304

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WXG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	HGSGSGHSSSYGQHGSGSGWSSSSGRHGS GSGQSSGFGHHESSSWQSSGYTQHGS GSGHS	2364

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104

sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SSYEQHGSRSQGSSRGERHGSSSGSSSSYGQHGSGSRQSLGHGQHGSGSGQSPSPSRGRH	2424

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	GSGSGQSSSYSPYSGSGWSSSRGPYESGSGHSSSGLGHRESRSGQSSGYGQHGSSSGHSS	2484

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	THGQHGSTSGQSSSCGQHGASSGQSSSHGQHGSGSSQSSGYGRQGSGSGQSPGHGQRGSG	2544

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101

sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SRQSPSYGRHSGSGSRSSSSQHGSGLGESSGFGHHESSSGQSSSYSQHGSGSGHSSGYG	2604

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	QHGSRSQGSSRGERHGSSSGSSSHYGQHGSGSRQSSGHGRQGSGSGQSPSRGRHGSGGLGH	2664

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	SSSHGQHGSGSGRSSSRGPYESRLGHSSVFGQHESGSGHSSAYSQHGSGSGHFCSQQQHG	2724

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	STSGQSSTFDQEGSSSTGQSSSYGHRGSGSSQSSGYGRHGAGSGQSLSHGRHGSQSSS	2784

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103
sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WYG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	YGQHGSQSSGYSQHGSGSGQDGYSYCKGGSNHDGGSSGSYFLSFPSSTSPYEYVQEQ	2844

sp P23297 S10A1_HUMAN	-----	94
sp P29034 S10A2_HUMAN	-----	98
sp P33764 S10A3_HUMAN	-----	101
sp P26447 S10A4_HUMAN	-----	101
sp P33763 S10A5_HUMAN	-----	92
sp P06703 S10A6_HUMAN	-----	90
sp P31151 S10A7_HUMAN	-----	101
sp Q86SG5 S1A7A_HUMAN	-----	101
sp Q5SY68 S1A7B_HUMAN	-----	101
sp P05109 S10A8_HUMAN	-----	93
sp P06702 S10A9_HUMAN	-----	114
sp P60903 S10AA_HUMAN	-----	97
sp P31949 S10AB_HUMAN	-----	105
sp P80511 S10AC_HUMAN	-----	92
sp Q99584 S10AD_HUMAN	-----	98
sp Q9HCY8 S10AE_HUMAN	-----	104
sp Q96FQ6 S10AG_HUMAN	-----	103

sp P04271 S100B_HUMAN	-----	92
sp P29377 S100G_HUMAN	-----	79
sp P25815 S100P_HUMAN	-----	95
sp Q8WVG8 S100Z_HUMAN	-----	99
sp Q5QJ38 TCHL1_HUMAN	-----	904
sp Q86YZ3 HORN_HUMAN	RCYFYQ	2850

Percent Identity Matrix - created by Clustal2.1

#

sp P23297 S10A1_HUMAN	100.00	50.00	40.43	48.94	46.15	43.33	20.88	23.08	20.88	37.78	36.17	47.25	40.43	36.96	34.07	24.42	32.98	57.61	40.51	52.69	57.45	23.91	32.26
sp P29034 S10A2_HUMAN	50.00	100.00	43.30	60.82	52.17	47.78	21.05	22.11	22.11	27.96	30.61	32.98	28.57	34.78	29.47	23.86	29.59	43.48	35.44	40.00	40.21	18.95	25.00
sp P33764 S10A3_HUMAN	40.43	43.30	100.00	44.55	40.22	45.56	16.33	18.37	19.39	21.51	29.70	25.77	27.00	30.43	26.60	18.68	23.23	36.96	25.32	31.58	34.34	22.22	25.00
sp P26447 S10A4_HUMAN	48.94	60.82	44.55	100.00	52.17	51.11	22.45	24.49	22.45	29.03	27.72	34.02	28.00	32.61	29.79	25.27	31.31	45.65	36.71	41.05	43.43	20.20	25.00
sp P33763 S10A5_HUMAN	46.15	52.17	40.22	52.17	100.00	51.69	24.72	25.84	19.10	30.68	32.61	33.71	32.61	34.83	36.67	21.43	29.35	42.70	35.06	38.46	42.39	22.22	28.57
sp P06703 S10A6_HUMAN	43.33	47.78	45.56	51.11	51.69	100.00	22.99	25.29	22.99	27.91	30.00	26.44	28.89	34.83	29.89	25.00	27.78	39.33	35.06	34.83	38.89	22.73	25.84
sp P31151 S10A7_HUMAN	20.88	21.05	16.33	22.45	24.72	22.99	100.00	94.06	52.48	24.44	24.00	22.68	32.65	25.84	19.57	19.10	25.77	25.84	28.95	27.17	25.00	16.67	19.59
sp Q86SG5 S1A7A_HUMAN	23.08	22.11	18.37	24.49	25.84	25.29	94.06	100.00	54.46	25.56	25.00	24.74	34.69	26.97	19.57	20.22	25.77	26.97	27.63	29.35	25.00	17.71	20.62
sp Q5SY68 S1A7B_HUMAN	20.88	22.11	19.39	22.45	19.10	22.99	52.48	54.46	100.00	23.33	24.00	24.74	23.47	24.72	16.30	16.85	18.56	22.47	25.00	30.43	20.83	12.50	22.68
sp P05109 S10A8_HUMAN	37.78	27.96	21.51	29.03	30.68	27.91	24.44	25.56	23.33	100.00	25.81	27.78	26.88	39.77	22.83	18.82	24.73	34.09	32.47	36.26	30.11	18.48	25.00
sp P06702 S10A9_HUMAN	36.17	30.61	29.70	27.72	32.61	30.00	24.00	25.00	24.00	25.81	100.00	29.90	32.04	46.74	30.93	30.85	23.53	36.96	29.11	35.79	34.34	22.33	25.69
sp P60903 S10AA_HUMAN	47.25	32.98	25.77	34.02	33.71	26.44	22.68	24.74	24.74	27.78	29.90	100.00	36.08	31.46	25.27	26.44	22.92	37.08	30.26	43.48	46.88	24.21	29.17
sp P31949 S10AB_HUMAN	40.43	28.57	27.00	28.00	32.61	28.89	32.65	34.69	23.47	26.88	32.04	36.08	100.00	35.87	31.63	25.26	24.51	34.78	34.18	38.95	31.31	23.47	26.26
sp P80511 S10AC_HUMAN	36.96	34.78	30.43	32.61	34.83	34.83	25.84	26.97	24.72	39.77	46.74	31.46	35.87	100.00	31.46	28.24	25.00	38.04	35.44	44.57	39.13	19.78	33.70
sp Q99584 S10AD_HUMAN	34.07	29.47	26.60	29.79	36.67	29.89	19.57	19.57	16.30	22.83	30.93	25.27	31.63	31.46	100.00	37.36	28.87	25.84	32.91	26.09	26.60	15.05	26.88
sp Q9HCY8 S10AE_HUMAN	24.42	23.86	18.68	25.27	21.43	25.00	19.10	20.22	16.85	18.82	30.85	26.44	25.26	28.24	37.36	100.00	21.74	27.06	21.79	23.53	19.10	21.11	16.67
sp Q96FQ6 S10AG_HUMAN	32.98	29.59	23.23	31.31	29.35	27.78	25.77	25.77	18.56	24.73	23.53	22.92	24.51	25.00	28.87	21.74	100.00	28.26	30.38	27.37	29.29	21.65	24.49
sp P04271 S100B_HUMAN	57.61	43.48	36.96	45.65	42.70	39.33	25.84	26.97	22.47	34.09	36.96	37.08	34.78	38.04	25.84	27.06	28.26	100.00	34.18	50.00	44.57	25.27	30.43
sp P29377 S100G_HUMAN	40.51	35.44	25.32	36.71	35.06	35.06	28.95	27.63	25.00	32.47	29.11	30.26	34.18	35.44	32.91	21.79	30.38	34.18	100.00	34.18	37.97	24.05	32.91
sp P25815 S100P_HUMAN	52.69	40.00	31.58	41.05	38.46	34.83	27.17	29.35	30.43	36.26	35.79	43.48	38.95	44.57	26.09	23.53	27.37	50.00	34.18	100.00	50.53	24.47	33.68
sp Q8WXG8 S100Z_HUMAN	57.45	40.21	34.34	43.43	42.39	38.89	25.00	25.00	20.83	30.11	34.34	46.88	31.31	39.13	26.60	19.10	29.29	44.57	37.97	50.53	100.00	24.74	28.57
sp Q5QJ38 TCHL1_HUMAN	23.91	18.95	22.22	20.20	22.22	22.73	16.67	17.71	12.50	18.48	22.33	24.21	23.47	19.78	15.05	21.11	21.65	25.27	24.05	24.47	24.74	100.00	20.92
sp Q86YZ3 HORN_HUMAN	32.26	25.00	25.00	25.00	28.57	25.84	19.59	20.62	22.68	25.00	25.69	29.17	26.26	33.70	26.88	16.67	24.49	30.43	32.91	33.68	28.57	20.92	100.00