```
HERK1       ---MGIEKFETFILISTISIILLCICHG----------------FTPVDNYLINCGSPTNGT--LMGRIFLSDKLSSKLLT---SSKEILASVG--GNSG-SDIYHTARVFTEVSSYK 90
HERK2       ---MSKLRKKYLEHLLCVLIFFTYVIG-----------------YGEAQSKSFLVDCGSNATTE--VDGRTWVGDLSPNKSVTLQGFDAITASTSK--GSSVYAEIYKTARVFDAVLNYT 96
THE1        -----MVFTKSLLVLLWFLSCYTTTTS-----------------SALFNPPDNYLISCGSSQNIT--FQNRIFVPDSLHSSLVLKIGNSSVATSTTS--NNST-NSIYQTARVFSSLASYR 94
ANX1        MSGKTR----FIF-FLTCLFSLFLVFPT----------------RSNG--QDLALSCGTSEASA-DQDKKWEPDTK---FLKTG--NSIHATATYQDPSLLSTVPYMTARIFTAPATYE 90
ANX2        MNEKLR----ILFSFLCFFYVLLVSPS-----------------QSNG--QDISLSCGASEPAV-DQDKKWEPDTK---FLKTP--NTVHAPATYQDPSLLSTVPYMTSRIFTAPATYE 91
FER         MKITEGRFRLSLLLLLLLISAATLISA-----------------ADYSPTEKILLNCGGASNLTDTDNRIWISDVK-SKFLSSSSEDSKTSPALTQDPSVP-EVPYMTARVFRSPFTYT 101
gi|56783691 MAGRVRCSPAVALALVVAAAAAAAATA----------------KLYSPADRILVNCGSTTDGL-DAEGRRWVADATNDTWLTDSGKSSIMAAADELETMLPSSIPYMTARVFTMDTVYN 102
gi|115462979 MASRR----HVLIAALIMVGVLEFANA----------------DKYKPTESILVNCGSDKEGQ-DIDGRKWLSDKD-SKWLIDGEKSSIMANADFQDPSLPSPVPYMTARVFTKETMYN 97
gi|25553554 MRRRGRMIPPALLLAAAVAAALATAVSGQGRPVTESGAQTAPTPSTFTPKDNFLIDCGSTSPVT--TGGKVYKTDAQSNSLLS--AKDAIKVATTD--ADVP-SPLYLTARIFRDEAVYS 113

HERK1       FSVTR-GRHWVRLYFNPFDYQNFKMGSAKFAVSSQ-SHVLLSDFTVT---------------SSK---VVKEYSLN-VTTNDLVLTFTPS---SGSFAFVNAIEVISIPDTLITG--SPR 184
HERK2       FEGITQGNYFVRLHFSPFAIENHNVNESSFSVFAD-GLRLMLDINIAGEIAHKNLILESTGHNATASSLVKEFLLP-TGPGKLVLSFIPE---KGSFGFVNAIEIVSVDDKLFKE--SVT 209
THE1        FKITSLGRHWIRLHFSPINNSTWNLTSASITVVTE-DFVLLNNFSFN--------------NFNGSYIFKEYTVN-VTSEFLTLSFIPS---NNSVVFVNAIEVVSVPDNLIPD--QAL 192
ANX1        IPIKGDKRHLLRLYFYPSTYTGLNISNSYFTVEAN-DVTLLSNFSAA-----------ITCQALTQAYLVKEYSLAPTDKDVLSIKFTPSDKYRDAFAFINGIEVIQMPELFD----TAA 194
ANX2        IPVKGDKRHMLRLHFYPSTYTGLNILDSYFSVAAN-DLTLLSNFSAA-----------ITCQALTQAYLVREYSLAPSEKDVLSIIFTPSDKHPKAFAFINGIEVIPMPELFD----TAS 195
FER         FPVA-SGRKFVRLYFYPNSYDGLNATNSLFSVSFG-PYTLLKNFSAS----------QTAEALTYAFIIKEFVVN-VEGGTLNMTFTPESAPSNAYAFVNGIEVTSMPDMYSSTDGTLT 207
gi|56783691 FTVNPRDRHWIRLHFYPSSYNGLEPQDFRFSVFTTTGYTLLHNFSVY-----------FTTKALTQAYLIREYSLPRVPEGHFGVTFSPSPMMNVTYAFVNGIEVISMPDMFNN---PAT 208
gi|115462979 FSVG-EERHWVRLHFYPASYHDLPAENFFFSVSTSTGITLLKNFSVY-----------ITAKALSQAYIIREFTLPPSTTGSLSLIFTPTAMNNASYAFVNGIEIISMPNIFSQ---AAA 202
gi|25553554 FPLTVPGWHFVRLYLFPLKNSDFDLTTATFTVSTD-TNVLLHSFTAE--------------NKP---VMKEFLVN-ATENHLAVKFYPL---KGSAAFINAIEVVNAPDELITD--MAM 208

HERK1       FVGNPAQFPDMSMQGLETIHRVNMGGPLVAS-NND-TLTRTWVPDSEFLLEKNLAKSMSKFSTVNFVPGYAT---EDSAPRTVYGSCTEMNSADNPNSIFNVTWEFDVDPGFQYYFRFHF 299
HERK2       KVGGSEVELGLGGRGIETMYRLNVGGPKLGP-SKDLKLYRTWETDLSYMVIENAGVEVKN-SSNITYALADD---SPVAPLLVYETARMMSNTEVLEKRFNISWKFEVDPNFDYLVRLHF 324
THE1        ALNPSTPFSGLSLLAFETVYRLNMGGPLLTS-QND-TLGRQWDNDAEYLHVNSSVLVVTANPSSIKYSPSVT---QETAPNMVYATADTMGDANVASPSFNVTWVLPVDPDFRYFVRVHF 307
ANX1        LVGFTDQTMDAKTANLQSMFRLNVGGQDIPGSQDSGGLTRTWYNDAPYIFSAGLGVTLQASNNFRINYQNMP---VSIAPADIYKTARSQGPNGDINLKSNLTWMFQIDKNFTYILRLHF 311
ANX2        LVGFSDQTSDTKTANLQTMFRLNVGGQDIPGSQDSGGLTRTWYNDAPYIFSAGLGVTLQASNNFRIDYQKMP---VSTAPADVYKTARSQGPNGDINMKSNLTWMFQVDTNFTYIMRLHF 312
FER         MVGSSGSVTIDNSTALENVYRLNVGGNDISPSADTG-LYRSWYDDQPYIFGAGLGIPETADPNMTIKYPTGT--PTYVAPVDVYSTARSMGPTAQINLNYNLTWIFSIDSGFTYLVRLHF 324
gi|56783691 MVGFADQTADVSAAAFQTMYRLNVGGAYIPPSNDSG-LTRPWYDDTPFVQGPLRGLVYNAGPHFHIKYPSD--AAEYAAPPEVYLGGRSMGRDQRLNQNSNLTWSLHVECNFTYVVRLHF 325
gi|115462979 SVDIAGNEVSTTDSSLQTIYRLNVGGSYVAPTNDSG-LSRDWYDDTPYIYGAAVGVTYQANDTVQIKYPKNDPDAEYAAPASVYLTSRSMGPDPKVNKNYKLTWVFEVDGNFTYIVRLHF 321
gi|25553554 GIAPVGEMTGLAEAAYQVVYRINVGGPAIAP-DKD-TLGRQWDVDAPYVQSKEAVKDVSVPVGNIKFPDGTS---KLVAPAQVYASCAKMADAGVGSPSFNMSWKMEVDPAFGYLVRLFF 323

HERK1       CDIVS--LSLNQLYFNLYVDSMVAATD---IDLSTLVDNTLAGAYSMDFVT--QTPKGS--NKVRVSIGPST-VHTDYPNAIVNGLEIMKMNNSKGQLSTGTFVPG---------------- 395
HERK2       CELLV--DKQNQRIFRIYINNQTAAGN---FDIFAHAG-GKNKGIYQDYLD--PVSSKN--DVLWIQLGPDS-SVGASGDALLSGLEIFKLSKN-GNLAHLIRFDTSTGHS---------- 422
THE1        CDIVS--QALNTLVFNLYVNDDLALGS---LDLSTLTN-GLKVPYFKDFIS--NGSVESS-GVLTVSVGPD--SQADITNATMNGLEVLKISNEAKSLSGVSSVKSLLPG---------- 406
ANX1        CEFQ--LSKINQKVFNIYINNRTAQADTTPADIIGWTG-EKGIPMYKDYAIYVDANNGG--EEITLQMTPSTFGQPEYYDSSLNGLEIFKMD-TMKNLAGPNPEPSPMQAEEEV------ 419
ANX2        CEFQ--LAKINQKVFNIFINNRTAQGDTNPADILGWTG-GKGIPTYKDYAYVDANTGGGGEEISLQMTPSTFGQPEYYDSQLNGLEIFKID-TMKNLAGPNPKPSPMQANEDV------ 422
FER         CEVSSNITKINQRVFTIYLNNQTAEPE---ADVIAWTS-SNGVPFHKDYVVNPPEGNGQ--QDLWLALHPNPVNKPEYYDSLLNGVEIFKMNTSDGNLAGTNPIPGPQVTADPSK---VL 435
gi|56783691 CELQ--LIHGNQRVFDIYINNRTAQTD---VDVLEMAT-ERGVPVYKDYAVRLSNDTAD--EHLWVAVHPSVMLRPQFYDAILNGLEVFKVNNTGGSLASPDPVPYKLLAEKELGWGGPP 437
gi|115462979 CELL--LSKPNQRVFDILINNKTAQSG---ADVIGWG--GQFVPVYKDYATIMPGGAGD--KVLWVQLMPNVGSGSEFFDSLLNGLEIFKMSDSSGNLAGPNPDPSKLLEEAESSAQG-- 430
gi|25553554 ADIVS--KSMNDLYFNVFVNGRKAISG---LDLSTVTG-ELSAAYYKDIVV--NSSIAT--DKLSIQVGPMG-EDTGRVDALLSGVEVLKMSNSVGSLDGEFGVDGKKADD--------- 423

HERK1       --SSSSSKSNLGLIVGSAIGSLLAVVFLGSCFVLYKKRKRGQDGHSKT-------WMPFSING----TSMGSKYSNGTTLTS---ITTNANYRIPFAAVKDATNNFDESRNIGVGGFGKV 499
HERK2       --VSDSKMRIIWISVGAGIAIIIFFVFLGILVVCLCKKRRSKSDESKN---NPPGWRPLFLHVN---NSTANAKATGGSLRLNTLAASTMGRKFTLAEIRAATKNFDDGLAIGVGGFGKV 534
THE1        --GSGSKSKKKAVIIGSLVGAVTLILLIAVCCYCCLVASRKQRSTSPQEGGNGHPWLPLPLYGLSQTLTKSTASHKSATASCISLASTHLGRCFMFQEIMDATNKFDESSLLGVGGFGRV 524
ANX1        KKEFKNEKR-HAFIIGSAGGVLAV-LIGALCFT-AYKKKQ----GYQGGDSHTSSWLPIYGNSTTSGTKST-ISGKSNNGSHLSNLAAGLCRRFSLPEIKHGTQNFDDSNVIGVGGFGKV 531
ANX2        KKDFQGDKRITAFVIGSAGGVAAV-LFCALCFT-MYQRKR----KFSGSDSHTSSWLPIYGNSHTSATKST-ISGKSNNGSHLSNLAAGLCRRFSLSEIKHGTHNFDESNVIGVGGFGKV 535
FER         RPTTRKSKSNTAIIAGAASGAVVLALIIGFCVFGAYRRRKRG--DYQPASDATSGWLPLSLYGNSHSAGSA-KTNTTGS--YASSLPSNLCRHFSFAEIKAATKNFDESRVLGVGGFGKV 550
gi|56783691 EFSTDNPANMASVMGGTAGGAAAAGIVAAICVV-VYSNKRSKKLGGGGADSHTSAWLPLY--HSHTS-------GKSSG--HITANIAGMCRHFSFAEIKAATKNFSNDLAIGVGGFGVV 545
gi|115462979 KFKSKPSNLKATVIGGAAGGAAAFGIVAAICIV-VYQSKKRKVLNN--SASHSSGWLPVYGGNSHTSTSKS-SGGRSAA--LINPNITAMCRHFSFGEIKSATKNFDESLVIGVGGFGKV 544
gi|25553554 --GSGSRKAVAAVGFAMMFGAFAGLGAMAVKWYKRPQDWERRNSFSS--------WLLPIHTGQSFTTSKGGSSKSGYTFS----STLGLGRFFSFAEIQAATKNFEESAIIGVGGFGNV 529

HERK1       YKGELND-GTKVAVKRGNPKSQQGLAEFRTEIEMLSQFRHRHLVSLIGYCDENNEMILIYEYMENGTVKSHLYG-SGLPSLTWKQRLEICIGAARGLHYLHTGDSKPVIHRDVKSANILL 617
HERK2       YRGELED-GTLIAIKRATPHSQQGLAEFETEIVMLSRLRHRHLVSLIGFCDEHNEMILVYEYMANGTLRSHLFG-SNLPPLSWKQRLEACIGSARGLHYLHTGSERGIIHRDVKTTNILL 652
THE1        YKGTLED-GTKVAVKRGNPRSEQGMAEFRTEIEMLSKLRHRHLVSLIGYCDERSEMILVYEYMANGPLRSHLYG-ADLPPLSWKQRLEICIGAARGLHYLHTGASQSIIHRDVKTTNILL 642
ANX1        YKGVIDG-TTKVAVKKSNPNSEQGLNEFETEIELLSRLRHKHLVSLIGYCDEGGEMCLVYDYMAFGTLREHLYN-TKKPQLTWKRRLEIAIGAARGLHYLHTGAKYTIIHRDVKTTNILV 649
ANX2        YKGVIDG-GTKVAIKKSNPNSEQGLNEFETEIELLSRLRHKHLVSLIGYCDEGGEMCLIYDYMSLGTLREHLYN-TKRPQLTWKRRLEIAIGAARGLHYLHTGAKYTIIHRDVKTTNILL 653
FER         YRGEIDGGTTKVAIKRGNPMSEQGVHEFQTEIEMLSKLRHRHLVSLIGYCEENCEMILVYDYMAHGTMREHLYK-TQNPSLPWKQRLEICIGAARGLHYLHTGAKHTIIHRDVKTTNILL 669
gi|56783691 YRGVVDG-DVKVAVKRSNPSSEQGITEFQTEVEMLSKLRHRHLVSLIGFCEEDGEMVLVYDYMEHGTLREHLYHNGGKPTLSWRHRLDICIGAARGLHYLHTGAKYTIIHRDVKTTNILV 664
gi|115462979 YRGVVDG-DTKVAIKRSNPSSEQGVLEFQTEIEMLSKLRHKHLVSLIGCCEDEGEMILVYDYMAHGTLREHLYK-GGKPALSWKQRLEITIGAARGLHYLHTGAKYTIIHRDVKTTNILV 662
gi|25553554 YIGEIDD-GTKVAVKRGNPQSEQGINEFNTEIQMLSKLRHRHLVSLIGYCDENAEMILVYEYMHNGPFRDHYG-KDLPALTWKQRLEICIGAARGLHYLHTGTAQGIIHRDVKTTNILL 647

HERK1       DENFMAKVADFGLSKTGPE-LDQTHVSTAVKGSFGYLDPEYFRRQQLTDKSDVYSFGVVLFEVLCARPVIDPTLPREMVNLAEWAMKWQKKGQLDQIIDQSLRGNIRPDSLRKFAETGEK 736
HERK2       DENFVAKMSDFGLSKAGPS-MDHTHVSTAVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEAVCARAVINPTLPKDQINLAEWALSWQKQRNLESIIDSNLRGNYSPESLEKYGEIAEK 771
THE1        DENLVAKVADFGLSKTGPS-LDQTHVSTAVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLMEVLCCRPALNPVLPREQVNIAEWAMAWQKKGLLDQIMDSNLTGKVNPASLKKFGETAEK 761
ANX1        DENWVAKVSDFGLSKTGPN-MNGGHVTTVVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEILCARPALNPSLPKEQVSLGDWAMNCKRKGNLEDIIDPNLKGKINAECLKKFADTAEK 768
ANX2        DENWVAKVSDFGLSKTGPN-MNGGHVTTVVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEVLCARPALNPSLSKEQVSLGDWAMNCKRKGTLEDIIDPNLKGKINPECLKKFADTAEK 772
FER         DEKWVAKVSDFGLSKTGPT-LDHTHVSTVVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEALCARPALNPTLAKEQVSLAEWAPYCYKKGMLDQIVDPYLKGKITPECFKKFAETAMK 788
gi|56783691 DDNWVAKVSDFGLSKSGPTTLNQSHVSTVVKGSFGYLDPEYYRRQQLTDKSDVYSFGVVLFEVLMARPALDPALPRDQVSLADYALACKRGGALPDVVDPAIRDQIAPECLAKFADTAEK 784
gi|115462979 DEKWVAKVSDFGLSKTGPTAMNQTHVSTMVKGSFGYLDPEYFRRQQLTEKSDVYSFGVVLFEVLCARPALNPSLPREQVSLADHAMSCQRKGTLHDIIDPLLNGKIAPDCLKKFAETAEK 782
gi|25553554 DDNFVAKVSDFGLSKDGPG-MNQLHVSTAVKGSFGYLDPEYFRCQQLTDKSDVYSFGVVLLETLCARPPIDPQLPREQVSLAEWGMQWKRKGLIEKIMDPKLAGTVNQESLNKFAEAAEK 766

HERK1       CLADYGVDRPSMGDVLWNLEYALQLQEAVID-G--------------EPEDNSTNMIGELPPQINNFSQGDTSVNVPGTAG-RFEESSIDDLSGVSMSKVFSQLVKSEGR 830
HERK2       CLADEGKNRPMMGEVLWSLEYVLQIHEAWLR-K--------------QNGENSFSSSQ-------AVEEAPESFT--------LPACSNQDSSETEQSQTGSALHNSA-- 849
THE1        CLAEYGVDRPSMGDVLWNLEYALQLEETSSALM--------------EPDDNSTNHIPGIP--MAPMEPFDNSMSIIDRGGVNSGTGTDDDAEDATTSAVFSQLVHPRGR 855
ANX1        CLNDSGLERPTMGDVLWNLEFALQLQETADGTRHRTP----------NNGGSSEDLGRGGMAVNV---AGRDDVS----------DLSSED-----NTEIFSQIVNPKGR 850
ANX2        CLSDSGLDRPTMGDVLWNLEFALQLQETADGSRHRTP----------SNGGGSVDLGGGGGGVTVNISAGESDLGD---------DLSSEE-----NSGIFSQIVNPKGR 858
FER         CVLDQGIERPSMGDVLWNLEFALQLQESAEENGKGVCGDMDMDEIKYDDGNCKGKNDKSSDVYEGNVTDSRSSGIDMSIGG---RSLASEDSDGLTPSAVFSQIMNPKGR 895
gi|56783691 CLSENGTERPTMGDVLWNLESAMHFQDAFDAAAGRPVPAL------DAAAGSSSHLDDGSTASINTLATSSTSHPHEPCVD---VVLEPDDV--VAERATFSQLVQPTGR 883
gi|115462979 CLADHGVDRPSMGDVLWNLEFALQMQETFENGG--------------KTEGADSTSDDSTTTSVADSMAANAAALS---LIS---EDMDEED---IANSVVFSQLVRPTGR 869
gi|25553554 CLAEFGSDRISMGDVLWNLEYALQLQDANPP----------------EGADKPADHDG-------AGAAPATSSG---------SGVSTVPDVSTTAAGEMFAQLADMKGR 845
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