

Numbering is for the alignment, not for FIX sequence

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      10      20      30      40      50      60      70      80      90     100
FIX_Human|47-461  YNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTEFEWKQYVDGDQCESNP-----CLNGGSCKDDINSYECWCPFGFEGKNCCEL----DVTC
FA10_Human|41-488 ANS-FLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDCETSP-----CQNQKCKDGLGEYTCCTCLEGFEGKNCLELF--TRKLC
FA7_Human|61-466  ANA-FLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQCASSP-----CQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDQLIC
PROC_Human|43-461 ANS-FLEELRHSSLERECIEEICDFEEAKEIFQNVDLTLAFWSKHVDGDQCLVLPLEHPCASLCCGHGTCLDGIIGSFSCDCRSGWEGRFQREV-SFLNC

      110     120     130     140     150     160     170     180     190     200
FIX_Human|47-461  NIKNGRCEQFCKNSADNKVVCSCTEGYRLAENQKSCEPAVPPFCGR--VSVSQTSKLTRAETV---FPD-----VDYVNSTEAETILD---NITQST
FA10_Human|41-488 SLDNNGDCDQFC-HEEQNSVVCSCARGYTLADNGKACIPTGYPYCGK--QTLERRKRSVAQATSSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTPQE
FA7_Human|61-466  VNENGGCEQYCSDHGTGRKRSRCHEGYSLADGVSCPTVEYPCGK--IPILEKR-----NASKPQ
PROC_Human|43-461 SLDNNGGCTHYCLEEVGWRR-CSCAPGYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKR-----DTEDQEDQVD-----

      210     220     230     240     250     260     270     280     290     300
FIX_Human|47-461  QSFNDFTRVVGGEDAKPGQFPWQVVL--NGKVDAFCGGSIVNEKWIIVTAAHCVEITGV--KITVVAGEHNIETEHEQKRNVIIRIIPHHNYAAINKYN
FA10_Human|41-488 RGDNNLTRIVGGQECKDGECPWQALL-INEENEGFCGGTILSEFYILTAACHLYQAK---RFKVRVGDNRTEQEEGGEAVHEVEVVIKHNRFTE--TYD
FA7_Human|61-466  -----GRIVGGKVC PKGECPWQVLLLVNGAQ--LCGGTLINTIWWVSAAHCFDKIKNWRNLI AVLGEHDLSEHDGDEQSRVAQVIIPSTYVPG--TTN
PROC_Human|43-461 -----PRLIDGKMTRRGDS PWQVVL-LDSKKKLACGAVLIHPSWVLTAAHCMDESK---KLLVRLGEYDLRRWEKWELDLDI KEV FVHPNYSKS--TTD

      310     320     330     340     350     360     370     380     390     400
FIX_Human|47-461  HDIALLELDEPLVLNSYVTPICIAADKEYTNIFL-KFGS-GYVSGWGRV FHKGRSA-----LVLYLRVPLVDRATCLRSTKFT-----IYNNMFCAGFHE
FA10_Human|41-488 FDI AVLRLKTPITFRMNVA PA CLPERDWAESTL-MTQKTGIVSGFGRTHEKGRQS-----TRLKMLEVPPYVDRNSCKLSSSFI-----ITQNMFCAGYDT
FA7_Human|61-466  HDIALLRLHQPVVLT DHV VPLCLPERTFSERTL-AFVRFSLVSGWGQLDRGATA-----LELMVLNVPRLMTQDCLQSRKVGDSPNITEYMF CAGYS D
PROC_Human|43-461 NDIALLLHLAQPATLSQTIVP ICLPDSGLAERELNQAQGETLVTGWGYHSSREKEAKRNRTFV LNF I KIPVVP HNECSEVMSNM-----VSENMLCAGILG

      410     420     430     440     450     460     470
FIX_Human|47-461  GGRDSCQGD SGGPHVTEVEGTSFLTGIISWGEECAMK GKYGIYTKVSRVNWIK EKTKLT-----
FA10_Human|41-488 KQEDACQGD SGGPHVTRFKDTYFVTGIVSWGEGCARK GKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK
FA7_Human|61-466  GSKDSCKGD SGGPHATHYRGTWYLTGIVSWGQCATVGHFGVYTRVSQYIEWLQKLMRSE--PR-----PGVLLRAPFP
PROC_Human|43-461 DRQDACEGD SGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRDKEAPQ-KSWAP-----
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