

Numbering is for the alignment, not for FX sequence

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      10      20      30      40      50      60      70      80      90     100
FX 41-488  . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . |
FVII 61-466 ANS-FLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKYKDGDCETSP-----CQNQKCKDGLGEYTCCTCLEGFEGKNCCELFT--RKLC
FIX 47-461  ANA-FLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQCASSP-----CQNGGCKDQLQSYICFCLPAFEGRNCETHKDDQLIC
Prot C 43-461 YNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTEFEWKQYVDGDQCESNP-----CLNGGCKDDINSYECWCPFFGFEKNCELDVI---TC
Chymo 34-261 ANS-FLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRSGWEGRFQREV-SFLNC
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      110     120     130     140     150     160     170     180     190     200
FX 41-488  . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . |
FVII 61-466 SLDNGDCDQFCHEEQNSVV-CSCARGYTLADNGKACIPTGPYPGCK--QTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTOPE
FIX 47-461  VNENGGCEQYCSDHGTGTRKSCRCHEGYSLLADGVSCPTVEYPCGK--IPILEKR-----NASKPQ
Prot C 43-461 NIKNGRCEQFCKNSADNKVVCSTEGYRLAENQKSCEPAVFPFCGR--VSVSQTSKLTRAETV---FPD-----VDYVNSTEAETILD---NITQST
Chymo 34-261 SLDNGGCTHYCLEEVGWRR-CSCAPGYKLGDDLLQHPAVKFPFCGRPWKRMEKKRSHLKR-----DTEDEQEDQVD-----
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      210     220     230     240     250     260     270     280     290     300
FX 41-488  . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . |
FVII 61-466 RGDNNLTRIVGGQECKDGECPWQALL-INEENEGFCGGTILSEFYILTAAHC---LYQAKRFKVRVGDNRTEQEEGGEAVHEVEVVIKHNRF--TKETYD
FIX 47-461  -----GRIVGGKVCPKGECPWQVLLLVNGAQ--LCGGTLINTIWWVSAAHCFDKIKNWRNLIQAVLGEHDLSEHDGDEQSRVAQVVIIPSTY--VPGTTN
Prot C 43-461 QSFNDFTRVVGEDAKPGQFPWQVVL--NGKVDAFCGGSIVNEKWIWVTAHC---VETGVKITVVAAGEHNIETEHETEQKRNVIRIIPHNYNAAINKYN
Chymo 34-261 -----PRLIDGKMTRRGDSPWQVVL-LDSKKKLACGAVLIHPSWVLTAAHC---MDESKLLVRLGEYDLRRWEKWEILDLDIKEVVFVHPNY--SKSTTD
-----IVNGEDAVPGSWPWQVSL-QDKTGFHFCGGSLLISEDVWVTAHC--GVRTSD--VVVAGEFDQGSDEENIQVLKIAKVFNPKF--SILTVN
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      310     320     330     340     350     360     370     380     390     400
FX 41-488  . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . |
FVII 61-466 FDIAVLRLKTPITFRMNVAPACLIP--ERDWAESTL-MTQKTGIVSGFGRTHEKGRQS-----TRLKMLEVPYVDRNSCKLSSSFI-----ITQNMFCAGY
FIX 47-461  HDIALLRLHQPVVLTDHVVPLCLIP--ERTFSERTL-AFVRFSLVSGWGQLDRGATA-----LELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFAGY
Prot C 43-461 HDIALLELEDEPLVLSYVTPICIA--DKEYTNIIFL-KFGS-GYVSGWRVVFHKGSA-----LVLQYLRVPLVDRATCLRSTKFT-----IYNNMFCAGF
Chymo 34-261 NDIALLLHLAQPATLSQTIVPICLIP--DSGLAERELNQAQGETLVTGWGYHSSREKEAKRNRTFVLFNFIKIPVVPHNECSEVMSNM-----VSENMLCAGI
NDITLLKLATPARFSQTVSAVCLPSADDDFPAGTL-----CATTGWGKTKYNANKT---PDKLQQAALPLLSNAECKKSWGRR-----ITDVMICAG-
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      410     420     430     440     450     460     470     480
FX 41-488  . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . | . . . . |
FVII 61-466 DTKQEDACQGDSSGGPHVTRFKDTYFVTGIVSWGEG-CARKGKYGIYTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK
FIX 47-461  SDGSKDCKGDSGGPHATHYRGTWYLTGIVSWGQG-CATVGHFGVYTRVSYIEWLQKLMRSEPRPGVLLRAPFP
Prot C 43-461 HEGGRDSCQGDSSGGPHVTEVEGTSFLTGIISWGEE-CAMKGYGIYTKVSRVYVNWIKETKLT
Chymo 34-261 LGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEG-CGLLHNYGVYTKVSRYLWDWIHGHIRDKEAPQKSWAP
-ASGVSSCMGDSGGPLVCQKDGAWTLVGIIVSWGSRTCSTT-TPAVYARVAKLIPVWQKILA

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