

Numbering is for the alignment, not for FXI sequence

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      10      20      30      40      50      60      70      80      90     100
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   MIFLYQVVHFI-LFTSVSGECVTQLLKDTCFEGGDITTVFTPSAKYQVVCYTHPRCLLFTFTAESPSEDPTRWFTCVLKDSVTEITLPRVNRATAAISGYS
CHY  -----
      110     120     130     140     150     160     170     180     190     200
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   FKQCSHQISACNKDIYVDLDMKGINYNSSVAKSAQECQERCTDDVHCHFFTYATRQFPSSLEHRNICLLKHTQTGTPTTRITKLDKVVSGFSLKSCALSNI
CHY  LKQCGHQISACHRDYKGVDMRGVNFVNSKVVSSVEECQKRCCTNNIRCOFFSYATQTFHKAERYNNCLLKYSPPGGTPTAIKVLNSVESGFSILKPCALSEIG
      210     220     230     240     250     260     270     280     290     300
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   CIRDIFPNTVFADSNIDSVMAPDAFVCGRICTHHPGCLFFTTFFSQEWPKESQRNLCLLKTSSEGLPSTRIKSKALSQSGFSLQSCRHSIPVFCSSFYHDT
CHY  CHMNIFQHIAFSDVDVARVLTDFAFVCRITICTYHPNCLFFFTYTNVWKIESQRNVCLLKTSSEGSTPSSSTPQENTISGYSLLTCKRTLPEPCHSKIYPGV
      310     320     330     340     350     360     370     380     390     400
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   DFLGEELDIVAAKSHEACQKLCNTAVRCQFFTYTPAQASCNEGKGCYKYLKSSNGSPTKILHGRGGISGYTLRLCKM-DN-ECTTKIKPRIVGGTASVRG
CHY  DFGGEEELNVTFFVKGVNVCQETCTKMIRCQFFTYSLLPEDCKEEKCKCFRLRLSMDGSPTRIAYGTOGSSGYSRLCNTGDNVCTTSTSTRIVGGTNSSWG
      410     420     430     440     450     460     470     480     490     500
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   EWPWQVTLHTTSPTQRHLCGGSIIGNQWILTAAHCFYGVESP KILRVYSGILNQSEIKEDTSFFGVQEIHHQYKMAESGYDIALLKLETTVNYTDSQR
CHY  SWPWQVSLQDKTG--FHFCGGSLISEDWVVTAHHC--GVRTSDVV--VAGEFDQGSDEENIQVLKIAKVFKNPKFSILTVNNDITLLKLATPARFSQTVS
      510     520     530     540     550     560     570     580     590     600
FXI  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PK   PICLPSKGDNRVIYTDWVGTGWGYRKL-RDKIQNTLQAKIPLVTNEECQKRYRGHKITHKMICAGYREGGKDACKGDSGGPLSCKHNEVWHLVGITSWG
CHY  AVCLPSADDDFPAGTLCATTGWGKTKYNANKTPDKLQQAALPLLSNAECKKSWG-RRITDVMICAG--ASGVSSCMGDSGGPLVCQKDGAWTLVGVISWG
      610     620     630
FXI  ....|....|....|....|....|....|....|
PK   EGCAQRERPGVYTNVVEYVDWILEKTQAV-----
CHY  SRTCSTTTPAVYARVAKLIPVWQKILA-----
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