

1B8F:A|PDBID|CHAIN|SEQUENCE

jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
-----T
1  -----MNTLLIHHWTALNNALSSNDI
1  -----ML-----DKH-----IPDGHLETTSAHWRDLNQ-VVQNG-
1  MADT PPNLS PDNSSLITHAEAMLSALMKVEKAVDEAGSGKNKPYDFTEAVLDATSKLEFILIVGK-
```

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jgi|Aspni7|1126350

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```
2  ELTLKPGTLTLAQLRAI-----HAAPVRLQLDASAAPAIDASVACVE
22 GRDL DGKTLDLATVVASARYGKRVS-----LSQSTRKHVQRSSEAVLR
29 ELSIDGYSLSLADVVAVAKYGC-----QPRLTDKPEPIDAINGSVIALA
66 I VSVNGRRLDLAEVVAVSKYVVVSFDET PRPHFEADSLSYLRHGVT PVVCDNGTIRPKMQSSVEFLS
```

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```
44 QIIAEDRTAYGIN TGFGLLASTRIASHDL ENLQRSVLVLSHAAGIGAPL-----
64 KHLADGELIYGVNTGFGGSADTTTD--AVNKLQENLLQMLQAGVKLDGSSPVVVKNP NEDILPLDD
73 ECLRDPGHHIYGVNTGFGGSADSR TN--QT TTLQSSLLQLLQSGILTASDTT-----NEGLQLNLQ
132 KHLKEGNTVYGVNTGFGGSADTRTD--NYRALQKALVQHHNAGVLLPAEQG-----LESTPI-QD
```

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```
92  -----DDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSV GASGDLAPLA
128 PISATIMPESWTRATMIIRLNCLASGSSGIRQSVLDVLLRMIEQHITPRVPLRGSISASGDL SPLS
131 GQSSHSMPEWVKATMLVRSNSVARGHSAVSLPAISAILRLIREDIIPVPLRGTISASGDL MPLA
189 RLKKHSMPASVYKAAMLIRCNSLINGHSAVRPVAIHHILKMAAADFTPVVPLRGSISASGDL TPLA
```

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```
151 HMSLVLLGEGK-----ARYKQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLF
194 YIGGAMQGHPSIHVWKRGRNSDCQVKGADVALKES SIPFVCLDAKEGLAIVNGTATSAAVGG LALH
197 YVVGAI EGS PG IYVRV-KNGSEHQVVT A QKALQTIAAKGVT L GPKEGLGLVNGT AAS GALAGLVLY
255 YIAGAIEGNPDIFVDC-GPNHNNMILPSDEALAKLSLKPISFFPK EGLGLLNGTAFSAGAASLVLF
```

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jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
210 Y AEDLYAAA IACGGLSVEAVLGSRS PF DARIHEARGQRGQ IDT AACFRDLLGDSSEVSL S---HKN
260 ETLGLAALSQVLAAM SVEALHGTSESFDPFFAKVRPHPGQTTAANNLYKFLSNSKLLNDG NDF-RQ
262 EAHQLAVLAQAVTAL TVEAIQGSTESFHPFIAQVRPHEGQIEAAENILSLLKGSLLARG S STTQTR
320 EANQLALFAQVVTAMCTEALMGT RRNFHPFISNARPHPGQKEVARNLYGILSDSKLASDS--IPEE
```

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jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
273 ADKVQDPYSLRRCQPQVMGACL TQLRQA AEVLGIEANAVSDNPLVFAA--EGDVISGGNFHAE PVAM
325 GSLRQDRYSIRTS AQWMGPLLEDLELAYQQISVELNSVT DNPLIDTAGDNARILHGGNFQAKS ITS
328 TGLVQDRYSLRTA SQWIGPQLEDLLADRQVQVELNST DNPLIDTG--SKTFYTGGNFQATS ITS
384 VGLAQDRYAIRT PQWIGPQIESLALATRQVECELNST DNPLLDTE--NGEVHHGGNYQAAS ITS
```

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jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
337 AADNLALAAIEIGSL SERRISLMMDKHMS-QLP PFLVENG-GVNSGFMIAQVTA AALAS ENKALSH
391 AMEKTRQAVQSMGRMLYAQCTEL IDSSKNNGLPNLSADEPSLSFTFKGVDIMIAALQS E LGLAN
392 AMEKTRLALQMF GKMLFVQC NEMIDPNL NGLPTNLVADDP SLSFTMKGVDINMAAYMS E LAYLAN
448 AMEKVMT CMQMI GKMIFAQCS ELLNPMFSKGLP PNL CADDPNLSFAFKGIDINMAS YMS E LAYLAH
```

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jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
401 PHSVDSLPTSANQEDHVS MAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTS AKLEKARQ
457 PIGSHVQTAEMGNQALNSLALIS SRYTLDAVAVLSQMAAAHLVATCQALDLRVINIQFMR---T--
458 PVS SHVQTAEMQNQALNSLAFVSARYTMKAVDIVSMMGACALYVACQALDLRVLQLRFFQ---R--
514 PVS NFVQSAEMHNQSINSLALLTARYAGDTVEILSLMMATHIYVLCQALDLRTLQLEFEE---S--
```

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jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
467 ALRSEVAHYDRDRFFAPDIEKA-V-----EL-----LAKGSL
518 -LEQDFMKLFGDSFQVNAV PFKNILAISKEAWDAFAKQVEQLQSV DSCSRFHQAARA ILPIFIMA-
519 -VQGVAKEIAHG-AFGKVL E PFEIDQVADHLSEAIQNSWPST SRLDLRDRCKRVAEMFIPVLF GAL
575 -AKPSVDETTRV-MCMDLVPEKRAAYIKVKIWNVLMQHWAKNSNLGLASRAATSTTHA----VGTL
```

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jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
498 TGLLPAGVLP S-----L-----
582 ---LPQS-----AASPAI IQSWIDRLGSQATETYRKTHEAYCKCPDATPYLGEASRKMYTHVRQN
583 LQMI PQNRQTS DL LT--AISACKMISVFKLEGVYREVFAEFCTSQPTADFLGTGTKEIYTFIRHD
635 INLITDECDESKIGEIPGKVL LWQKEVKSKL CDEYEMTREKYFLDPSTPDYLC TSCIKLYNYVRKT
```

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jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
639 LKL PFI VEGTLWRPS DSAKTPDGEATPPPLPTMGDVVGIAYDAIRRGSLYTVAVECIRDVEQ-DMG
646 LRV PFHQ-GFVEHPSASQTDLPETINGRVKKT VGGWISVVYEALRNGT LSGTILNSFRQ*-----
701 LEV PMHK-GVVDHPTFL----PPHTIPSEKQTIGSLISTIYVDLREGDLMHTLKGCFEVP LVG SVG
```

1B8F:A|PDBID|CHAIN|SEQUENCE

jgi|Aspni7|1129557

jgi|Aspni7|1126350

jgi|Aspni7|1081533

```
704 KYPHCLVNYPTCASRT*
762 KDDEE*-----
```