


[illegible]



| Sequence  | Score |
|---|-------|
| CPDYDGDGDDKAEDWLRVGTDSRVKAAAL <del>EME</del> .QYAYTSVGMAS <del>C</del> WEFVEL.....  | 86    |
| CPDYDGDGDDKAEDWLRVGTDSRVKAAAL <del>EME</del> .QYAYTSVGMAS <del>C</del> WEFVEL.....  | 85    |
| ELAE <del>GG</del> GAPARNAAFK <del>W</del> IGSQSAGPVV <del>REL</del> Q.ALGRV <del>C</del> AGMCSGWEFVEL.....                   | 92    |
| VSVEPGAAGVQAVRA <del>W</del> IESPGAAPVV <del>REL</del> Q.ALGRVT <del>I</del> GMCSG <del>W</del> QFVEQ.....                    | 87    |
| ALLDYDADAPGALAAATDDQRLAPT <del>V</del> RRLQ.ALGQV <del>S</del> AGMCGAWEFVEL.....  | 133   |
| DFGGQDGPTRADAQTA <del>I</del> DEPVLAPT <del>V</del> RHLQ.ALGSV <del>H</del> MGMLSG <del>W</del> AFVEL.....                    | 103   |
| DFGGQDGPTRADAQTA <del>I</del> DEPVLAPT <del>V</del> RHLQ.ALGSV <del>H</del> MGMLSG <del>W</del> AFVEL.....                    | 147   |
| .LIPDFADTVEAAPSIGDNARVAQVARALEKDFG <del>F</del> VRVGVIVSSWEFCEL.....  | 85    |
| HLPIGAEQAAEVIRR <del>W</del> DTLPASSVVD <del>EL</del> Q.QLGRIT <del>V</del> GMCHEG <del>Q</del> FL <del>EC</del> .....        | 95    |
| DENFDGLEPEIIYYDV <del>V</del> ASQACKEVAYRYE.EMGEFT <del>F</del> GLCSWEFNV <del>M</del> .....                                  | 91    |
| .FAYDPDLEASQREQ <del>F</del> G...VYRQKCR <del>D</del> YLSSKGR <del>I</del> ESGHCSWEFSTTNAYYCEAESLLAAIESEREYME <del>LN</del> T | 117   |
| AYPQDD <del>S</del> ISQEDLIEFYFSNDFEYDPD <del>D</del> V.....GRLMR <del>W</del> .....  | 92    |

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- ☐ non conserved
- ☒ similar
- ☒  $\geq 50\%$  conserved