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logo
NTDB id 1184 GTF74 RS02335 WP 000649326.1     ...MKAYKNKQQKGFTLIELMIVVAVIGVLAAIAIPQYQNYVKKSAIGVGLANITALKTNIEDYIATEGSFPATTAGTAA   77
NTDB id 1167 A1552VC RS11065 WP 000649326.1   ...MKAYKNKQQKGFTLIELMIVVAVIGVLAAIAIPQYQNYVKKSAIGVGLANITALKTNIEDYIATEGSFPATTAGTAA   77
NTDB id 1160 ABDM36 RS02330 WP 000649326.1    ...MKAYKNKQQKGFTLIELMIVVAVIGVLAAIAIPQYQNYVKKSAIGVGLANITALKTNIEDYIATEGSFPATTAGTAA   77
NTDB id 1197 PSJM300 03940 AFN76866.1         ......MKAQMQKGFTLIELMIVVAIIGILAAIALPAYQDYTVRSNAAAALAEITPGKIGFE.QAINEGKTPSLTSTDEG   73
NTDB id 1204 PSJM300 03935 AFN76865.1         ....MKPVKSSCRGFSLIELMIVVAIIGILAAIALPAYQNYTVRSTAASALAEITPAKAAFE.QAISEGHTPSLVSSLPG   75
NTDB id 1191 AAC28468.1 484..945( )           ......MLKKVQKGFTLIELMIVIAIIGILAAIALPAYQDYTARAQATEGFKATAGLQTDLGAWRADRGSFPNAAALVAG   74
NTDB id 1424 RS RS02795 WP 011000517.1        MKSMRHLNKRVQKGFTLIELMIVVAIVGILAAIAIPAYQDYTVRARVTEGLSLAAQAKALVSENAANAQSDLSV....GS   76
NTDB id 1002 ACIAD RS15100 WP 004923779.1     ........MNAQKGFTLIELMIVIAIIGILAAIAIPAYTDYTVRARVSEGLTAASSMKTTVSENILNAGALVAGTPSTAG   72
NTDB id 183636 A9E97 RS09325 WP 015444381.1  .........MRMKGFTLIELMIVAAILGILVAIAIPAYQDYTIRARVVEGLEMASAAKLAVVETSLIDNTLPANQADTGY   71
NTDB id 1274 LPP RS09530 WP 011214168.1       .........MRQKGFTLIELMIVVAIIGILAAIAIPAYQDYTIRARVTEGLTLADSAKLAVSETAITNNALPATQAATGY   71
NTDB id 1258 GC085 RS09745 WP 014844212.1    .........MRQKGFTLIELMIVVAIIGILAAIAIPAYQDYTIRARVTEGLTLADSAKLAVSETAITNNALPATQAATGY   71
consensus                                       **!!*!!!!!!!*!**!*!*!!!*!*!**!**** * ***   * **  * *  ***** **  * ***

logo
NTDB id 1184 GTF74 RS02335 WP 000649326.1     G........FTRLGTVEDMGDGKIVIAPTASGALGGTIKYTFD...AGVVSSSK.............IQLARDANGLWTC   133
NTDB id 1167 A1552VC RS11065 WP 000649326.1   G........FTRLGTVEDMGDGKIVIAPTASGALGGTIKYTFD...AGVVSSSK.............IQLARDANGLWTC   133
NTDB id 1160 ABDM36 RS02330 WP 000649326.1    G........FTRLGTVEDMGDGKIVIAPTASGALGGTIKYTFD...AGVVSSSK.............IQLARDANGLWTC   133
NTDB id 1197 PSJM300 03940 AFN76866.1         .........YIGITDST...S.YCDVD..LDTAADGHIECTAKGGNAGKFDGKTITLNRT.............ADGEWSC   125
NTDB id 1204 PSJM300 03935 AFN76865.1         .........FIGIGAST...N.YCTVT..LIATATGSITCTTQNGMPDRFNGKTITIART............TDGLWDC   127
NTDB id 1191 AAC28468.1 484..945( )           NVIFDSANGLDGK.YFAPGGV.T.......VTPDTGAINIAFD...AGANAGKTMTITPTVI.......AASGQISTWTC   135
NTDB id 1424 RS RS02795 WP 011000517.1        S............VFTPTKN.VANLTIAGTGTVPGQI.TVTY...TTAAGGGTLALVPTAAGTALPVSSAPSGPIMWTC   138
NTDB id 1002 ACIAD RS15100 WP 004923779.1     S....SCVGVQEISASNATTN.VATATCGA..SSAGQIIVTMD...TTKAKGANITLTPTY.........ASGAVTWKC   132
NTDB id 183636 A9E97 RS09325 WP 015444381.1  T............SPAPTIN.VASIAIGN....QGII.TITY...TANAGNGTITMVPTI........DATNRILTWDC   121
NTDB id 1274 LPP RS09530 WP 011214168.1       V............SPAATPN.VASIAIGA....NGVI.TITY...TAAAGGGTIVMTPTL........QAN.GDVTWTC   120
NTDB id 1258 GC085 RS09745 WP 014844212.1    V............SPAATPN.VQSIAIGA....NGVI.TITY...TAAAGGGTIIMTPTL........QAN.GDVTWTC   120
consensus                                       * *     *    **  *     ! !  *      *   * ** * **          *  *   !*!

   <0
logo
NTDB id 1184 GTF74 RS02335 WP 000649326.1     STT................VTSEIAPKGCTAGATIN   153
NTDB id 1167 A1552VC RS11065 WP 000649326.1   STT................VTSEIAPKGCTAGATIN   153
NTDB id 1160 ABDM36 RS02330 WP 000649326.1    STT................VTSEIAPKGCTAGATIN   153
NTDB id 1197 PSJM300 03940 AFN76866.1         AST................LDAKYKPGKCS......   139
NTDB id 1204 PSJM300 03935 AFN76865.1         TSD................LDSRYKPGKCL......   141
NTDB id 1191 AAC28468.1 484..945( )           APGAANG............IETRRLPTSCQ*.....   153
NTDB id 1424 RS RS02795 WP 011000517.1        YAQNKAQAASSVAPSGTMSLAAKYAPAECR......   168
NTDB id 1002 ACIAD RS15100 WP 004923779.1     TTT................SDKKYVPSECRG.....   147
NTDB id 183636 A9E97 RS09325 WP 015444381.1  TGG...............TLISKYRPAYCRP.....   137
NTDB id 1274 LPP RS09530 WP 011214168.1       TGG...............TLLAKYRPASCRP.....   136
NTDB id 1258 GC085 RS09745 WP 014844212.1    TGG...............TLLAKYRPASCRP.....   136
consensus                                     **                 * *** !* !
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X non conserved

X similar

X ≥ 50% conserved