```
logo
NTDB id 1127 NGFG RS10560 WP 003703428.1       MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.F..................VLF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1126 NGFG RS09375 WP 003703428.1       MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.F..................VLF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1125 NGFG RS07215 WP 003703428.1       MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.F..................VLF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1108 NGFG RS06525 WP 003703428.1       MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.F..................VLF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1014 ACIAD RS13855 WP 004924483.1      ......MSIRHFFTFFWATLLTLFSMQIVFAQGFDQQYDAWKTQQKAHDTRLNSSASHHSLSKPTQQSGTGVKVNINSAT   74
NTDB id 1159 ABDM36 RS04765 WP 001166105.1     ......MQIKTKIVTLFLSLCLPTLPLLANAEETAP.......AAQ...................VEEGIVITVNINTAS   48
NTDB id 1150 A1552VC RS08580 WP 001166105.1    ......MQIKTKIVTLFLSLCLPTLPLLANAEETAP.......AAQ...................VEEGIVITVNINTAS   48
NTDB id 1294 VP RS04495 WP 021449594.1         .............MKWILTLCLVVFAPLSLAA..DT.......KAD...................KYEGIEITVNINTAS   39
NTDB id 1072001 ACI3L8 RS02665 WP 103410106.1  .............MKWMLTLCLLILTPMSWAE.TKT.......KAD...................KYEGIEITVNVNSAT   40
NTDB id 1395 DSB67 RS04445 WP 010649155.1      .............MKWMLTLCLLILAPMSWAE.TKT.......KAD...................KYEGIEITVNVNSAT   40
NTDB id 1362 HI 1008 AAC22669.1                ........MKTL..FTSVVLCGALVVSSSFAEEKAT.......XQTAQ......SVVTTQAEAQVAPAVVSDKLNINTAT   57
NTDB id 1382 A4U84 RS07375 WP 062924234.1      ........MKKLSRYTFSLLFG.LFSATTFAEEKVT.......TSTEH......TPVVMQQ.VAATQKVNANVVNINTAT   57
consensus                                               *   ** ** ** **   *  *                                          *!*!*!*

logo
NTDB id 1127 NGFG RS10560 WP 003703428.1       QQELEA.LPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK   131
NTDB id 1126 NGFG RS09375 WP 003703428.1       QQELEA.LPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK   131
NTDB id 1125 NGFG RS07215 WP 003703428.1       QQELEA.LPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK   131
NTDB id 1108 NGFG RS06525 WP 003703428.1       QQELEA.LPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK   131
NTDB id 1014 ACIAD RS13855 WP 004924483.1      AKELQQ.LHGVGEKKALAIVEYRQQYGKFASVDDLQKVKGIGPKFIEKNRDRLAI...................   128
NTDB id 1159 ABDM36 RS04765 WP 001166105.1     AEELATLLKGIGLKKAQAIVDYREANGPFTHIDDLTNVKGIGEATVRNNAARILL...................   103
NTDB id 1150 A1552VC RS08580 WP 001166105.1    AEELATLLKGIGLKKAQAIVDYREANGPFTHIDDLTNVKGIGEATVRNNAARILL...................   103
NTDB id 1294 VP RS04495 WP 021449594.1         AEEIATMLKGIGEKKAQSIVDYRTEHGPFKTAADLTNVKGIGEATIKKNEDRILL...................    94
NTDB id 1072001 ACI3L8 RS02665 WP 103410106.1  AEEIATLLNGIGEKKAQDIVEYRNEHGPFKTAADLTKVKGIGEATVKKNEDRILL...................    95
NTDB id 1395 DSB67 RS04445 WP 010649155.1      AQEIATLLIGIGEKKAQDIVEYRNEHGPFKTAADLTKVKGIGEATVRKNEDRILL...................    95
NTDB id 1362 HI 1008 AAC22669.1                ASEIQKSLTGIGAKKAEAIVQYREKHGNFXNAEQLLEVQGIGKATLEKNRDRIIF...................   112
NTDB id 1382 A4U84 RS07375 WP 062924234.1      ASEIQDKLVGIGAKKAQAIVEYREKNGKFLNVEQLTEVSGIGKATLEKNRDCIVIE...................   113
consensus                                      * !*   ! !*! *!! *!**!!  *! !*****! *!*!!! *** ********
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X non conserved

X similar

X ≥ 50% conserved