```
logo

NTDB id 1127 NGFG RS10560 WP 003703428.1      MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.FV..................LF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1126 NGFG RS09375 WP 003703428.1      MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.FV..................LF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1125 NGFG RS07215 WP 003703428.1      MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.FV..................LF..CMLFSCAFSLAAVNINAAS   59
NTDB id 1108 NGFG RS06525 WP 003703428.1      MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.FV..................LF..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 975494 AADH43 RS11290 WP 021449594.1  .............MKWILTLCLVVFAPLSLAA..DT.......KAD...................KYEGIEITVNINTAS   39
NTDB id 1294 VP RS04495 WP 021449594.1        .............MKWILTLCLVVFAPLSLAA..DT.......KAD...................KYEGIEITVNINTAS   39
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 975494 AADH43 RS11290 WP 021449594.1  AEEIATMLKGIGEKKAQSIVDYRTEHGPFKTAADLTNVKGIGEATIKKNEDRILL...................    94
NTDB id 1294 VP RS04495 WP 021449594.1        AEEIATMLKGIGEKKAQSIVDYRTEHGPFKTAADLTNVKGIGEATIKKNEDRILL...................    94
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                                     * !*    ! !*! *!! *!**!!  *! !*****!  !*!!! *** ********
```

X non conserved

X similar

X ≥ 50% conserved