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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 1082092 ACK2V6 RS04540 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                                                *   ** ** ** **** *  *                                          *!*!*!*
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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 1082092 ACK2V6 RS04540 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                                       * !*   ! !*! *!! *!**!!  *! !*****!  !*!!! *** ********
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X non conserved

X similar

X ≥50% conserved