```
logo
                                                  MSRGGATPYRFLLIRHIVARCGLLFATLKGKTMKKM.F..................VLF..CMLFSCAFSLAAVNINAAS
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 1395 DSB67 RS04445 WP 010649155.1         .............MKWMLTLCLLILAPMSWAE.TKT.......KAD...................KYEGIEITVNVNSAT   40
NTDB id 96818 OO774 RS11155 WP 264906106.1        .............MKWVLTLLLCVFTPFGLAA..DT.......TAD...................KYEGIEITVNINSAT   39
NTDB id 1294 VP RS04495 WP 021449594.1            .............MKWILTLCLVVFAPLSLAA..DT.......KAD...................KYEGIEITVNINTAS   39
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
                                                  QQELEA.LPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK   131
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 1395 DSB67 RS04445 WP 010649155.1         AQEIATLLIGIGEKKAQDIVEYRNEHGPFKTAADLTKVKGIGEATVRKNEDRILL...................    95
NTDB id 96818 OO774 RS11155 WP 264906106.1        AEEIATMLKGIGEKKAQDIVDYRSEHGPFKTVSDLGKVKGIGDATLKKNEGRIIL...................    94
NTDB id 1294 VP RS04495 WP 021449594.1            AEEIATMLKGIGEKKAQSIVDYRTEHGPFKTAADLTNVKGIGEATIKKNEDRILL...................    94
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