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logo
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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 132009 FORC6 RS11125 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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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 132009 FORC6 RS11125 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 $\geq$ 50% conserved