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logo
NTDB id 105 BSU 25590 NP 390437.1          ........MNWLNQHKKAIILAASAAVFTAIM.IFLATGKNKEPVK...................QAVPTETENTVVKQEANNDES   58
NTDB id 595 KW2 RS08725 WP 021037687.1     ....MEKILDKLKEYWKIMLLVVCALIAGGIFYIFTNSPKPAETL........SVENLSSSSTKSSVS......KFNSSSSEKN   66
NTDB id 521 SMSK321 RS04960 WP 000443804.1 ....MESIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPHTPV.KETNLQAEVVAISKDSST.......EKDVKKEEKEEPVE   70
NTDB id 493 SM12261 RS04300 WP 000387351.1 ....MEAIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPQTPV.KETNLQAEVVAVSKDSVS.......EKEVKKEEKEEPLE   70
NTDB id 263 KZH43 RS04195 WP 000387330.1   ....MEAIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPQTPV.KETNLQAEVAAVSKDLVS.......EKEVNKEEKEEPLE   70
NTDB id 222 SPD RS04535 WP 000387330.1     ....MEAIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPQTPV.KETNLQAEVAAVSKDLVS.......EKEVNKEEKEEPLE   70
NTDB id 188 SPR RS04295 WP 000387330.1     ....MEAIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPQTPV.KETNLQAEVAAVSKDLVS.......EKEVNKEEKEEPLE   70
NTDB id 153 SP RS04730 WP 000387344.1      ....MEAIIEKIKEYKIIVICTG.LGLLVG..GFFLLKPAPQTPV.KETNLQAEVAAVSKDSST.......EKEVKKEEKEEPLE   70
NTDB id 49735 SSUD9 RS04070 WP 002935348.1 .MDTIKTYIEMLKEYKWQIALPAVAGLLMATFLIF...SQPAKSD......QTGLTDFPQTAQTSSSSDLVEET...S.TEASEE   71
NTDB id 300 STER RS07485 WP 011681496.1    MKEKILAYV...KDNRLFVS...VIAVLMVIFCFFLWMTCGAGNSMEAETSYTDVTALSTSSSKQSSQSLSEASSQSKTEGSEKV   79
consensus                                      ******************** ******  **!********** ********* ****** *        **** *********
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logo
NTDB id 105 BSU 25590 NP 390437.1          NETIVIDIKGAVQHPGVYEMRTGDRVSQAIEKAGGTSEQADEAQVNLAEILQDGTVVYIPKKGEETAVQQGGGGS.....VQSDG   138
NTDB id 595 KW2 RS08725 WP 021037687.1     KNEIMVDLKGAVAKPNVYQISSDERLVDLIRQAGGFTDQADQKSINLSAKLKDEEVIYVPKVGESSSSESTDSPTGSSVSNQIST   151
NTDB id 521 SMSK321 RS04960 WP 000443804.1 QDLITVDVKGAVKSPGIYDLSVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEESASQ.HTGSG.....APSST   149
NTDB id 493 SM12261 RS04300 WP 000387351.1 QDLITVDVKGAVKSPGIYDLPVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEEAASQ.QAGPG.....TASST   149
NTDB id 263 KZH43 RS04195 WP 000387330.1   QDLITVDVKGAVKSPGIYDLPVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEEAVSQ.QTGLG.....TASSI   149
NTDB id 222 SPD RS04535 WP 000387330.1     QDLITVDVKGAVKSPGIYDLPVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEEAVSQ.QTGLG.....TASSI   149
NTDB id 188 SPR RS04295 WP 000387330.1     QDLITVDVKGAVKSPGIYDLPVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEEAVSQ.QTGLG.....TASSI   149
NTDB id 153 SP RS04730 WP 000387344.1      QDLITVDVKGAVKSPGIYDLPVGSRVNDAVQKAGGLTEQADSKSLNLAQKVSDEALVYVPTKGEEAVSQ.QTGSG.....TASST   149
NTDB id 49735 SSUD9 RS04070 WP 002935348.1 PSQLVVDVKGAVVKPGLYTLEADARVNDAVEAAGGLTSQADPKSINLAQKLSDEAVVYVASKDENISVVASTTASSAMS...SEE   153
NTDB id 300 STER RS07485 WP 011681496.1    KSKVTVDVKGAVVNPGVYTLKAGARVTDVIQEAGGMTEDADAKSVNLAASLSDEEVIYVANKDENVSVLDQTGTGQVSDKGGQAV   164
consensus                                  ******!*!!!!**!**!******!*******!!!****!!****!!*****!****!*****!** ** *** *      ****
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logo
NTDB id 105 BSU 25590 NP 390437.1          GKGALVNINTATLEELQGISGVGPSKAEAIIAYREENGRFQTIEDITKVSGIGEKSFEKIKSSITVK   205
NTDB id 595 KW2 RS08725 WP 021037687.1     TSGPKVNINKADLTELQKLTGIGQKKAQDIIDFRMKNGDFKSIEDLGKVSGFGDKTLEKLKDEISID   218
NTDB id 521 SMSK321 RS04960 WP 000443804.1 SKDKKINLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGAKTIEKLKDYVTVD   216
NTDB id 493 SM12261 RS04300 WP 000387351.1 SKEKKVNLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGAKTIEKLKDYVTVD   216
NTDB id 263 KZH43 RS04195 WP 000387330.1   SKEKKVNLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGGKTIEKLKDYVTVD   216
NTDB id 222 SPD RS04535 WP 000387330.1     SKEKKVNLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGGKTIEKLKDYVTVD   216
NTDB id 188 SPR RS04295 WP 000387330.1     SKEKKVNLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGGKTIEKLKDYVTVD   216
NTDB id 153 SP RS04730 WP 000387344.1      SKEKKVNLNKASLEELKQVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGGKTIEKLKDYVTVD   216
NTDB id 49735 SSUD9 RS04070 WP 002935348.1 KSTSQVNLNTATEADLQTISGIGAKRATDIIAYREANGGFKSVDDLNNVSGIGDKTMESIRPYVTVE   220
NTDB id 300 STER RS07485 WP 011681496.1    SKDGKINLNTATSEQLQTISGIGAKRAEDVIAYRESHGGFQSVDDLKNVSGIGDKTLDKIRESLYVA   231
consensus                                  ******!*!*!****!****!*!***!***!**!***!*!********!!!*!*!************
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X non conserved

X similar

X ≥ 50% conserved