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logo
NTDB id 425 SGO RS10525 WP 012131081.1          .MKNSSNFFKKTLQVFIVLLVGFIGGVAGTWGFSYFSTPHSATNNNQKTATTVTTSYKNSNSTTEAVDKVKDAVVSVITY   79
NTDB id 539 SM12261 RS09395 WP 000681587.1      .MKHLKTFYKKGFQLLVVIVISFFSGALGSFSINQLTQKSTEST.SNNNSTITQTAYKNENSTTQAVNKVKDAVVSVITY   78
NTDB id 256 KZH43 RS10270 WP 000681597.1        .MKHLKTFYKKWFQLLVVIVISFFSGALGSFSITQLTQKSSVNN.SNNNSTITQTAYKNENSTTQAVNKVKDAVVSVITY   78
NTDB id 215 SPD RS10945 WP 000681597.1          .MKHLKTFYKKWFQLLVVIVISFFSGALGSFSITQLTQKSSVNN.SNNNSTITQTAYKNENSTTQAVNKVKDAVVSVITY   78
NTDB id 181 SPR RS10425 WP 000681597.1          .MKHLKTFYKKWFQLLVVIVISFFSGALGSFSITQLTQKSSVNN.SNNNSTITQTAYKNENSTTQAVNKVKDAVVSVITY   78
NTDB id 145 SP RS11450 WP 000681597.1           .MKHLKTFYKKWFQLLVVIVISFFSGALGSFSITQLTQKSSVNN.SNNNSTITQTAYKNENSTTQAVNKVKDAVVSVITY   78
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    MKKKLVSSLLK...CSLIIIVSFAGGAFASFV...MNHNDNIPNGG..VTKTSKVNYNNITPTTKAVKKVQNSVVSVINY   72
NTDB id 381 SMU RS09890 WP 002262650.1          MNNTKSHPFLKWFIPFLVIFLTFILGVISTLTFNWITGNKSFSNNG..KTTVSNVIYDTKSNTTKAVKNVKNTVVSVINY   78
consensus
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logo
NTDB id 425 SGO RS10525 WP 012131081.1          SESNSDAI........FDNN..NSGNFNDQVASEGSGVIYRKDKDYAYLVTNTHVINGAKKVDIRLADGNKVPGEIVGTD   149
NTDB id 539 SM12261 RS09395 WP 000681587.1      SANRQNSV........FGND..DTDTDSQQISSEGSGVIYKKNDKEAYIVTNNHVINGASKVDIRLSDGTKVPGEIVGAD   148
NTDB id 256 KZH43 RS10270 WP 000681597.1        SANRQNSV........FGND..DTDTDSQRISSEGSGVIYKKNDKEAYIVTNNHVINGASKVDIRLSDGTKVPGEIVGAD   148
NTDB id 215 SPD RS10945 WP 000681597.1          SANRQNSV........FGND..DTDTDSQRISSEGSGVIYKKNDKEAYIVTNNHVINGASKVDIRLSDGTKVPGEIVGAD   148
NTDB id 181 SPR RS10425 WP 000681597.1          SANRQNSV........FGND..DTDTDSQRISSEGSGVIYKKNDKEAYIVTNNHVINGASKVDIRLSDGTKVPGEIVGAD   148
NTDB id 145 SP RS11450 WP 000681597.1           SANRQNSV........FGND..DTDTDSQRISSEGSGVIYKKNDKEAYIVTNNHVINGASKVDIRLSDGTKVPGEIVGAD   148
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    KQQESRSDLSDFYSHFFG.NQGGNTDKGLQVYGEGSGVIYKKDGKNAYVVTNNHVIDGAKQIEIQLADGSKAVGKLVGSD   151
NTDB id 381 SMU RS09890 WP 002262650.1          QKTDNS.....YYNYDSGSQEKNKSEDGLGVYGEGSGVIYKKDGDSAYLVTNNHVVKDAEKLEIMMANGKKVVGKLVGSD   153
consensus
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logo
NTDB id 425 SGO RS10525 WP 012131081.1          TYSDISVVRIPADKVKNVAEFGDSSKLTVGETAIAIGSPLGSDYANTVTQGIVSSLSRNVSSRSEDGQTIATQAIQTDAA   229
NTDB id 539 SM12261 RS09395 WP 000681587.1      TFSDIAVVKISSEKVTTVAEFGDSSKLTVGETAIAIGSPLGSEYANTVTQGIVSSLNRNVSLKSEDGQAISTKAIQTDTA   228
NTDB id 256 KZH43 RS10270 WP 000681597.1        TFSDIAVVKISSEKVTTVAEFGDSSKLTVGETAIAIGSPLGSEYANTVTQGIVSSLNRNVSLKSEDGQAISTKAIQTDTA   228
NTDB id 215 SPD RS10945 WP 000681597.1          TFSDIAVVKISSEKVTTVAEFGDSSKLTVGETAIAIGSPLGSEYANTVTQGIVSSLNRNVSLKSEDGQAISTKAIQTDTA   228
NTDB id 181 SPR RS10425 WP 000681597.1          TFSDIAVVKISSEKVTTVAEFGDSSKLTVGETAIAIGSPLGSEYANTVTQGIVSSLNRNVSLKSEDGQAISTKAIQTDTA   228
NTDB id 145 SP RS11450 WP 000681597.1           TFSDIAVVKISSEKVTTVAEFGDSSKLTVGETAIAIGSPLGSEYANTVTQGIVSSLNRNVSLKSEDGQAISTKAIQTDTA   228
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    TYSDLAVVKIPSDKVSNIAEFADSSKLNIGETAIAIGSPLGTEYANSVTQGIVSSLKRTVTMTNEEGQTVSTNAIQTDAA   231
NTDB id 381 SMU RS09890 WP 002262650.1          TYSDLAVIKISSKYVTTVAEFANSDKIKVGEPAIAIGSPLGSDYANSVTEGIVSSLSRTVTSQNENGETISTNAIQTDAA   233
consensus
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logo
NTDB id 425 SGO RS10525 WP 012131081.1          INPGNSGGPLVNIQGQVIGITSSKIANTNN......GSTSVEGMGFAIPSNDVVNIIEQLEKNGKVIRPALGIQMVNLSS   303
NTDB id 539 SM12261 RS09395 WP 000681587.1      INPGNSGGPLINIQGQVIGITSSKIAT..N......GGTSVEGLGFAIPANDAINIIEQLEKNGKVTRPALGIQMVNLSN   300
NTDB id 256 KZH43 RS10270 WP 000681597.1        INPGNSGGPLINIQGQVIGITSSKIAT..N......GGTSVEGLGFAIPANDAINIIEQLEKNGKVTRPALGIQMVNLSN   300
NTDB id 215 SPD RS10945 WP 000681597.1          INPGNSGGPLINIQGQVIGITSSKIAT..N......GGTSVEGLGFAIPANDAINIIEQLEKNGKVTRPALGIQMVNLSN   300
NTDB id 181 SPR RS10425 WP 000681597.1          INPGNSGGPLINIQGQVIGITSSKIAT..N......GGTSVEGLGFAIPANDAINIIEQLEKNGKVTRPALGIQMVNLSN   300
NTDB id 145 SP RS11450 WP 000681597.1           INPGNSGGPLINIQGQVIGITSSKIAT..N......GGTSVEGLGFAIPANDAINIIEQLEKNGKVTRPALGIQMVNLSN   300
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    INPGNSGGALINIEGQVIGINSSKISSTSNQTSGQSSGNSVEGMGFAIPSNDVVKIINQLESNGQVERPALGISMAGLSN   311
NTDB id 381 SMU RS09890 WP 002262650.1          INPGNSGGALINIKGQVIGINSSKIASSNNS....NSGVAVEGMGFAIPSNDVVSIINQLEENGEVVRPALGISMANLSE   309
consensus
```

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logo

NTDB id 425 SGO RS10525 WP 012131081.1          LSSSSSDRLKLPDNVKNGVVVRSTQTGMPADGKLEKYDVITKIDDTEISSASDIQSALYKHSINEEIKVTYYRDGKEQTT   383
NTDB id 539 SM12261 RS09395 WP 000681587.1      INTSDIRRLNIPSNVTSGVVVRSVQSNMPANGHLEKYDVITKVDDKEIASSTDLQSALYNHSIGDTIKITYYRNGKEETT   380
NTDB id 256 KZH43 RS10270 WP 000681597.1        VSTSDIRRLNIPSNVTSGVIVRSVQSNMPANGHLEKYDVITKVDDKEIASSTDLQSALYNHSIGDTIKITYYRNGKEETT   380
NTDB id 215 SPD RS10945 WP 000681597.1          VSTSDIRRLNIPSNVTSGVIVRSVQSNMPANGHLEKYDVITKVDDKEIASSTDLQSALYNHSIGDTIKITYYRNGKEETT   380
NTDB id 181 SPR RS10425 WP 000681597.1          VSTSDIRRLNIPSNVTSGVIVRSVQSNMPANGHLEKYDVITKVDDKEIASSTDLQSALYNHSIGDTIKITYYRNGKEETT   380
NTDB id 145 SP RS11450 WP 000681597.1           VSTSDIRRLNIPSNVTSGVIVRSVQSNMPANGHLEKYDVITKVDDKEIASSTDLQSALYNHSIGDTIKITYYRNGKEETT   380
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    LPSDVISKLKIPSNVTNGIVVASIQSGMPAQGKLKKYDVITKVDDKEVASPSDLQSLLYGHQVGDSITVTFYRGENKQTV   391
NTDB id 381 SMU RS09890 WP 002262650.1          ASTSGRDTLKIPSDVTSGIVVLSTQSGMPADGKLKKYDVITEIDGKKVASISDLQSILYKHKKGDKIKLTFYREKDKQTV   389
consensus                                       ********!**!**!**!**!*!*!**!!!*!*!*!!!!!!**!*****!**!*!!*!!*!*****!**!*!!*****!*

logo

NTDB id 425 SGO RS10525 WP 012131081.1          TIKLTKSTDDLSSE....   397
NTDB id 539 SM12261 RS09395 WP 000681587.1      SIKLDKSSGDLES.....   393
NTDB id 256 KZH43 RS10270 WP 000681597.1        SIKLNKSSGDLES.....   393
NTDB id 215 SPD RS10945 WP 000681597.1          SIKLNKSSGDLES.....   393
NTDB id 181 SPR RS10425 WP 000681597.1          SIKLNKSSGDLES.....   393
NTDB id 145 SP RS11450 WP 000681597.1           SIKLNKSSGDLES.....   393
NTDB id 1159266 QOR52 RS10645 WP 000728357.1    TIKLTKTSKDLAKQRANN   409
NTDB id 381 SMU RS09890 WP 002262650.1          EIQLTKTSQDLNH.....   402
consensus                                       *!*! !***!!**
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X non conserved

X similar

X ≥ 50% conserved