logo

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NTDB id 509 SM12261 RS00130 WP 078228442.1   MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 279 KZH43 RS00140 WP 074017595.1     MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 238 SPD RS00140 WP 074017595.1       MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 204 SPR RS00140 WP 074017595.1       MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 169 SP RS00155 WP 074017595.1        MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 537 SMSK321 RS07120 WP 080550752.1   MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVS...LTGEKTKPMKLAEVTSINVNRTKTEMEEF   77
NTDB id 969375 MHI32 RS27900 WP 036680472.1  MAKAKTKFFCTDCGYESPKWFGKCPGCQAWNSMVEETESVVKTQGM..NAPIFHSKEKAQSIISIESDKEPRILTGIGEL   78
NTDB id 125 BSU 00870 NP 387968.1            MAKTKSKFICQSCGYESPKWMGKCPGCGAWNTMVEEMIKKAPANRRAAFSHSVQTVQKPSPITSIETSEEPRVKTQLGEF   80
consensus                                    !!!*!**!*!**!!!*!!!**!*!!*!**!***!!!**********    ******!**********!**!***!*
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logo

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NTDB id 509 SM12261 RS00130 WP 078228442.1   NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 279 KZH43 RS00140 WP 074017595.1     NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 238 SPD RS00140 WP 074017595.1       NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 204 SPR RS00140 WP 074017595.1       NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 169 SP RS00155 WP 074017595.1        NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 537 SMSK321 RS07120 WP 080550752.1   NRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQVG.TVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQSVR   156
NTDB id 969375 MHI32 RS27900 WP 036680472.1  NRVLGGGIVPGSLVLVGGDPGIGKSTLLLQTSHALTTQGLRVLYISGEESVRQTKLRADRLDALSTELYVLCETNMESIE   158
NTDB id 125 BSU 00870 NP 387968.1            NRVLGGGVVKGSLVLIGGDPGIGKSTLLLQVSAQLSGSSNSVLYISGEESVKQTKLRADRLGINNPSLHVLSETDMEYIS   160
consensus                                    !!!!!!!*!*!!!!!*!!!!!!!!!!!!!!*!**!****  *!!!*!!!!!!**!*!!!!*!!***********!!*!****
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logo

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NTDB id 509 SM12261 RS00130 WP 078228442.1   TEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 279 KZH43 RS00140 WP 074017595.1     AEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 238 SPD RS00140 WP 074017595.1       AEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 204 SPR RS00140 WP 074017595.1       AEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 169 SP RS00155 WP 074017595.1        AEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 537 SMSK321 RS07120 WP 080550752.1   AEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVLYF   236
NTDB id 969375 MHI32 RS27900 WP 036680472.1  EAIEQIQPQFLVIDSIQTVFMPEVTSAPGSVTQVRECTTRFMRIAKIRGIATVLVGHVTKEGAIAGPRMLEHMVDCVLYF   238
NTDB id 125 BSU 00870 NP 387968.1            SAIQEMNPSFVVVDSIQTVYQSDITSAPGSVSQVRECTAELMKIAKTKGIPIFIVGHVTKEGSIAGPRLLEHMVDTVLYF   240
consensus                                    ********!*!***!!!!!*********!!!*!!!!*!***!**!!***!****!!!!!!!!**!!!!*!!!!!!*!!!!
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logo

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NTDB id 509 SM12261 RS00130 WP 078228442.1   EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 279 KZH43 RS00140 WP 074017595.1     EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 238 SPD RS00140 WP 074017595.1       EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 204 SPR RS00140 WP 074017595.1       EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 169 SP RS00155 WP 074017595.1        EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 537 SMSK321 RS07120 WP 080550752.1   EGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPTMF   316
NTDB id 969375 MHI32 RS27900 WP 036680472.1  EGERHHTYRLLRAVKNRFGSTNEIGIFEMGEAGLTEVENPSELFLSERPLGVAGSTVVASMEGTRPVLVELQALVAATHF   318
NTDB id 125 BSU 00870 NP 387968.1            EGERHHTFRILRAVKNRFGSTNEMGIFEMREEGLTEVLNPSEIFLEERSAGSAGSSITASMEGTRPILVEIQALISPTSF   320
consensus                                    !!!!!!!*!*!!!!!!!!!!!!!!*!!!!!***!!*!!*!!!**!!*!!**!**!!*****!!!!!!*!*!*!!!***!*!
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logo
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NTDB id 509 SM12261 RS00130 WP 078228442.1     GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 279 KZH43 RS00140 WP 074017595.1       GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 238 SPD RS00140 WP 074017595.1         GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 204 SPR RS00140 WP 074017595.1         GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 169 SP RS00155 WP 074017595.1          GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 537 SMSK321 RS07120 WP 080550752.1     GNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELGLT   396
NTDB id 969375 MHI32 RS27900 WP 036680472.1   PSPRRMCTGMDHQRMALIIAVLEKRMGMFLQNQDAYLNVAGGVKLDEPAIDLAVAISIASSFRDISTKPYDVFFGEVGLT   398
NTDB id 125 BSU 00870 NP 387968.1             GNPRRMATGIDHNRVSLLMAVLEKRVGLLLQNQDAYLKVAGGVKLDEPAIDLAIVISIASSFRDTPPNPADCFIGEVGLT   400
consensus                                      ****!**!!*!**!**!**!!!!!!*!**!!!!!!!!**!!!!!!!!!!!!!!****!!!!**!****!***!*!!*!!!
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logo
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NTDB id 509 SM12261 RS00130 WP 078228442.1     GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 279 KZH43 RS00140 WP 074017595.1       GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 238 SPD RS00140 WP 074017595.1         GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 204 SPR RS00140 WP 074017595.1         GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 169 SP RS00155 WP 074017595.1          GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 537 SMSK321 RS07120 WP 080550752.1     GEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPMEIQVIGVTTIQEVLKKVFA.   453
NTDB id 969375 MHI32 RS27900 WP 036680472.1   GEVRGVSRAEMRVKEAAKLGFRRVIMPEKSMKGWKHPQDIQIIGVSTVADALSVALD.   455
NTDB id 125 BSU 00870 NP 387968.1             GEVRRVSRIEQRVKEAAKLGFKRMIIPAANLDGWTKPKGIEVIGVANVAEALRTSLGG   458
consensus                                      !!*!*!*!*!*!**!!!!!!!*****!*****!** !**!**!!!******!*****
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X non conserved

X similar

X ≥ 50% conserved