```
logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 238 SPD RS00140 WP 074017595.1        ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 204 SPR RS00140 WP 074017595.1        ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 169 SP RS00155 WP 074017595.1         ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 537 SMSK321 RS07120 WP 080550752.1   ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 509 SM12261 RS00130 WP 078228442.1   ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTG....EKTKPMKLAEVTSINVNRTKTEM   74
NTDB id 247571 CNY62 RS06335 WP 029091568.1  MAKKKASTKFVCNACGYESPKWMGRCPNCSEWNQMVEFVEAKVQKGR.TSFNHTEEMESQQALPLSKITSETEQRILTDM   79
NTDB id 125 BSU 00870 NP 387968.1             ..MAKTKSKFICQSCGYESPKWMGKCPGCGAWNTMVEEMIKKAPANRRAAFSHS.VQTVQKPSPITSIETSEEPRVKTQL   77
consensus                                       **!****!*!**!!!*!!!**!*!!*!**!***!!*****************    *****************!**!**
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logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 238 SPD RS00140 WP 074017595.1        EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 204 SPR RS00140 WP 074017595.1        EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 169 SP RS00155 WP 074017595.1         EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 537 SMSK321 RS07120 WP 080550752.1   EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 509 SM12261 RS00130 WP 078228442.1   EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQ   153
NTDB id 247571 CNY62 RS06335 WP 029091568.1  PELNRVLGGGLVKGSLVLVGGDPGIGKSTLLLQVSAQLTTAKRKGLYVSGEESIKQTKLRAERLNVDGDLLYVYAQTDLE   159
NTDB id 125 BSU 00870 NP 387968.1             GEFNRVLGGGVVKGSLVLIGGDPGIGKSTLLLQVSAQLSGSSNSVLYISGEESVKQTKLRADRLGINNPSLHVLSETDME   157
consensus                                     *!*!!!!!!!*!*!!!!!*!!!!!!!!!!!!!!!!!*!!*** ***!!*!!!!!**!*!!!!*!!*************!***
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logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      SVRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 238 SPD RS00140 WP 074017595.1        SVRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 204 SPR RS00140 WP 074017595.1        SVRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 169 SP RS00155 WP 074017595.1         SVRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 537 SMSK321 RS07120 WP 080550752.1   SVRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 509 SM12261 RS00130 WP 078228442.1   SVRTEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTV   233
NTDB id 247571 CNY62 RS06335 WP 029091568.1  VISKTIQTLQPEFVVIDSIQTIYHPDVTSAAGSVTQVRECTSELMRLAKTLNIAIFIVGHVTKEGTIAGPRMLEHMVDTV   239
NTDB id 125 BSU 00870 NP 387968.1             YISSAIQEMNPSFVVVDSIQTVYQSDITSAPGSVSQVRECTAELMKIAKTKGIPIFIVGHVTKEGSIAGPRLLEHMVDTV   237
consensus                                     **********!*!***!!!!!*********!!!*!!!!*!*!!!*!!!!*!*!!!!!!!!!!!*!!!!*!!!!!!!!
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logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 238 SPD RS00140 WP 074017595.1        LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 204 SPR RS00140 WP 074017595.1        LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 169 SP RS00155 WP 074017595.1         LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 537 SMSK321 RS07120 WP 080550752.1   LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 509 SM12261 RS00130 WP 078228442.1   LYFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTP   313
NTDB id 247571 CNY62 RS06335 WP 029091568.1  LYFEGERHHAYRILRAVKNRFGSTNEMGIFEMRDVGLVEVDNASEVFLEERLEGAAGSAVVTSMEGTRPVLVEIQALVSP   319
NTDB id 125 BSU 00870 NP 387968.1             LYFEGERHHTFRILRAVKNRFGSTNEMGIFEMREEGLTEVLNPSEIFLEERSAGSAGSSITASMEGTRPILVEIQALISP   317
consensus                                     !!!!!!!!!**!!!!!!!!!!!!!!!!!*!!!!!***!!*!!*!*!**!!!!!**!**!!*****!!!!!!*!*!*!!!**!
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logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 238 SPD RS00140 WP 074017595.1        TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 204 SPR RS00140 WP 074017595.1        TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 169 SP RS00155 WP 074017595.1         TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 537 SMSK321 RS07120 WP 080550752.1    TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 509 SM12261 RS00130 WP 078228442.1    TMFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGEL   393
NTDB id 247571 CNY62 RS06335 WP 029091568.1   TVYGNARRMATGMDYNRVSLIMAVLEKREGLMLQNQDAYLKAAGGVKLDEPAIDLAIAISIASSYYDTPTAAMDCFIGEV   399
NTDB id 125 BSU 00870 NP 387968.1             TSFGNPRRMATGIDHNRVSLLMAVLEKRVGLLLQNQDAYLKVAGGVKLDEPAIDLAIVISIASSFRDTPPNPADCFIGEV   397
consensus                                     !**!!**!**!!*!*!!*!!*!!!!!!!!*!!*!!!!!!!!!!*!!!!!!!!!!!!!!!!***!!!!**!*!*****!!*!!*
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logo
NTDB id 279 KZH43 RS00140 WP 074017595.1      GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA..   453
NTDB id 238 SPD RS00140 WP 074017595.1        GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA..   453
NTDB id 204 SPR RS00140 WP 074017595.1        GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA..   453
NTDB id 169 SP RS00155 WP 074017595.1         GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA..   453
NTDB id 537 SMSK321 RS07120 WP 080550752.1    GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPMEIQVIGVTTIQEVLKKVFA..   453
NTDB id 509 SM12261 RS00130 WP 078228442.1    GLTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPKEIQVIGVTTIQEVLKKVFA..   453
NTDB id 247571 CNY62 RS06335 WP 029091568.1   GLTGELRRVARIDQRVQEAAKLGFKRIIIPANNIGGWTFPAEIEVVGVSTLKDAIHKAFPNR   461
NTDB id 125 BSU 00870 NP 387968.1             GLTGEVRRVSRIEQRVKEAAKLGFKRMIIPAANLDGWTKPKGIEVIGVANVAEALRTSLGG.   458
consensus                                     !!!!!*!!!*!!*!!**!!!!!!!*****!*****!*!  !**!*!*!!***********
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X non conserved

X similar

X $\geq$ 50% conserved