```
logo

NTDB id 279 KZH43 RS00140 WP 074017595.1      ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 238 SPD RS00140 WP 074017595.1        ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 204 SPR RS00140 WP 074017595.1        ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 169 SP RS00155 WP 074017595.1         ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 509 SM12261 RS00130 WP 078228442.1    ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 537 SMSK321 RS07120 WP 080550752.1    ..MAKKKATFVCQNCGYNSPKYLGRCPNCGSWSSFVEEVEVAEVKNARVSLTGEK...TKPMKLAEVTSINVNRTKTEME   75
NTDB id 396679 GH758 RS13395 WP 003723898.1  MAKAKRTTKFVCQACGYESAKWMGKCPNCNEWNQMVEALEPSK..KSRSAFNHTG.EPSKATPITQIASETEKRVETNMP   77
NTDB id 125 BSU 00870 NP 387968.1             ..MAKTKSKFICQSCGYESPKWMGKCPGCGAWNTMVEEMIKKAPANRRAAFSHSVQTVQKPSPITSIETSEEPRVKTQLG   78
consensus                                       *!!****!*!!*!!!*!*!**!*!!*!**!***!!*********!*******    *!*************!**!***
```

```
logo

NTDB id 279 KZH43 RS00140 WP 074017595.1      EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 238 SPD RS00140 WP 074017595.1        EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 204 SPR RS00140 WP 074017595.1        EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 169 SP RS00155 WP 074017595.1         EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 509 SM12261 RS00130 WP 078228442.1    EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 537 SMSK321 RS07120 WP 080550752.1    EFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLSQV.GTVLYVSGEESAQQIKLRAERLGDIDSEFYLYAETNMQS   154
NTDB id 396679 GH758 RS13395 WP 003723898.1  ELNRVLGGGVVPGSMVLVGGDPGIGKSTLLLQVSAQLTLTNKKVLYISGEESIKQTKLRAERLQVSGDNLYVYAETNLEA   157
NTDB id 125 BSU 00870 NP 387968.1             EFNRVLGGGVVKGSLVLIGGDPGIGKSTLLLQVSAQLSGSSNSVLYISGEESVKQTKLRADRLGINNPSLHVLSETDMEY   158
consensus                                     !*!!!!!!!!!*!!*!!*!!!!!!!!!!!!!!!!!!*!!*** **!!!*!!!!!**!*!!!!*!!*********!!****
```

```
logo

NTDB id 279 KZH43 RS00140 WP 074017595.1      VRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 238 SPD RS00140 WP 074017595.1        VRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 204 SPR RS00140 WP 074017595.1        VRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 169 SP RS00155 WP 074017595.1         VRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 509 SM12261 RS00130 WP 078228442.1    VRTEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 537 SMSK321 RS07120 WP 080550752.1    VRAEVERIQPDFLIIDSIQTIMSPEISGVQGSVSQVREVTAELMQLAKTNNIAIFIVGHVTKEGTLAGPRMLEHMVDTVL   234
NTDB id 396679 GH758 RS13395 WP 003723898.1  VQETIDFVKPDFVVIDSIQTVYHPDVTSAAGSVSQVRECTATLMRIAKMQNIAIFIVGHVTKEGAIAGPRLLEHMVDTVL   237
NTDB id 125 BSU 00870 NP 387968.1             ISSAIQEMNPSFVVVDSIQTVYQSDITSAPGSVSQVRECTAELMKIAKTKGIPIFIVGHVTKEGSIAGPRLLEHMVDTVL   238
consensus                                     *********!*!***!!!!!!*************!!!!!!!!*!!*!!**!***!*!!!!!!!!!!!**!!!!*!!!!!!!!!
```

```
logo

NTDB id 279 KZH43 RS00140 WP 074017595.1      YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 238 SPD RS00140 WP 074017595.1        YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 204 SPR RS00140 WP 074017595.1        YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 169 SP RS00155 WP 074017595.1         YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 509 SM12261 RS00130 WP 078228442.1    YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 537 SMSK321 RS07120 WP 080550752.1    YFEGERHHTFRILRAVKNRFGSTNEIGIFEMQSGGLVEVLNPSQVFLEERLDGATGSSIVVTMEGTRPILAEVQALVTPT   314
NTDB id 396679 GH758 RS13395 WP 003723898.1  YFEGERHHAYRILRAVKNRFGSTNEMGIFEMRDVGLVEVANPSEVFLEERLEGASGSTVVASMEGTRPVLVEIQALVSPT   317
NTDB id 125 BSU 00870 NP 387968.1             YFEGERHHTFRILRAVKNRFGSTNEMGIFEMREEGLTEVLNPSEIFLEERSAGSAGSSITASMEGTRPILVEIQALISPT   318
consensus                                     !!!!!!!!**!!!!!!!!!!!!!!!!*!!!!!***!!*!!*!!!**!!!!!**!**!!****!!!!!!*!*!*!!!**!!
```

```
logo
```

```
NTDB id 279 KZH43 RS00140 WP 074017595.1      MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 238 SPD RS00140 WP 074017595.1        MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 204 SPR RS00140 WP 074017595.1        MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 169 SP RS00155 WP 074017595.1         MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 509 SM12261 RS00130 WP 078228442.1    MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 537 SMSK321 RS07120 WP 080550752.1    MFGNAKRTTTGLDFNRASLIMAVLEKRAGLLLQNQDAYLKSAGGVKLDEPAIDLAVAVAIASSYKDKPTNPQECFVGELG   394
NTDB id 396679 GH758 RS13395 WP 003723898.1   MFGNAKRMATGIDYNKVSLIMAVLEKRVGLMLQNQDAYLKAAGGVKLDEPAVDLAVAVSVASSYRDKPTRSTDCFIGELG   397
NTDB id 125 BSU 00870 NP 387968.1             SFGNPRRMATGIDHNRVSLLMAVLEKRVGLLLQNQDAYLKVAGGVKLDEPAIDLAIVISIASSFRDTPPNPADCFIGEVG   398
consensus                                     *!!!**!**!!*!*!**!!*!!!!!!!*!!*!!!!!!!!!*!!!!!!!!!!!*!!!*****!!!**!*!*****!!*!!*!
```

```
logo
```

```
NTDB id 279 KZH43 RS00140 WP 074017595.1      LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 238 SPD RS00140 WP 074017595.1        LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 204 SPR RS00140 WP 074017595.1        LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 169 SP RS00155 WP 074017595.1         LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITLPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 509 SM12261 RS00130 WP 078228442.1    LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPKEIQVIGVTTIQEVLKKVFA.   453
NTDB id 537 SMSK321 RS07120 WP 080550752.1    LTGEIRRVNRIEQRINEAAKLGFTKIYVPKNSLTGITPPMEIQVIGVTTIQEVLKKVFA.   453
NTDB id 396679 GH758 RS13395 WP 003723898.1   LTGEIRRVARIEQRVQEAAKLGFKRIFIPKNNEGNWKIPKDVQVVGVETIGEALKKALPD   457
NTDB id 125 BSU 00870 NP 387968.1             LTGEVRRVSRIEQRVKEAAKLGFKRMIIPAANLDGWTKPKGIEVIGVANVAEALRTSLGG   458
consensus                                     !!!!*!!!!*!!!!!**!!!!!!!*****!********!****!*!!****!*!*****
```

X non conserved

X similar

X $\geq$ 50% conserved