```
logo
NTDB id 108 BSU 35470 NP 391427.1          MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEW..HIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSSGKNKLY   83
NTDB id 615 LCA RS02545 WP 011374200.1     ............MGQQVIACGRQFTAAQLADTQNN.....NYSLPQIKRRPAFLRVKHRLVCQRCQQV.VPPQT...CLPDGRHY   64
NTDB id 593 KW2 RS05130 WP 021037147.1     ...........MNLILENLLGHLLLEKDISAFNNFTDQVNNENKL.IKIGAMTSVNANKVRCNRCGIIHIKTNV...KLPIGAFF   70
NTDB id 24732 SAK RS02015 WP 000432961.1   ...............MENYLGRLWTKAQLSEQ.........LRKIAISLPS.FIKKGSDYICTRCSSS.VAKNC...QLPTGNYY   56
NTDB id 277 KZH43 RS10090 WP 000867601.1   ............MKVNLDYLGRLFTENELTEE.........ERQLAEKLPA.MRKEKGKLFCQRCNST.ILEEW...YLPIGAYY   59
NTDB id 236 SPD RS10765 WP 000867601.1     ............MKVNLDYLGRLFTENELTEE.........ERQLAEKLPA.MRKEKGKLFCQRCNST.ILEEW...YLPIGAYY   59
NTDB id 202 SPR RS10250 WP 000867601.1     ............MKVNLDYLGRLFTENELTEE.........ERQLAEKLPA.MRKEKGKLFCQRCNST.ILEEW...YLPIGAYY   59
NTDB id 167 SP RS11275 WP 000867616.1      ............MKVNLDYLGRLFTENELTEE.........ERQLAEKLPA.MRKEKGKLFCQRCNST.ILEEW...YLPIGAYY   59
NTDB id 507 SM12261 RS09240 WP 000867722.1 ............MKVNPNYLGRLFTENELTEE.........ERQLAEKLPA.MRKEKGKLFCQRCNST.ILEEW...YLPIGTYY   59
NTDB id 535 SMSK321 RS10515 WP 000867726.1 ............MKVNPNYLGRLFTENELTKE.........ERQLAEKLPA.MRKEKGKLFCQRCDSA.ILDEW...YLPIGAYY   59
consensus                                               *****  **************          **********  *********!*!!***  *****    ********

logo
NTDB id 108 BSU 35470 NP 391427.1          CRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFPGIESALNQGL  168
NTDB id 615 LCA RS02545 WP 011374200.1     CAQCLLFGRLVEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEMLFQGILVALQKGQ  149
NTDB id 593 KW2 RS05130 WP 021037147.1     CPTCLELGRVRSDEYFYHLPQQDFPEKT..YLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMIYQLIEQILSHGG  153
NTDB id 24732 SAK RS02015 WP 000432961.1   CRECIVFGRVTSNENLYYFPQKTFSKTN..SLKWKGELTPYQNEVSEELLKGISSKENLLVHAVTGAGKTEMIYHSVAKVIDTGG  139
NTDB id 277 KZH43 RS10090 WP 000867601.1   CRECLLMKRVRSDQTLYYFPQEDFPKQD..VLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGG  142
NTDB id 236 SPD RS10765 WP 000867601.1     CRECLLMKRVRSDQTLYYFPQEDFPKQD..VLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGG  142
NTDB id 202 SPR RS10250 WP 000867601.1     CRECLLMKRVRSDQTLYYFPQEDFPKQD..VLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGG  142
NTDB id 167 SP RS11275 WP 000867616.1      CRECLLMKRVRSDQTLYYFPQEDFPKQD..VLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGG  142
NTDB id 507 SM12261 RS09240 WP 000867722.1 CRECLLMKRVRSDQSLYYFPQEDFPKQD..VLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMIYQVVAKVINAGG  142
NTDB id 535 SMSK321 RS10515 WP 000867726.1 CRECLLMKRVRSDQVLYYFPQEDFAKQD..ILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMIYQVVAKVINAGG  142
consensus                                  !**!****!******!***********  *!*!*!*!***!*******************!!*!!!!!!!***********!*

logo
NTDB id 108 BSU 35470 NP 391427.1          RVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAFPYSADQTLQFAVQKA  253
NTDB id 615 LCA RS02545 WP 011374200.1     RVCLAAPRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVDAFPFVDNPVLATAVEQA  234
NTDB id 593 KW2 RS05130 WP 021037147.1     SVGLASPRIDVCIELHQRLSRDFTC.QIPLLYHE.GDSYFRSPLVVMTSHQLLRFKEAFDLLIIDEVDAFPFRDNDMLYFALENA  236
NTDB id 24732 SAK RS02015 WP 000432961.1   SVCIASPRIDVCLELYKRLSNDFRC.AITLMHGE.SPSYQRSPLTIATTHQLLKFYHAFDLLIVDEVDAFPYVDNPILYQGVKQA  222
NTDB id 277 KZH43 RS10090 WP 000867601.1   AVCLASPRIDVCLELYKRLQQDFSC.GIALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
NTDB id 236 SPD RS10765 WP 000867601.1     AVCLASPRIDVCLELYKRLQQDFSC.GIALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
NTDB id 202 SPR RS10250 WP 000867601.1     AVCLASPRIDVCLELYKRLQQDFSC.GIALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
NTDB id 167 SP RS11275 WP 000867616.1      AVCLASPRIDVCLELYKRLQQDFSC.GIALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
NTDB id 507 SM12261 RS09240 WP 000867722.1 AVCLASPRIDVCLELYKRLQKDFAC.EIALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
NTDB id 535 SMSK321 RS10515 WP 000867726.1 AVCLASPRIDVCLELYKRLQDDFAC.EISLLYGE.SEPYFRTPLVVSTTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
consensus                                  *!**!*!!**!**!!**!!***!** *!******  ********!***!*!!!!****!*!**!*!!!!!!!******!*******
```

```
logo
```

```
NTDB id 108 BSU 35470 NP 391427.1          RKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAVKRWIEFHVKEGRPVFLFVPS   338
NTDB id 615 LCA RS02545 WP 011374200.1     CKPQCALLYLTATPTPAIKRAIAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPKRLERDCQTYL.KTQQILLFVPQ   318
NTDB id 593 KW2 RS05130 WP 021037147.1     KKINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYK.............KFIEQRKTGFPLLIFVAE   308
NTDB id 24732 SAK RS02015 WP 000432961.1   LKENGTSIFLTATSTTELERKVARKELKKLHLARRFHANPLVIPEMVWVSGIQKSLQTQKLPPKLYQLINKQRQTRYPLLLFFPH   307
NTDB id 277 KZH43 RS10090 WP 000867601.1   VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASE   310
NTDB id 236 SPD RS10765 WP 000867601.1     VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASE   310
NTDB id 202 SPR RS10250 WP 000867601.1     VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASE   310
NTDB id 167 SP RS11275 WP 000867616.1      VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASE   310
NTDB id 507 SM12261 RS09240 WP 000867722.1 VKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSPKLKSYIEKQRKTGYPLLIFASE   310
NTDB id 535 SMSK321 RS10515 WP 000867726.1 VKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSPKLKSYIEKQRKTGYPLLIFASE   310
consensus                                  *!*******!*!!** ************** ***!*!***!**!*****************************!***
```

```
logo
```

```
NTDB id 108 BSU 35470 NP 391427.1          VSILEKAAACFKGV..HCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQTGVLGAESSIFTESALVQIAGRTG   421
NTDB id 615 LCA RS02545 WP 011374200.1     VRLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFKNVAVLVLGAEHMVFNEAVLVQIAGRAG   403
NTDB id 593 KW2 RS05130 WP 021037147.1     IDFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILERGVTFSSIDVFVINSEHPNFTKSALIQMAGRVG   393
NTDB id 24732 SAK RS02015 WP 000432961.1   ISEGQVFTEILRQAFPMEKIGFVSSKSTSRLKLVQDFRDNKLSILVSTTILERGVTFPSVDVFVIQANHHLFTKSSLVQISGRVG   392
NTDB id 277 KZH43 RS10090 WP 000867601.1   IKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
NTDB id 236 SPD RS10765 WP 000867601.1     IKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
NTDB id 202 SPR RS10250 WP 000867601.1     IKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
NTDB id 167 SP RS11275 WP 000867616.1      IKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
NTDB id 507 SM12261 RS09240 WP 000867722.1 IKKGEQLKEILQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
NTDB id 535 SMSK321 RS10515 WP 000867726.1 IKKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVG   395
consensus                                  ***************************************!!*********!*!!!!!!!*******!*******!****!*!**!!*!
```

```
logo
```

```
NTDB id 108 BSU 35470 NP 391427.1          RHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
NTDB id 615 LCA RS02545 WP 011374200.1     RHKDYAQNPVHFYYQDYTRAIKGACRQIKTQNQRGRRLQSTV   445
NTDB id 593 KW2 RS05130 WP 021037147.1     RDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF.....   430
NTDB id 24732 SAK RS02015 WP 000432961.1   RALERPEGLLYFLHDGKSKSMHQAIKEIKNMNHIGGF.....   429
NTDB id 277 KZH43 RS10090 WP 000867601.1   RSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 236 SPD RS10765 WP 000867601.1     RSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 202 SPR RS10250 WP 000867601.1     RSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 167 SP RS11275 WP 000867616.1      RSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 507 SM12261 RS09240 WP 000867722.1 RSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
NTDB id 535 SMSK321 RS10515 WP 000867726.1 RSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
consensus                                  !***************** ****!***!* *!*****
```

X non conserved

X similar

X ≥ 50% conserved