```
logo
NTDB id 615 LCA RS02545 WP 011374200.1          .MGQQVIACGRQFTAAQLADTQNN....NYSLPQIKRRPAFLRVKHRLVCQRCQQVPP.QTCLPDGRHYCAQCLLFGRL   74
NTDB id 593 KW2 RS05130 WP 021037147.1          MNLLILENLLGHLLLEKDISAFNNFTDQVNNENKLIKIGAMTSVNANKVRCNRCGTIHIKTNVKLPIGAFFCPTCLELGRV   80
NTDB id 1029419 AB4X21 RS03040 WP 369088160.1  .MKI.EDSYGRLLTESQMT.........NDLKEIAQEFPAIEKGNGRYQCFRCGSLINQKLWKLSEEVLYCRACIQLGRI   69
NTDB id 277 KZH43 RS10090 WP 000867601.1        .MKVNLDYLGRLFTENELT.........EEERQLAEKLPAMRKEKGKLFCQRCNSTILE.EWYLPIGAYYCRECLLMKRV   69
NTDB id 236 SPD RS10765 WP 000867601.1          .MKVNLDYLGRLFTENELT.........EEERQLAEKLPAMRKEKGKLFCQRCNSTILE.EWYLPIGAYYCRECLLMKRV   69
NTDB id 202 SPR RS10250 WP 000867601.1          .MKVNLDYLGRLFTENELT.........EEERQLAEKLPAMRKEKGKLFCQRCNSTILE.EWYLPIGAYYCRECLLMKRV   69
NTDB id 167 SP RS11275 WP 000867616.1           .MKVNLDYLGRLFTENELT.........EEERQLAEKLPAMRKEKGKLFCQRCNSTILE.EWYLPIGAYYCRECLLMKRV   69
NTDB id 507 SM12261 RS09240 WP 000867722.1      .MKVNPNYLGRLFTENELT.........EEERQLAEKLPAMRKEKGKLFCQRCNSTILE.EWYLPIGTYYCRECLLMKRV   69
NTDB id 535 SMSK321 RS10515 WP 000867726.1      .MKVNPNYLGRLFTENELT.........KEERQLAEKLPAMRKEKGKLFCQRCDSAILD.EWYLPIGAYYCRECLLMKRV   69
consensus                                        ********!*********         **********************!*!!******  ***!******!**!****!*

logo
NTDB id 615 LCA RS02545 WP 011374200.1          VEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEMLRQGILVALQKGQRVCLA  154
NTDB id 593 KW2 RS05130 WP 021037147.1          RSDEYFYHLPQQDFPEK..TYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMIYQLIEQILSHGGSVGLA  158
NTDB id 1029419 AB4X21 RS03040 WP 369088160.1  RSDQKLYAIGQQDFEGK..EVLNWKGTLTSYQQEVSEGLIHAVKAGKHALVHAVTGAGKTEMMYQVVATAIKAGKAVCIA  147
NTDB id 277 KZH43 RS10090 WP 000867601.1        RSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
NTDB id 236 SPD RS10765 WP 000867601.1          RSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
NTDB id 202 SPR RS10250 WP 000867601.1          RSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
NTDB id 167 SP RS11275 WP 000867616.1           RSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
NTDB id 507 SM12261 RS09240 WP 000867722.1      RSDQSLYYFPQEDFPKQ..DVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
NTDB id 535 SMSK321 RS10515 WP 000867726.1      RSDQVLYYFPQEDFAKQ..DILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMIYQVVAKVINAGGAVCLA  147
consensus                                        ******!**********  **!*!*!*!!**!*******************!!!!!!!!!!**!********!**!**!

logo
APRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVDAFPFVDNPVLATAVEQA  234
SPRIDVCIELHQRLSRDFTCQ.IPLLYHE.GDSYFRSPLVVMTSHQLLRFKEAFDLLIIDEVDAFPFRDNDMLYFALENA  236
TPRIDVCIELYGRMEEDFSCS.ISLLHGE.SEPYFRTPLVIATTHQLLKFYQAFDLLIIDEVDAFPYVDNPILYKAAQNA  225
SPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQKDFACE.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
SPRIDVCLELYKRLQDDFACE.ISLLYGE.SEPYFRTPLVVSTTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNS  225
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logo
CKPQCALLYLTATPTPAIKRAIAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPKRLERDCQTYLK.TQQIL  313
KKINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYKK.............FIEQRKTGFPLL  303
IKKEGNTLYLTATSTDELDKKVKKKEIIRYSLPRRFHGNPLVVPKIKWVPKIREKIEKGRIPYELLQLIKKQRQTHYPLL  305
VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLL  305
VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLL  305
VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLL  305
VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLL  305
VKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLL  305
VKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSPKLKSYIEKQRKTGYPLL  305
VKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSPKLKSYIEKQRKTGYPLL  305
consensus
*!*******!!!!*! ************** !!*!!!!**!**!************** ******************!
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logo

NTDB id 615 LCA RS02545 WP 011374200.1          LFVPQVRLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFKNVAVLVLGAEHMVFNEA   393
NTDB id 593 KW2 RS05130 WP 021037147.1          IFVAEIDFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILERGVTFSSIDVFVINSEHPNFTKS   383
NTDB id 1029419 AB4X21 RS03040 WP 369088160.1  IFVSEIELGQQFTENLKKYFPKETVGFVSSQTTDRLRMVEEFRNRAITMLVSTTILERGVTFPFVDVFVLESNHKLFTKS   385
NTDB id 277 KZH43 RS10090 WP 000867601.1        IFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
NTDB id 236 SPD RS10765 WP 000867601.1          IFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
NTDB id 202 SPR RS10250 WP 000867601.1          IFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
NTDB id 167 SP RS11275 WP 000867616.1           IFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
NTDB id 507 SM12261 RS09240 WP 000867722.1      IFASEIKKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
NTDB id 535 SMSK321 RS10515 WP 000867726.1      IFASEIKKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKS   385
consensus                                       *!*****************!*******************!!*********!*!!!!!!!!****!*!****!**!***

logo

NTDB id 615 LCA RS02545 WP 011374200.1          VLVQIAGRAGRHKDYAQNPVHFYYQDYTRAIKGACRQIKTQNQRGRRLQSTV   445
NTDB id 593 KW2 RS05130 WP 021037147.1          ALIQMAGRVGRDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF.....   430
NTDB id 1029419 AB4X21 RS03040 WP 369088160.1  TLVQISGRVGRSKERPTGKLLFLSDGITREMKKAIKEIKEMNQEAGF.....   432
NTDB id 277 KZH43 RS10090 WP 000867601.1        SLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 236 SPD RS10765 WP 000867601.1          SLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 202 SPR RS10250 WP 000867601.1          SLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 167 SP RS11275 WP 000867616.1           SLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 507 SM12261 RS09240 WP 000867722.1      SLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
NTDB id 535 SMSK321 RS10515 WP 000867726.1      SLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
consensus                                       *!*!**!!*!!**********!****** ****!***!* *!*****
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X non conserved

X similar

X $\geq$ 50% conserved