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logo

NTDB id 108 BSU 35470 NP 391427.1          MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWH.IKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSSGK   79
NTDB id 593 KW2 RS05130 WP 021037147.1     MNLILE...........NLLGHLLLEKDISAFNNFTDQVNNENKLIKIGAMTSVNANKVRCNRCGTIHIKTNVK...LPI   66
NTDB id 261186 SPSF3K RS09600 WP 004234978.1 MGKNY............YEQGRLFTEQQMKN.......VIT.ARTFSMKGSMSMESGKQCCNRCFQEVAKT.NL...LPN   56
NTDB id 277 KZH43 RS10090 WP 000867601.1   MKVNL............DYLGRLFTENELTE.......EER.Q.LAEKLPAMRKEKGKLFCQRCNSTILEE.WY...LPI   55
NTDB id 236 SPD RS10765 WP 000867601.1     MKVNL............DYLGRLFTENELTE.......EER.Q.LAEKLPAMRKEKGKLFCQRCNSTILEE.WY...LPI   55
NTDB id 202 SPR RS10250 WP 000867601.1     MKVNL............DYLGRLFTENELTE.......EER.Q.LAEKLPAMRKEKGKLFCQRCNSTILEE.WY...LPI   55
NTDB id 167 SP RS11275 WP 000867616.1      MKVNL............DYLGRLFTENELTE.......EER.Q.LAEKLPAMRKEKGKLFCQRCNSTILEE.WY...LPI   55
NTDB id 507 SM12261 RS09240 WP 000867722.1 MKVNP............NYLGRLFTENELTE.......EER.Q.LAEKLPAMRKEKGKLFCQRCNSTILEE.WY...LPI   55
NTDB id 535 SMSK321 RS10515 WP 000867726.1 MKVNP............NYLGRLFTENELTK.......EER.Q.LAEKLPAMRKEKGKLFCQRCDSAILDE.WY...LPI   55
consensus                                  !****             *************       *** * ****************!*!!******* **    ***

logo

NTDB id 108 BSU 35470 NP 391427.1          NKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFPG   159
NTDB id 593 KW2 RS05130 WP 021037147.1     GAFFCPTCLELGRVRSDEYFYHLPQQDFP..EKTYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMIYQL   144
NTDB id 261186 SPSF3K RS09600 WP 004234978.1 GKTYCRFCIAFGRVESESQLYYFAPQAFP..KGDYLSWNGQLTPYQEKISEFLLGNYLNKKNSLVHAVTGAGKTEMIYKL   134
NTDB id 277 KZH43 RS10090 WP 000867601.1   GAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQV   133
NTDB id 236 SPD RS10765 WP 000867601.1     GAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQV   133
NTDB id 202 SPR RS10250 WP 000867601.1     GAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQV   133
NTDB id 167 SP RS11275 WP 000867616.1      GAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMIYQV   133
NTDB id 507 SM12261 RS09240 WP 000867722.1 GTYYCRECLLMKRVRSDQSLYYFPQEDFP..KQDVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMIYQV   133
NTDB id 535 SMSK321 RS10515 WP 000867726.1 GAYYCRECLLMKRVRSDQVLYYFPQEDFA..KQDILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMIYQV   133
consensus                                  ****!**!****!!******!********  ****!*!*!*!***!*!****!**********!**!!*!!!!!!!****

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NTDB id 108 BSU 35470 NP 391427.1          IESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAFP   239
NTDB id 593 KW2 RS05130 WP 021037147.1     IEQILSHGGSVGLASPRIDVCIELHQRLSRDFT.CQIPLLYHEGDS.YFRSPLVVMTSHQLLRFKEAFDLLIIDEVDAFP   222
NTDB id 261186 SPSF3K RS09600 WP 004234978.1 IESVINQGGWVCFTSPRVDVCIDIKNRLVRDFS.CPITIMYGGSEE.YRPAPLIVSTTHQLLKFYRAFDLLIIDEVDAFP   212
NTDB id 277 KZH43 RS10090 WP 000867601.1   VAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGESEP.YFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFP   211
NTDB id 236 SPD RS10765 WP 000867601.1     VAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGESEP.YFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFP   211
NTDB id 202 SPR RS10250 WP 000867601.1     VAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGESEP.YFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFP   211
NTDB id 167 SP RS11275 WP 000867616.1      VAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGESEP.YFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFP   211
NTDB id 507 SM12261 RS09240 WP 000867722.1 VAKVINAGGAVCLASPRIDVCLELYKRLQKDFA.CEIALLHGESEP.YFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFP   211
NTDB id 535 SMSK321 RS10515 WP 000867726.1 VAKVINAGGAVCLASPRIDVCLELYKRLQDDFA.CEISLLYGESEP.YFRTPLVVSTTHQLLKFYQAFDLLIVDEVDAFP   211
consensus                                  *******!**!****!!*!!******!!* *!* * !********* ****!!***!*!!!!****!*!**!*!!!!!!!

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NTDB id 108 BSU 35470 NP 391427.1          YSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAVK   319
NTDB id 593 KW2 RS05130 WP 021037147.1     FRDNDMLYFALENAKKINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYKKF..........   292
NTDB id 261186 SPSF3K RS09600 WP 004234978.1 FLGNVVLNKATQSCLKEEGKVVCLTATSTNELEQKVSDGHYEKIRLSRRFHNQPLVVPKFQLIYPLSKQFEKNKFPNLLS   292
NTDB id 277 KZH43 RS10090 WP 000867601.1   YVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLK   291
NTDB id 236 SPD RS10765 WP 000867601.1     YVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLK   291
NTDB id 202 SPR RS10250 WP 000867601.1     YVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLK   291
NTDB id 167 SP RS11275 WP 000867616.1      YVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLK   291
NTDB id 507 SM12261 RS09240 WP 000867722.1 YVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSPKLK   291
NTDB id 535 SMSK321 RS10515 WP 000867726.1 YVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSPKLK   291
consensus                                  ******!**!*****!*******!*!!****!************ ***!*!**!!**!**********************
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NTDB id 108 BSU 35470 NP 391427.1              RWIEFHVKEGRPVFLFVPSVSILEKAAACFKGV..HCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQ   397
NTDB id 593 KW2 RS05130 WP 021037147.1         ...IEQRKTGFPLLIFVAEIDFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILERGVTFSSID   369
NTDB id 261186 SPSF3K RS09600 WP 004234978.1   NLISQQRQTAFPLLIFYPLITEGEKFTKILQKASPKEKIAFVSSKSDDRKEKIDAFKKRQIDILVTTTILERGVTFPEVD   372
NTDB id 277 KZH43 RS10090 WP 000867601.1       SYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVD   371
NTDB id 236 SPD RS10765 WP 000867601.1         SYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVD   371
NTDB id 202 SPR RS10250 WP 000867601.1         SYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVD   371
NTDB id 167 SP RS11275 WP 000867616.1          SYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVD   371
NTDB id 507 SM12261 RS09240 WP 000867722.1     SYIEKQRKTGYPLLIFASEIKKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFPCVD   371
NTDB id 535 SMSK321 RS10515 WP 000867726.1     SYIEKQRKTGYPLLIFASEIKKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVD   371
consensus                                      ***********!***!**********************!******!******!*******!**!*!!!!!!!*****
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NTDB id 108 BSU 35470 NP 391427.1              TGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
NTDB id 593 KW2 RS05130 WP 021037147.1         VFVINSEHPNFTKSALIQMAGRVGRDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF.....   430
NTDB id 261186 SPSF3K RS09600 WP 004234978.1   VYVILANHKLFTSSSLIQIAGRVGRSVSRPSGQLLFIHEGVSLQMKKARKQIIEMNKEAYGE....   434
NTDB id 277 KZH43 RS10090 WP 000867601.1       VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 236 SPD RS10765 WP 000867601.1         VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 202 SPR RS10250 WP 000867601.1         VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 167 SP RS11275 WP 000867616.1          VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 507 SM12261 RS09240 WP 000867722.1     VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
NTDB id 535 SMSK321 RS10515 WP 000867726.1     VFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
consensus                                      **!*******!!*!*!*!**!!*!!******!*****!*!** ****!*!*!* !!*****
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X non conserved

X similar

X $\geq$ 50% conserved