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logo

NTDB id 593 KW2 RS05130 WP 021037147.1          MNLIL...........ENLLGHLLLEKDISAFN.NFTDQVNNE..NKLIKIGAMTSVNANKVRCNRCGTIHIKT...NVK   63
NTDB id 277 KZH43 RS10090 WP 000867601.1        MKVN............LDYLGRLFTENELT..........EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY   52
NTDB id 236 SPD RS10765 WP 000867601.1          MKVN............LDYLGRLFTENELT..........EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY   52
NTDB id 202 SPR RS10250 WP 000867601.1          MKVN............LDYLGRLFTENELT..........EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY   52
NTDB id 167 SP RS11275 WP 000867616.1           MKVN............LDYLGRLFTENELT..........EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY   52
NTDB id 507 SM12261 RS09240 WP 000867722.1      MKVN............PNYLGRLFTENELT..........EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY   52
NTDB id 535 SMSK321 RS10515 WP 000867726.1      MKVN............PNYLGRLFTENELT..........KEE..RQLAEKLPAMRKEKGKLFCQRCDSAI.LD...EWY   52
NTDB id 615 LCA RS02545 WP 011374200.1          ....................MGQQVIACGRQFTAAQLADTQNNNYSLPQIKRRPAFLRVKHRLVCQRCQQVVPPQ....TC   57
NTDB id 983946 NSQ70 RS16260 WP 251185086.1     ......................................................................................    0
NTDB id 108 BSU 35470 NP 391427.1               MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGY....ITAENSISINKRRYRCNRCGQTDQRYFSFYHS   76
consensus                                       ****               ************          ***   ************************ **    ***

logo

NTDB id 593 KW2 RS05130 WP 021037147.1          LPIGAFFCPTCLELGRVRSDEYFYHLPQQDFP..EKTYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMI  141
NTDB id 277 KZH43 RS10090 WP 000867601.1        LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 236 SPD RS10765 WP 000867601.1          LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 202 SPR RS10250 WP 000867601.1          LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 167 SP RS11275 WP 000867616.1           LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 507 SM12261 RS09240 WP 000867722.1      LPIGTYYCRECLLMKRVRSDQSLYYFPQEDFP..KQDVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMI  130
NTDB id 535 SMSK321 RS10515 WP 000867726.1      LPIGAYYCRECLLMKRVRSDQVLYYFPQEDFA..KQDILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMI  130
NTDB id 615 LCA RS02545 WP 011374200.1          LPDGRHYCAQCLLFGRLVEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEML  137
NTDB id 983946 NSQ70 RS16260 WP 251185086.1     ............MLGKVSECGFLYEWTGPQKKETRQVELTWQGELSKGQKRASDRLVEAIQNKFDLLVWAVCGAGKTEVL   68
NTDB id 108 BSU 35470 NP 391427.1               SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML  156
consensus                                       **********************!********  ****!*!*!*!***!*******************!!*!!!!!!**

logo

NTDB id 593 KW2 RS05130 WP 021037147.1          YQLIEQILSHGGSVGLASPRIDVCIELHQRLSRDFT.CQIPLLYHEG.DSYFRSPLVVMTSHQLLRFKEAFDLLIIDEVD  219
NTDB id 277 KZH43 RS10090 WP 000867601.1        YQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD  208
NTDB id 236 SPD RS10765 WP 000867601.1          YQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD  208
NTDB id 202 SPR RS10250 WP 000867601.1          YQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD  208
NTDB id 167 SP RS11275 WP 000867616.1           YQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD  208
NTDB id 507 SM12261 RS09240 WP 000867722.1      YQVVAKVINAGGAVCLASPRIDVCLELYKRLQKDFA.CEIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD  208
NTDB id 535 SMSK321 RS10515 WP 000867726.1      YQVVAKVINAGGAVCLASPRIDVCLELYKRLQDDFA.CEISLLYGES.EPYFRTPLVVSTTHQLLKFYQAFDLLIVDEVD  208
NTDB id 615 LCA RS02545 WP 011374200.1          FQGILVALQKGQRVCLAAPRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVD  217
NTDB id 983946 NSQ70 RS16260 WP 251185086.1     FHGIKYALNNGMSVCIATPRTDVVLELEPRMRKAFQGLNIAALYGGSSQRFQMAPLMIATTHQLMRYKNAFDVLIVDEVD  148
NTDB id 108 BSU 35470 NP 391427.1               FPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVD  236
consensus                                       **********!**!**!*!!**!**!!**!** *!* * !******* *******!***!*!!!*****!*!**!*!!!!
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logo
NTDB id 593 KW2 RS05130 WP 021037147.1          AFPFRDNDMLYFALENAKKINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYKK........  291
NTDB id 277 KZH43 RS10090 WP 000867601.1        AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSP  288
NTDB id 236 SPD RS10765 WP 000867601.1          AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSP  288
NTDB id 202 SPR RS10250 WP 000867601.1          AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSP  288
NTDB id 167 SP RS11275 WP 000867616.1           AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSP  288
NTDB id 507 SM12261 RS09240 WP 000867722.1      AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSP  288
NTDB id 535 SMSK321 RS10515 WP 000867726.1      AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSP  288
NTDB id 615 LCA RS02545 WP 011374200.1          AFPFVDNPVLATAVEQACKPQCALLYLTATPTPAIKRAIAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPK  297
NTDB id 983946 NSQ70 RS16260 WP 251185086.1    AFPYSMDERLQFAVLKSMKKTGVRIYLSATPSKKMQKDVARRQLEAIKIPLRFHQKPLPVPTFQWVGDWKKKLKRNRLPA  228
NTDB id 108 BSU 35470 NP 391427.1               AFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPP  316
consensus                                       !!!******!**!*****!*******!*!!** ************** *!*!*!***!**!*****************
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logo
NTDB id 593 KW2 RS05130 WP 021037147.1          .....FIEQRKTGFPLLIFVAEIDFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILERGVTFS  366
NTDB id 277 KZH43 RS10090 WP 000867601.1        KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 236 SPD RS10765 WP 000867601.1          KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 202 SPR RS10250 WP 000867601.1          KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 167 SP RS11275 WP 000867616.1           KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 507 SM12261 RS09240 WP 000867722.1      KLKSYIEKQRKTGYPLLIFASEIKKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFP  368
NTDB id 535 SMSK321 RS10515 WP 000867726.1      KLKSYIEKQRKTGYPLLIFASEIKKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 615 LCA RS02545 WP 011374200.1          RLERDCQTY.LKTQQILLFVPQVRLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFK  376
NTDB id 983946 NSQ70 RS16260 WP 251185086.1    STMNWLHEHITKKKRVLLFVPSISTMKKVTHILQG..QDVNVQGVSADDQERKQKVQHFRDHRYDVLVTTTILERGVTIQ  306
NTDB id 108 BSU 35470 NP 391427.1               AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKG..VHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVP  394
consensus                                       ******************!*************************************!!*********!*!!!!!!!**
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logo
NTDB id 593 KW2 RS05130 WP 021037147.1          SIDVFVINSEHPNFTKSALIQMAGRVGRDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF.....  430
NTDB id 277 KZH43 RS10090 WP 000867601.1        CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....  432
NTDB id 236 SPD RS10765 WP 000867601.1          CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....  432
NTDB id 202 SPR RS10250 WP 000867601.1          CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....  432
NTDB id 167 SP RS11275 WP 000867616.1           CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....  432
NTDB id 507 SM12261 RS09240 WP 000867722.1      CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....  432
NTDB id 535 SMSK321 RS10515 WP 000867726.1      CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....  432
NTDB id 615 LCA RS02545 WP 011374200.1          NVAVLVLGAEHMVFNEAVLVQIAGRAGRHKDYAQNPVHFYYQDYTRAIKGACRQIKTQNQRGRRLQSTV  445
NTDB id 983946 NSQ70 RS16260 WP 251185086.1    DVQVGVLGAESPIFTESALVQISGRAGRHPDFFNGDVYFFHFGLTRSMKQAKKHIVKMNNTAEKEFSEK  375
NTDB id 108 BSU 35470 NP 391427.1               KVQTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                       *****!*******!****!*!**!!*!!*****************  ****!***!*  *!*****
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X non conserved

X similar

X ≥ 50% conserved