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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          ...................MGQQVIACGRQFTAAQLADTQNNNYSLPQIKRRPAFLRVKHRLVCQRCGQVVPPQ....TC   57
NTDB id 996943 AAH687 RS07125 WP 346395552.1    ......................................................................................    0
NTDB id 108 BSU 35470 NP 391427.1               MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGY....ITAENSISINKRRYRCNRCGQTDQRYFSFYHS   76
consensus                                       ****              ************          ***  ************************ **    ***

logo

NTDB id 593 KW2 RS05130 WP 021037147.1          LPIGAFFCPTCLELGRVRSDEYFYHLPQQDFPEK..TYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMI  141
NTDB id 277 KZH43 RS10090 WP 000867601.1        LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 236 SPD RS10765 WP 000867601.1          LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 202 SPR RS10250 WP 000867601.1          LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 167 SP RS11275 WP 000867616.1           LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMI  130
NTDB id 507 SM12261 RS09240 WP 000867722.1      LPIGTYYCRECLLMKRVRSDQSLYYFPQEDFPKQ..DVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMI  130
NTDB id 535 SMSK321 RS10515 WP 000867726.1      LPIGAYYCRECLLMKRVRSDQVLYYFPQEDFAKQ..DILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMI  130
NTDB id 615 LCA RS02545 WP 011374200.1          LPDGRHYCAQCLLFGRLVEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEML  137
NTDB id 996943 AAH687 RS07125 WP 346395552.1    ...............................MKETRRVELTWQGELSKGQKRASDRLVEAIQNKFDLLVWAVCGAGKTEVL   50
NTDB id 108 BSU 35470 NP 391427.1               SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML  156
consensus                                       ***********************************  **!*!*!*!***!*******************!!*!!!!!!**

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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 996943 AAH687 RS07125 WP 346395552.1    FHGIKYALNNGMSVCIATPRTDVVLELEPRMRKAFQGLNIAALYGGSSQRFQMAPLMIATTHQLMRYKNAFDVLIVDEVD  130
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 996943 AAH687 RS07125 WP 346395552.1   AFPYSIDERLQFAVLKSMKKTGVRIYLSATPSKKMQKDVARRQLEAIKIPLRFHQKPLPVPTFQWVGDWKKRLKRNRLPA  210
NTDB id 108 BSU 35470 NP 391427.1               AFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPP  316
consensus                                       !!!******!**!*****!*******!*!!** ************** *!*!*!***!**!******************

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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 996943 AAH687 RS07125 WP 346395552.1   STMNWLHEHITKKKRVLLFVPSISTMKKVTHILQG..QDVNVQGVSADDQERKQKVQHFRDHRYDVLVTTTILERGVTIQ  288
NTDB id 108 BSU 35470 NP 391427.1               AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKG..VHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVP  394
consensus                                       ******************!*************************************!!*********!*!!!!!!!**

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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 996943 AAH687 RS07125 WP 346395552.1   DVQVGVLGAESPIFTESALVQISGRAGRHPDFFNGDVYFFHFGLTRSMKQAKKHIVKMNNTAEKEFSEK  357
NTDB id 108 BSU 35470 NP 391427.1               KVQTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD  463
consensus                                       *****!*******!****!*!**!!*!!****************** ****!***!* *!*****
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X non conserved

X similar

X ≥ 50% conserved