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logo

NTDB id 108 BSU 35470 NP 391427.1          MNVPVEKNSSFSKELQQTLRSRHLLRTE..........LSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRY   70
NTDB id 277 KZH43 RS10090 WP 000867601.1   MKVN............LDYLGRLFTENELTE...................EERQLAEKLPAMRKEKGKLFCQRCNSTI.LE   49
NTDB id 236 SPD RS10765 WP 000867601.1     MKVN............LDYLGRLFTENELTE...................EERQLAEKLPAMRKEKGKLFCQRCNSTI.LE   49
NTDB id 202 SPR RS10250 WP 000867601.1     MKVN............LDYLGRLFTENELTE...................EERQLAEKLPAMRKEKGKLFCQRCNSTI.LE   49
NTDB id 167 SP RS11275 WP 000867616.1      MKVN............LDYLGRLFTENELTE...................EERQLAEKLPAMRKEKGKLFCQRCNSTI.LE   49
NTDB id 535 SMSK321 RS10515 WP 000867726.1 MKVN............PNYLGRLFTENELTK...................EERQLAEKLPAMRKEKGKLFCQRCDSAI.LD   49
NTDB id 507 SM12261 RS09240 WP 000867722.1 MKVN............PNYLGRLFTENELTE...................EERQLAEKLPAMRKEKGKLFCQRCNSTI.LE   49
NTDB id 183268 LLUC77 RS07790 WP 021214546.1 MSTNQ..........EKLFGRLLLKNDILQLIKNTDKISVSKIFSNFLLETKVNPILGMTSISSNKIKCNRCGTVHIKN   69
NTDB id 593 KW2 RS05130 WP 021037147.1     MNLIL...........ENLLGHLLLEKDISAFNNFTDQV.........NNENKLIKIGAMTSVNANKVRCNRCGTIHIKT   60
consensus                                  !***             ************                    ********************!*!!**** **

logo

NTDB id 108 BSU 35470 NP 391427.1          FSFYHSSGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGA  150
NTDB id 277 KZH43 RS10090 WP 000867601.1   EW.Y..LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGA  124
NTDB id 236 SPD RS10765 WP 000867601.1     EW.Y..LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGA  124
NTDB id 202 SPR RS10250 WP 000867601.1     EW.Y..LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGA  124
NTDB id 167 SP RS11275 WP 000867616.1      EW.Y..LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGA  124
NTDB id 535 SMSK321 RS10515 WP 000867726.1 EW.Y..LPIGAYYCRECLLMKRVRSDQVLYYFPQEDFA..KQDILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGA  124
NTDB id 507 SM12261 RS09240 WP 000867722.1 EW.Y..LPIGTYYCRECLLMKRVRSDQSLYYFPQEDFP..KQDVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGA  124
NTDB id 183268 LLUC77 RS07790 WP 021214546.1 SV.K..LPIGVFYCPSCIQLGRVRSDDFLYFLPQKNFP..KKSYINWSGKLTENQKSISNALCQEINSHQQIIVQAVTGA  144
NTDB id 593 KW2 RS05130 WP 021037147.1     NV.K..LPIGAFFCPTCLELGRVRSDEYFYHLPQQDFP..EKTYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGA  135
consensus                                  ** *  *******!**!****!!******!*******  ******!*!*!***!******!******* *****!!*!!

logo

NTDB id 108 BSU 35470 NP 391427.1          GKTEMLFPGIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVM  230
NTDB id 277 KZH43 RS10090 WP 000867601.1   GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFSC.GIALLHGESE.PYFRTPLVVATTHQLLKFYQAFDLL  202
NTDB id 236 SPD RS10765 WP 000867601.1     GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFSC.GIALLHGESE.PYFRTPLVVATTHQLLKFYQAFDLL  202
NTDB id 202 SPR RS10250 WP 000867601.1     GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFSC.GIALLHGESE.PYFRTPLVVATTHQLLKFYQAFDLL  202
NTDB id 167 SP RS11275 WP 000867616.1      GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFSC.GIALLHGESE.PYFRTPLVVATTHQLLKFYQAFDLL  202
NTDB id 535 SMSK321 RS10515 WP 000867726.1 GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQDDFAC.EISLLYGESE.PYFRTPLVVSTTHQLLKFYQAFDLL  202
NTDB id 507 SM12261 RS09240 WP 000867722.1 GKTEMIYQVVAKVINAGGAVCLASPRIDVCLELYKRLQKDFAC.EIALLHGESE.PYFRTPLVVATTHQLLKFYQAFDLL  202
NTDB id 183268 LLUC77 RS07790 WP 021214546.1 GKTEMIYQVIEQILESGGVVGLASPRIDVCLELHQRLSRDFSC.KIPLLYHDGD.SYFRAPLIIMTSHQLLRFKEAFDLL  222
NTDB id 593 KW2 RS05130 WP 021037147.1     GKTEMIYQLIEQILSHGGSVGLASPRIDVCIELHQRLSRDFTC.QIPLLYHEGD.SYFRSPLVVMTSHQLLRFKEAFDLL  213
consensus                                  !!!!!***********!**!**!*!!*!!**!!**!!* *!**  !**!***** *****!!***!*!!!!****!*!**

logo

NTDB id 108 BSU 35470 NP 391427.1          IIDEVDAFPYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLN  310
NTDB id 277 KZH43 RS10090 WP 000867601.1   IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLD  282
NTDB id 236 SPD RS10765 WP 000867601.1     IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLD  282
NTDB id 202 SPR RS10250 WP 000867601.1     IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLD  282
NTDB id 167 SP RS11275 WP 000867616.1      IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLD  282
NTDB id 535 SMSK321 RS10515 WP 000867726.1 IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLE  282
NTDB id 507 SM12261 RS09240 WP 000867722.1 IVDEVDAFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLE  282
NTDB id 183268 LLUC77 RS07790 WP 021214546.1 IIDEVDAFPFRDNEMLYVAAEKARKIEGNLIYLTATSTDKLEKDIKKQKLYPLFLPRRFHNFPLVVPKFFWKNKFDKKL.  301
NTDB id 593 KW2 RS05130 WP 021037147.1     IIDEVDAFPFRDNDMLYFALENAKKINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYKKF.  292
consensus                                  !*!!!!!!!******!**!*****!*******!*!!** *!************ *!*!*!**!!**!***!*********
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logo

NTDB id 108 BSU 35470 NP 391427.1                RNKIPPAVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKG..VHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILE   388
NTDB id 277 KZH43 RS10090 WP 000867601.1         KNRLSPKLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILE   362
NTDB id 236 SPD RS10765 WP 000867601.1           KNRLSPKLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILE   362
NTDB id 202 SPR RS10250 WP 000867601.1           KNRLSPKLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILE   362
NTDB id 167 SP RS11275 WP 000867616.1            KNRLSPKLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILE   362
NTDB id 535 SMSK321 RS10515 WP 000867726.1       KKCLSPKLKSYIEKQRKTGYPLLIFASEIKKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILE   362
NTDB id 507 SM12261 RS09240 WP 000867722.1       KSRLSPKLKSYIEKQRKTGYPLLIFASEIKKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILE   362
NTDB id 183268 LLUC77 RS07790 WP 021214546.1    ............IEQRNSGFPLLIFAAEIEFGQEFAKQLQLKFPKEKIASVASTTKDRLEIVKAFRNKEITILIATSILE   369
NTDB id 593 KW2 RS05130 WP 021037147.1           ............IEQRKTGFPLLIFVAEIDFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILE   360
consensus                                        ********************!***!************************!******!***!**!!******!!*!*!!!

logo

NTDB id 108 BSU 35470 NP 391427.1                RGVTVPKVQTGVLGAESSIFTESALVQIAGRTGFHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
NTDB id 277 KZH43 RS10090 WP 000867601.1         RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 236 SPD RS10765 WP 000867601.1           RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 202 SPR RS10250 WP 000867601.1           RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 167 SP RS11275 WP 000867616.1            RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL.....   432
NTDB id 535 SMSK321 RS10515 WP 000867726.1       RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
NTDB id 507 SM12261 RS09240 WP 000867722.1       RGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL.....   432
NTDB id 183268 LLUC77 RS07790 WP 021214546.1    RGVTFPNVDVFVINSEHPNFTKSALIQMAGRVGRSPERPTGLVSFFHYGKSKAMCQAVREIKKMNQLGGFS....   440
NTDB id 593 KW2 RS05130 WP 021037147.1           RGVTFSSIDVFVINSEHPNFTKSALIQMAGRVGRDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF.....   430
consensus                                        !!!!*******!********!!*!*!*!**!!*!!******!****!!*!** ****!***!* !!*****
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X non conserved

X similar

X $\geq$ 50% conserved