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logo
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NTDB id 626 LCA RS04960 WP 011374694.1        MLTKNQLLLKVHLAAGFGTISELRLAAWLSTSHNWALSALEIAQI......ARLPERYWPTFQASFQSTTLQRQCIDHEV   74
NTDB id 599 KW2 RS05940 WP 021037268.1        .MITNFDLFRWK.KAGMTNLGVNKLLKFFRKY.DRKISLRQMGQVAQVKSIPNFIEQYKNQDVK.........KLRADYK   68
NTDB id 407 SMU RS04605 WP 002262865.1        ..MDNFQLFKLK.KAGLTNLNILNIIDYEERT.QKSLSLRDMAVVSKNKKPLIFMEHYKNLDSK.........ALRKEFN   67
NTDB id 1152595 NBW44 RS03940 WP 349815551.1  MKIDNFEIYKLK.KAGLSNLQVLKVLQYGEIY.DQELTLETIAEASECRNPVVFMERYYKLTFESME......KLKTDFE   72
NTDB id 525 SMSK321 RS06295 WP 000705298.1    MKITNYEIYKLK.KSGLTNQQILKVLEYGENV.DQELLLGDIADISGCRNPAVFMERYFQIDDA.........HLEKEFK   69
NTDB id 497 SM12261 RS05565 WP 000705318.1    MKITNYEIYKLK.KSGLTNQQVLAVLEYGENV.DQELLLGDIAEISGCRNPAVFMERYFQIDDA.........HLEKEFQ   69
NTDB id 267 KZH43 RS05590 WP 000705306.1      MKITNYEIYKLK.KSGLTNQQILKVLEYGENV.DQELLLGDIADISGCRNPAVFMERYFQIDDA.........HLSKEFQ   69
NTDB id 226 SPD RS05990 WP 000705306.1        MKITNYEIYKLK.KSGLTNQQILKVLEYGENV.DQELLLGDIADISGCRNPAVFMERYFQIDDA.........HLSKEFQ   69
NTDB id 192 SPR RS05715 WP 000705306.1        MKITNYEIYKLK.KSGLTNQQILKVLEYGENV.DQELLLGDIADISGCRNPAVFMERYFQIDDA.........HLSKEFQ   69
NTDB id 157 SP RS06205 WP 000705306.1         MKITNYEIYKLK.KSGLTNQQILKVLEYGENV.DQELLLGDIADISGCRNPAVFMERYFQIDDA.........HLSKEFQ   69
consensus                                     ****!******* **!**************** **********************!*!******         ** ****
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NTDB id 626 LCA RS04960 WP 011374694.1        RTTYLTILDKDYPQRLLETYLPPVLLFYRGDLRLLKQPCLAVVGARQATHYSKQSLEQLLQGLTA.TTIISGLAQGADAM  153
NTDB id 599 KW2 RS05940 WP 021037268.1        KFSSFSILDDLYPERLREIYNPPVLIFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVQKIVTELNQSFTIVSGLAKGIDTA  148
NTDB id 407 SMU RS04605 WP 002262865.1        RFPSLSILDKEYPLELKNIYNPPVLLFYQGDLDLLARPKLAVVGSRNASQMGVAAVKKIIQDLSKQFVIISGLARGIDTA  147
NTDB id 1152595 NBW44 RS03940 WP 349815551.1  KFPSFSILDDVYPFSLCEIYDAPVLLFYKGDLNLLKLPKVAVVGSRSCSQVGIKSVGKVIQGLENELVIVSGLARGIDTA  152
NTDB id 525 SMSK321 RS06295 WP 000705298.1    KIPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRSCSKQGAKSVEKIIQGLENELVIVSGLAKGIDTA  149
NTDB id 497 SM12261 RS05565 WP 000705318.1    KFPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTA  149
NTDB id 267 KZH43 RS05590 WP 000705306.1      KFPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTA  149
NTDB id 226 SPD RS05990 WP 000705306.1        KFPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTA  149
NTDB id 192 SPR RS05715 WP 000705306.1        KFPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTA  149
NTDB id 157 SP RS06205 WP 000705306.1         KFPSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLENELVIVSGLAKGIDTA  149
consensus                                     ******!!!**!!**!***!**!!!*!!*!***!!**!**!*!!*!****************!*****!*!!!!*!*!**
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logo
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NTDB id 626 LCA RS04960 WP 011374694.1        AHEVALQRGLAPIGVIGTGINCSYPPQNEHLQQVVAEKGLLLSEYALGTPARRYQFPARNKIIAGLCHSLIVTEARHKSG  233
NTDB id 599 KW2 RS05940 WP 021037268.1        SHLSAIKTKTPTIAVIGTGLDIFYPLENRKIQEYLAKYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVVEAKLRSG  228
NTDB id 407 SMU RS04605 WP 002262865.1        AHLASLKSGGATIAVIGTGLDVHYPKENRRLQDYIAKNHLLLSEYEAQSQPLKYHFPERNRIIAGLSQGVMVAEAKIRSG  227
NTDB id 1152595 NBW44 RS03940 WP 349815551.1  AHMSILQNGGKTIAVIGTGLDNFYPKSNKRLQNYIGEHHLLLSEYGPGEEPLKYHFPARNRIIAGLCRGVIVAEAKMRSG  232
NTDB id 525 SMSK321 RS06295 WP 000705298.1    AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYISNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
NTDB id 497 SM12261 RS05565 WP 000705318.1    AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
NTDB id 267 KZH43 RS05590 WP 000705306.1      AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
NTDB id 226 SPD RS05990 WP 000705306.1        AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
NTDB id 192 SPR RS05715 WP 000705306.1        AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
NTDB id 157 SP RS06205 WP 000705306.1         AHMAALQNGGKTIAVIGTGLDVFYPKANKRLQDYIGNDHLVLSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEAKMRSG  229
consensus                                     *!**********!*!!!!!****!!**!***!*******!*!!!!**********!!*!!*!!!!!*****!*!!***!!
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logo
                                                  SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLYTSGQDYLAEFEF
NTDB id 626 LCA RS04960 WP 011374694.1            SLITANLALQANRNVYAIPGRIDQSLSQGCNQLIAAGATPLLDKNILIEELRYFD   288
NTDB id 599 KW2 RS05940 WP 021037268.1            SLITCERALEEGRDIFAIPGNIADGTSDGCNHLIQQGAKLVYQAQDILEEYLYN.   282
NTDB id 407 SMU RS04605 WP 002262865.1            SLITCERAMEEGRDVFVVPGNILDGQSEGCHHLIQEGAKCITSGFDILNEFNF..   280
NTDB id 1152595 NBW44 RS03940 WP 349815551.1      SLITCERAMEEGRDVFAIPGSILDGRSDGCHHLIQEGAKLITSGQDVLAEFEF..   285
NTDB id 525 SMSK321 RS06295 WP 000705298.1        SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 497 SM12261 RS05565 WP 000705318.1        SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 267 KZH43 RS05590 WP 000705306.1          SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 226 SPD RS05990 WP 000705306.1            SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 192 SPR RS05715 WP 000705306.1            SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
NTDB id 157 SP RS06205 WP 000705306.1             SLITCERAMEEGRDVFAIPGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF..   282
consensus                                         !!!!***!****!*****!!*!****!*!!**!!**!!**********!***
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X non conserved

X similar

X $\geq$ 50% conserved