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logo
NTDB id 84110 JG741 RS11790 WP 032950503.1   MLTAIDENNKIINLLELERKELTGKFYCPSCHAELLIKNGQIKVLHFAHKSLKSCNLWLENESEQHLGLKKILYQWFKRTDKVEI   85
NTDB id 598 KW2 RS08500 WP 021037660.1       MRTAIDENNKIINLLELDRKELTGKFYCPSCHSELLIKNGQIKVLHFAHKSLKSCNLWLENESEQHLGLKKILYQWFKRTDKVEI   85
NTDB id 155 SP RS04850 WP 000495909.1        MFVARDARGELVNVLE..DKLEKQAYTCPACGGQLHLRQGPSVRTHFAHKSLKDCDFFFENESPEHLANKESLYHWLKKETKVQL   83
NTDB id 265 KZH43 RS04315 WP 000495911.1     MFVARDARGELVNVLE..DKLEKQAYTCPACGGQLHLRQGPSVRTHFAHKSLKDCDFFFENESPEHLANKESLYHWLKKETKVQL   83
NTDB id 224 SPD RS04655 WP 000495911.1       MFVARDARGELVNVLE..DKLEKQAYTCPACGGQLHLRQGPSVRTHFAHKSLKDCDFFFENESPEHLANKESLYHWLKKETKVQL   83
NTDB id 190 SPR RS04415 WP 000495911.1       MFVARDARGELVNVLE..DKLEKQAYTCPACGGQLHLRQGPSVRTHFAHKSLKDCDFFFENESPEHLANKESLYHWLKKETKVQL   83
NTDB id 495 SM12261 RS04415 WP 000495920.1   MFVARDSRGELVNVLE..DKLEKQAYTCPACGGQLRLRQGPSVRIHFAHKTLKDCDFSSENESPEHLENKEVLYHWLKKEAEVQL   83
consensus                                    !**!*!******!*!!  *!*******!!*!***!****!*****!!!!!*!!*!****!!!!**!!**!**!!*!*!****!**

logo
NTDB id 84110 JG741 RS11790 WP 032950503.1   ERYLPELNQRPDLLVNDKIAIEIQCSHLSIKRLKERTENYKAHGFKVLWLMGKDLWLAEQVTKLQKNLVYFSENRGFFYWELDFQ   170
NTDB id 598 KW2 RS08500 WP 021037660.1       ERYLPELNQRPDLLVNDKIAIEIQCSHLSIKRLKERTENYKTHGFKVLWLMGKDLWLAEQVTELQKNLVYFSENRGFFYWELDFQ   170
NTDB id 155 SP RS04850 WP 000495909.1        EYPLSELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGQKLWLKERLTRLQQGFLYFSQNMGFYVWELDKE   168
NTDB id 265 KZH43 RS04315 WP 000495911.1     EYPLSELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGQKLWLKERLTRLQQGFLYFSQNMGFYVWELDKG   168
NTDB id 224 SPD RS04655 WP 000495911.1       EYPLSELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGQKLWLKERLTRLQQGFLYFSQNMGFYVWELDKG   168
NTDB id 190 SPR RS04415 WP 000495911.1       EYPLSELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGQKLWLKERLTRLQQGFLYFSQNMGFYVWELDKG   168
NTDB id 495 SM12261 RS04415 WP 000495920.1   EYLLPELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGKKLWLKERLTRLQQGFLYFSQNMGFYVWELDSE   168
consensus                                    !**!*!!*!**!**!!***!*!*!!!!*!**!*!!!!*!*!***!**!!!!*!**!!!!*!**!*!!****!!!*!*!!**!!!!*

logo
NTDB id 84110 JG741 RS11790 WP 032950503.1   RKKLRLKSLIHEDLRGRIICLQEEIPFGKGRLIAHLRLPYLAQKLVKIPTFKDPKLSSFIRQQLYYQSPKWMKIQEKYYQKGENL   255
NTDB id 598 KW2 RS08500 WP 021037660.1       RKKLRLKSLIHEDLRGRIICLQEEIPFGKGRLIAHLRLPYLAQKLVKIPTFKDSKLSSFIRQQLYYQSPKWMKIQEKYYQKGENL   255
NTDB id 155 SP RS04850 WP 000495909.1        KQVLRLKYLIYQDLRGKLHYQIKEFSYGQGSLLEILRLPYKRQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI   253
NTDB id 265 KZH43 RS04315 WP 000495911.1     KQVLRLKYLIYQDLRGKLHYQIKEFSYGQGSLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI   253
NTDB id 224 SPD RS04655 WP 000495911.1       KQVLRLKYLIYQDLRGKLHYQIKEFSYGQGSLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI   253
NTDB id 190 SPR RS04415 WP 000495911.1       KQVLRLKYLIYQDLRGKLHYQIKEFSYGQGSLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI   253
NTDB id 495 SM12261 RS04415 WP 000495920.1   KQVLRLKYLIHQDLRGKLHYQIKEFPYGHGSLLEILRFPYKKQKISHFTVSQDKDICRYIRQQLYYQNPIWMKEQAEAYKKGENL   253
consensus                                    ***!!!!*!!**!!!!*******!***!*!*!***!!*!!**!!********!******!!!!!!!!***!!!!*!***!*!!!!*

logo
NTDB id 84110 JG741 RS11790 WP 032950503.1   LTKKFEGPYIAPLGLNLLESFTDEMTITTFTQIDQNVKLYYENFLINFQ...RNSLEMLYPPCFYAIMGKQKKEK   327
NTDB id 598 KW2 RS08500 WP 021037660.1       LTKKFEGPYIAPLGLNLLENFTDEMTITTFTQIDQNVKLYYENFLINFQ...RNSLEMLYPPRSYAIMGKQKKEK   327
NTDB id 155 SP RS04850 WP 000495909.1        LTYGLKEWYPQI...........RPIVGKFFQIEQDLTSYYQHFYTYYQKNPQNDWQKLYPPAFYQQYFLKNMVE   317
NTDB id 265 KZH43 RS04315 WP 000495911.1     LTYGLKEWYPQI...........RPIVGKFFQIEQDLTSYYQHFYTYYQKNPQNDWQKLYPPAFYQQYFLKNMVE   317
NTDB id 224 SPD RS04655 WP 000495911.1       LTYGLKEWYPQI...........RPIVGKFFQIEQDLTSYYQHFYTYYQKNPQNDWQKLYPPAFYQQYFLKNMVE   317
NTDB id 190 SPR RS04415 WP 000495911.1       LTYGLKEWYPQI...........RPIVGKFFQIEQDLTSYYQHFYTYYQKNPQNDWQKLYPPAFYQQYFLKNMVE   317
NTDB id 495 SM12261 RS04415 WP 000495920.1   LTYGLKEWYPQI...........RPLVGNFCQIEQDLIRYYLYFQTYYQENPQNDWQMLYPPAFYQQYFLKNMVE   317
consensus                                    !!******!***           ******!*!!*!****!!**!****!****!****!!!!**!**********
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X non conserved

X similar

X ≥ 50% conserved