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logo

NTDB id 424 SGO RS10430 WP 012130755.1          ..........................MKFEDVYKQVEGIVKRCYKDYYLHLWEYADWRQEGMLVLYELLKSHPNLLEDQ   53
NTDB id 423 SGO RS08370 WP 012130755.1          ..........................MKFEDVYKQVEGIVKRCYKDYYLHLWEYADWRQEGMLVLYELLKSHPNLLEDQ   53
NTDB id 44 SMU RS09085 WP 002263585.1           ........................MEEDFEIVFNKVKPIVWKLSRYYFIKMWTREDWQQEGMLILHQLLREHPELEEDD   55
NTDB id 1128493 FQT45 RS07970 WP 077322504.1    ...MFFFVTFFYNMTIILKEGIIKKPMYELNQLFSQVKPIVFKLMRTYFIQLWETDDWLQEGRLVLYSLIESNPELLTNQ   77
NTDB id 442 SPYM3 RS08515 WP 011106595.1        MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAVFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 441 SPYM3 RS01385 WP 011106595.1        MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAVFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 450 SPYM18 RS08475 WP 011018214.1       MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAAFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 449 SPYM18 RS01395 WP 011018214.1       MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAAFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1   MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAAFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1   MSCCFFVVLFIL..GIVK.KKRRLKMSIETRAAFEKVKPIILKLKRHYYIQLWDRDDWLQEGHIILLQLLERYPELIEEE   77
NTDB id 554 STRINF RS00370 WP 115283725.1       ..........................MDFERYFQTVKPIILKLRRHYFVKLWDYEDWIQEGRIVFFQLLEEHPDLLNNE   53
consensus                                       ************  **** ****************!**!*******!****!***!!*!!******!****!*!****
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NTDB id 424 SGO RS10430 WP 012130755.1          PRLYRYFKTKFRNRIHDLIRRQESQKRKLDRQPYEEVSEIGHRLRMKEL.YLDELVAFRSAMSEYRSRLSPEEAKQYERL   132
NTDB id 423 SGO RS08370 WP 012130755.1          PRLYRYFKTKFRNRIHDLIRRQESQKRKLDRQPYEEVSEIGHRLRMKEL.YLDELVAFRSAMSEYRSRLSPEEAKQYERL   132
NTDB id 44 SMU RS09085 WP 002263585.1           TKLYIYFKTRFSNYIKDVLRQQESQKRRFNRMSYEEVGEIEHCLSSGGM.QLDEYILFRDSLLAYKQGLSTEKQELFERL   134
NTDB id 1128493 FQT45 RS07970 WP 077322504.1    KKLLVYFKTKFSSHIKDTIRHQESFKRKLNRLPYQEISEVSHRIPEKGL.ILDDFVAYQSIIEELKPYLTMKEQNQFKAL   156
NTDB id 442 SPYM3 RS08515 WP 011106595.1        ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFQAL   156
NTDB id 441 SPYM3 RS01385 WP 011106595.1        ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFQAL   156
NTDB id 450 SPYM18 RS08475 WP 011018214.1       ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFKAL   156
NTDB id 449 SPYM18 RS01395 WP 011018214.1       ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFKAL   156
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1   ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFQAL   156
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1   ERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGL.WLDDYVAYQEVIASLENQLNSQERMQFQAL   156
NTDB id 554 STRINF RS00370 WP 115283725.1       GKCYSYFKTKFSNHVKDIIRHQESFKRKFNRMPYEEISDISHCVPQVFFFEVEDYVAYQDSLACLRRTLGREDRLKLEKV   133
consensus                                       *****!!!!*!*****!**!*!!!*!!******!*!*****!******* ******************!******** **
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logo

NTDB id 424 SGO RS10430 WP 012130755.1          MADERFKGRKAMLKDLSYHLRDFNPRLD   160
NTDB id 423 SGO RS08370 WP 012130755.1          MADERFKGRKAMLKDLSYHLRDFNPRLD   160
NTDB id 44 SMU RS09085 WP 002263585.1           VAGEHFLGRQSMLKDLRKKLSDFKEK..   160
NTDB id 1128493 FQT45 RS07970 WP 077322504.1    LRGERFSGRKSLLRKLKPFFIDFQ....   180
NTDB id 442 SPYM3 RS08515 WP 011106595.1        IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 441 SPYM3 RS01385 WP 011106595.1        IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 450 SPYM18 RS08475 WP 011018214.1       IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 449 SPYM18 RS01395 WP 011018214.1       IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1   IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1   IRGERFKGRRALLRKISPYFKEFAQQL.   183
NTDB id 554 STRINF RS00370 WP 115283725.1       IRGERFEGKKAFLKSIELYFSDFRP...   158
consensus                                       ***!*!*!****!*********!****
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X non conserved

X similar

X ≥50% conserved