

logo

NTDB id 320 STU RS10340 WP 002949220.1
 NTDB id 47 STER RS00925 WP 002949220.1
 NTDB id 468 HSISS4 RS00725 WP 021143466.1
 NTDB id 50 STRSA0001 RS07545 WP 002885610.1
 NTDB id 44 SMU RS09085 WP 002263585.1
 NTDB id 1155332 QNH74 RS00080 WP 011921639.1
 NTDB id 461 GPW51 RS00080 WP 011921639.1
 NTDB id 454 SSU RS00080 WP 011921639.1
 NTDB id 457 SSUD9 RS00080 WP 002936602.1
 NTDB id 424 SGO RS10430 WP 012130755.1
 NTDB id 423 SGO RS08370 WP 012130755.1
 NTDB id 141 SP RS10155 WP 000588925.1
 NTDB id 140 SP RS00070 WP 000588925.1
 NTDB id 252 KZH43 RS09050 WP 000588897.1
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 NTDB id 211 SPD RS09675 WP 000588897.1
 NTDB id 210 SPD RS00065 WP 000588897.1
 NTDB id 177 SPR RS09210 WP 000588897.1
 NTDB id 176 SPR RS00065 WP 000588897.1
 NTDB id 489 SM12261 RS01070 WP 000471940.1
 NTDB id 488 SM12261 RS00065 WP 000471939.1
 NTDB id 516 SMSK321 RS09125 WP 000471944.1
 NTDB id 517 SMSK321 RS10700 WP 000471945.1
 NTDB id 582 DLJ51 RS00505 WP 002962720.1
 NTDB id 554 STRINF RS00370 WP 115283725.1
 NTDB id 450 SPYM18 RS08475 WP 011018214.1
 NTDB id 449 SPYM18 RS01395 WP 011018214.1
 NTDB id 442 SPYM3 RS08515 WP 011106595.1
 NTDB id 441 SPYM3 RS01385 WP 011106595.1
 NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1
 NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1



LD.MVDRLAYDEQLNAFREQLSSEDSLKLDRLIGGECFRGRKKMIRELRFWMVDFDPCNEED 165
 LD.MVDRLAYDEQLNAFREQLSSEDSLKLDRLIGGECFRGRKKMIRELRFWMVDFDPCNEED 165
 LD.AVDRLVYDEQLNAFRNQLSSEDATEKLDRLLAGECFRGRKKMIRELRFWMVDFDPYNEDD 165
 LD.AVDRLVYDEQLNAFRNQLSSEDATEKLDRLLAGECFRGRKKMIRELRFWMVDFDPYNEDD 165
 MQ.LDEYILFRDLSLAYKQGLSTEQELFERLVAGEHFLGRQSMKDLRKKLSDFKKEK... 160
 LI.NDELLMLRGAIRDYRKNLSNDQLDKYEKLISSGCFNGRREMIRDQLIHLKDFR..... 156
 LI.NDELLMLRGAIRDYRKNLSNDQLDKYEKLISSGCFNGRREMIRDQLIHLKDFR..... 156
 LI.NDELLMLRGAIRDYRKNLSNDQLDKYEKLISSGCFNGRREMIRDQLIHLKDFR..... 156
 LY.LDELVAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMKDL SYHLRDFNPRLD.. 160
 LY.LDELVAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMKDL SYHLRDFNPRLD.. 160
 LW.LDDYYLFHETLRDYRNKQSKQEKQEELELRLVLSNERFRGRQRVLRDLRIVFKEFTIRTH.. 159
 MD.TADYCALKEKIKELKQKLAPEDYAKILLLMRGGAFKGRSAFIKDIKVEFEDFDEDN... 207
 FFEVEYVAVQDSLACLRLTGREDRLEKVIKGERFECCKAFKSLIYFSDFRP..... 158
 LW.LDDYVAYQEVIASLENQLNSQERMQFKALIRGERFKGRHALLRKTSPYFKEFAAQL... 183
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consensus

** ***** * ***** ** * * ***** ***!*** ***** **!

non conserved
 similar
 ≥ 50% conserved