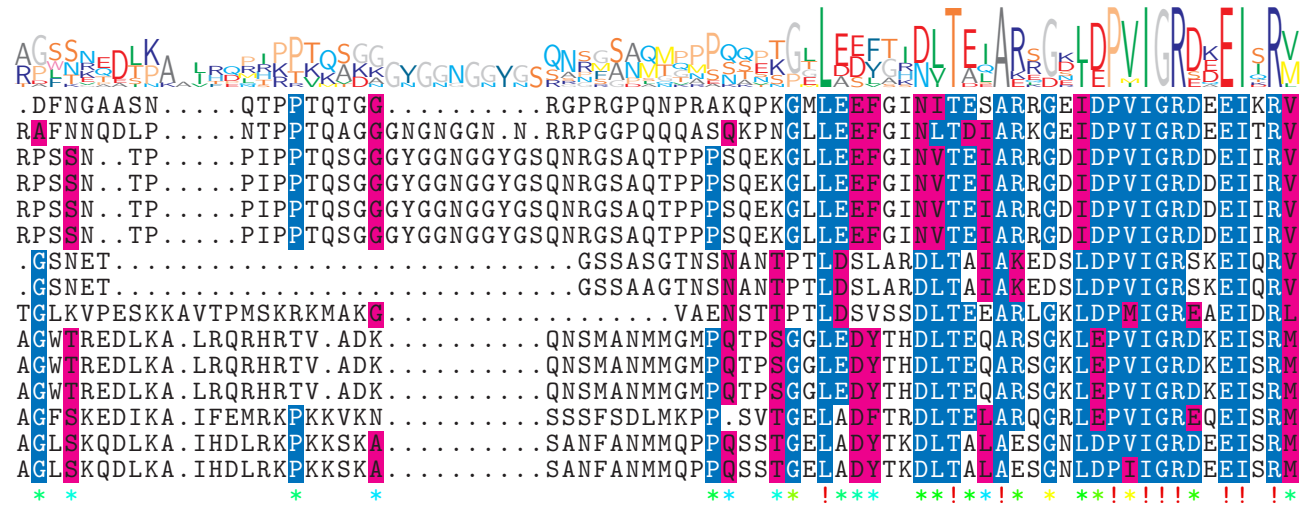




logo

NTDB id 601 KW2 RS02615 WP 021036805.1  
 NTDB id 378 SMU RS02690 WP 002263569.1  
 NTDB id 241 SP RS04015 WP 000882523.1  
 NTDB id 281 KZH43 RS03550 WP 000882517.1  
 NTDB id 245 SPD RS03860 WP 000882517.1  
 NTDB id 243 SPR RS03635 WP 000882517.1  
 NTDB id 1056108 ACFBUK RS00580 WP 015239036.1  
 NTDB id 85 BSU 00860 NP 387967.1  
 NTDB id 610 V4T04 RS10165 WP 012897346.1  
 NTDB id 290 KZH43 RS10025 WP 001109677.1  
 NTDB id 289 SPD RS10700 WP 001109677.1  
 NTDB id 287 SP RS11210 WP 001109712.1  
 NTDB id 377 SMU RS09275 WP 002262344.1  
 NTDB id 297 STER RS00545 WP 011680614.1  
 NTDB id 329 STU RS10020 WP 011225298.1  
 consensus



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 NTDB id 377 SMU RS09275 WP 002262344.1  
 NTDB id 297 STER RS00545 WP 011680614.1  
 NTDB id 329 STU RS10020 WP 011225298.1  
 consensus









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NTDB id 601 KW2 RS02615 WP 021036805.1	LVDLGYNPAMGARPLRRTIQENTIEDSTADFYIEHPEYKQ.LVADLIDDKIVISNQTQETAETDDEEVP	AE	748
NTDB id 378 SMU RS02690 WP 002263569.1	LVDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKE.LKAIMTSNGKIVIKASNK.VETVTKATSD.	AE	753
NTDB id 241 SP RS04015 WP 000882523.1	LVDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	AE	752
NTDB id 281 KZH43 RS03550 WP 000882517.1	LVDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	AE	752
NTDB id 245 SPD RS03860 WP 000882517.1	LVDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	AE	752
NTDB id 243 SPR RS03635 WP 000882517.1	LVDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKD.LKAVMTSKGNIQIKSAKK.AEVKSSEKEK.	AE	752
NTDB id 1056108 ACFBUK RS00580 WP 015239036.1	VAEEGVLDLEYGARPLRRRAIQKHVEDRLSEELLRGNIDKQGHIVLDVEDGEFVVKTTAKTN.....	AE	810
NTDB id 85 BSU 00860 NP 387967.1	VAEEGVLDLEYGARPLRRRAIQKHVEDRLSEELLRGNIDKQGHIVLDVEDGEFVVKTTAKTN.....	AE	810
NTDB id 610 V4T04 RS10165 WP 012897346.1	IAEVGFDPPEYGARPLRKAALQKEVEDLLSEQLLSGETKAGNHVSIIGASNKKTKIAQIV.....	AE	816
NTDB id 290 KZH43 RS10025 WP 001109677.1	LANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA.....	AE	810
NTDB id 289 SPD RS10700 WP 001109677.1	LANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA.....	AE	810
NTDB id 287 SP RS11210 WP 001109712.1	LANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIIGVKAGQLKFDIA.....	AE	810
NTDB id 377 SMU RS09275 WP 002262344.1	LALAGYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIIGIQKEKLKFDIV.....	AE	813
NTDB id 297 STER RS00545 WP 011680614.1	LAKDGYDIEMGARPLRRTIQTVEDKLSLELLGGQVVSQTLLKIGCSKDKLTFTVV.....	AE	816
NTDB id 329 STU RS10020 WP 011225298.1	LAKDGYDIEMGARPLRRTIQTVEDKLSLELLGGQVVSQTLLKIGCSKDKLTFTVV.....	AE	816
consensus	*** !*****!!!!!!***! *!! *** ** * * * * * * * * * *		

- X non conserved
- X similar
- X ≥ 50% conserved