

NTDB id 1253 GC085 RS04835 WP 011215094.1
NTDB id 75781 H7X90 RS18270 WP 057496791.1
NTDB id 1010 ACIAD RS15195 WP 004923715.1
NTDB id 1054 ABD1 RS15870 WP 002014066.1
NTDB id 1084 FDQ49 RS11070 WP 004711654.1
consensus

MLRLYRKPNKGLVGVDSSTSVKLELSVKNNKYWVESYALMPLPENSWEKNILNPEAVAEALERAMNLANPQTTHAAIAVPTS
MGLIPKSKQSPLVGVDSISTAVKLLQLSRSGNRFRVEHYAVEPLPPNAVVEKNIVEVEAVGEAIRRAMNRSKSAKLAAAIAVAGS
MLRLYRPPKKGVLGVDSISTSVKLVLELSVKNNQYRVESYGLVPLLENSVVEKNILNPEAVADALTPSINLANPQAINAAIAVPTS
MLRLYRKPNKGLMGVDISSTSVKLELSVKNGKYWVESYALMPLPENSVEKNILNPEAVAEALERAMNLANPQTTTHAAIAVPTS
MLRLYRKPNKGLMGVDISSTSVKLELSVKNGKYWVESYALMPLPENSVEKNILNPEAVAEALERAMNLANPQTTTHAAIAVPTS

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[illegible]

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ESYAVERAFAESVFADSLPMPGANTYVGLDIGHMTTILSVMQNGKLIYTREQVFGGKQLTLEIQRYGLSLEEA SRAKKDGS L PDD	255
AFIMNSVALYISTXSSIDKYALVIANYPFLKMPLEFSIEKIMVBAVAETHHNYQATLIRQRKDS	
ESYAVERSVQQIAQELPASQDKIIVAVDIGANYTHLFLVHGMRLIFSREHKFGGMQLVEATAEHYHMLNLEQAIALKNQGKLPED	255
EAFAVENAYALVAELPV.SIDGVVALVDIGATMTTLNVLRGGRSLYSREQVFGGKQLTDEIMRRYGLSYEEAGLAKFQGGGLPES	253
ESYAMERAFSVFADTLPM.GVNT.VGILDIGHTMTTLSVMQK GKLIYTREQVFGGKQLTQEVQKRYCMSYEEAGRAKKDGS L PDD	253
ESYAVERAFAFSVFADSLPM.GANT.IGILDIGHTMTTLSVMQNGKLIYTREQVFGGKQLTLEIQSRYGLSLEEA SRAKKDRSLPDD	253
ESYAVERAFAFSVFADSLPM.GANT.IGILDIGHTMTTLSVMQNGKLIYTREQVFGGKQLTLEIQSRYGLSLEEA SRAKKDRSLPDD	253

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YE EVLEPFLDAVQQAAARSLQFFSSQFNEIDHILLAGGNANIPGLAKLLQQKLG YRVTIANPFLQMGFSPQVDVQKIENDAS 340
 FMAFDYKEMTLLIRILYAGEHGFVYKLSKPMYEEQLVPTVWLAHIELGKKNIDALASDA 341
 YESAVLEPFKDMILLQIKRTLQFFYSTSQHGFVDHILLAGGMARQPGLAALIQEQLGVTTVANPLSHMSFGKKVNLDVINSAP 342
 YEMEVLEPFKEATVQQISRLQLQFFYAGSEFNVRVDHIVLAGGC AVLGLPEMVEEQLGVP TVANPLAQMTLGPKNWAHALAQDAP 343
 FTQEVFEPYLEALVQQAARSLQFFSSSQYNEIDHILLAGGNANILGLSRLQKLG YRVTIANPFLQMGFSPQVDIKKVENDAA 344
 YEIEVLDPFLDAVVQQAARSLQFFSSSQFNEIDHILLAGGNANIPGLAKLLQQKLG YRVTIANPFLQMGFSPQVDVQKIENDAS 345
 YEIEVLDPFLDAVVQQAARSLQFFSSSQFNEIDHILLAGGNANIPGLAKLLQQKLG YRVTIANPFLQMGFSPQVDVQKIENDAS 346
 ***** 347
 ***** 348
 ***** 349
 ***** 350
 ***** 351
 ***** 352
 ***** 353
 ***** 354
 ***** 355
 ***** 356
 ***** 357
 ***** 358
 ***** 359
 ***** 360

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TLMVACGLALRHVE.	354
ALMTATGLALRSFD.	352
SLMVACGLALRSFDE	353
SLMVACGLALRSFD.	352
SLMVACGLALRSFD.	352

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 non conserved
 similar
 $\geq 50\%$ conserved