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NTDB id 1253 GC085 RS04835 WP 011215094.1
NTDB id 125164 HV99 RS04835 WP 003110888.1
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
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**MLR**LYRKPNKGLMGVDISSTSVKLELSVKNGKYWVESYALMPLPENSVEKNILNPEAVAEALERAMNLANPQTTHAAIAVPTS  
85  
**ML**GLIKKKANTLLGDISSTSVKLELSRSGGRYKVEAYAVEPLPPNAVVEKNIVELEGVGQALSRLVKAKTNLKSAVVAVAGS  
85  
MLRLYRRPKKGLVGVDISSTSVKVLELSVKNNQYRVESYGLVPLENSVVEKNILNPEAVADALT~~RS~~INLANPQA~~I~~NAAIAVPTS  
85  
MLRLYRKPNKGLMGVDISSTSVKLELSVKNGKYWVESYALMPLPENSVEKNILNPEAVAEALERAMNLANPQTTHAAIAVPTS  
85  
MLRLYRKPNKGLMGVDISSTSVKLELSVKNGKYWVESYALMPLPENSVEKNILNPEAVAEALERAMNLANPQTTHAAIAVPTS  
85

T V I H K T I E M D A D M S D D E R E V Q I R Y D A E Q Y I P F P L D E V S L D F E V L P D R L A N P N R V N V L L V A T R T E N V E T R V E V L E A G L N P K V A D V  
 A V I S K V V Q I N E G L T D L E M E E L V V I E A D K Y I P Y P I D E I N L D F E V L G H S A K S S S L D V L I V A S R A E N V N T R V E A A H R A G L E P K V V D V  
 A V I T K T I E M E A G L S E D E L E N Q L K I E A D Q Y I P Y P L E E V A I D F E V Q G L S A R N P E R V D V L L A A C R K E N V E V R E A A L A L A G L T A K V V D V  
 M V V H K T I E M D A D M T D D E R E V Q I R M D A E R Y I P F P L D E V S L D F E V M S E P L A N P N R V S V L I A A T R T E N V D T R I E V L E L A G L T P K V A D V  
 T V I H K T I E M D A D M S D D E R E V Q I R V D A E Q Y I P F P L D E V S L D F E V L P D R L A N P N R V N V L L V A T R T E N V E T R V E V L E L A D L N P K L A D V  
 T V I H K T I E M D A D M S D D E R E V Q I R V D A E Q Y I P F P L D E V S L D F E V L P D R L L A N P N R V N V L L V A T R T E N V E T R V E V L E L A D L N P K L A D V

ESYAVERA FSVFADSLPMGA...NTVGILDIGHTMTTLSVMQNGKIIYTREQVFGGKQLTLEIQRYGLSLEEASRAKKDGLPDD 255

EYALERSYALLSSQLGADTDQLTVAVVDIGATMTTLSVLHNGRTIYTREQVFGGKQLTLEIQRYGLSVEEAGLAKKQGGPLDD 255

ESYAMERAFSVFADTLPMGV...NTVGILDIGHTMTTLSVMQNGKIIYTREQVFGGKQLTLEIQRYGLSVEEAGLAKKQGGPLDD 253

ESYAVERA FSVFADSLPMGA...NTIGILDIGHTMTTLSVMQNGKIIYTREQVFGGKQLTLEIQRYGLSLEEASRAKKDRSLPDD 253

ESYAVERA FSVFADSLPMGA...NTIGILDIGHTMTTLSVMQNGKIIYTREQVFGGKQLTLEIQRYGLSLEEASRAKKDRSLPDD 253

[illegible]

S L M V A C G L A L R S F D  
A L M I A C G L A L R S F D E  
T L M V A C G L A L R H V E . 354  
A L M I A C G L A L R S F D . 354  
S L M V A C G L A L R S F D E 353  
S L M V A C G L A L R S F D . 352  
S L M V A C G L A L R S F D . 352

 non conserved  
 similar  
  $\geq 50\%$  conserved