

```
NTDB id 1253 GC085 RS04835 WP 011215094.1
NTDB id 168941 PcP3B5 RS28180 WP 009613650.1
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
```

MLRLYRKPNKGLMGYDSSSTSVKLELSVKNKYVESYALMLPLPNSWEKNLNPEAVAALEFAMNLANPQITTHAAI
GFKPKARTSTVSALYITSSGEDIKWRCAIRVETLASALEGNMKEVDLGGBCTRKETARLRFRGATHVLY
MLKLLPKPHRSILGIDISSAVKILEISGSGEDICVGGYGREEIPASALEGNMTKVDVVANCIKKLVERLKFTSKNVAL 80
MLGLFTKKANTLLGIDISSTSVKLELSRSGCRYKVEAYAVEPLPPNSVVEKNIAELEGGQALSRVAKARTGVKTTAAV 80
MLRLYRRPKKGLVGVDISSTSVKVLELSVKNNQYRVESYGLVPLLENSVVEKNILNPEAVADALTRSTINLANPQAINAAI 80
MLRLYRKPNKGLMGVDISSTSVKLELSVKNKYWVESYALMLPLPNSVVEKNILNPEAVAEALERAMNLANPQITTHAAI 80
MLRLYRKPNKGLMGVDISSTSVKLELSVKNKYWVESYALMLPLPNSVVEKNILNPEAVAEALERAMNLANPQITTHAAI 80
!!!!!!!! **!!!!!!*!*!*!!!!!!*!*!*!!!!!!*!*!*!!!!!!*!*!*!!!!!!*!*!*!!!!!!*!*!*!!!!!!

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consensus
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[illegible]

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[illegible]

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NTDB id 1253 GCO85 RS04835 WP 011215094.1
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consensus
```

Row	Sequence	Score
1	L S H M S F G K K V N L D V I N S D A P T L M V A C G L A L R H V E .	354
2	F A D M V L S N K V N A G A I A S D A P A L M I A C G L A M R S F D .	354
3	F L Q M E F S P Q V D I K K V E N D A A S L M V A C G L A L R S F D E	353
4	F L Q M G F S P Q V D V Q K I E N D A S S L M V A C G L A L R S F D	352
5	F L Q M G F S P Q V D V Q K I E N D A S S L M V A C G L A L R S F D .	352

 non conserved
 similar
 $\geq 50\%$ conserved