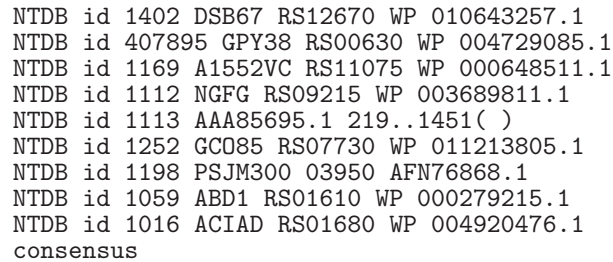
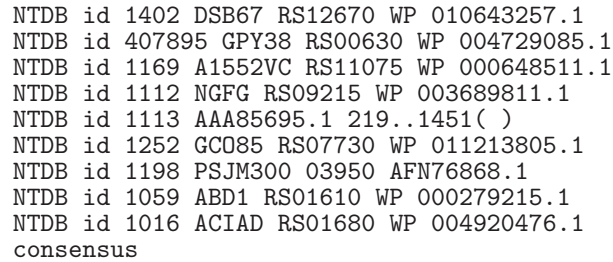
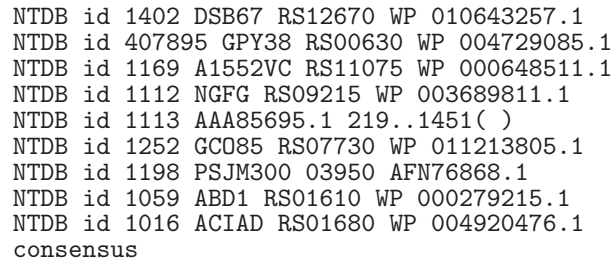


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NTDB id 407895 GPY38 RS00630 WP 004729085.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

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consensus

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logo

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NTDB id 1402 DSB67 RS12670 WP 010643257.1
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

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Sequence logo and sequence alignment for the 407-408 region. The sequence logo at the top shows the conservation of residues V, T, I, L, F, N, L, G, S, V, and A. Below it, the sequence alignment shows 10 sequences with positions 407 to 408 indicated on the right. The sequences are: VTAMYLPIFNLMSV LG., VVAMYLPIFNLMSV LG., VVAMYLPIFNLMSV LG., LVAMYLPIFNLGNVVA., LVAMYLPIFNLGNVVA*, VVAMYLPIFKLGS AV., ITAMYLPIFQMGSVV., VTAMYLPIFQMGSVV., VTAMYLPIFQMGSVV., and VTAMYLPIFQMGSVV. The asterisk under the 5th position of the 5th sequence indicates a mutation.

- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved