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NTDB id 1081 FDQ49 RS05335 WP 006581387.1
NTDB id 1060 ABD1 RS04380 WP 000355489.1
NTDB id 1040 HQN27 RS13360 WP 000355489.1

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MEFEKLLRLMVEKGGSDLFITAGVPPSMKVNGKILPVNKTPTMSPEMTRETIVHGVMNEQQRREFTENHECNFAISAR	76
MDFNDLNLMAKHKASDLFITAGVEPSLKINGEITTPVSKTKLDGDMIAQLIDSITTTQKQRQFEIETHECNFAILNR	76
MTSGIDITDILRLADKGSADIILAGLPPQFKLSGDYDAQGFEPLEASDTRKLMYSMMNNEQRRIFEKRELDDFSFAIG	80
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MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLEHKDVIKIITYDIMNDRQRKEYEEFFETDFSFEIA	76
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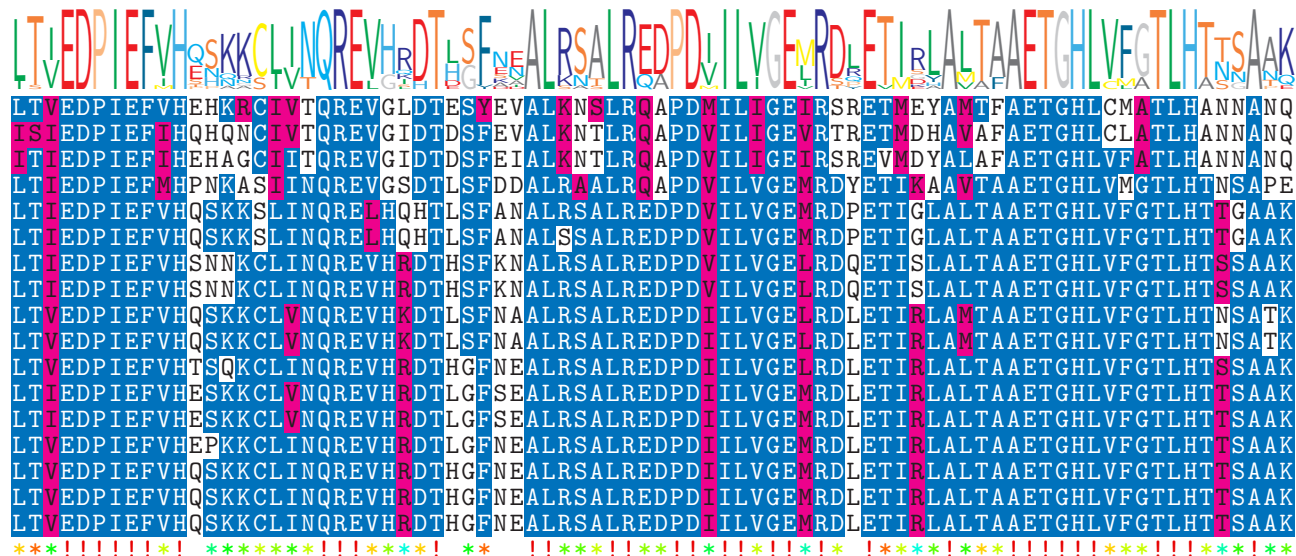


Sequence	Position
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EKNERFRVSAFQQRDMPCGMVIRRIETKIPSPDDLHLPLLEKELAMSKRGIIIFSCATGTGKSTSLASMIQHRNQHSGKHI	156
D. KARFRVNAFMQRGNVCGVMRLIPTTVRTIAEMGLPQTVIDIANAPRGVLVTGPTGSGKSTTLASMDIHINTTKLHI	159
N. VARFRVNAFNIIGRGPAAVFRTIPSTVLSLEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
N. VARFRVNAFNTGRGPAAVFRTIPSTVLSLEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
N. VGRFRVNAFHQARGCSAVFRTIPTVPIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
N. VGRFRVNAFHQARGCSAVFRTIPTVPIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
N. LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
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S. LARFRVNAFNQNRGAGAVFRTIPSEVLTLIEDLGCPPIFRQLIDQPQGLILVTGPTGSGKSTTLACMIDYINKNEYGHI	155
G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKTIIDVPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
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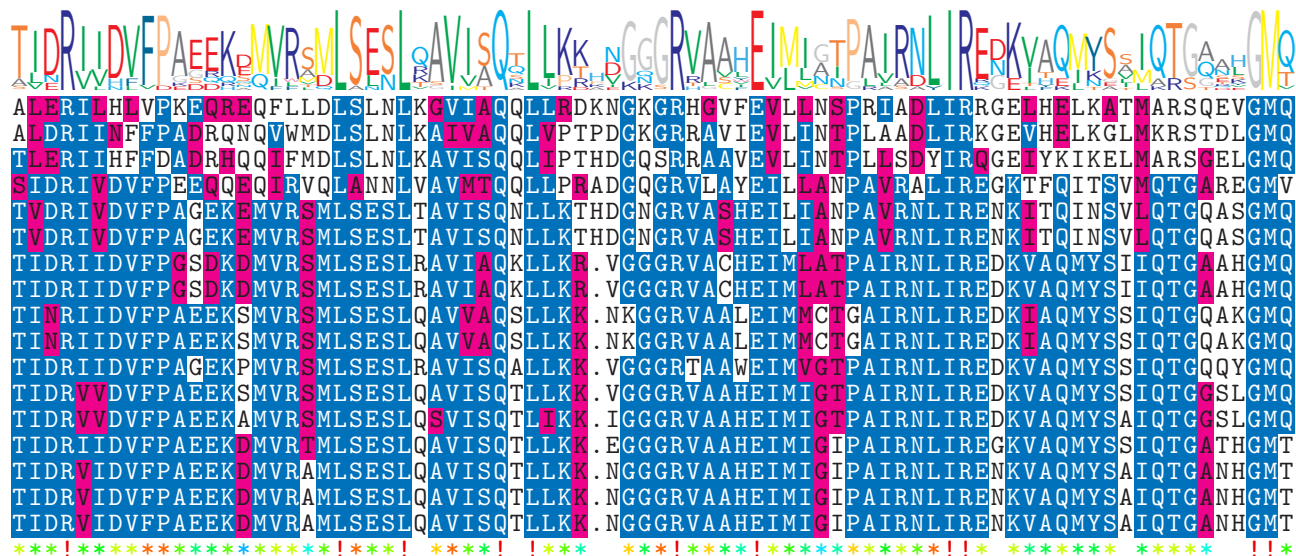
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consensus



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NTDB id 1177 A1552VC RS01165 WP 000422572.1
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consensus



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NTDB id 1177 A1552VC RS01165 WP 000422572.1	TFDQALYQLVVDKISEQDALHSADSANDLRLMLKTKRGDDY...GSGSLQNVKI.....DME.....	368
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consensus	!*** * !* ***** * *	

logo

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consensus		

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