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NTDB id 1019 ACIAD RS04205 WP 004922051.1
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NTDB id 1185 GTF74 RS11940 WP 000350195.1
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NTDB id 1202 PSJM300 01600 AFN76400.1
NTDB id 1194 PAKAF RS01995 WP 003084552.1
NTDB id 1020 ACIAD RS04210 WP 011182164.1
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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Sequence	Position 12
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MEFEKLLRLMVEKGGSDLFITAGVPPSMKVNGKILPWNKTPMSPEMTRETIVHGVMNEQQRREFTENHECNFAISAR	76
MDFNDLLNLMAHKHASDLFITAGVEPSLKINGEITPVSKTCLDGDMLAQILDSITTTQKQRQFEIETHECNFAILNR	76
MTSGIDITDILRLAADKGSADIILAGLPPQFKLSGDYDAQGFEP.LASDTRKLMYSMMNRRQQRIFEKRELDDFSFAIG	80
MQITDLLAFGAKNKASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MQITDLLAFGAKNKASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MDIAELLEFSVKHNASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MDIAELLEFSVKHNASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MDIAELLEFSVKHNASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
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MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPELHKDVIKIITYDIMNDRQRKEYEEFFETDFSFEIA	76
MDIAELLAFSVKNKASDLHLSSGISPMIRVDGTVRRINLPALDHKQVHALIYDIMNDKQRKDYEFFLEVDDFSFEIP	76
MDITELLAFSAKQGASDLHLSSGLPPMIRVDGTVRRINLPALDHKQVHALIYDIMNDKQRKDFEEFLETDFSFEVP	76
MDITELLAFSAKQGASDLHLSSGLPPMIRVDGTVRRINLPALDHKQVHALIYDIMNDKQRKDFEEFLETDFSFEVP	76
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MDITELLAFSVKNKASDLHLSSGLPPMIRVDGTVRRINLPALDHSEVHNLIYDIMNDKQRKDYEEKLETDFSFEVP	76
MDITELLAFSVKNKASDLHLSSGLPPMIRVDGTVRRINLPALDHSEVHNLIYDIMNDKQRKDYEEKLETDFSFEVP	76



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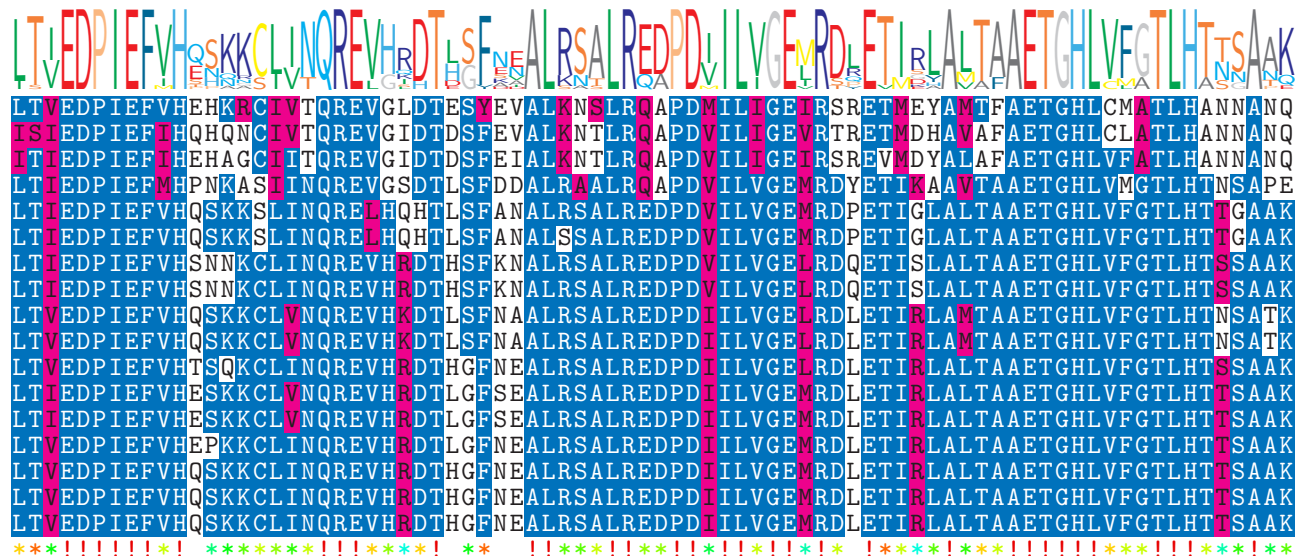


Position	Sequence	Conservation Score
153	. SGRFRVSAFFQRELP GAVIRRTETRIPTFEELKLPVLQNLAIAKRGVLVVGATGSGKSTTMAAMTGYRNQHRITGHI	153
155	G. IGRFRVSAFYQRNLAGMVLRRITETNIPTIEDLKLPDVLKKLALTKRGLVLFVGATGTGKSTSLAAMIGYRNKNSSGHI	155
156	EKNERFRVSAFQQRDMPCGMVIRRIETKIPSPDDLHLPLLEKELAMSKRGIIIFSGATGTGKSTSLASMIQHRNQHSKGI	156
159	D. KARFRVNAFMQRGNVCGVMRLIPTTVRTIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLASMDIHINTTKLHI	159
155	N. VARFRVNAFNIIGRGPAAVFRTIPSTVLSEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VARFRVNAFNTGRGPAAVFRTIPSTVLSEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VGRFRVNAFHQARGCSAVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
155	N. VGRFRVNAFHQARGCSAVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
155	N. LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
155	N. LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
155	S. LARFRVNAFNQNRGAGAVFRTIPSEVLTLIEDLGCPPIFRQLIDQPQGLILVTGPTGSGKSTTLACMIDYINKNEYGHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKTIIDVPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKTVSDVPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	N. LARFRVNVFNQNRGAGAVFRTIPSQVLTLEELGLGKIFRDICDYPRGLVLVTGPTGSGKSTTLAAMDYINNHRDYHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKIDICDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
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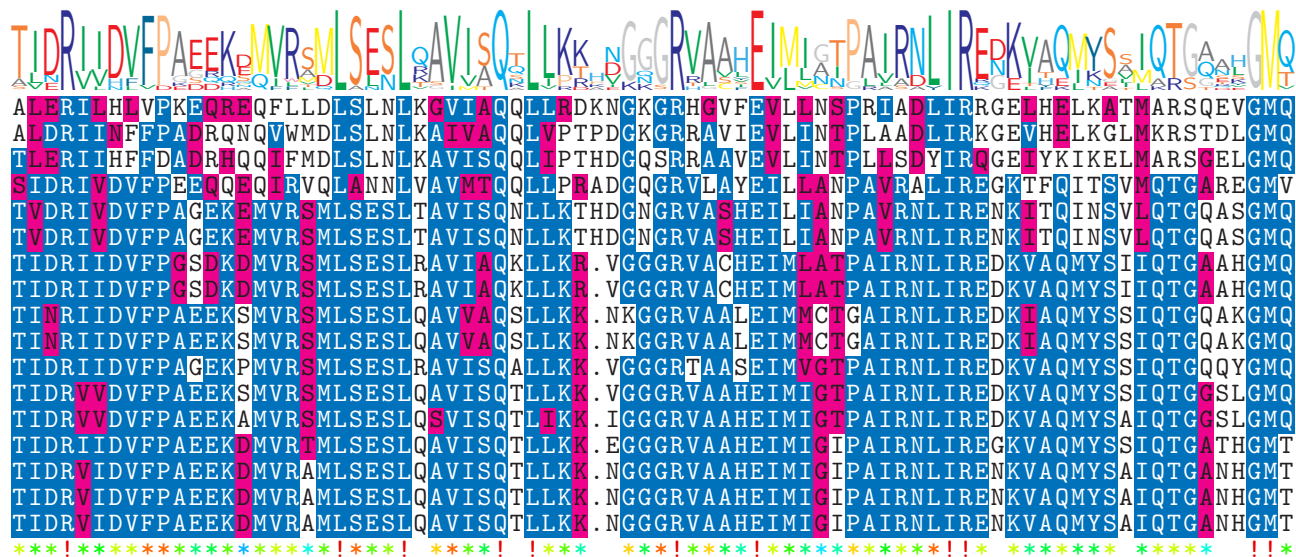
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consensus



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consensus



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NTDB id 1177 A1552VC RS01165 WP 000422572.1	TFDQALYQLVVDKISEQDALHSADSANDLRLMLKTKRGDDY...GSGSLQNVKI.....DME.....	368
NTDB id 1203 PSJM300 01605 AFN76401.1	TFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLGSETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR.....	381
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NTDB id 1185 GTF74 RS11940 WP 000350195.1	TMEQNAKQLIARGVVDAQEVQSKIELDLKA..F.....	345
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NTDB id 1259 GC085 RS10305 WP 010947729.1	TLDQHLTELVNKNIISKHTAHEAAL.NKSL..F.....	344
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NTDB id 1202 PSJM300 01600 AFN76400.1	TLDSCCLKGLLAKGLISRDSAKEKAK.QPEN..F.....	344
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NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TLDQSLKGLVSRGVISPQTARTAAK.QPES..FL.....	345
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consensus	!*** * !* ***** * *	

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	PATPAAPAAACRSEPCRCACCFRR	368
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consensus		

- non conserved
- similar
- ≥ 50% conserved