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NTDB id 1020 ACIAD RS04210 WP 011182164.1
NTDB id 1060 ABD1 RS04380 WP 000355489.1
NTDB id 1040 HON27 RS13360 WP 000355489.1
NTDB id 1081 FDQ49 RS05335 WP 006581387.1
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 ... MEINCYLDGMTHKASDLYITVGCAPILYRVDGELRAQGEALSVADVITALHAMMODARQAETKQTREANFAVVRD 73
 ... MFEKILLRLMVEKGGSDLFITAGVPPSMKVNGKILPVNKTTPMSPEMTRETIVHGVMNEQQRREFTENHECNFAISAR 76
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NTDB id 1081 FDQ49 RS05335 WP 006581387.1

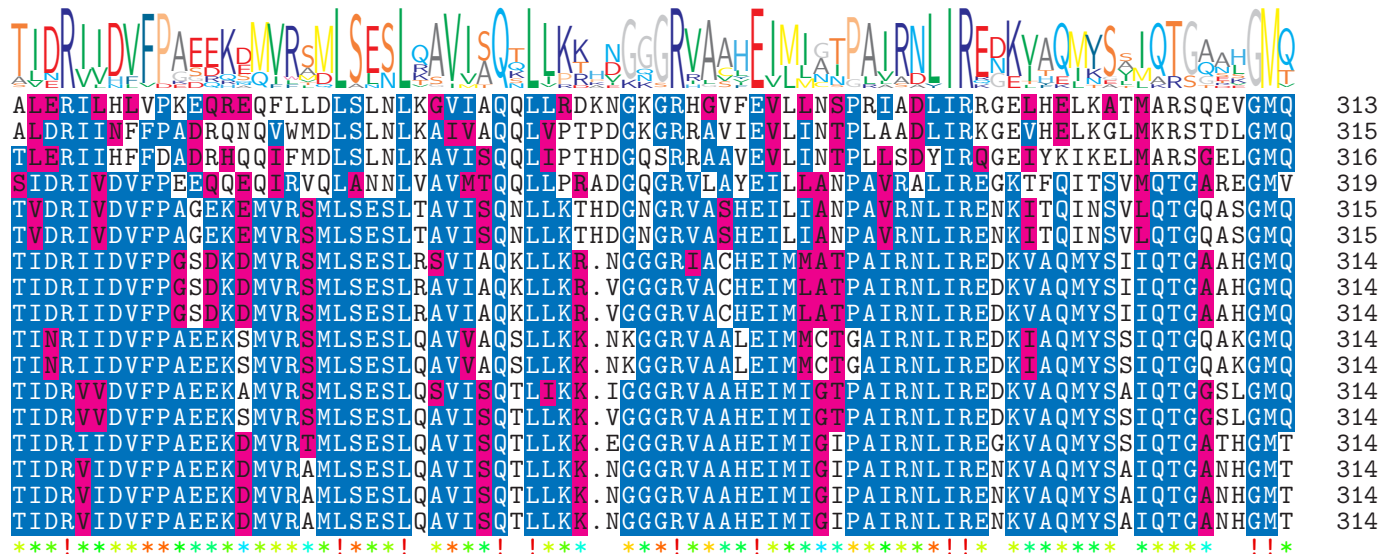
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Position	Sequence	Conservation Score (bits)
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155	G. IGRFRVSAFYQRNLAGMVLRRITETNIPTIEDLKLPDVLKKLALTK RGLVLVFGATGTGKSTSLAAMIGYRNKNSSGHI	155
156	EKNERFRVSAFQQRDMPCGMVIRRIETKIPSPDDHLPLLELAKELAMSKRG I IIFSGATGTGKSTSLASMIQHRNQHSGKHI	156
159	D. KARFRVNAFMQRGNVCGVMRLIPTTVRTIAEMGLPQTVIDIANAP RGLVLVTGPTGSGKSTTLASMDIHNTTKLHI	159
158	N. VARFRVNAFNIIGRGAIAVFRPTIPSTVLSLEELKAPSI FQKIAESP RGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	158
155	N. VARFRVNAFNTGRGPAAVFRPTIPSTVLSLEELKAPSI FQKIAESP RGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VGRFRVNAFNQSRGCAAVFRPTIPSSIPTLEELAEPEIFK KIANAEKGLVLVTGPTGSGKSTTLAAITVDYINRNHNKHI	155
155	N. VGRFRVNAFHQAARGCSAVFRPTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155
155	N. VGRFRVNAFHQAARGCSAVFRPTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155
155	N. LARFRVNAFNQSRGAAAVFRPTIPSEILSMEDLGLPIFKEMASFS RGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
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155	G. VARFRVNAFNQNRGAGAVFRPTIPSKVLTMEELGMGEVFRKIVSDVPRGLVLVTGPTGSGKSTTLAAMDYINNTKYHHI	155
155	G. VARFRVNAFNQNRGAGAVFRPTIPSKVLTMEELGMGEVFRKITDVP RGLVLVTGPTGSGKSTTLAAMDYINNTKYHHI	155
155	N. LARFRVNVFNQNRGAGAVFRPTIPSKVLTLEELGLGKIFRDCIDYPRGLVLVTGPTGSGKSTTLAAMDYINNHRDYHI	155
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consensus



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consensus



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

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NTDB id 1185 GTF74 RS11940 WP 000350195.1		345
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consensus		

- ☒ non conserved
- ☒ similar
- ☒ ≥ 50% conserved