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NTDB id 1177 A1552VC RS01165 WP 000422572.1
NTDB id 1203 PSJM300 01605 AFN76401.1
NTDB id 1019 ACIAD RS04205 WP 004922051.1
NTDB id 1307 DR RS10055 WP 010888596.1
NTDB id 1086 NMV RS00245 WP 002218487.1
NTDB id 1116 NFGF RS10615 WP 003690200.1
NTDB id 1185 GTF74 RS11940 WP 000350195.1
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NTDB id 1283 ACE17W RS02630 WP 010947729.1
NTDB id 1259 GCO85 RS10305 WP 010947729.1
NTDB id 21997 XCC RS14275 WP 003489919.1
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
MEINCYLDGMTHKASDLYITVGCAPILYRVDGELRAQGEALSVADVTAALHAMMODARQAETKQTR EANFAVVRD	73
MEFEKILRLMVEKGGSDLFITAGVPPSMKVNGKILPWNKTPMSPEMTRETIVHGVMNEQQRREFTENHECNFAISAR	76
MDFNDLNLMAKHKASDLFITAGVEPSLKINGEITTPVSKTKLDGDMIAQLIDSITTTQKQRQFEIETHECNFAILNR	76
MTSGIDITDILRLADKGSADIILAGLPPQFKLSGQYDAQGFEPLEASDTRKLMYSMMNNEQRRIFEKRELDDFSFAIG	80
MQITDLLAFGAKNKASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFEIP	76
MQITDLLAFGAKNKASDLHLSSGISPMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFEIP	76
MDIAELLEFSVKHNASDLHLSSAGVPPMVRIDGVRKLGVPFATHSDVHRLIFEIMNDAQRSEYEKKLEVDFSFEIP	76
MDIAELLEFSVKHNASDLHLSSAGVPPMVRIDGVRKLGVPFATHSDVHRLIFEIMNDAQRSEYEKKLEVDFSFEIP	76
MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLEHKDVIKIIYDIMNDRQRKEYEEFFETDFSFEIA	76
MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLEHKDVIKIIYDIMNDRQRKEYEEFFETDFSFEIA	76
MDIAELLAFSVKNKASDLHLSSAGLPPMIRVDGTVRRINLPALDHKQVHALIYDIMNDKQRKDYEFFLEVDFSFEIP	76
MDITELLAFSAKQGASDLHLSSGLPPMIRVDGDVRRINLPAMDHKQVHALIYDIMNDKQRKDFEEFLETDFSFEVP	76
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MDITELLAFSVQNRASDLHLSSAGIPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRRDYEKKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSAGMPPMIRVDGEVRRINLPALHKDVHRLVYDIMNDKQRRDYEKKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSAGMPPMIRVDGEVRRINLPALHKDVHRLVYDIMNDKQRRDYEKKLETDFSFEVP	76



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NTDB id 1040 HQN27 RS13360 WP 000355489.1

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Position	Sequence	Conservation Score
153	. . SGRFRVSAFFQRELP GAVIRRTETRIPTFEELKLPVLQNLAIAKRGVLVVGATGSGKSTTMAAMTGYRNQHRGTGHI	153
155	G. IGRFRVSFAFYQRNLACMVLRRITETINPTIEDILKLPDVLKKLALTKRGLVLFVGATGTGKSTSLAAMIGYRNKNSSGHI	155
156	EKNERFRVSAFQQRDMPGMVIIRRIETIKIPSPDDLHLPLLKLAMSKRGITIFSGATGTGKSTSLASMIQHRNQHSKGI	156
159	D. KARFRVNAFMQRGNVCGVMRLIPTITVTRTIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLASMDIHNTTKLHI	159
155	N. VARFRVNAFNI GRGPA AVFRTIPSTVLSLEELKAPSI FQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VARFRVNAFNTGRGPA AVFRTIPSTVLSLEELKAPSI FQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VGRFRVNAFHQARGCS AVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
155	N. VGRFRVNAFHQARGCS AVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHHNKHI	155
155	N. LARFRVNAFNQSRGAA AVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
155	N. LARFRVNAFNQSRGAA AVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEHI	155
155	S. LARFRVNAFNQNRGAGAVFRTIPSEVLTLIEDLGCPPIFRQLIDQPQGLILVTGPTGSGKSTTLACMIDYINKNEYGHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKLTIDVPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEELGMGEVFRKVS D VPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	N. LARFRVNVFNQNRGAGAVFRTIPSQVLTLEELGLGKIFRDI CDYPRGLVLVTGPTGSGKSTTLAAMDYINNHRDYHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGITVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGITVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGITVLVTGPTGSGKSTTLAAMDYINENRYDHI	155



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NTDB id 1060 ABD1 RS04380 WP 000355489.1
NTDB id 1040 HON27 RS13360 WP 000355489.1
consensus

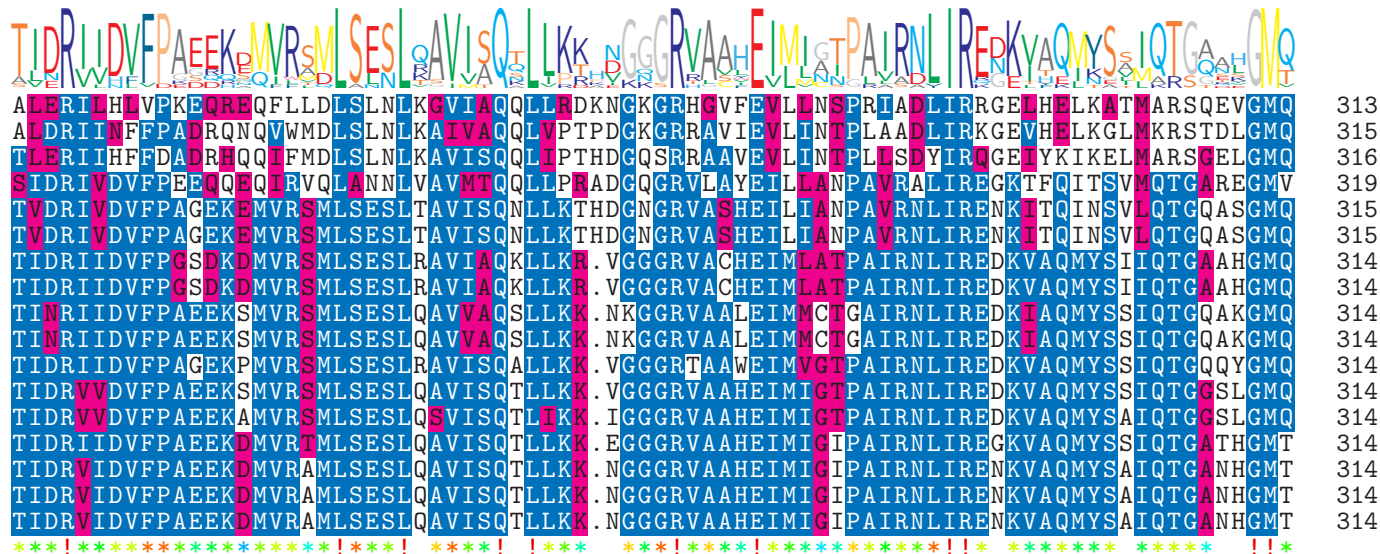
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NTDB id 1040 HON27 RS13360 WP 000355489.1
consensus

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logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	TFDQALYQLVVDKISEQDALHSADSANDLRLMLKTKRGDDY...GSGSLQNVKI.....DME.....	368
NTDB id 1203 PSJM300 01605 AFN76401.1	TFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLGSETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR.....	381
NTDB id 1019 ACIAD RS04205 WP 004922051.1	TFDQALFDLYDHQHSYADALKHADSPNNLRLQIKLSEEANKPLDNRERMSEMER.....KMTFDGQRRNLK.....	383
NTDB id 1307 DR RS10055 WP 010888596.1	TMDAYLAGLFRHLLITYDKGLERAI.DPKE..FARLANDASAGL.GGASMTPAAPPVPAYNSASSSSTGRGGDFGRGAAA	395
NTDB id 1086 NMV RS00245 WP 002218487.1	TMDQSLQSLVRQGLIAPEVARRRAQNSESM..SF.....	347
NTDB id 1116 NGFG RS10615 WP 003690200.1	TMDQSLQSLVRQGLIAPEAAARRRAQNSESM..SF.....	347
NTDB id 1185 GTF74 RS11940 WP 000350195.1	TMEQNAKQLIARGVVDAQEVQSKIELDLKA..F.....	345
NTDB id 1176 A1552VC RS01160 WP 000350195.1	TMEQNAKQLIARGVVDAQEVQSKIELDLKA..F.....	345
NTDB id 1283 ACE17W RS02630 WP 010947729.1	TLDQHLTELVNKNIISKHTAHEAAL.NKSL..F.....	344
NTDB id 1259 GC085 RS10305 WP 010947729.1	TLDQHLTELVNKNIISKHTAHEAAL.NKSL..F.....	344
NTDB id 21997 XCC RS14275 WP 003489919.1	TLDQHLQDLVKRSLITRNQAREYAK.DKRI..FE.....	345
NTDB id 1202 PSJM300 01600 AFN76400.1	TLDSCCLKGLLAKGLISRDSAKEKAK.QPEN..F.....	344
NTDB id 1194 PAKAF RS01995 WP 003084552.1	TLDMLKGLVAKGLISRENAREKAK.IPEN..F.....	344
NTDB id 1020 ACIAD RS04210 WP 011182164.1	TLDQSLKQLLAKGIINLPTARAVAK.SPES..F.....	344
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TLDQSLKGLVSRGVISPQTARTAAK.QPES..FL.....	345
NTDB id 1060 ABD1 RS04380 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAK.QPES..FL.....	345
NTDB id 1040 HON27 RS13360 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAK.QPES..FL.....	345
consensus	!*** * !* ***** * *	

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	PATPAAPAAACRSEPCRRACCFRR	368
NTDB id 1203 PSJM300 01605 AFN76401.1		381
NTDB id 1019 ACIAD RS04205 WP 004922051.1		383
NTDB id 1307 DR RS10055 WP 010888596.1	PATPAAPAAAGRSEPGRAGGFRR	418
NTDB id 1086 NMV RS00245 WP 002218487.1		347
NTDB id 1116 NGFG RS10615 WP 003690200.1		347
NTDB id 1185 GTF74 RS11940 WP 000350195.1		345
NTDB id 1176 A1552VC RS01160 WP 000350195.1		345
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NTDB id 1040 HON27 RS13360 WP 000355489.1		345
consensus		

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