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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 NGFG RS10615 WP 003690200.1
NTDB id 1185 GTF74 RS11940 WP 000350195.1
NTDB id 1176 A1552VC RS01160 WP 000350195.1
NTDB id 1283 ACE17W RS02630 WP 010947729.1
NTDB id 1259 GC085 RS10305 WP 010947729.1
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 201001 KAB03 RS04695 WP 000355489.1
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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Sequence	Position
MEINQYLDGMTHKASDLYITVGAPILYRVDGELRAQGEAL.SVADVTALEHAMMDARQAEFKQTREANFAVVRD	75
MEFEKILRLMVEKGCSDLFITAGVPPSMKVNGKILPWNKTPMSPEMTRETIVHGVNNEQQRREFTENHECNFAISAR	76
MDFNDLLNLMAHKHASDLFITAGVEPSLKINGEITTPVSKTKLDGDMIAQLIDSITTTQKQRQEFIEHTECNFAILNR	76
MTSGIDITDILRLADKAGSDIILAAGLPQFKLSGDYDAQGFEPLSDATRKLMSYMMNERQQRIFEKRELDFSFALP	80
MQITDLLAFGAKNKASDLHLSSGISPIMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MQITDLLAFGAKNKASDLHLSSGISPIMIRVHGDMMRRINLPPEMSAEVGNMVTSMNDHQRKIYQQNLEVDFSFELP	76
MDIAELLEFSVKHNASDLHLSSGVPPIVRIDGEVRKLGVPFATHSDVHRLIFEIMNDAQRSEYEKLEVDFSFELP	76
MDIAELLEFSVKHNASDLHLSSGVPPIVRIDGEVRKLGVPFATHSDVHRLIFEIMNDAQRSEYEKLEVDFSFELP	76
MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLLEHKDVIKIIYDIMNDRQRKEYEEFFETDFSFEIA	76
MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLLEHKDVIKIIYDIMNDRQRKEYEEFFETDFSFEIA	76
MDITELLAFSAKCGASDLHLSSGLPPMIRVDGVDRRINLPAMDHKQVHALIYDIMNDKQRKDFFEEFLETDFSFEVP	76
MDITELLAFSAKCGASDLHLSSGLPPMIRVDGVDRRINLPAMDHKQVHALIYDIMNDKQRKDFFEEFLETDFSFEVP	76
MDITELLAFSVQNRASDLHLSSGLPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRDYEEKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSGLPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRDYEEKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSGLPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRDYEEKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSGLPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRDYEEKLETDFSFEVP	76
MDITELLAFSVKNGASDLHLSSGLPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRDYEEKLETDFSFEVP	76



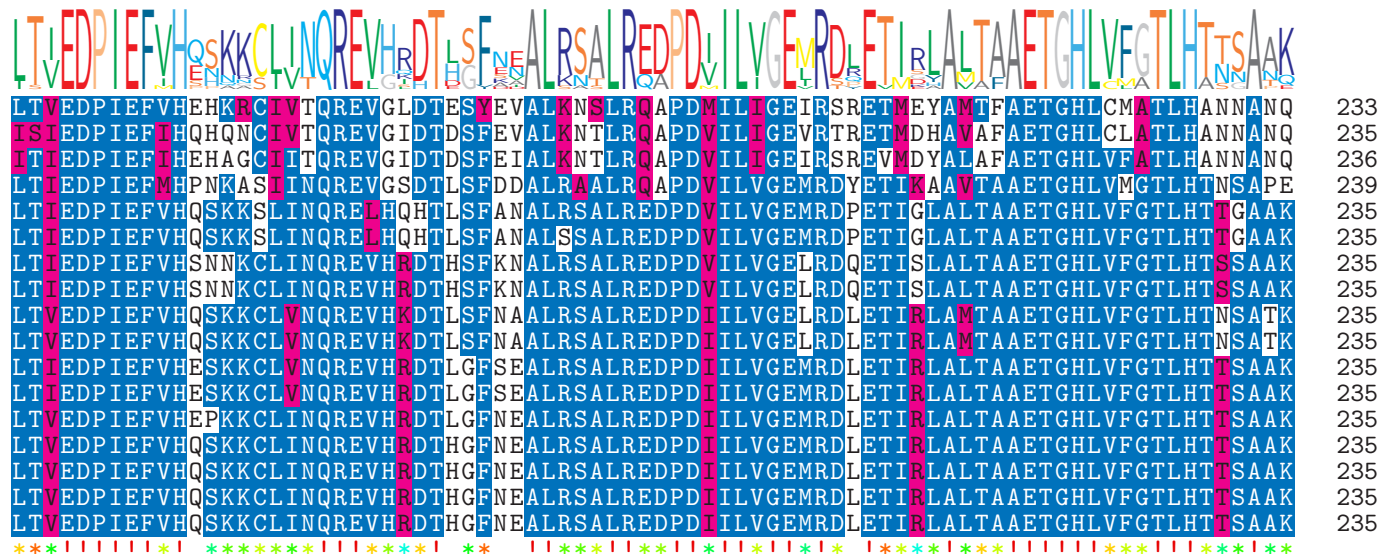
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NTDB id 1040 HON27 RS13360 WP 000355489.1
NTDB id 1081 FDQ49 RS05335 WP 006581387.1
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Position	Sequence	Conservation Score
153	. . SGRFRVSAFFQRELP GAVIRRTETRIPTFEELKLPVLQNLAIAKRGVLVVGATGSGKSTTMAAMTGYRNQHRITGHI	153
155	G. IGRFRVSFAFYQRNLAGMVLRRITETNIPTIEDLKLDPVLKKLALTKRGLVLFVGATGTGKSTSLAAMIGYRNKNSSGHI	155
156	EKNERFRVSAFQQRDMPCGMVIRRIETKIPSPDDLHLPLLKLKELAMSKRGIIIFSGATGTGKSTSLASMIQHRNQHSKGI	156
159	D. KARFRVNAFMQRGNVCGVMRLIPTTVRTIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLASMDIHINTTKLHI	159
159	N. VARFRVNAFNIGRGPAAVFRTIPSTVLSLEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	159
155	N. VARFRVNAFNTGRGPAAVFRTIPSTVLSLEELKAPSIFFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAHI	155
155	N. VGRFRVNAFHQARGCSAVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155
155	N. VGRFRVNAFHQARGCSAVFRTIPTV IPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155
155	N. LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAV IDYINSSRYEHI	155
155	N. LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAV IDYINSSRYEHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKITDVPRLGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	G. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKIVSDVPRGLVLVTGPTGSGKSTTLAAMDYLNNTKYHHI	155
155	N. LARFRVNVFNQNRGAGAVFRTIPSKVLTLEELGLGKIFRDI CDYPRGLVLVTGPTGSGKSTTLAAMDYINNHRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155
155	N. VARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYPRGIVLVTGPTGSGKSTTLAAMDYINENRYDHI	155

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consensus

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NTDB id 1081 FDQ49 RS05335 WP 006581387.1
consensus

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logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	TFDQALYQLVVDKKISEQDALHSADSANDLRLMLKTK.RGDDY...GSGSLQNVKI.....DME.....	368
NTDB id 1203 PSJM300 01605 AFN76401.1	TFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLG.SETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR....	381
NTDB id 1019 ACIAD RS04205 WP 004922051.1	TFDQALFDLYDHQHISYADALKHADSPNNLRQLIKLS.EEANKPLDNRRERMSEMER.....KMTFDGQRRNLK....	383
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NTDB id 1086 NMV RS00245 WP 002218487.1	TMDQSLQSLVRQGLIAPEVARRRAQNSESMSF.....	347
NTDB id 1116 NGFG RS10615 WP 003690200.1	TMDQSLQSLVRQGLIAPEAARRRAQNSESMSF.....	347
NTDB id 1185 GTF74 RS11940 WP 000350195.1	TMEQNAKQLIARGVVDAQEVQSKIELDLKAF.....	345
NTDB id 1176 A1552VC RS01160 WP 000350195.1	TMEQNAKQLIARGVVDAQEVQSKIELDLKAF.....	345
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NTDB id 1259 GC085 RS10305 WP 010947729.1	TLDQHLTELNVNKNIISKHTAHEAALNK.SLF.....	344
NTDB id 1202 PSJM300 01600 AFN76400.1	TLDQSLKGLIAKGLISRDSAKEKAKQP.ENF.....	344
NTDB id 1194 PAKAF RS01995 WP 003084552.1	TLDQSLKGLIAKGLISRDSAKEKAKQP.ENF.....	344
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NTDB id 201001 KAB03 RS04695 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1060 ABD1 RS04380 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1040 HON27 RS13360 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
consensus	!*** * !* ***** * *	

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	APATPAAPAAAGRSEPGRAGGFGRR	368
NTDB id 1203 PSJM300 01605 AFN76401.1		381
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NTDB id 1307 DR RS10055 WP 010888596.1	APATPAAPAAAGRSEPGRAGGFGRR	418
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NTDB id 1116 NGFG RS10615 WP 003690200.1		347
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NTDB id 1081 FDQ49 RS05335 WP 006581387.1		345
consensus		

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