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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
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NTDB id 1116 NGFG RS10615 WP 003690200.1
NTDB id 1185 GTF74 RS11940 WP 000350195.1
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NTDB id 1283 ACE17W RS02630 WP 010947729.1
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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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[illegible]

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The sequence logo displays the following amino acid sequences (residues 1-198) aligned vertically:
1. SGRFRVSAFFQRELP GAVIRRTETRIPTFEELKPLEVLQNLAIAKRGLVLVVGATGSGKSTTMAAMTG YRNQHRTGHI
2. IGRFRVSFAFYQRNLACMVLRRITETINPTIEDILKLPDVLKKALTKRGLVLFVGATGTGKSTSLAAMI GYRNKNSSGHI
3. EKNERFRVSAFQQRDMPCGMVIRRIETIKIPSPDDLHLPLLKL EAMSKRGIIIFSGATGTGKSTSLASMI QHRNQHSGKI
4. KAFRVNAFMQRGNVCGVMRLIPTTVRTIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLAS MIDHINTTKLHI
5. VARFVNFAFNIGRGPAAVFRTIPSTVLSLEELKAPSIFQKIAESPRGMVLVTGPTGSGKSTTLAAM INYINETQPAHI
6. VARFVNFAFNTGRGPA AVFRTIPSTVLSLEELKAPSIFQKIAESPRGMVLVTGPTGSGKSTTLAAM INYINETQPAHI
7. VGRFVNFAFHQAARGCSAVFRTIPTVIPTLEQLDAPEIFS KIANYEKG LVLVTGPTGSGKSTTLAAMVNYVA HHNKHI
8. VGRFVNFAFHQAARGCSAVFRTIPTVIPTLEQLDAPEIFS KIANYEKG LVLVTGPTGSGKSTTLAAMVNYVA HHNKHI
9. LARFVNFAFNQSRGA AVFRTIPSEILSMEDLGLPIPFKE MASFSRGLVLVTGPTGSGKSTTLAAV IDYINSSRYEHI
10. LARFVNFAFNQSRGA AVFRTIPSEILSMEDLGLPIPFKE MASFSRGLVLVTGPTGSGKSTTLAAV IDYINSSRYEHI
11. MARFVNFAFCQAARGSAVFRTIPSTVLTLDLGLAPEIFRK IAEPYRGLVLVTGPTGSGKSTTLAAMDYINDNFHHI
12. VARFVNFAFNQNRGAGAVFRTIPS KVLTMEDLG MGEVFRK ITDVPRGLVLVTGPTGSGKSTTLAAMDY LNNTKYHI
13. VARFVNFAFNQNRGAGAVFRTIPS KVLTMEDLG MGEVFRK RSDVPRGLVLVTGPTGSGKSTTLAAMDY LNNTKYHI
14. LARFVN VFNQNRGAGAVFRTIPS QVLTLEELGLGKIFRD IC DYP RGLVLVTGPTGSGKSTTLAAMDY INNHR YDHI
15. VARFVNFAFNQNRGAGAVFRTIPS KVLTMEDLGLGQIFKD IC DYP RG IVLVTGPTGSGKSTTLAAMDY INENR YDHI
16. VARFVNFAFNQNRGAGAVFRTIPS KVLTMEDLGLGQIFKD IC DYP RG IVLVTGPTGSGKSTTLAAMDY INENR YDHI

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consensus



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consensus



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NTDB id 1177 A1552VC RS01165 WP 000422572.1	TFDQALYQLVVDKISEQDALHSADSANDLRLMLK.TKRGDDY...GSGSL..QNV.KIDME.....	368
NTDB id 1203 PSJM300 01605 AFN76401.1	TFDQALYNLYVQGEITYEDALLHADSSNDLRLMIK.LGSETDGEHLTSVS...QGL.TLEMSDDDPGRSFR.....	381
NTDB id 1019 ACIAD RS04205 WP 004922051.1	TFDQALFDLYDHQHSYADALKHADSPNNLRLQIK.LSEEANKPLDNRERM..SEM.ERKMTFDGQRRNLK.....	383
NTDB id 1307 DR RS10055 WP 010888596.1	TMDAYLAGLFRHLITYDKGLERAIDPKFEARLANDASAGLGASMTPAAPPVPAYNSASSSSTGRGGDFGRGAAAPATP	399
NTDB id 1086 NMV RS00245 WP 002218487.1	TMDQSLQSLVRQGLIAPEVARRRAQNSESMSF.....	347
NTDB id 1116 NGFG RS10615 WP 003690200.1	TMDQSLQSLVRQGLIAPEAAARRRAQNSESMSF.....	347
NTDB id 1185 GTF74 RS11940 WP 000350195.1	TMEQNAKQLIARGVVDQAEVQSKIELDLKAF.....	345
NTDB id 1176 A1552VC RS01160 WP 000350195.1	TMEQNAKQLIARGVVDQAEVQSKIELDLKAF.....	345
NTDB id 1283 ACE17W RS02630 WP 010947729.1	TLDQHLTELVNKNIISKHTAHEAALNK.SLF.....	344
NTDB id 1259 GC085 RS10305 WP 010947729.1	TLDQHLTELVNKNIISKHTAHEAALNK.SLF.....	344
NTDB id 77338 H7R78 RS02750 WP 010673050.1	TMDQSLKQLVNRGVVASLDAKAKAVDP.NTI.....	344
NTDB id 1202 PSJM300 01600 AFN76400.1	TLDSCCLKGLLAKGLISRDSAKEKAKQP.ENF.....	344
NTDB id 1194 PAKAF RS01995 WP 003084552.1	TLDMCLKGLVAKGLISRENAREKAKIP.ENF.....	344
NTDB id 1020 ACIAD RS04210 WP 011182164.1	TLDQSLKQLLAKGIINLPTARAVAKSP.ESF.....	344
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TLDQSLKGLVSRGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1060 ABD1 RS04380 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1040 HON27 RS13360 WP 000355489.1	TLDQSLKGLVARGVISPQTARTAAKQP.ESFL.....	345
consensus	!*** * !* ***** * *	

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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	AAPAAGRSEPGRAGGFGRR	418
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consensus		

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