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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 47242 FNFX1 RS08300 WP 014550254.1
NTDB id 1116 NGFG RS10615 WP 003690200.1
NTDB id 1086 NMV RS00245 WP 002218487.1
NTDB id 1185 GTF74 RS11940 WP 000350195.1
NTDB id 1176 A1552VC RS01160 WP 000350195.1
NTDB id 1283 ACE17W RS02630 WP 010947729.1
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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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	MDIT	TE	AF	SV	VK	NG	AS	DL	HL	SAG	PP	MM	VR	ID	GE	VR	RR	IN	PA	LE	HK	DV	HR	LV	YD	IM	ND	QR	RD	YE	EE	KL	ET	DF	SF	FE	V
...	ME	LN	QY	LD	GM	LT	HK	AS	DL	YI	TV	GA	PIL	Y	RV	DG	EL	RA	QGE	AL	SV	AD	VT	AL	LH	AM	MD	AR	QA	EF	KQ	TR	EA	NF	AV	VR	
...	ME	FE	KL	LR	LM	VE	KG	GS	DL	FI	TA	GV	PP	SM	KV	NG	KI	LP	VNK	TP	MS	PE	MT	RE	TV	HG	VM	NE	EQ	QR	RE	FT	EN	HE	CN	FA	IS
...	MD	FN	DL	LL	NL	MA	HK	AS	DL	FI	TA	GV	EP	SL	KI	NG	ET	IP	VS	TK	LD	GM	LA	QL	ID	SI	TT	QK	QR	QF	ET	HE	CN	FA	IL	N	
MTSGI	DI	TD	IT	DL	RL	LA	DG	AS	DL	II	LA	GL	PQ	FK	LS	GD	YA	QGF	EP	LS	AS	DT	RK	LY	SM	YN	ND	QK	RI	FE	KE	RL	DF	SF	AL		
...	MIR	KLL	TL	CL	VQ	KK	AS	DL	HL	SS	GK	AK	YR	ID	GD	LI	DE	SS	SV	LD	KM	IS	QM	LE	IM	TD	QK	RI	FE	KE	RL	DF	SF	AL			
...	MQ	IT	DL	LA	FA	GA	KN	AS	DL	HL	SS	GI	SP	MIR	VH	GD	MR	RI	NL	PE	MS	AE	EV	GN	MV	TS	VM	ND	HQ	RK	KI	YQ	QN	LE	VD	FS	FE
...	MQ	IT	DL	LA	FA	GA	KN	AS	DL	HL	SS	GI	SP	MIR	VH	GD	MR	RI	NL	PE	MS	AE	EV	GN	MV	TS	VM	ND	HQ	RK	KI	YQ	QN	LE	VD	FS	FE
...	MD	IA	EL	LE	FE	SV	KN	AS	DL	HL	SAG	VP	PM	VR	ID	GE	VR	KL	GV	PA	FT	HS	DV	HR	LI	FE	IM	ND	AQ	RS	YE	EE	KL	ET	DF	SF	
...	MD	IA	EL	LE	FE	SV	KN	AS	DL	HL	SAG	VP	PM	VR	ID	GE	VR	KL	GV	PA	FT	HS	DV	HR	LI	FE	IM	ND	AQ	RS	YE	EE	KL	ET	DF	SF	
...	MD	IA	EL	LA	FA	SV	KN	AS	DL	HL	SS	GI	SP	MIR	VD	GE	DL	RK	IN	PP	LE	HK	DV	IK	II	YD	IM	ND	QR	KE	YE	EE	FF	ET	DF	SF	
...	MD	IA	EL	LA	FA	SV	KN	AS	DL	HL	SAG	VP	PM	VR	ID	GE	VR	KL	IN	PP	LE	HK	DV	IK	II	YD	IM	ND	QR	KE	YE	EE	FF	ET	DF	SF	
...	MD	IT	EL	LA	FA	SA	KQ	AS	DL	HL	SS	GL	PP	MIR	VD	GD	VR	RI	NL	PA	MD	HK	QV	HA	LI	YD	IM	ND	KQ	RD	FE	EF	FLET	DF	SF	EV	
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...	MD	IT	EL	LA	FA	SV	QNR	AS	DL	HL	SAG	I	PP	MIR	VD	GE	VR	RI	NL	PA	MD	H	SE	VH	N	LI	YD	IM	ND	KQ	RD	YE	EE	KLET	DF	SF	
...	MD	IT	EL	LA	FA	SV	KN	AS	DL	HL	SAG	I	PP	MIR	VD	GE	VR	RI	NL	PA	LE	HK	DV	HR	LV	YD	IM	ND	KQ	RD	YE	EE	KLET	DF	SF		
...	MD	IT	EL	LA	FA	SV	KN	AS	DL	HL	SAG	I	PP	MIR	VD	GE	VR	RI	NL	PA	LE	HK	DV	HR	LV	YD	IM	ND	KQ	RD	YE	EE	KLET	DF	SF		
...	MD	IT	EL	LA	FA	SV	KN	AS	DL	HL	SAG	I	PP	MIR	VD	GE	VR	RI	NL	PA	LE	HK	DV	HR	LV	YD	IM	ND	KQ	RD	YE	EE	KLET				

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Sequence	Score
D..SGRFRVSAFFQRELPGAVIRRIETRIPTFEELKLPVLQNLAIAKRGLVLVVGATGSGKSTTMAAMTGYRNQHRTGH	152
RG.IGRFRVSAFYQRNLAGMVLRRRIETINIPTIEDLKLPDVLKLLALTKRGLVLFVGGATGTGKSTSLAAMIGYRNKNSSGH	154
REKNERFRVSAFQQRDMPCGMVIRRIETIKIPSPDDLHLPPILKELAMSKRGITIFSGATGTGKSTSLASMIQHRNHQSKGH	155
.GDKARFRVNAFMQRGNVGVMLRIPTTVRTIAEMGLPQTVIDIANAPRGLVLVTGPTGSGKSTTLASMDIHNTTKLKLH	158
RDNDARFRVNAFFHNRGYGAFLRRLENTIPTLDQFGAPRLTIKEVQAQKGGILVTGPTGSGKSTTLAALVNEINHKKDGH	155
.PNVARFRVNAFNTRGRPAAVFRTIPSTVLSLEELKAPSIQFKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAH	154
.PNVARFRVNAFNIGRPAAVFRTIPSTVLSLEELKAPSIQFKIAESPRGMVLVTGPTGSGKSTTLAAMINYINETQPAH	154
.PNVGRFRVNAFHQARGCSAVFRTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKH	154
.PNVGRFRVNAFHQARGCSAVFRTIPTVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKH	154
.ANLARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEH	154
.ANLARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYINSSRYEH	154
.PGVARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGMGEVFRKITDVP RGLVLVTGPTGSGKSTTLAAMDYINNTKYHH	154
.PGVARFRVNAFNQNRGAGAVFRTIPSKVLTMEELGMGEVFRKVS DVP RGLVLVTGPTGSGKSTTLAAMDYINNTKYHH	154
.PNLARFRVNVFNQNRGAGAVFRTIPSKVLTLEELGLGKIFRDI CDYP RGLVLVTGPTGSGKSTTLAAMDYINNHRYPH	154
.PNVARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYP RGLVLVTGPTGSGKSTTLAAMDYINENRYPH	154
.PNVARFRVNAFNQNRGAGAVFRTIPSKVLTMEDLGLGQIFKDI CDYP RGLVLVTGPTGSGKSTTLAAMDYINENRYPH	154

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consensus

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consensus

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logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	QTFDQALYQLVVDKISEQDALHSADLANDRLMLKTK.RGDDY...GSGSLQNVKI.....DME.....	368
NTDB id 1203 PSJM300 01605 AFN76401.1	QTFDQALYNLYVQGEITYEDALLHADSSNDLRLMIKLG.SETDGEHLTSVS.QGLTL.....EMSDDDPGRSFR...	381
NTDB id 1019 ACIAD RS04205 WP 004922051.1	QTFDQALFDLYDHQHISYADALKHADSPNNLRLQIKLS.EEANKPLDNRRERMSEMER.....KMTFDGQRRNLK...	383
NTDB id 1307 DR RS10055 WP 010888596.1	VTMDAYLAGLFRHLLITYDKGLERAIDPKEFARLANDASAGLGG.....ASMTPAAPPVPAYNASASSSSTGRGGDFGRGA	393
NTDB id 47242 FNFX1 RS08300 WP 014550254.1	ATMEQSTIENLLKAGTITPEEAACYIVVR.....	342
NTDB id 1116 NGFG RS10615 WP 003690200.1	QTMDDQLQSLVRQGLIAPEAAARRRAQNSESMSF.....	347
NTDB id 1086 NMV RS00245 WP 002218487.1	QTMDDQLQSLVRQGLIAPEVARRRAQNSESMSF.....	347
NTDB id 1185 GTF74 RS11940 WP 000350195.1	QTMEQNAKQLIARGVVDQEVQSKIELDLKAF.....	345
NTDB id 1176 A1552VC RS01160 WP 000350195.1	QTMEQNAKQLIARGVVDQEVQSKIELDLKAF.....	345
NTDB id 1283 ACE17W RS02630 WP 010947729.1	QTLDDQHLTELVNKNIISKHTAHEAALNK.SLF.....	344
NTDB id 1259 GC085 RS10305 WP 010947729.1	QTLDDQHLTELVNKNIISKHTAHEAALNK.SLF.....	344
NTDB id 1202 PSJM300 01600 AFN76400.1	QTLDDSLKGLLAKGLISRDSAKEKAKQP.ENF.....	344
NTDB id 1194 PAKAF RS01995 WP 003084552.1	QTLDDMLKGLVAKGLISRRENAKEKAKIP.ENF.....	344
NTDB id 1020 ACIAD RS04210 WP 011182164.1	TTLDDQLKQLLAKGIINLPTARAVAKSP.ESF.....	344
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TTLDDQLKGLVSRGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1060 ABD1 RS04380 WP 000355489.1	TTLDDQLKGLVARGVISPQTARTAAKQP.ESFL.....	345
NTDB id 1040 HON27 RS13360 WP 000355489.1	TTLDDQLKGLVARGVISPQTARTAAKQP.ESFL.....	345
consensus	*!*** * !* ***** * *	

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1		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	AAPATPAAPAAGRSEPGRAGGFGR	418
NTDB id 47242 FNFX1 RS08300 WP 014550254.1		342
NTDB id 1116 NGFG RS10615 WP 003690200.1		347
NTDB id 1086 NMV RS00245 WP 002218487.1		347
NTDB id 1185 GTF74 RS11940 WP 000350195.1		345
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NTDB id 1040 HON27 RS13360 WP 000355489.1		345
consensus		

- [X] non conserved
- [X] similar
- [X] ≥ 50% conserved