

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	MSALTTSPKLTGFRRVVEKLYSATIMQALAKAKQSvYLIENYLSPSTLAETISSEFGEPYLDLVYDAIT	72
NTDB id 1251 GC085 RS07725 WP 011946523.1	MLINLVAILRQAELISATQEQAIVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSRYDYANL	80
NTDB id 126159 AMD12 RS16880 WP 005915819.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYIVKNKILSAEQIALTAQAQNFVPMPLDINCIDVGTI	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPYPLIDNFSISPLTTAEIISLEFGEPLLDLGVFDPALF	80
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRRLVEEKHVSAAATMQTALDAAKRAKQDTPVAYLIEEVHLSPSLLAETISAEFAEPYFDLDVYDTSQI	80
consensus	* *	

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	PKDLYDEKLTIRYBILPLYSRGILVYATSNPTNLEAIDEIRFNTKLVEPLIVEHKL EALLSSLEFEESSENFENE	152
NTDB id 1251 GC085 RS07725 WP 011946523.1	CQQLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEEEFRFATGLQVELALADHRALQAATIRRLYGRSIQGAANQGKE	160
NTDB id 126159 AMD12 RS16880 WP 005915819.1	PVNLYVNEKLIKPHAMVPLFSRGTNLYLATDDPSKQASLIKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	LKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSKCLKVEPTIVEHDKLERLLSEHFVEETHFNFDTE..	158
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSKLLVEPVIVEHHKLEKVLGQHF AEESSFDFNDE..	158
consensus	* *	

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	ISQD...ELANLVKVSDDDELQSI EDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGILVETQQPASHL	230
NTDB id 1251 GC085 RS07725 WP 011946523.1	DSGDLEGLEISAD.DEDQDIDTATSVTD DAPIVKFVNKILLDAIRQGASDIHFEPYEREYRIRYRQDGLILHEVATPPASL	239
NTDB id 126159 AMD12 RS16880 WP 005915819.1	ELD...LDVEVDPHTTDDDEDKCLKDEAPIVKYINKLLIDAIRMSASDLHFEPYEKSYRVRVYRVDGVLRLIATPPLQL	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	..EFD...LDVNLDGPTAQEDEEEAPQGDEAPIVKYINKLLIDAIRMGASDLHFEPYEKSYRVRVYRVDGVLRLQIANPPLQL	234
NTDB id 1058 ABD1 RS01615 WP 001274986.1	consensus	* *

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	SRRLAARIKILSKLIDIAERRLPQDGRIKLRISRDTAIDMRVSTLPTLWGEKIVLRLLDSSAANLIDDKLGYNPQQKQLYL	310
NTDB id 1251 GC085 RS07725 WP 011946523.1	SSRITARIKVMNSLDISERRIPQDGGFKMKISKSRaidFRVSTCPTSAGEKVVMRVLDSGAAKLGIEALGFNPVQRTNFL	319
NTDB id 126159 AMD12 RS16880 WP 005915819.1	ATRLASRLKVMSQMDISEKRVPPQDGRIKLRKMSKSKTIDFRVNSLPTLFGEKIVLRILDPASAMLGIDALGYEPEQKALFM	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ANRLASRLKVMSQMDISEKRVPPQDGRIKLRKLSKSKAIDFRVNSLPTLFGEKIVLRILDPSSAMLGIDALGYEEDQKALFM	314
NTDB id 1058 ABD1 RS01615 WP 001274986.1	consensus	* *

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	NALKRPQGMILMTGPTGSGKTVSLYTGLNRLNTESSNISTAEDPVEINLGINQVNVNPKVGLTFAAALRSFLRQDPDI	390
NTDB id 1251 GC085 RS07725 WP 011946523.1	KAIQRPQGMILVTGPTGSGKTVTLTYALNRLNTEIEVNISTAEDPVEIKVPGINQVNVNPKAGLTFSGALRSFLRQDPDI	399
NTDB id 126159 AMD12 RS16880 WP 005915819.1	EALNKPQGMILLITGPTGSGKTVSLYTGLNRLNTEHANISTAEDPVEINLEGVNQVNVNPKVGLTFAAALRSFLRQDPDI	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EALDKPQGMILLITGPTGSGKTVSLYTGLNRLNTESSNISTAEDPVEINLEGINQVNVNPKVGLTFAAALKSFLRQDPDI	394
NTDB id 1058 ABD1 RS01615 WP 001274986.1	consensus	* *

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	MVGEIRDLETAETIAKAAQTGHLV	STLHTNSAAET	IRLNMGYPSFNIA	TSVNL	YIAQRLARRL	C	SQCK	IP	RYDPNQ		467
NTDB id 1251 GC085 RS07725 WP 011946523.1	MVGEIRDLETAETIAKAAQTGHLV	STLHTNSAAET	IRLNMGV	EPFNLASSL	SL	IAQRLARRL	CKHCK	IAVRP	...	S	479
NTDB id 126159 AMD12 RS16880 WP 005915819.1	MVGEIRDLETAETIAKAAQTGHLV	STLHTNSAAET	LNRLVNMGI	PTFN	IASSVTL	IAQRLARRL	CK	AVR	DDFTNQ		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MVGEIRDLETAETIAKAAQTGHLV	STLHTNSAAET	TLRLNMGV	ASFNI	ATSVNL	VIAQRLARRL	CSQCK	RPI	QVPER		473
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MVGEIRDLETAETIAKAAQTGHLV	STLHTNSAAET	TLRLNMGV	PSFNI	ATSVNL	VIAQRLARRL	CSQCK	IPA	DIPKQ		473
consensus	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	ALLQSQFAFQPN	ET	...	LYEANAAGCN	ECTGGYS	GRVGIY	EVMAFNT	ELAEAIMQR	ASIHQ	IERLAKANG	MQTLQES	SGI	543
NTDB id 1251 GC085 RS07725 WP 011946523.1	GLIE	...	LGFK	EADLV	...	NLKL	YKAVGCE	QCTSGYR	GRVGLFEVLP	MTKELGQL	LIMSGGNSLD	ILKLAQSE	555
NTDB id 126159 AMD12 RS16880 WP 005915819.1	GLIE	...	LGFK	EADLV	...	NLKL	YKAVGCE	QCTSGYR	GRVGLFEVLP	MTKELGQL	LIMSGGNSLD	ILKLAQSE	20
NTDB id 1018 ACIAD RS01685 WP 004920473.1	SLLE	...	MGFTPE	DLAQPEFQ	IFEP	VGCHD	CREGYK	GRVGIY	EVMMK	ITPEISK	IIMEDGNALE	IAATAETL	551
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SLLE	...	MGFTPE	DLAHPDFR	VFQP	VGCL	ECREGYK	GRVGIY	EVMMK	VTPEISK	IIMEDGNALE	IAAA	551
consensus	***	***	***	***	***	***	***	***	***	***	***	***	

logo

NTDB id 1168 A1552VC RS11070 WP 000957200.1	EKLREG	GITSFAELQ	RVLYF	562
NTDB id 1251 GC085 RS07725 WP 011946523.1	EKVKEG	ITITIEE	VNRVTVD	574
NTDB id 126159 AMD12 RS16880 WP 005915819.1	MKAAH	GVTS	LA	39
NTDB id 1018 ACIAD RS01685 WP 004920473.1	KKVMQ	GVTS	LQ	570
NTDB id 1058 ABD1 RS01615 WP 001274986.1	KKVMQ	GVTS	LQ	570
consensus	!*	!***	!***!	*

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