

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	MELNQYLDGMLTHKASDLYITVGA	PILYRVDGELRAQGEAL.SVADVTALLHAMDDARQAEFKQ	TREANFAVVRD	75							
NTDB id 1203 PSJM300 01605 AFN76401.1	MEFEKLLRLMVEKGGSDLFITAGV	PPSMKVNGKILPVNKT	TPMSPEMTRET	76							
NTDB id 1019 ACIAD RS04205 WP 004922051.1	MDFNDLLNLMAKHKASDLFITAGV	EPSLKINGEITPVSKTKLDGDMIAQL	IDSITTQKQRQEF	76							
NTDB id 323878 EBB51 RS08000 WP 123053986.1	...MISLRELLNITINQNASDLHLTVGV	PPVIRVDGQLLYISNEKLNPD	TEAYAKEILDNDLYGDYMKIGEID	77							
NTDB id 1307 DR RS10055 WP 010888596.1	MTSGIDITDILRLAADKGASDITILAA	GLPPQFKLSG	YDAQGFEL	80							
NTDB id 1086 NMV RS00245 WP 002218487.1	MQITDLLAFGAKNKASDLHLSSG	ISPMIRVHGD	MRRINLPEMSAE	76							
NTDB id 1116 NGFG RS10615 WP 003690200.1	MQITDLLAFGAKNKASDLHLSSG	ISPMIRVHGD	MRRINLPEMSAE	76							
NTDB id 1185 GTF74 RS11940 WP 000350195.1	MDIAELLEFSVKHNASDLHLSAGV	PPMVRIDG	EVRLKGVPAFT	76							
NTDB id 1176 A1552VC RS01160 WP 000350195.1	MDIAELLEFSVKHNASDLHLSAGV	PPMVRIDG	EVRLKGVPAFT	76							
NTDB id 1283 ACE17W RS02630 WP 010947729.1	MDIAELLAFSVKKNSSDLHISAGM	PPMIRVDG	DLRKNINLP	76							
NTDB id 1259 GC085 RS10305 WP 010947729.1	MDIAELLAFSVKKNSSDLHISAGM	PPMIRVDG	DLRKNINLP	76							
NTDB id 1202 PSJM300 01600 AFN76400.1	MDITELLAFSAKQGGASDLHLSSG	LPPMIRVDG	DVRRINLP	76							
NTDB id 1194 PAKAF RS01995 WP 003084552.1	MDITELLAFSAKQGGASDLHLSSG	LPPMIRVDG	DVRRINLP	76							
NTDB id 1020 ACIAD RS04210 WP 01182164.1	MDITELLAFSVQNRASDLHLSAGI	PPMIRVDG	EVRRINLP	76							
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	MDITELLAFSVKNGASDLHLSAGM	PPMIRVDG	EVRRINLP	76							
NTDB id 1060 ABD1 RS04380 WP 000355489.1	MDITELLAFSVKNGASDLHLSAGM	PPMIRVDG	EVRRINLP	76							
NTDB id 1040 HON27 RS13360 WP 000355489.1	MDITELLAFSVKNGASDLHLSAGM	PPMIRVDG	EVRRINLP	76							
consensus	***	***!*****	*!*****!*****	*****	*	*	*	*****	*****	!!	*****

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	..	SCRFRVSAFFQRELP	GAVIRRIETRIPTFEELKLPEVLQNLAI	AKRGLVLVVGATGSGKSTTMAAMTGYRNQHR	TGHI	153				
NTDB id 1203 PSJM300 01605 AFN76401.1	G.	IGRFRVSAFYQRNL	LAGMVLRR	IETNIPTIEDLKL	PDVLKKLALTKRGLVLFVGATGTGKSTSLAAMIGYRNKNSSGHI	155				
NTDB id 1019 ACIAD RS04205 WP 004922051.1	EKNERFRVSAFYQRDMPCGMVIRRIETKIPSPDDL	HLP	PILKELAMSKRG	IIIFS	GATGTGKSTSLASMIQHRNQHSGKHI	156				
NTDB id 323878 EBB51 RS08000 WP 123053986.1	G.	VGRFRVNL	FKQRGSA	AIIRA	VGLKVPS	INELKVSTVIKDLT	LSKRGLILVTGPTGSGKSTTLAAMINEINITRAAHI	156		
NTDB id 1307 DR RS10055 WP 010888596.1	D.	KARFRVNAFMQR	GNVGGVMRLIPT	TVRTIAEMGLPQT	VIDIANAPRGLVLVTGPTGSGKSTTLAS	MIDHINTTKKLHI	159			
NTDB id 1086 NMV RS00245 WP 002218487.1	N.	VARFRVNAFNIGRGPAAVFRTIP	STVLSLEELKAPSIFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYNINETQPAHI	155						
NTDB id 1116 NGFG RS10615 WP 003690200.1	N.	VARFRVNAFNIGRGPAAVFRTIP	STVLSLEELKAPSIFQKIAESPRGMVLVTGPTGSGKSTTLAAMINYNINETQPAHI	155						
NTDB id 1185 GTF74 RS11940 WP 000350195.1	N.	VGRFRVNAFHQA	RGC	SAVFRTIPT	TVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155				
NTDB id 1176 A1552VC RS01160 WP 000350195.1	N.	VGRFRVNAFHQA	RGC	SAVFRTIPT	TVIPTLEQLDAPEIFSKIANYEKGLVLVTGPTGSGKSTTLAAMVNYVNAHNNKHI	155				
NTDB id 1283 ACE17W RS02630 WP 010947729.1	N.	LARFRVNAFNQSRGAAAVFRTIP	SEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAMVIDYINSSRYEHI	155						
NTDB id 1259 GC085 RS10305 WP 010947729.1	N.	LARFRVNAFNQSRGAAAVFRTIP	SEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAMVIDYINSSRYEHI	155						
NTDB id 1202 PSJM300 01600 AFN76400.1	G.	VARFRVNAFNQNRGAGAVFRTIP	SKVLTMEDLGMGEVFRKITDVP	RGLVLVTGPTGSGKSTTLAAMLDYLNNTKYHHI	155					
NTDB id 1194 PAKAF RS01995 WP 003084552.1	G.	VARFRVNAFNQNRGAGAVFRTIP	SKVLTMEDLGMGEVFRKVS	DVPRGLVLVTGPTGSGKSTTLAAMLDYLNNTKYHHI	155					
NTDB id 1020 ACIAD RS04210 WP 01182164.1	N.	LARFRVNVFNQNRGAGAVFRTIP	SKVLTLEELGLGKIFRD	ICDYP	RGLVLVTGPTGSGKSTTLAAMLDYINNHRDHI	155				
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	N.	VARFRVNAFNQNRGAGAVFRTIP	SKVLTMEDLGLGQIFKD	ICDYP	RGLVLVTGPTGSGKSTTLAAMLDYINENRYDHI	155				
NTDB id 1060 ABD1 RS04380 WP 000355489.1	N.	VARFRVNAFNQNRGAGAVFRTIP	SKVLTMEDLGLGQIFKD	ICDYP	RGLVLVTGPTGSGKSTTLAAMLDYINENRYDHI	155				
NTDB id 1040 HON27 RS13360 WP 000355489.1	N.	VARFRVNAFNQNRGAGAVFRTIP	SKVLTMEDLGLGQIFKD	ICDYP	RGLVLVTGPTGSGKSTTLAAMLDYINENRYDHI	155				
consensus	*	***!!!!!!*	*****!*****	*****	***	***	*****	*****	!!	*****

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	LTIVEDPIEFVHEHKKRCIVTQREVGLDTESYEVALKNSLRQAPDMILIGEIRSRRETMEYAMTFAETGHL ^{CM} ATLHANNANQ	233
NTDB id 1203 PSJM300 01605 AFN76401.1	ISIEDPIEFITHQHQCIVTQREVGIDTDSFEVALKNTLRQAPDVILIGEVRTRETMDHAVAF ^{AF} ETGHLCLATLHANNANQ	235
NTDB id 1019 ACIAD RS04205 WP 004922051.1	ITIEDPIEFIEHAGCIITQREVGIDTDSFEIALKNTLRQAPDVILIGEIRSRREVMDYALAF ^{AF} ETGHLVFA ^{AT} LHANNANQ	236
NTDB id 323878 EBB51 RS08000 WP 123053986.1	ITLEDPIEY ^{YL} LHKHNKSIINQREIG RD TRSYANALRAVLREDPDVILIGEMRDLETISIALTAAETGHLVFS ^{TL} LHTIGAAK	236
NTDB id 1307 DR RS10055 WP 010888596.1	LTIEDPIEFMHPNKASIIINQREVGS ^{DT} LSFDDALRAALRQAPDVILVGEMRDYETIKA ^{AV} TAAETGHLVMGTLHTNSAPE	239
NTDB id 1086 NMV RS00245 WP 002218487.1	LTIEDPIEFVHQSKKSLINQRELHQHTLSFANALRSALREDPDVILVGEMRDPETIGLALTA ^{AA} ETGHLVFGTLHTTGA ^{AA} K	235
NTDB id 1116 NGFG RS10615 WP 003690200.1	LTIEDPIEFVHQSKKSLINQRELHQHTLSFANALSSALREDPDVILVGEMRDPETIGLALTA ^{AA} ETGHLVFGTLHTTGA ^{AA} K	235
NTDB id 1185 GTF74 RS11940 WP 000350195.1	LTIEDPIEFVHSNNKCLINQREVHRDTHSFKNALRSALREDPDVILVGLERDQETISLALTA ^{AA} ETGHLVFGTLHTSSA ^{AA} K	235
NTDB id 1176 A1552VC RS01160 WP 000350195.1	LTIEDPIEFVHSNNKCLINQREVHRDTHSFKNALRSALREDPDVILVGLERDQETISLALTA ^{AA} ETGHLVFGTLHTSSA ^{AA} K	235
NTDB id 1283 ACE17W RS02630 WP 010947729.1	LTVEDPIEFVHQSKKCLV ^N QREVHK ^{DT} LSFNAALRSALREDPDII ^L VGLERDLETIRLAM ^{TA} AETGHLVFGTLHTNSAT ^K	235
NTDB id 1259 GC085 RS10305 WP 010947729.1	LTVEDPIEFVHQSKKCLV ^N QREVHK ^{DT} LSFNAALRSALREDPDII ^L VGLERDLETIRLAM ^{TA} AETGHLVFGTLHTNSAT ^K	235
NTDB id 1202 PSJM300 01600 AFN76400.1	LTIEDPIEFVHESKKCLV ^N QREVHRD ^{TL} GFSEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
NTDB id 1194 PAKAF RS01995 WP 003084552.1	LTIEDPIEFVHESKKCLV ^N QREVHRD ^{TL} GFSEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
NTDB id 1020 ACIAD RS04210 WP 01182164.1	LTVEDPIEFVHEPKKCLINQREVHRD ^{TL} GFNEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	LTVEDPIEFVHQSKKCLINQREVHRD TH GFNEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
NTDB id 1060 ABD1 RS04380 WP 000355489.1	LTVEDPIEFVHQSKKCLINQREVHRD TH GFNEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
NTDB id 1040 HON27 RS13360 WP 000355489.1	LTVEDPIEFVHQSKKCLINQREVHRD TH GFNEALRSALREDPDII ^L VGEMRDLETIRLALTA ^{AA} ETGHLVFGTLHTTSA ^{AA} K	235
consensus	***!!!!*!* *****!!!!*!* * * !!!!!*!*!*!*!*!*!*!* *!* *!*****!!!!*!*!*!*!*!*!*!* *	

logo

NTDB id 1177 A1552VC RS01165 WP 000422572.1	TIDRIIDVFP ^{AE} EKK ^{WVR} ML ^{SES} L ^Q AVIS ^Q LLKK ^{GG} RVAAH ^E IM ^L ATPAIRN ^L IRE ^K YAQMYS ^I QTGA ^{AA} HGMQ	313
NTDB id 1203 PSJM300 01605 AFN76401.1	ALERTIH ^{LV} PKEQREQFLLDLSLNLKGVIAQQLLR ^{DK} NGKGRHGVFEVLINSPRIADLI ^{RR} GE ^L HELKA TM MARSQEVGMQ	315
NTDB id 1019 ACIAD RS04205 WP 004922051.1	ALDRIINFFPADRQ ^{NQ} VWMDLSLNLKAIV ^{AQ} QLVPTPDGKGRRAVIEVLINTPLAADLIRKGEV ^{HE} LKGLMKRSTDLGMQ	316
NTDB id 323878 EBB51 RS08000 WP 123053986.1	TLERIIHFFDADR ^{HQ} QIFMDLSLNLKAVISQQLIP TH DGQSRRAAVEVLINTPL ^{LS} DYIRQGEIYKIKELMARS ^{GE} LGMQ	316
NTDB id 1307 DR RS10055 WP 010888596.1	TIDRIIDVFP ^{PH} Q ^{QQ} QVRIQLAGVMKGIISQQLIP ^K ADGSGRIA ^{AE} IMVATT ^{AI} KNMIREGKTYQIESSMQTGSKYGM ^L	316
NTDB id 1086 NMV RS00245 WP 002218487.1	SIDRIVDVFP ^{EE} Q ^{QE} QIRVQLANNLVAVMTQQLLP ^{RA} DGQGRVLAYEILLANPAVRALIREGKTFQITSVMQTGA ^{RE} GMV	319
NTDB id 1086 NMV RS00245 WP 002218487.1	TVDRIVDVFPAGEKEMVRSMLSESLTAVISQNLK TH DGNGRVASHEILIANPAVRNLIRENKITQINSVLQTGQASGMQ	315
NTDB id 1116 NGFG RS10615 WP 003690200.1	TVDRIVDVFPAGEKEMVRSMLSESLTAVISQNLK TH DGNGRVASHEILIANPAVRNLIRENKITQINSVLQTGQASGMQ	315
NTDB id 1185 GTF74 RS11940 WP 000350195.1	TIDRIIDVFP ^{GS} DKDMVRSMLSESLRAVIAQKLLK ^R .VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGA ^{AA} HGMQ	314
NTDB id 1176 A1552VC RS01160 WP 000350195.1	TIDRIIDVFP ^{GS} DKDMVRSMLSESLRAVIAQKLLK ^R .VGGGRVACHEIMLATPAIRNLIREDKVAQMYSIIQTGA ^{AA} HGMQ	314
NTDB id 1283 ACE17W RS02630 WP 010947729.1	TINRIIDVFP ^{AE} EKSMVRSMLSESLQAVVAQSLLK ^K .NKGGRVAALEIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGMQ	314
NTDB id 1259 GC085 RS10305 WP 010947729.1	TINRIIDVFP ^{AE} EKSMVRSMLSESLQAVVAQSLLK ^K .NKGGRVAALEIMMCTGAIRNLIREDKIAQMYSIIQTGQAKGMQ	314
NTDB id 1202 PSJM300 01600 AFN76400.1	TIDRVVDVFP ^{AE} EKSMVRSMLSESLQAVISQTL ^{LK} K.VGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGS ^L GMQ	314
NTDB id 1194 PAKAF RS01995 WP 003084552.1	TIDRVVDVFP ^{AE} EKAMVRSMLSESLQSVISQTL ^{LK} K.IGGGRVAAHEIMIGTPAIRNLIREDKVAQMYSIIQTGGS ^L GMQ	314
NTDB id 1020 ACIAD RS04210 WP 01182164.1	TIDRIIDVFP ^{AE} EKDMVRTMLSESLQAVISQTL ^{LK} K.EGGGRVAAHEIMIGIPAIRNLIREDKVAQMYSIIQTGA TH GM ^T	314
NTDB id 1081 FDQ49 RS05335 WP 006581387.1	TIDRV ^I IDVFP ^{AE} EKDMVRAMLSESLQAVISQTL ^{LK} K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGAN ^H GM ^T	314
NTDB id 1060 ABD1 RS04380 WP 000355489.1	TIDRV ^I IDVFP ^{AE} EKDMVRAMLSESLQAVISQTL ^{LK} K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGAN ^H GM ^T	314
NTDB id 1040 HON27 RS13360 WP 000355489.1	TIDRV ^I IDVFP ^{AE} EKDMVRAMLSESLQAVISQTL ^{LK} K.NGGGRVAAHEIMIGIPAIRNLIRENKVAQMYSIIQTGAN ^H GM ^T	314
consensus	***!********** *!***** ***** !*** *****!*****!**********!*! ***** ***** !**	

Protein	Sequence	Score
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	368
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	381
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	383
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	352
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	395
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	347
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	347
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	344
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	344
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	344
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	344
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345
TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	TMDQSLQSLVRRQGLIAPEVARRRAQNSESMSF	345

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 323878	EBB51 RS08000 WP 123053986.1	352
NTDB id 1307	DR RS10055 WP 010888596.1	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
NTDB id 1283	ACE17W RS02630 WP 010947729.1	344
NTDB id 1259	GC085 RS10305 WP 010947729.1	344
NTDB id 1202	PSJM300 01600 AFN76400.1	344
NTDB id 1194	PAKAF RS01995 WP 003084552.1	344
NTDB id 1020	ACIAD RS04210 WP 011182164.1	344
NTDB id 1081	FDQ49 RS05335 WP 006581387.1	345
NTDB id 1060	ABD1 RS04380 WP 000355489.1	345
NTDB id 1040	HON27 RS13360 WP 000355489.1	345
consensus		

- X non conserved
- X similar
- X > 50% conserved