

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 201082 KAB06 RS01815 WP 001274990.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1410 SGL RS13950 WP 010873519.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 201082 KAB06 RS01815 WP 001274990.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1410 SGL RS13950 WP 010873519.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVDPDPSAALLL	0
NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVDPDPSAALLL	240
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 201082 KAB06 RS01815 WP 001274990.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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consensus

[illegible]

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consensus

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MSA	TT	DM	ET	GL	Vo	G	Y	A	Q	AL	Q	V	K	A	G	S	P	E	X	L	T	SG	L	SP	EL	LA	E	T	TS	S	E	FG	P				
SKKSRAVALRNYP	SPFGNK	LVAG	GHV	DAEQ	RQALV	QV	K	T	GRS	LPEL	KAVT	GRE	LSP	EL	LR	QY	KN	Q	LF	E	KV	L	Y	G	V	D	96										
KEA	EVQ	KG	LP	RAK	P	GE	IL	VE	L	G	AR	P	DE	VE	EA	L	Q	K	R	R	G	G	R	L	E	D	LT	V	Q	SG	K	R	PE	AL	QA	97	
.....	ML	T	N	L	V	A	I	L	R	Q	A	E	L	I	S	A	T	Q	E	A	V	T	Q	V	S	A	S	G	T	V	P	E	A	L	E	98	
.....	M	H	S	N	L	S	T	I	L	R	Q	K	G	L	T	F	S	Q	E	E	S	L	I	E	Q	V	K	A	S	G	I	S	M	P	E	A	99
.....	ML	T	N	L	V	A	I	L	R	Q	A	E	L	I	S	A	T	Q	E	A	V	T	Q	V	S	A	S	G	T	V	P	E	A	L	E	100	
.....	MS	V	G	L	L	R	I	L	V	Q	N	V	I	V	E	Q	A	E	H	Y	N	E	S	Q	A	G	K	E	V	I	P	M	L	F	S	101	
.....	MA	L	A	T	E	E	Y	R	L	Q	G	I	L	V	L	E	K	I	D	K	T	A	I	E	L	H	K	L	A	A	A	E	K	I	102		
.....	MS	A	L	H	T	S	P	K	F	T	G	F	R	R	L	V	E	E	K	H	V	S	A	A	T	Q	T	A	D	A	A	K	R	A	K	103	
.....	MS	A	L	H	T	S	P	K	F	T	G	F	R	R	L	V	E	E	K	H	V	S	A	A	T	Q	T	A	D	A	A	K	R	A	K	104	
.....	MS	A	F	T	T	P	P	K	F	S	G	F	I	R	L	V	E	E	G	Y	N	A	Q	N	Q	A	L	E	K	A	K	F	K	Q	I	105	

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

Position	Sequence	Score
1	SVDPEVAP	164
2	YVDPEEDPPDP	463
3	ETDLSRYDYAN	127
4	QPELSQY EYAS	127
5	CTSLNQY EYAS	127
6	ILDRLHYPRHR	126
7	MDINCIDVGT	135
8	YFDLDVYDTSQ	135
9	YFDLDVYDTSQ	135
10	ILDGLGVDPAL	135

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NTDB id 1410 SGL RS13950 WP 010873519.1	QDDFNQLIEQYVAIREEWFAAQEKRDQERALDKLNDLTDIVGSIDMNLG	EDKEDVDNALDSNDANQAPVINLVNKILAKA	244
NTDB id 1028 TT RS08215 WP 011173991.1	EAAITTKLIERFYGKAELSEIAKEF.....	AKKQAEIEVPSPLELDESAAQKFVKQVIREA	518
NTDB id 1168 A1552VC RS11070 WP 000957200.1	HRALQAAIRRLYGRSISQGAANQGK..EI.SQDELANL.....	VKVSDDQLQSTIEDLSQDDSPVSRFINQVLLDA	193
NTDB id 1293 VP RS12240 WP 005479695.1	FRELSTAIRRLYGRSLSHEKSGLK..EI.NQEELASL.....	VDVGADEIDNIEDLSQDESVPVSRYINQILLDA	193
NTDB id 1401 DSB67 RS12665 WP 010643259.1	FRELTAAIRRLYGRSLGQEKSGLK..EI.NQDELAGL.....	VDIGEDEIENIEDLSQDESVPVSRYINQILLDA	193
NTDB id 1110 NGFG RS09235 WP 003689817.1	DDQLAGLLDWVGSFSTSL..LQEL.....	GEG.....QEEEEHSHTLYIDNEEAEDGPVPRFIHKHTLSDA	183
NTDB id 1251 GC085 RS07725 WP 011946523.1	TDKLSALIDNLLTAKESQGLSEYVEDSG.DLEGLEIS.....	AD.DEDQDIDTATSVTDDAPIVKFVNKILLDA	202
NTDB id 201082 KAB06 RS01815 WP 001274990.1	HHKLEKVLGQHFEESSFDFNDE...EF.D...LDVN.....	LDGPTTQEDEEEAPQGDEAPIVKYINKLLIDA	197
NTDB id 1058 ABD1 RS01615 WP 001274986.1	HHKLEKVLGQHFEESSFDFNDE...EF.D...LDVN.....	LDGPTAQEDEEEAPQGDEAPIVKYINKLLIDA	197
NTDB id 1018 ACIAD RS01685 WP 004920473.1	HDKLERLLSEHFVEETHFNFDTE...EL.D...LDVE.....	VDPHTTDDDDDEDKDKLDEAPIVKYINKLLIDA	197
consensus	* ** **** * *	** ***** *	*****!!!!!!

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NTDB id 1410 SGL RS13950 WP 010873519.1	LQEGTSDIHVEPQEETLRIRFRKDGVLNQAFDPLPRKITPAVVARFKIMADMDIAERRSPQDGKIRRIYQ..GRKVDFRV	322
NTDB id 1028 TT RS08215 WP 011173991.1	FLQDASDIHIEPRQNDVQVRLRIDGALRPYSTL.PKGALNAVISVVKIMGGLNIAEKRLPQDGRVRYR..EGAIDVDLRL	595
NTDB id 1168 A1552VC RS11070 WP 000957200.1	VRKGASDIHFEPYENQYRIRLRCDGILVETQQP.ASHLSRRLAARIKILSKLDIAERRLPQDGRIKLRLSR.DTAIDMRV	271
NTDB id 1293 VP RS12240 WP 005479695.1	VRKGASDIHFEPYEKMYRVRLRCDGILVETQQP.PNHLSRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRV	271
NTDB id 1401 DSB67 RS12665 WP 010643259.1	VRKGASDIHFEPYENMYRVRLRCDGILVETQQP.PSHLSRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRV	271
NTDB id 1110 NGFG RS09235 WP 003689817.1	LRSGASDIHFEFYEHNNARIRFRVDGQLREVVQP.PIAVRGQLASRIKVM SRLDISEKRIPQDGRMQLTFQKGGKPVDFRV	262
NTDB id 1251 GC085 RS07725 WP 011946523.1	IRQGASDIHFEPYEREYRIRYRQDGLHEVATP.PASLSRITARIKVM SNLDISERRIPQDGGFKMKISK.SRAIDFRV	280
NTDB id 201082 KAB06 RS01815 WP 001274990.1	IRMGASDLHFEPYEKSYRVRYRVDGMLRQIANP.PLQLANRLASRLKVM SQMDISEKRVPPQDGRIKLKLSK.SKAIDFRV	275
NTDB id 1058 ABD1 RS01615 WP 001274986.1	IRMGASDLHFEPYEKSYRVRYRVDGVLRLQIANP.PLQLANRLASRLKVM SQMDISEKRVPPQDGRIKLKLSK.SKAIDFRV	275
NTDB id 1018 ACIAD RS01685 WP 004920473.1	IRMSASDLHFEPYEKSYRVRYRVDGVLRLIATP.PLQLATRLASRLKVM SQMDISEKRVPPQDGRIKLKMSK.SKIDFRV	275
consensus	** **!!*!*!*!* * * * * *	* *

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NTDB id 1410 SGL RS13950 WP 010873519.1	NTLPSRYGEKVCLRILDNSATQLGLDFLITNPETLQTVRELAARPYGLMLVTGPTGSGKSTTLYSVLAERNSPEVNINTA	402
NTDB id 1028 TT RS08215 WP 011173991.1	STLPTVYGEKAVMRLLKKASDIPEIEDLGFAPGVFERFKEVTSKPYGIFLITGPTGSGKSFTTFSILKRIATPDKNTQTI	675
NTDB id 1168 A1552VC RS11070 WP 000957200.1	STLPTLWGEKIVLRLLDSSAANLDDIDKLGYNPQQKQLYLEALNRKPQGMILMTGPTGSGKTVSLYTGLRILNTSQINISTA	351
NTDB id 1293 VP RS12240 WP 005479695.1	STLPTLFGEKIVLRLLDSSASLDDIDKLGYSSEQKQLYLEALRRPQGMILMTGPTGSGKTVSLYTGLNILNKPEINISTA	351
NTDB id 1401 DSB67 RS12665 WP 010643259.1	STLPTLFGEKIVLRLLDSSAALDDINKLGYSDSQKQLYLDALRRPQGMILMTGPTGSGKTVSLYTGLSILNKPEINISTA	351
NTDB id 1110 NGFG RS09235 WP 003689817.1	STLPTLFGEKIVMRILNSDAASLNIDQLGFEPFQKKLLLEATHRPYGMVLVTGPTGSGKTVSLYTCLNILNTESVNIATA	342
NTDB id 1251 GC085 RS07725 WP 011946523.1	STCPTSAGEKIVMRVLDSGAAKLGIEALGFNPVQRTNFLKAIQRPQGMILVTGPTGSGKTVTLYTALNILNTIEVNISTA	360
NTDB id 201082 KAB06 RS01815 WP 001274990.1	NSLPTLFGEKIVLRILDPSSAMLGIDALGYEEDQKALFMEALDKPQGMILLITGPTGSGKTVSLYTGLNILNTESVNISTA	355
NTDB id 1058 ABD1 RS01615 WP 001274986.1	NSLPTLFGEKIVLRILDPSSAMLGIDALGYEEDQKALFMEALDKPQGMILLITGPTGSGKTVSLYTGLNILNTESVNISTA	355
NTDB id 1018 ACIAD RS01685 WP 004920473.1	NSLPTLFGEKIVLRILDPASAMLGIDALGYEPEKQALFMEALNKPQGMILLITGPTGSGKTVSLYTGLNILNTEHANISTA	355
consensus	***!***!!*!***!*!***** **** *!*** * * * * * *!***!!*!	

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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
NTDB id 1028 TT RS08215 WP 011173991.1		889
NTDB id 1168 A1552VC RS11070 WP 000957200.1		562
NTDB id 1293 VP RS12240 WP 005479695.1		561
NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 201082 KAB06 RS01815 WP 001274990.1		570
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved