

logo

NTDB id 1028 TT RS08215 WP 011173991.1	MSXLSIGDRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQG YLGDN DLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 149800 IY0 RS23865 WP 017684778.1		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 1028 TT RS08215 WP 011173991.1	RLTPEERKELRPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEYPSPGK	158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPALE..GDLRLVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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
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consensus

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NTDB id 1028	TT RS08215 WP 011173991.1	AELSEIAKEF.....AKKQAEEEV..PSPLELDESAAQKFVKQVIREAFLQDASDIHIEPRQNDVQVRLRIDGA	544
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NTDB id 1110	NGFG RS09235 WP 003689817.1	STSLQLQELGEGQEE.....EESHTLYIDNEEAEDGPVPRFIHKHTLSDALRSGASDIHFEFYEHNARIRFRVDGQ	209
NTDB id 1168	A1552VC RS11070 WP 000957200.1	SIQGAANQGKEISQDELA..NLVKVSDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGI	219
NTDB id 1293	VP RS12240 WP 005479695.1	SLSHEKSGLKEINQEELA..SLVDVGADEIDNIEDLSQDESPVSRYINQILDAVRKGASDIHFEPYEKMYRVRLRCDGI	219
NTDB id 1401	DSB67 RS12665 WP 010643259.1	SLGQEKSGLKEINQDELA..GLVDIGEDEIENIEDLSQDESPVSRYINQILDAVRKGASDIHFEPYENMYRVRLRCDGI	219
NTDB id 1251	GC085 RS07725 WP 011946523.1	KESQGLSEYV.EDSGDLEGLEISADDEDDIDTATSVTDDAPIVKFVNKILLDAIRQGASDIHFEPYEREYRIRYRQDGI	228
NTDB id 149800	IYO RS23865 WP 017684778.1	ESGLGE.LAD.ID....LGLDIEPASDKETSLANQSDADAPVVRVFNKMLMDAIRLGSSDLHFEPYEKIFRVRLRTDGI	219
NTDB id 1058	ABD1 RS01615 WP 001274986.1	ESSFDNFDEE.FD....LDVNLDGPTAQE.DEEEAPQGDEAPIVKYINKLLIDAIRMGASDLHFEPYEKSYRVRYRVDGV	223
NTDB id 1018	ACIAD RS01685 WP 004920473.1	ETHFNFDTEE.LD....LDVEVDPHTTDD.DDEDKCLKDEAPIVKYINKLLIDAIRMSASDLHFEPYEKSYRVRYRVDGV	223
consensus		*****!*** **!*!***!*** **!*!***!***	

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NTDB id 1028	TT RS08215 WP 011173991.1	LRPYSTLPKGALNAVISVVKIMGGNLIAEKRLPQDGRVRY..REGAIDVDLRLSTLPTVYGEKAVMRLKKASDIPEIED	622
NTDB id 1306	DR RS10060 WP 027479822.1	LREQNSFPKGAAQQTIMARLKIMGHLDIAERRVPQDGRVRF..KKGSIDLDLRLSTLPTVYGEKAVMRLQKASNIPLEIQ	619
NTDB id 1110	NGFG RS09235 WP 003689817.1	LREVVPPIAVRGQLASRIKVMRSLDISEKRIPQDGRMQLTFQKGGKPVDFRVSTLPTLFGEKVVMRILNSDAASLNDIQ	289
NTDB id 1168	A1552VC RS11070 WP 000957200.1	LVETQQPASHLSRRLAARIKILSKLDIAERRLPQDGRIKRLRSR.DTAIDMRVSTLPTLWGEKIVLRLLDSSAANLDIDK	298
NTDB id 1293	VP RS12240 WP 005479695.1	LIETQQPPNHLRSRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRVSTLPTLFGEKIVLRLLDSSASLDIDK	298
NTDB id 1401	DSB67 RS12665 WP 010643259.1	LIETQQPPSHLSRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.DTAIDMRVSTLPTLFGEKIVLRLLDSSAALDINK	298
NTDB id 1251	GC085 RS07725 WP 011946523.1	LHEVATPPASLSSRITARIKVMSNLDISERRIPQDGGFKMKISK.SRAIDFRVSTCPTSAGEKVVMRVLDSGAAKLGIEA	307
NTDB id 149800	IYO RS23865 WP 017684778.1	LHELARPPIHLANRIAARLKVMASLDISERRKPDGRVKLRVSK.NKAIDFRMNTLPTLWGEKIVMRILDP TSAQM GIDA	298
NTDB id 1058	ABD1 RS01615 WP 001274986.1	LRQIANPPLQLANRLASRLKVMSQMDISEKRVPPQDGRIKLKLKSK.SK AIDFRVNSLPTLFGEKLVLRILDPSAAMLGIDA	302
NTDB id 1018	ACIAD RS01685 WP 004920473.1	LRLIATPPLQLATRLASRLKVMSQMDISEKRVPPQDGRIKLKMSK.SKTIDFRVNSLPTLFGEKIVLRILDPA SAMLGIDA	302
consensus		!*** ** * *****!*** **! !*!***** *****!*****!*****!*****!*****	

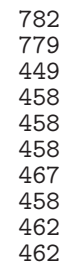
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NTDB id 1028	TT RS08215 WP 011173991.1	LGFAFGVFERFKEVISKPYGIFLITGPTGSGKSFTTFSILKRIATPDKNQTIEDPVEYEIPGINQTQVNPQAGLTFARA	702
NTDB id 1306	DR RS10060 WP 027479822.1	LGfSEYNYARYTEIIERPNIGIFLVTGPTGSGKSFTCFSTLKRIAKPEKNTTTIEDPIEYEVPGIVQSQVNNSTGMTFARA	699
NTDB id 1110	NGFG RS09235 WP 003689817.1	LGFEFPQKKLLLEAIHRPYGMVLVTGPTGSGKTVSLYTCLNILNTESVNIATAEDPAEINLPGINQVNVNDKQGLTFAAA	369
NTDB id 1168	A1552VC RS11070 WP 000957200.1	LGYNPQQKQLYLNALKRPQGMILMTGPTGSGKTVSLYTGLRILNTSQINISTAEDPVEINLSGINQVQVQPKIGFGFAEA	378
NTDB id 1293	VP RS12240 WP 005479695.1	LGyseQQKQLYLEALRRPQGMILMTGPTGSGKTVSLYTGLNILNKPEINISTAEDPVEINLSGINQVQVQPKIGFGFAEA	378
NTDB id 1401	DSB67 RS12665 WP 010643259.1	LGYSDSQKQLYLDALRRPQGMILMTGPTGSGKTVSLYTGLSILNKPEINISTAEDPVEIYLPGINQVQVQPKIGFGFAEA	378
NTDB id 1251	GC085 RS07725 WP 011946523.1	LGfNPVQRtNfLkAIQRpQGMILVTGPTGSGKTVLYTALNlilNTIEVNIStaEDPVEIKVPGINQVNIINPKAGLTFSGA	387
NTDB id 149800	IYO RS23865 WP 017684778.1	LGyePEQKALYMEALKQPQGMILVTGPTGSGKTVSlyTGLNlilNTIEVNIStaEDPVEINLEGINQVNVNPKGLDFsQA	378
NTDB id 1058	ABD1 RS01615 WP 001274986.1	LGyeEDQKALFMEALDKPQGMILLITGPTGSGKTVSlyTGLNlilNTESSNIStaEDPVEINLEGINQVNVNPKVGLTFAAA	382
NTDB id 1018	ACIAD RS01685 WP 004920473.1	LGyePEQKALFMEALNKPQGMILLITGPTGSGKTVSlyTGLNlilNTEHANISTAEDPVEINLEGVNQVNVNPKVGLTFAAA	382
consensus		!!* * ** ***** *!*****!*****!*****!*****!*****!*****!*****!*****!	

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consensus

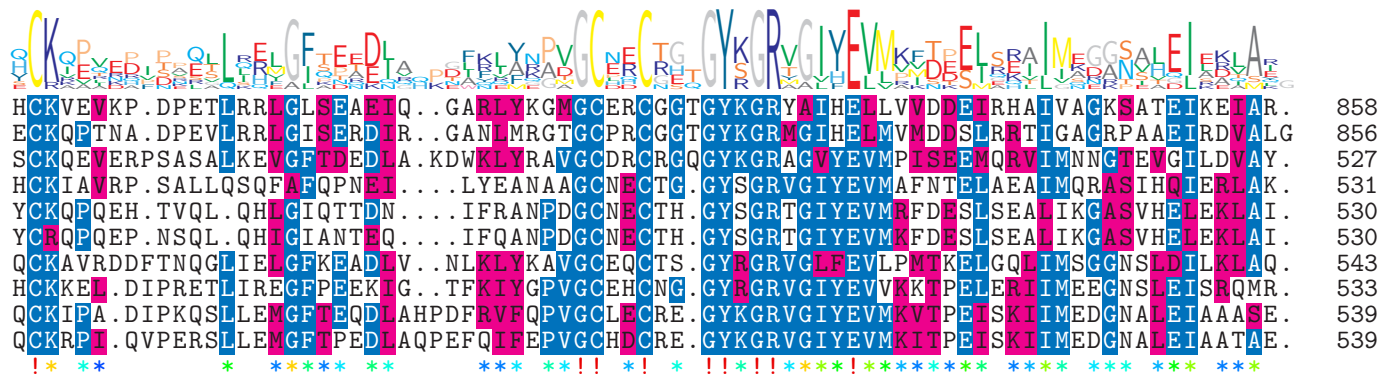
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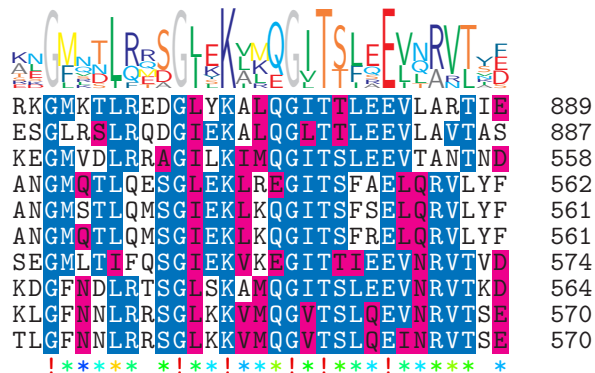
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consensus
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-  non conserved
-  similar
-  >50% conserved