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NTDB id 1306 DR RS10060 WP 027479822.1	MALSIIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	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 1076849 ACJHFE RS07770 WP 011408072.1		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 1306 DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	160
NTDB id 1168 A1552VC RS11070 WP 000957200.1	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	0
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEEGTTFLPNPSGFHPGEEVLGSM	240
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEEGTTFLPNPSGFHPGEEVLGSM	0
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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 1306 DR RS10060 WP 027479822.1	LRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRIGEQLVQEGTLSRDQL	320
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQ.	19
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSLILRQKGLLTFSQ.	19
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQ.	19
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQ.	19
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGITQLLVLEKLLDKTK.	27
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFTGFFRRLVEEKHVSAAAT.	27
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MS..AFTTPPKFTSGFIRRLVEEGYVNAQN.	27
consensus	*** *!***** **	

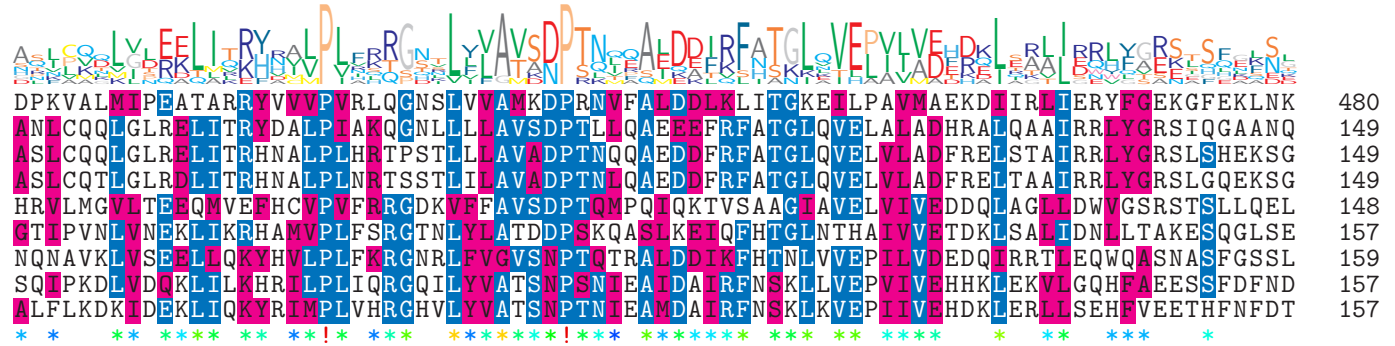
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consensus



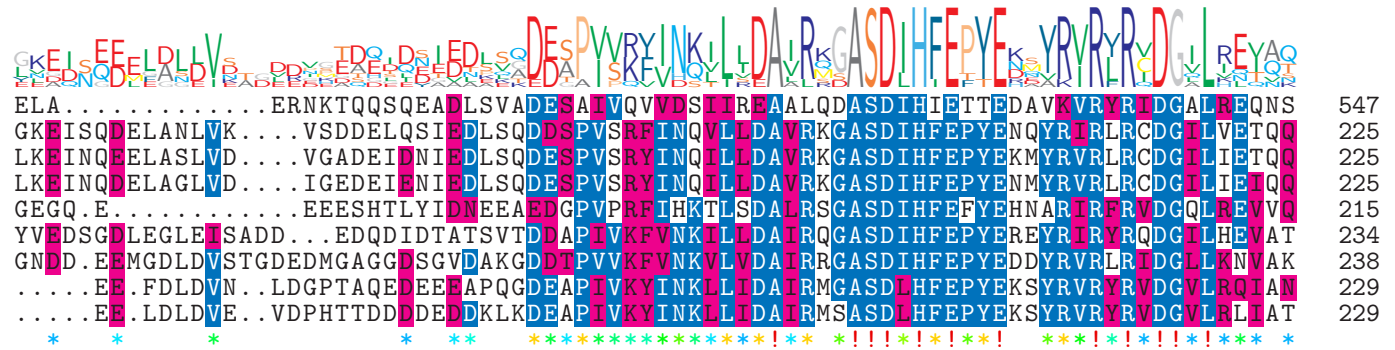
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consensus
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NYARYTEIERPNGIFLVTGPTGSGKSFICFSTLKRILAKPEKNTITIEDPIEYVPGIVQSQVMNSTGMTFARALRAFLLR	705
QKQLYLNALKRPPQGMILMTGPTGSGKTVSLYTLGILRLNTSQINISTAEDPVEINLPGINQVQVQPKIGFGFAEALRSFLR	384
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QRTNFLKAIQRPQGMILVTGPTGSGKTVTLTYALNLTIEVNISTAEDPVEIKVPGINQVNIINPKACLTFSGALRSFLR	393
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QKALFMEALNKPPQGMILITGPTGSGKTVSLYTLGILNLTESVNIATAEDPVEINLPGINQVNVNPKVGLTFAAALRSFLR	388
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QDPDIIMVGEIRDLETAETIAKAAQTGHLVLSLTHTNAAETLRLRMGVAFNIASSVLLIAQRLARRLCCKQKRP	785
QDPDIIMVGEIRDLETAETIAKAAQTGHLVLSLTHTNAAETLRLRMGVAFNIASSVLLIAQRLARRLCCKQKIAV	464
QDPDIIMVGEIRDLETAETIAKAAQTGHLVLSLTHTNAAETLRLRMGVAFNIASSVLLIAQRLARRLCCKQKCPY	464
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consensus
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[illegible]

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L	R	S	G	L	K	K	Q	G	T	S	L	E	V	N	R	V	T	D							
Q	R	S	G	L	K	K	Q	G	T	S	L	E	V	N	R	V	T	D							
L	R	Q	D	G	I	E	K	A	L	Q	L	T	T	L	E	V	L	A	V	T	887				
L	R	Q	D	G	L	E	K	I	R	E	G	I	T	S	F	A	L	Q	R	V	L	Y	F		
L	Q	M	S	G	I	E	K	L	K	Q	G	I	T	S	F	S	E	L	Q	R	V	L	Y	F	
L	Q	M	S	G	I	E	K	L	K	Q	G	I	T	S	F	R	E	L	Q	R	V	L	Y	F	
L	R	R	A	G	I	L	K	I	M	Q	G	I	T	S	L	E	V	N	R	V	T	D		558	
I	F	Q	S	G	I	E	K	V	K	E	G	I	T	T	I	E	V	N	R	V	T	D		574	
L	R	Q	S	A	L	M	K	K	A	S	Q	G	V	T	S	L	A	E	I	N	R	V	T	K	D
L	R	R	S	G	L	K	K	V	M	Q	G	V	T	S	L	Q	E	V	N	R	V	T	S	E	
L	R	R	S	G	L	K	K	V	M	Q	G	V	T	S	L	Q	E	I	N	R	V	T	S	E	

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 non conserved
 similar
 $\geq 50\%$ conserved