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NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
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NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		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	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPVPP..P	158
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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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		SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	
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NTDB id 1293	VP RS12240 WP 005479695.1		0
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NTDB id 1251	GCO85 RS07725 WP 011946523.1		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	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRDPIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGLGEQLVQEGTLSR	317
NTDB id 1028	TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
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NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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NTDB id 1410	SGL RS13950 WP 010873519.1	SSSSKKSRRAVALRNYFSPFGNKLIVAGCHVDAEQLRQALVQVVKTKGRSLPEELKAVTGRELSPELLRQYKKNQLFELKVLY	83
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NTDB id 1436	BW25113 RS00530 WP 001025145.1	M	1
NTDB id 1168	A1552VC RS11070 WP 000957200.1	MLTNLVALILRQAEILISATQEQAVVTQVSASGTSVPEALLE..LSIFHAQELTEQ.....LSHIF	57
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLSTVLRLQAGILTFSGEESLLEQVKASGISMPEALLS..SGFFQSHELTEH.....LSSVF	57
NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSGEESLIEQVKASGISMPEALLS..SGFFTSSSELAEH.....LSSIF	57
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMLFS..DGVISPKSALAAL.....IARVF	56
NTDB id 1251	GC085 RS07725 WP 011946523.1	MALATEEYRLQGITQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
NTDB id 1058	ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAET.....ISAEF	65
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consensus		*****	

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NTDB id 1410	SGL RS13950 WP 010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPPSVLVAMVDPDNLAAQDELNRILRVKGF..ELRRL	161
NTDB id 1306	DR RS10060 WP 027479822.1	GYEFLDPIQNPPD.....PKVALMPEATARRVVVVPVRLQG...NSLVVAMKDPRNVFALDDDLKLITG.....KEILPA	455
NTDB id 1028	TT RS08215 WP 011173991.1	GYPYVDPEEDPPD.....PGAPLLLPEDLCRRYGVFPHRLEG...NRLVLMLMKDPRNILALDDVRLALKRKGLNYEVAPA	460
NTDB id 1436	BW25113 RS00530 WP 001025145.1	NIPQL.....TALCLRYHGVLLDASE...EVVHVAVVDAPSHELLDALHFATT.....KRIEIT	52
NTDB id 1168	A1552VC RS11070 WP 000957200.1	GLPETDLRSYDYA.....NLCQQGLRLRLITRYDALPIAKQG...NLLLLAVSDPTLLQAEEEFRFATG.....LQVELA	124
NTDB id 1401	DSB67 RS12665 WP 010643259.1	GLSCTSLNQYEYA.....SLCQTLGLRDLITRHNAIPLNRTS...STLILAVADPTNLQAEDDFRFATG.....LQVELV	124
NTDB id 1293	VP RS12240 WP 005479695.1	GLSQPELSQYEYA.....SLCQQGLRLRLITRHNAIPLHRTPT...STLLLAVADPTNQQAEDDFRFATG.....LQVELV	124
NTDB id 1110	NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH.....RVLMGVITEEQMVEFHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG.....IAVELV	123
NTDB id 1251	GC085 RS07725 WP 011946523.1	GVPMLDINCIDVG.....TIPVNLVNEKLIKRRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAI	132
NTDB id 1058	ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS.....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNASK.....LLVEPV	132
NTDB id 1018	ACIAD RS01685 WP 004920473.1	GEPLLDLGVFDPA.....LFLKDKLIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFNASK.....LKVEPI	132
consensus		*****	

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NTDB id 1410 SGL RS13950 WP 010873519.1
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
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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REAAFLQDASDIHIETTEDAVKVRVIRLDGALREQNSF.PKGAQAQIMARLKIMGHLDIAERRVPDQGRVRF..KKGSIDLD	589
REAFLLQDASDIHIEPRQNDVQVYRLRIDGALRPYSTL.PKGALNAVISVVKIMGGI.NIAEKRLPDQGRVRY..REGAIDVD	592
QSALEQRASDIHIEPADNAYRIRLRIDGVLHLP.LPDV.SPDGVALTARLKVLGNLDIAEHRLLPDQGQFTVELA..GNVVS	166
LDAVRKQGASDIHFEPYENQYRIRLRCDGILVETQQP.ASHLSRRLAARIKILSKLDIAERRLPDQGRIKLRLSR.DTAID	268
LDAVRKQGASDIHFEPYENMYRVRRLRCDGILIEIQQP.PSHLSRRLSARIKILSKLDIAERRLPDQGRIKLKLNQ.DTAID	268
LDAVRKQGASDIHFEPYEKMYRVRRLRCDGILIEITQQP.PNHLSRRLSARIKILSKLDIAERRLPDQGRIKLKLNQ.DTAID	268
SDALRSGASDIHFEFYEHNARIRFRVDGQLREVVP.PIAVRGQLASRIKVM SRLDISEKRIPDQGRMQLTFQKGGKPV	259
LDAIRQGASDIHFEPYEREYRIRYRQDGIILHEVATP.PASLSSRTTARIKVM SNLDISERRIPDQGGFKMKITSK.SRAID	277
IDAIRMQASDIHFEPYEKSYRVRVYRVDGVLRLQIANP.PLQLANRLASRIKVM SQMDISEKRVDPDQGRIKLKLSK.SK AID	272
IDAIRMSASDLHFEPYEKSYRVRVYRVDGVLRLLIATP.PLQLATRLASRIKVM SQMDISEKRVDPDQGRIKLKMSK.SKTID	272

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

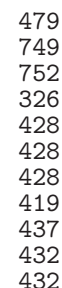
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LRLSTLPTVYGEKAVMRLLKQASDIPEIEDLGFAPGVFERFEVISKPYGIFLITGPTGSGKSFITFSLIKRIATPDKNT	672	
FRIATLPCRGEKVVLRLLQQVGQALDVNTLGMQPLQLADFAHALQQPQGLVLVTGPTGSGKTVTLYSALQKLNTADINI	246	
MRVSTLPTLWGEKIVLRLLDSSAANLDIDKLGYNPQQKQLYLINALKRPQGMILMTGPTGSGKTVSLYTGLRILNTSQINI	348	
MRVSTLPTLWGEKIVLRLLDSSAALDINKLGYSDSQKQLYLDALRRPQGMILMTGPTGSGKTVSLYTGLSILNKPEINI	348	
MRVSTLPTLWGEKIVLRLLDSSASALDIDKLGYSQEQKQLYLEALRRPQGMILMTGPTGSGKTVSLYTGLNILNKPEINI	348	
FRVSTLPTLWGEKIVMRILNSDAASLNIDQLGFEPQFKLLLEATHRPYGMVLVTGPTGSGKTVSLYTGLNILNKTESVNI	339	
FRVSTCPTSAAGEKVMRVLDSGAAKLGIEALGFNPVQRTNFKAIQRPQGMILVTGPTGSGKTVTLYTALNILNTIEVNI	357	
FRVNSLPTLWGEKIVLRLDPSAMLGIDALGYEEDQKALFMEALDKPQGMILITGPTGSGKTVSLYTGLNILNTESSNI	352	
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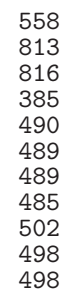
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consensus

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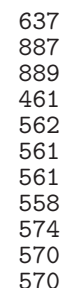
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consensus



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NTDB id 1410 SGL RS13950 WP 010873519.1
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consensus

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NTDB id 1018	ACIAD RS01685 WP 004920473.1		570
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved