

logo

		MSXLSIGDRRLGAALLDQGYLDNBLQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	
NTDB id 1410	SGL RS13950 WP 010873519.1		0
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	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	GCO85 RS07725 WP 011946523.1		0
NTDB id 400890	KRP1 RS24845 WP 021205142.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		SLTPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP.P	
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NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP.P	158
NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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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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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1028	TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFGHPGEEVL	237
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
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NTDB id 400890	KRP1 RS24845 WP 021205142.1		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	MTS	3
NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARYLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1306 DR RS10060 WP 027479822.1	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGETLVELGIARPEDVEEALQKQRRGGGRLEDTLVQ..SGKLRPEALAAQ.....VATQL	388
NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGDEVITELGFASPDDEVDSALQKQNVGGGRLEDTLVQ..SGKLSPEMLARS.....LAAQL	388
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYYNES.QAGKEVLPMLFS..DGVISPKSLAAL.....IARVF	56
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQEQAVVTQVSASGTSVPEALLE..LSIFHAQELTEQ.....LSHIF	57
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSLTLRQKGLLTFSGEESLIEQVKASGISMPEALLS..SGFFTSSSELAEH.....LSSIF	57
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSGEESLIEQVKASGISMPEALLS..SGFFQSHELTEH.....LSSVF	57
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
NTDB id 400890 KRP1 RS24845 WP 021205142.1	MNDSTPLSLAKQLVLNELLDEKSARQAQVQAARNKQSLVSHLVQ..AKLVQSRALVEV.....AAEQF	62
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAET.....TSAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPVPLYID..NFSISPLTTAEI.....ISLEF	65
consensus	* * * * *	

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NTDB id 1410 SGL RS13950 WP 010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPPSVLVAMVDPDNLAAQDELNRILRVKG..FELRRL	161
NTDB id 1028 TT RS08215 WP 011173991.1	GYPYVDPEEDPPD.....PGAPLLLPEDLCRRYGVFPHRLEG...NRLVLMLKDPNRNIALDDVRLALKRKGKLNVEVAPA	460
NTDB id 1306 DR RS10060 WP 027479822.1	GYEFLDPIQNPPD.....PKVALMPEATARRVVPVRLQG...NSLVVAMKDPNRNVFALDDLKLIITG....KEILPA	455
NTDB id 1110 NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH.....RVLMLGVLTTEEQMVFEHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAQ.....IAVELV	123
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GLPETDLSDYDYA.....NLCQQGLGLRELITRYDALPIAKQG...NLLLLAVSDPTLLQAEFFFRFATG.....LQVELA	124
NTDB id 1293 VP RS12240 WP 005479695.1	GLSQPELSQYEYA.....SLCQQGLGLRELITRHNAIPLHRTP...STLLAVADPTNQQAEDDFRFATG.....LQVELV	124
NTDB id 1401 DSB67 RS12665 WP 010643259.1	GLSCTSLNQYEYA.....SLCQTGLGLRLITRHNAIPLNRTS...STLILAVADPTNLQAEDDFRFATG.....LQVELV	124
NTDB id 1251 GC085 RS07725 WP 011946523.1	GVPMILDINCIDVG.....TIPVNLVNEKLIKRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAI	132
NTDB id 400890 KRP1 RS24845 WP 021205142.1	GIAYCDLNSLDRE.....SIPKDVISERLVRQHRVPLPWKRG...NKLFIGLSDPTNHQAVTDIQFSTG.....LTTEAL	129
NTDB id 1058 ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS.....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNASK.....LKVEPV	132
NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLIDLGVFDPA.....LFLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFNASK.....LKVEPI	132
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
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consensus

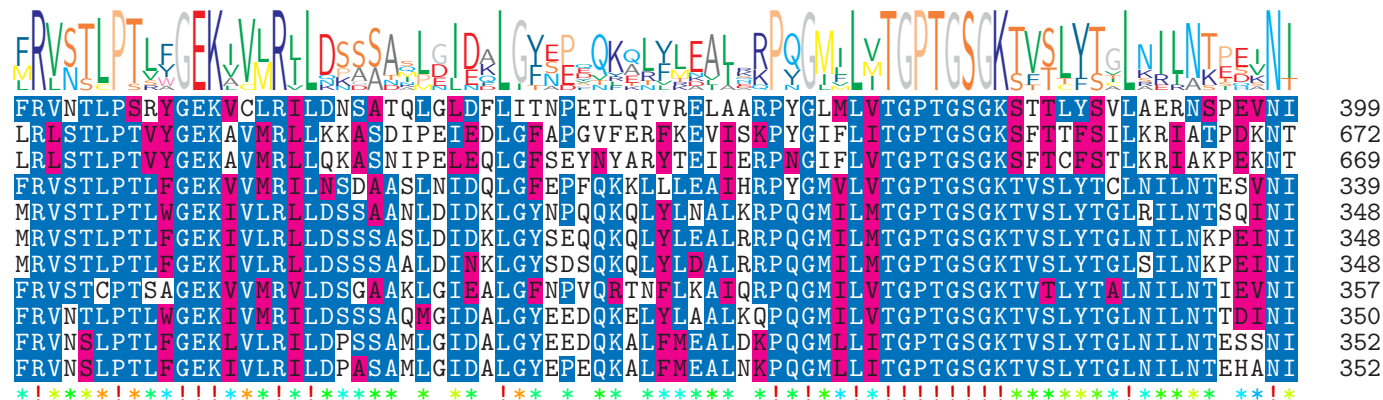
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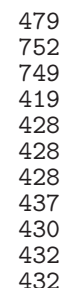
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consensus

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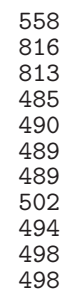
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consensus



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consensus

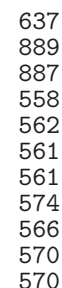
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1	EMRAKRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1293 VP RS12240 WP 005479695.1		561
NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

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