

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	.MALSIGDRRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL		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 415425 GVI48 RS07845 WP 003107297.1			0
NTDB id 1058 ABD1 RS01615 WP 001274986.1			0
NTDB id 1018 ACIAD RS01685 WP 004920473.1			0
consensus			0

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		SLTPAEKAKELRAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLEIVVPSGA	
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NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLEIVVPSGA		158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA		157
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NTDB id 1018 ACIAD RS01685 WP 004920473.1			0
consensus			0

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL		237
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NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARYLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1306 DR RS10060 WP 027479822.1	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLGEQLVQEGTLSR	317
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGETLVELGLIARPEDVEEALQKQRGGGRIEDTLVQ..SGKLRPEALAAQ.....VATQL	388
NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGDEVITELGFASPDDEVDSALQKQNVGGGRIEDTLVQ..SGKLSPEMLARS.....LAAQL	388
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYNE.SQAGKEVLPMLFS..DGVISPKSLAAL.....IARVF	56
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NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSLTLRQKGLLTFSGEESLIEQVKASGISMPEALLS..SGFFTSSSLAEH.....LSSIF	57
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSGEESLIEQVKASGISMPEALLS..SGFFQSHLTHE.....LSSVF	57
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
NTDB id 415425 GVI48 RS07845 WP 003107297.1	MNDSTPLSLAKQLVLNELLDEKTARQAQVQAARNKQSLVSHLVQ..AKLVQSRALVEV.....AAEQF	62
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAET.....TSAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMMQALEKAKKFKQDTPVPLYID..NFSISPLTTAEI.....ISLEF	65
consensus	* * * * *	

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NTDB id 1410 SGL RS13950 WP 010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPPSVLVAMVDPDNLAAQDELNRILRVKG..FELRRL	161
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NTDB id 1110 NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH.....RVLMLGVLTTEEQMVFEHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAQ.....IAVELV	123
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GLPETDLSDYDYA.....NLCQQGLGLRELITRYDALPIAKQG...NLLLLAVSDPTLLQAEFFRFATG.....LQVELA	124
NTDB id 1293 VP RS12240 WP 005479695.1	GLSQPELSQYEYA.....SLCQQGLGLRELITRHNAIPLHRT...STLLAVADPTNQAEEDDFRFATG.....LQVELV	124
NTDB id 1401 DSB67 RS12665 WP 010643259.1	GLSCTSLNQYEYA.....SLCQTLGLRLDLITRHNAIPLNRTS...STLLAVADPTNLQAEEDDFRFATG.....LQVELV	124
NTDB id 1251 GC085 RS07725 WP 011946523.1	GVPMILDINCIDVG.....TIPVNLVNEKLIKRRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAI	132
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS.....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNASK.....LKVEPV	132
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consensus	* * * * *	

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consensus

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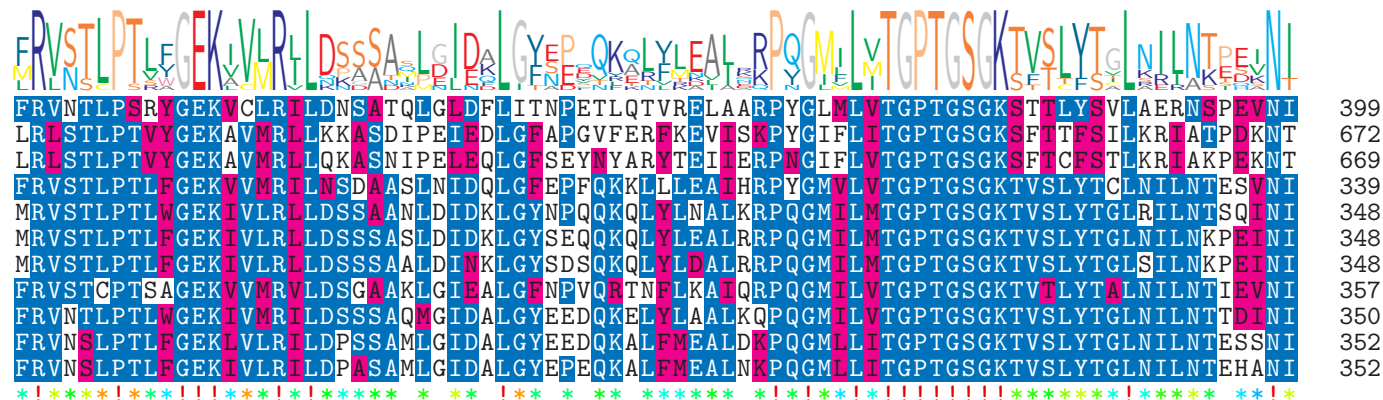
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consensus



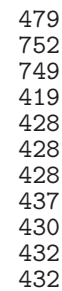
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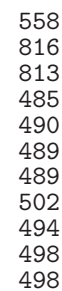
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consensus



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consensus

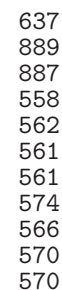
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consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1	EMRAKRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

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