

logo

		MSXLSIGDRRLGAALLDQGYLDNBLQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	
NTDB id 1410	SGL RS13950 WP 010873519.1		0
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 366484	FF962 RS28885 WP 021264132.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		SLTPAEKAKELRAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP.P	
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NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIIVVPSGA	157
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NTDB id 1293	VP RS12240 WP 005479695.1		0
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NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 366484	FF962 RS28885 WP 021264132.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFGHPGEEVL	237
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NTDB id 366484	FF962 RS28885 WP 021264132.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
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consensus			

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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	SSSSKKSRVALRNYFSPFGNKLIVAGCHVDAEQLRQALVQVVKTKGRSLPEELKAVTGRELSPPELLRQYKKNQLFELKVLV	83
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILSATQEAVVTQVSASGTSVPEALL..ELSFHAQELTEQL.....SHIF	57
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSGEESLIEQVKASGISMPEALL..SSGFFTSSSLAEHL.....SSIF	57
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALL..SSGFFQSHELTEHL.....SSVF	57
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAHEHYNES.QAGKEVLPMLF..SDGVIISPKSLAALI.....ARVF	56
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIV..KNKILSAEQIALTA.....AQNF	65
NTDB id 366484 FF962 RS28885 WP 021264132.1	MNDSIQLSGLSRQLVQANLLDEKTALQAQAQARNKLSLVTHLV..QNKLVSGLALAEELS.....AEQF	62
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLI..EEVHLSPSLLAETI.....SAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPVPLYI..DNFSISPLTTAEI.....SLEF	65
consensus	* * * * *	

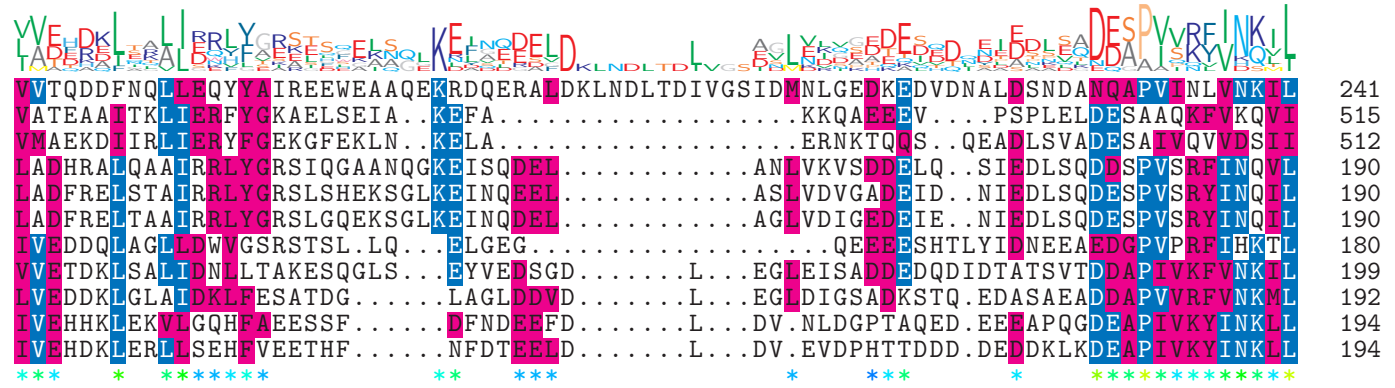
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NTDB id 1110 NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH....RVLMLGVLTEEQMVVEFHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG....IAVELV	123
NTDB id 1251 GC085 RS07725 WP 011946523.1	GVPMLDINCIDVG....TIPVNLVNEKLIKRRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG....LNTHAI	132
NTDB id 366484 FF962 RS28885 WP 021264132.1	GIAYCDLNSLDKE....SFPRDAISEKLVQRHVIPLWRRG...NKLFGVTSDPANHQAINDVQFSTG....LTTEAI	129
NTDB id 1058 ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNASK....LKVPEV	132
NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLLDLGVFDPA....LFLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFNASK....LKVPEI	132
consensus	* * * * *	

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consensus

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consensus
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consensus

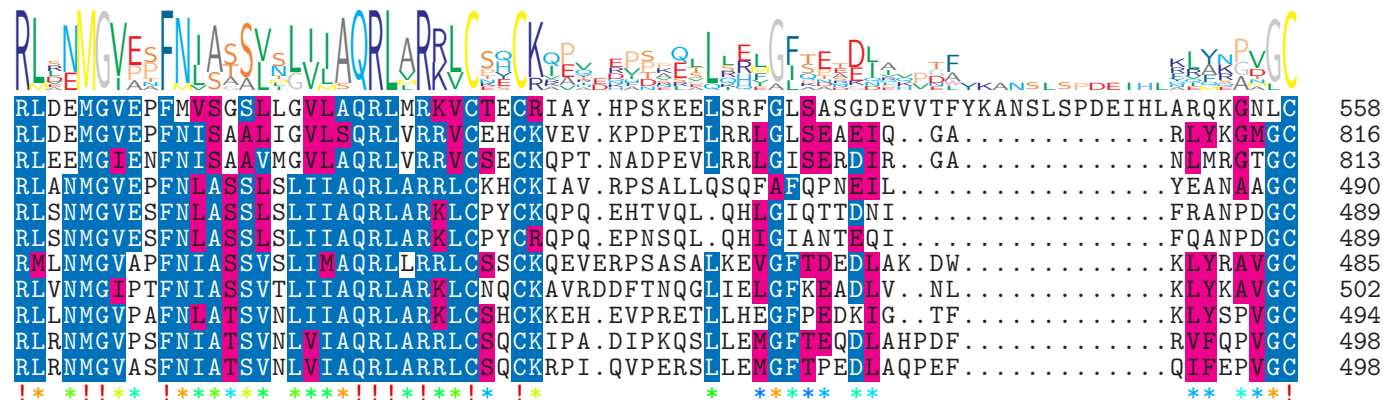
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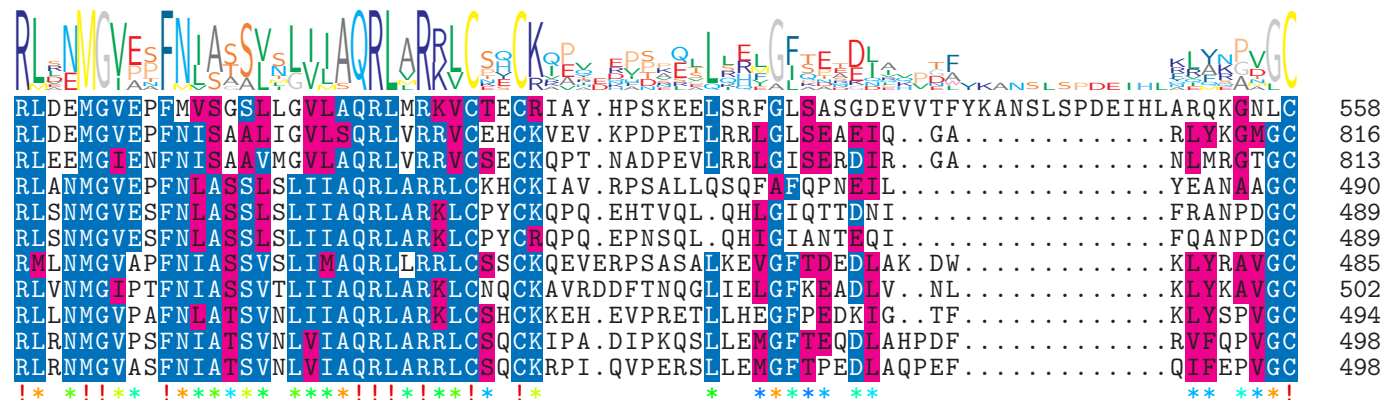
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consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1
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consensus



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consensus

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NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

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