

logo

		MSXLEIGDRRLGAALLDQGYLDNQLQRALERHREVGGLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	
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NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
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NTDB id 408591	GPY16 RS03330 WP 158104985.1		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 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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consensus			

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consensus		

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NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPVPLYLID..NFSISPLTIAEI.....LSAEF	65
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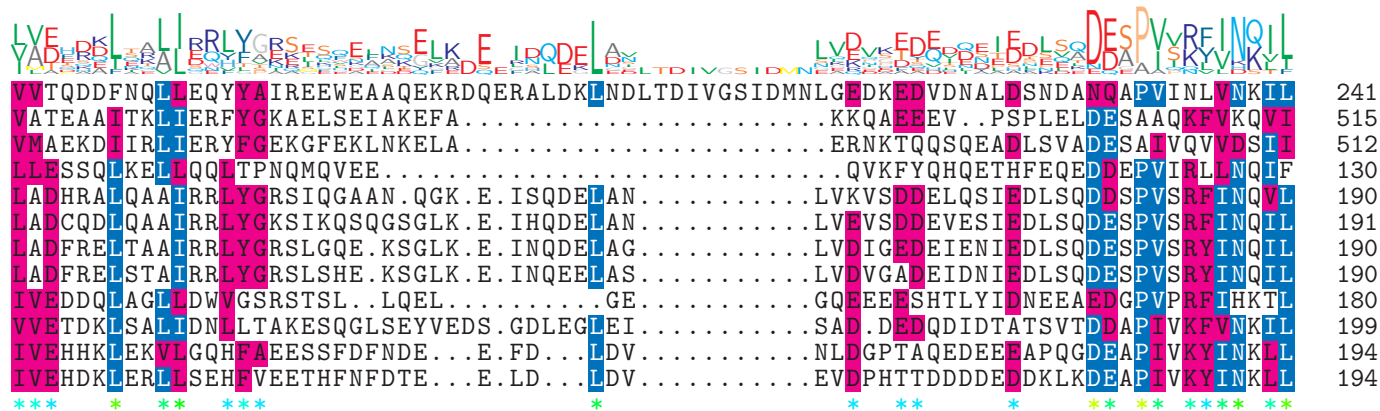
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	GLPETDLSRYDYA....NLCQQGLGRELITRYDALPIAKQG...NLLLLAVSDPTLLQAEFEFRFATG.....LQVELA	124
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NTDB id 1251 GC085 RS07725 WP 011946523.1	GVPMLDINCIDVG....TIPVNLVNEKLIKRHAMVPLFSRG...TNLYLATDDPSKQASLKEITQFHTG.....LNTHAI	132
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLLDLGVFDPA....LFLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMD AIRFNSK.....LKVEPT	132
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consensus

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consensus

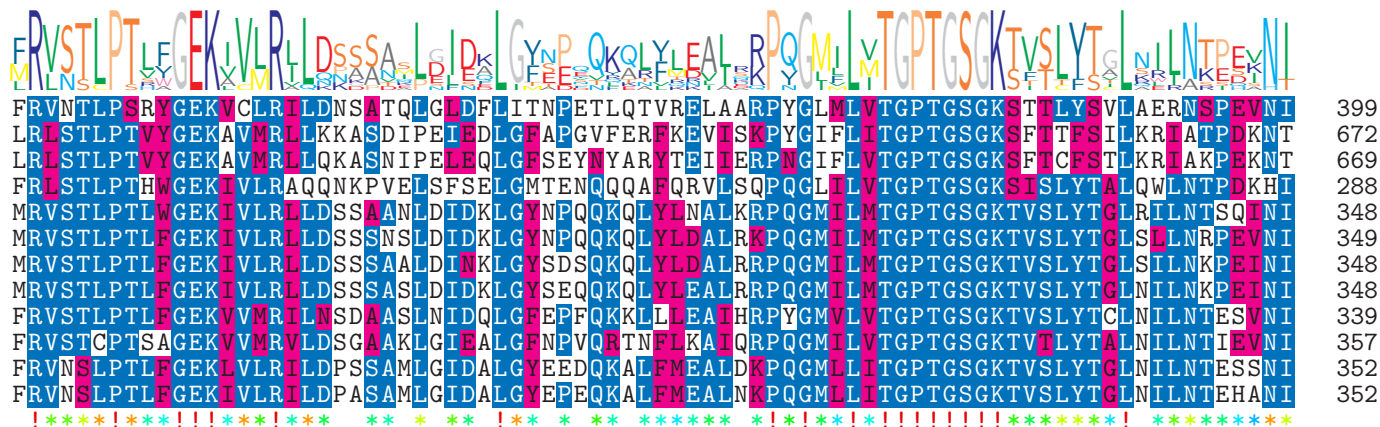
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consensus

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consensus

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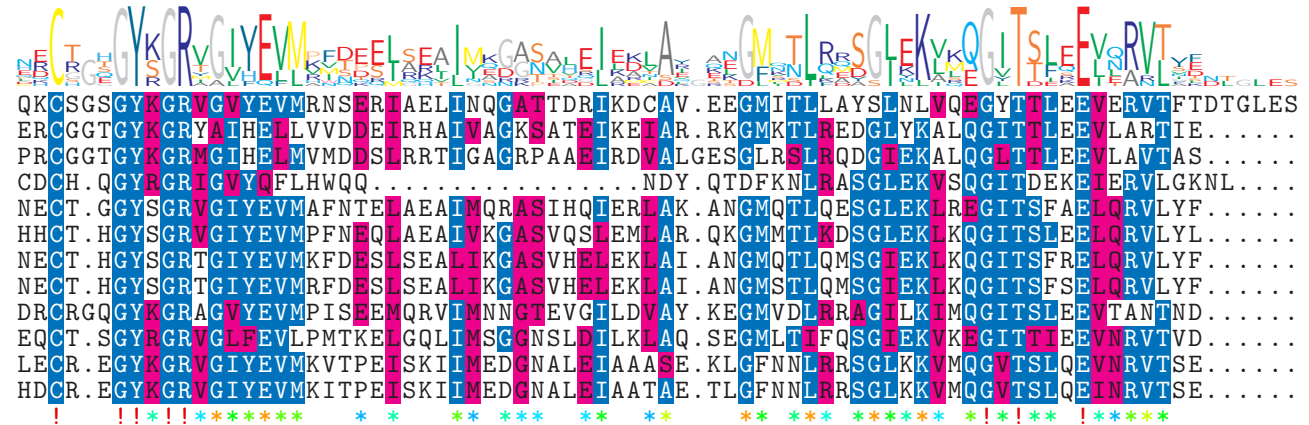
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consensus

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NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved