

logo

		MSXLSIGDRRLGAALLDQGYLDNBLQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKK	
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NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKK	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
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 125029	HV95 RS05810 WP 003107297.1		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 1251	GCO85 RS07725 WP 011946523.1		0
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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	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEGTTFLPNPSGFHPGEEVL	237
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consensus			

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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGDEVITELGFASPDVEVDSALQKQNVGGGRIEDTLVQ..SGKLSPEMLARS.....LAAQL	388
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NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSLTLRQKGLLTFSGEESLIEQVKASGISMPEALLS..SGFFTSSSELAEH.....LSSIF	57
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NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAET.....TSAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPVPLYID..NFSISPLTTAEI.....ISLEF	65
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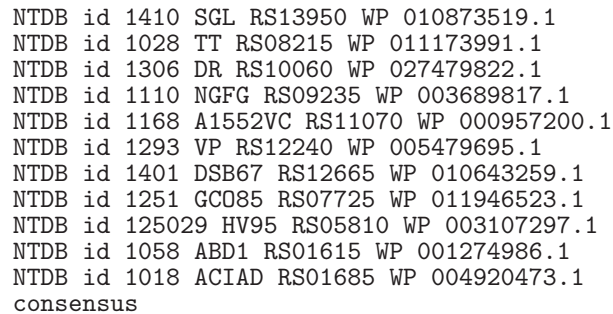
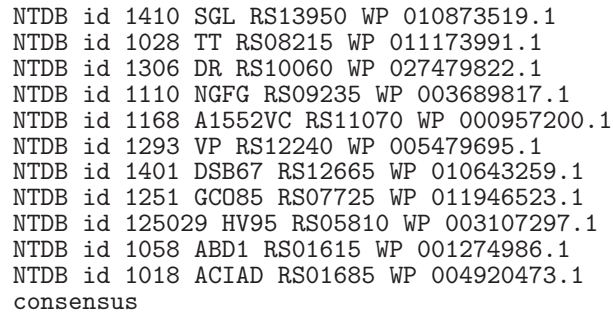
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLIDLGVFDPA....LFLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFNASK....LKVEPI	132
consensus	* * * * *	

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consensus

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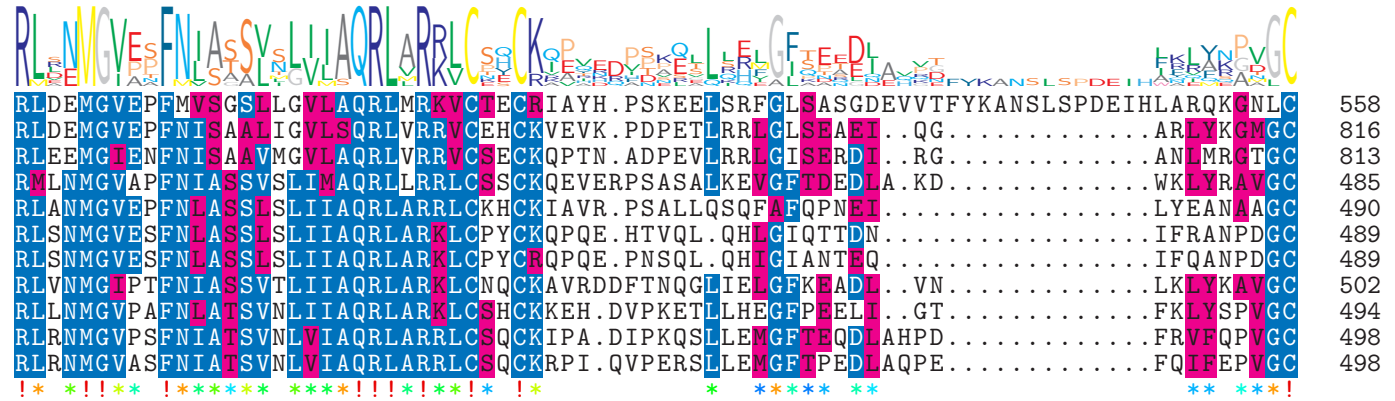
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consensus
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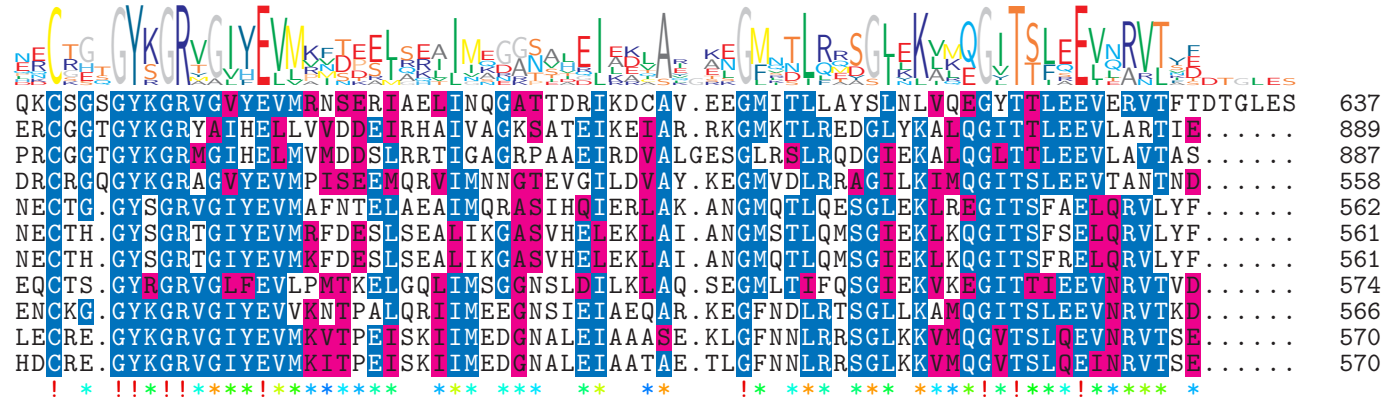
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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved