

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 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 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GCO85 RS07725 WP 011946523.1		0
NTDB id 405970	GO602 RS24250 WP 024914668.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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		SLTPAEKAKELRAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLEIVVPSGA	
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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			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQEGTTFLPNPSGFGHPGEEVL	237
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consensus			

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NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARYLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
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consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGETLVELGLIARPEDVEEALQKQRRGGGRLEDTLV..QSGKLRPEALAAQA.....VATQL	388
NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGGEVITELGFASPDEVDLSALQKQNVGGGRLEDTLV..QSGKLSPEMLARS.....LAAQL	388
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQEAVVTQVSASGTSVPEALL..ELSFHAQELTEQ.....LSHIF	57
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NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALL..SSGFFQSHELTEH.....LSSVF	57
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAHEHYNES.QAGKEVLPMLF..SDGVIISPKSLAAL.....IARVF	56
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIV..KNKILSAEQIALT.....AAQNF	65
NTDB id 405970 G0602 RS24250 WP 024914668.1	MNDSIQLSGLSRQLVQANLLDEKTAVQAQAQAQRNKLSLVTHLV..QNKLVSGLALAEEL.....SAEQF	62
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQD TVAYLI..EEVHLSPSLLAET.....ISAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDTPVPLYI..DNFSLISPLTIAEI.....ISLEF	65
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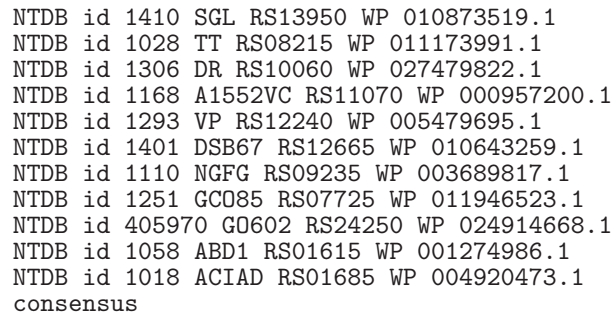
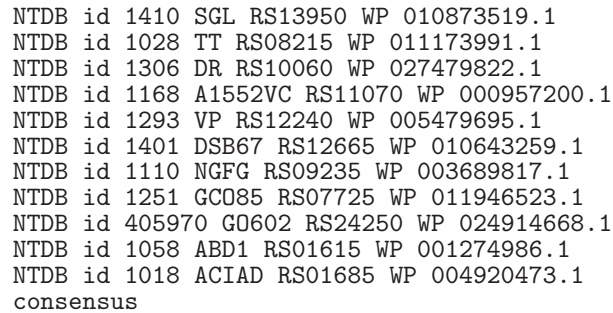
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NTDB id 1110 NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH....RVLMLGVLTEEQMVFEHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG....IAVELV	123
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNSK....LKVPEV	132
NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLIDLGVFDPA....LFLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFNSK....LKVEPI	132
consensus	* * * * *	

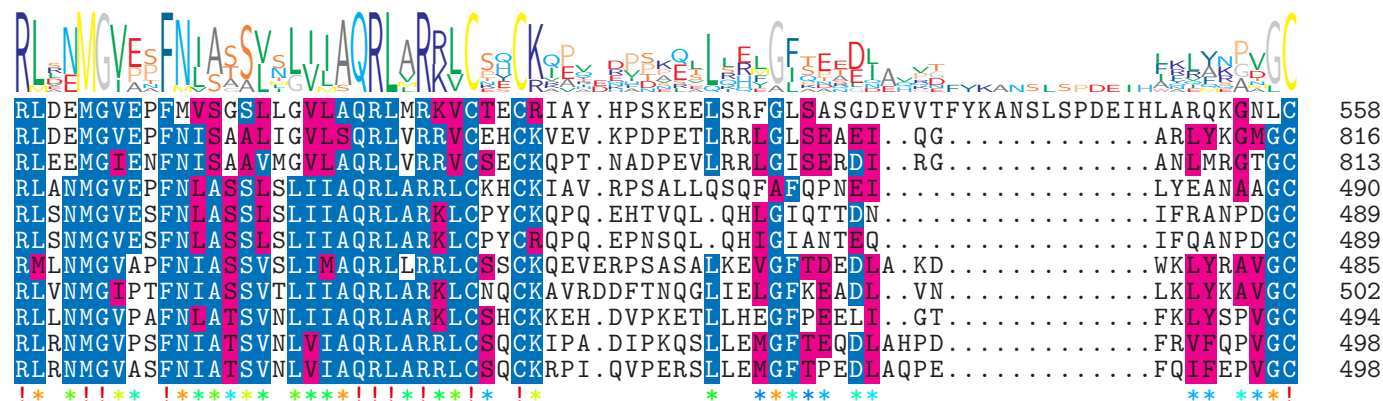
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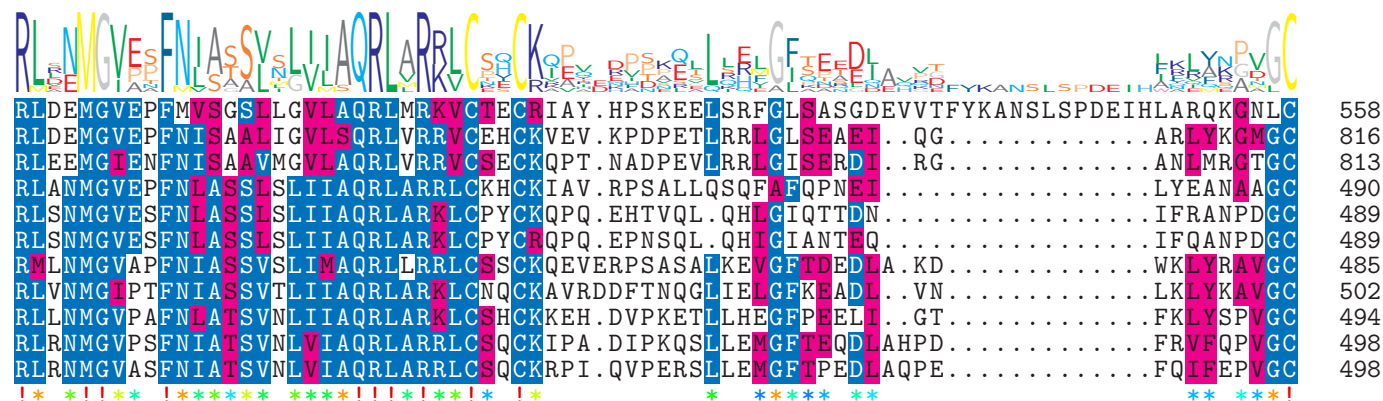
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consensus



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consensus



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consensus



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NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved