

logo

	MSXLRIGDRRLGAALLDQGYLGDNDLQRALERHSEVGGRLADVLDISGMVGEKRIARAIEEALGIPLVNLAVQPDPAAAL	
NTDB id 1410 SGL RS13950 WP 010873519.1	.....	0
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLDISGMVGEKRIARAIEEALGIPLVNLAVQPDPAAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1	.....	0
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NTDB id 392661 GBK02 RS05205 WP 203468688.1	.....	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	.....	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	.....	0
consensus		

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	RSIRPQTALNLQAFPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIIVVPSGA	
NTDB id 1410 SGL RS13950 WP 010873519.1	.....	0
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLISLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPP..P	158
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NTDB id 1110 NGFG RS09235 WP 003689817.1	.....	0
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consensus		

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	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQEGTTFLPNPSGFHPGEEVL	
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NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVDPDSAA	237
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NTDB id 1110 NGFG RS09235 WP 003689817.1	.....	0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	.....	0
consensus		

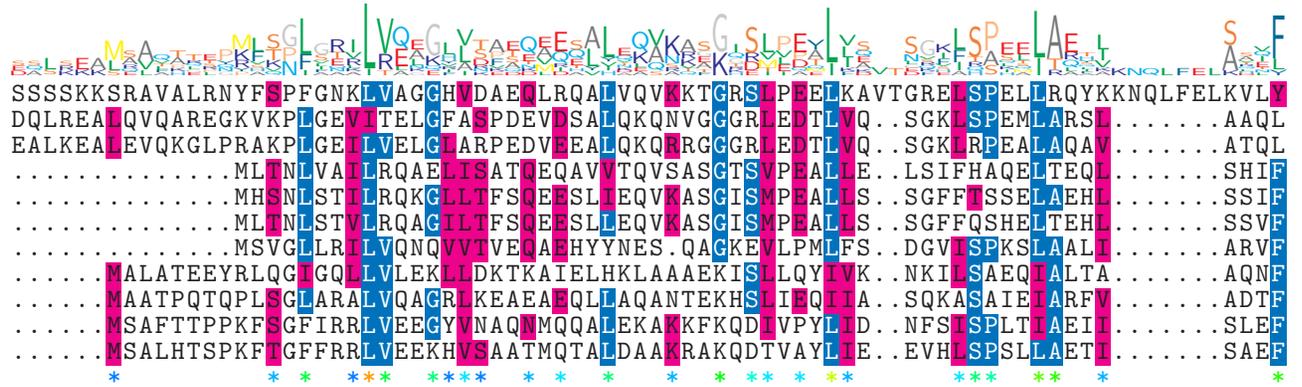
logo

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 NTDB id 1018 ACIAD RS01685 WP 004920473.1  
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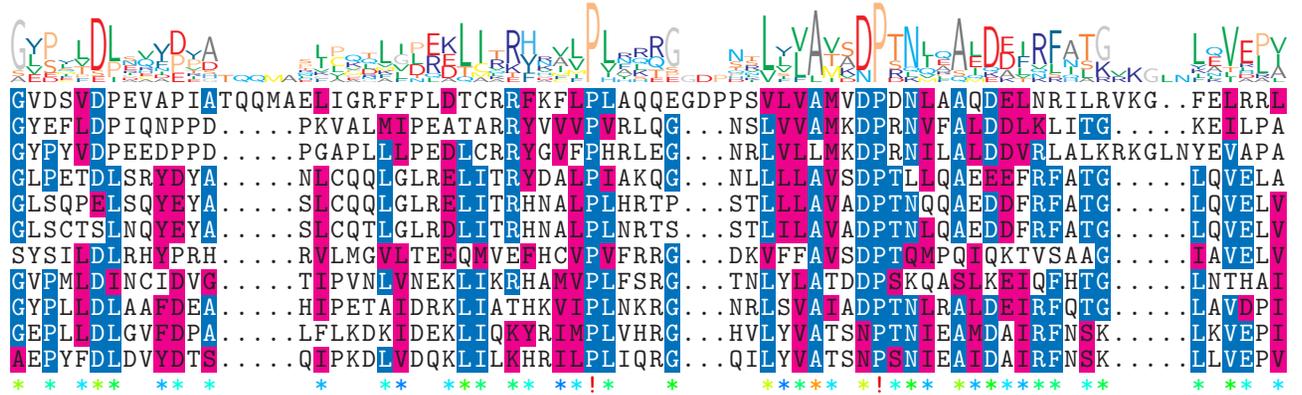
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NTDB id 1410 SGL RS13950 WP 010873519.1  
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 NTDB id 1168 A1552VC RS11070 WP 000957200.1  
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NTDB id 1410 SGL RS13950 WP 010873519.1  
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 NTDB id 1251 GCO85 RS07725 WP 011946523.1  
 NTDB id 392661 GBK02 RS05205 WP 203468688.1  
 NTDB id 1018 ACIAD RS01685 WP 004920473.1  
 NTDB id 1058 ABD1 RS01615 WP 001274986.1







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NTDB id 1410 SGL RS13950 WP 010873519.1	EMRAKRKRSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	.....	570
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consensus		

 non conserved  
 similar  
 ≥ 50% conserved