

logo

	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAALR	
NTDB id 1306 DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAALR	80
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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 404731 IX0597 RS16520 WP 075243394.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
consensus	

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	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIEWVPSGASDA	
NTDB id 1306 DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIEWVPSGASDA	160
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NTDB id 1110 NGFG RS09235 WP 003689817.1	0
NTDB id 1251 GCO85 RS07725 WP 011946523.1	0
NTDB id 404731 IX0597 RS16520 WP 075243394.1	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
NTDB id 1018 ACIAD RS01685 WP 004920473.1	0
consensus	

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	CRTGGKLGGERLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSCGFHPGEEVLGSM	
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consensus	

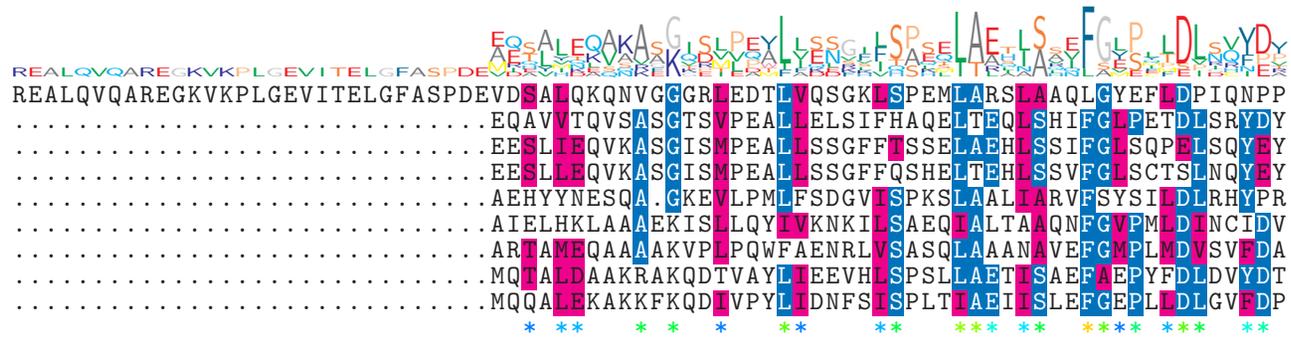
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	LRADALRLLAVPVDETEQGVTVLTSDFRKRDPDIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGEGQLVQEGTISRDL	
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NTDB id 404731 IX0597 RS16520 WP 075243394.1 MNSVSTTNLVGITARRLVQDGALEETA	29
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NTDB id 1018 ACIAD RS01685 WP 004920473.1 MS..AFTTPPKFSCFIRRLVEEGYVNAQN	27
consensus	

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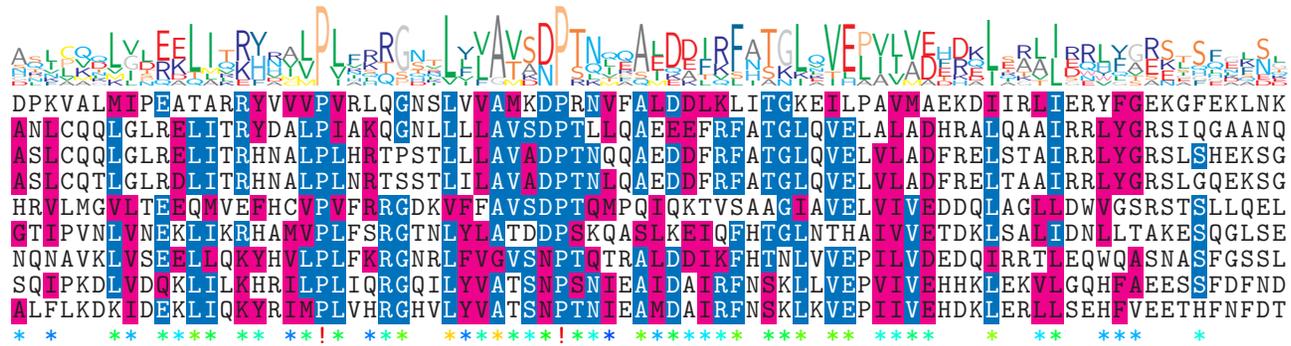
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logo

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225
215
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238
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625
304
304
304
295
313
317
308
308

 non conserved
 similar
 $\geq 50\%$ conserved