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Accession	Protein	Sequence	Score
NTDB id 125660	DR96 RS07075 WP 040132695.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGSSSEKLYSYGLNLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	31
NTDB id 1410	SGL RS13950 WP 010873519.1	MNSGLLDITSL...TTLHGVGASQSEKLSKIGLN.....	0
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGSSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
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NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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Accession	Protein	Sequence	Score
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consensus			

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NTDB id	Accession	Protein	Sequence	Score
NTDB id 125660	DR96	RS07075 WP 040132695.1	.GTTATIVGEVLQTKVVFGRKRMMTCLIT.DGTGNLT.....LRFFNFSAAMKN.....SLA	108
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NTDB id 1058	ABD1	RS01615 WP 001274986.1		0
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consensus				

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NTDB id 125660 DR96 RS07075 WP 040132695.1	ESRBXTRYGAVBRGQNEEYEWLTHPEYKESVAQLLSBFAFNTALPQALWEENTFRXYPTQENYSEXTLRKLI EQALKL	173
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NTDB id 1028 TT RS08215 WP 011173991.1	LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYLALPQAWHEELFRRAYPQKNRLGEV.....L	309
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consensus		

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NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALLS..SGFFQS	46
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMLFS..DGVISP	45
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLIE..EVHLSP	54
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIPYPLID..NFSISP	54
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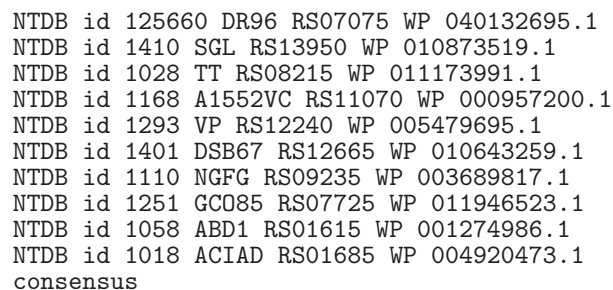
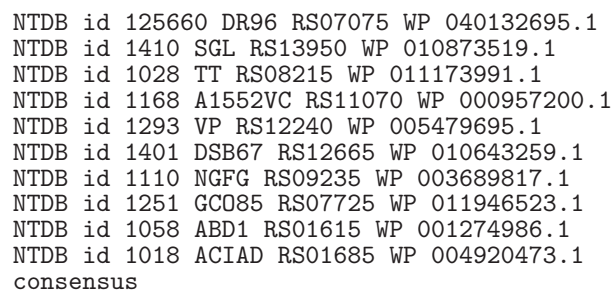
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	LTIAEI.....ISLEFGEPLLDLG.....VFDPAL.....FLKDKID EKLIQKYRIMPLVHRG....HVLV....	106
consensus	*** ** ***** *** ** * * ** *** ** *** * ** *	

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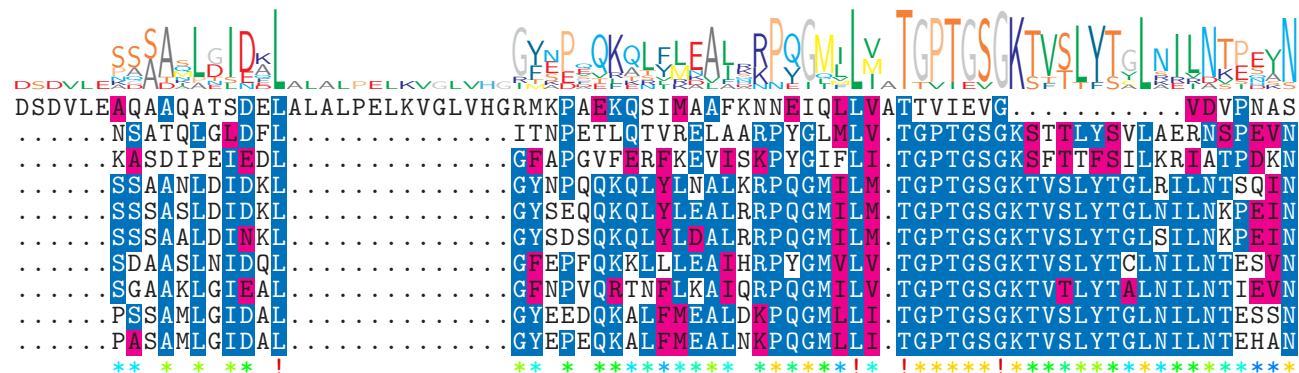


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consensus

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consensus

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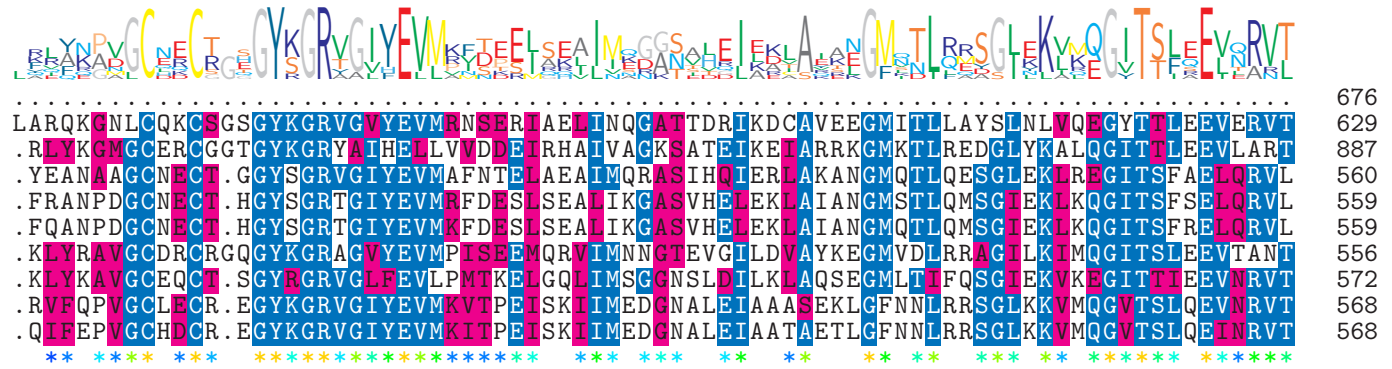
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consensus
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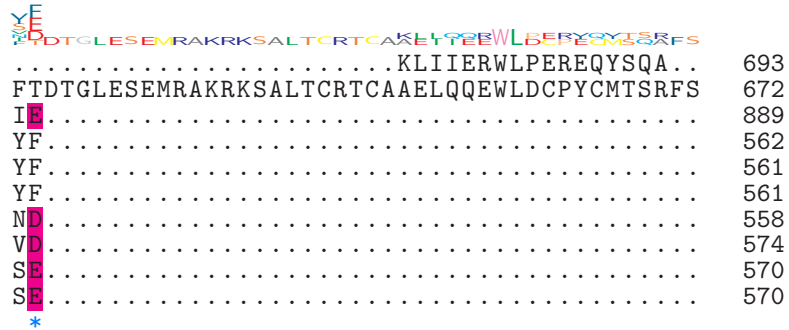


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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus
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-  non conserved
-  similar
-  $\geq 50\%$ conserved