

NTDB id	Accession	Protein	Sequence	Score
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80	
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	GC085 RS07725 WP 011946523.1		0	
NTDB id 1101869	Q9276 RS15340 WP 011408072.1		0	
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0	
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0	
consensus				

NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	160
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consensus			

NTDB id	Accession	Length	Consensus
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1168	A1552VC RS11070 WP 000957200.1	0	0
1293	VP RS12240 WP 005479695.1	0	0
1401	DSB67 RS12665 WP 010643259.1	0	0
1110	NGFG RS09235 WP 003689817.1	0	0
1251	GC085 RS07725 WP 011946523.1	0	0
1101869	Q9276 RS15340 WP 011408072.1	0	0
1058	ABD1 RS01615 WP 001274986.1	0	0
1018	ACIAD RS01685 WP 004920473.1	0	0
consensus			

NTDB id	Accession	Protein	Sequence	Score
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NTDB id 1168	A1552VC RS11070 WP 000957200.1	MLTNLVAIILRQAELISATQ.		19
NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSQ.		19
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQ.		19
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQ.		19
NTDB id 1251	GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTK.		27
NTDB id 1101869	Q9276 RS15340 WP 011408072.1	MNSVSTTNLVGITGIARRLVQDGALEETA.		29
NTDB id 1058	ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFTGFFRRLVEEKHVSAAAT.		27
NTDB id 1018	ACIAD RS01685 WP 004920473.1	MS..AFTTPPKFSGFIRRLVEEGYVNAQN.		27
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	EQAVVTQVSASGTSVPEALLSIFHAQELTEQLSHIFG	69
NTDB id 1293 VP RS12240 WP 005479695.1	EESLIEQVKASGISMPEALLSSGFFISSELAEHLSSIF	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EESLLIEQVKASGISMPEALLSSGFFQSHLTHSSVFC	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	AEHYYNESQA.CKEVLPMLFSDGVI.SPKSLAALIA	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQ	77
NTDB id 1101869 Q9276 RS15340 WP 011408072.1	ARTAMEQAAA.AKVPLPQWFAENRLVSASQLAAANA	79
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MQTALDAAKRAKQDVTAYLIEEVHLSPSLAEETIS	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MQQALEKAKKFQKD.VPPLYLDNFS.SPLTTABEIS	77
consensus	*****	

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NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTIEHQMVFEHCVVFFRGDKVFFAVSDPTQ	148
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NTDB id 1101869 Q9276 RS15340 WP 011408072.1	NQNAVKLVSEELIQKYHVLPLFKRCNRLFVGVSNPTQ	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLIKLRHRLPLLIQRGQILYVATSNPS	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTN	157
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NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIEDLSQDES	225
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consensus	*****	

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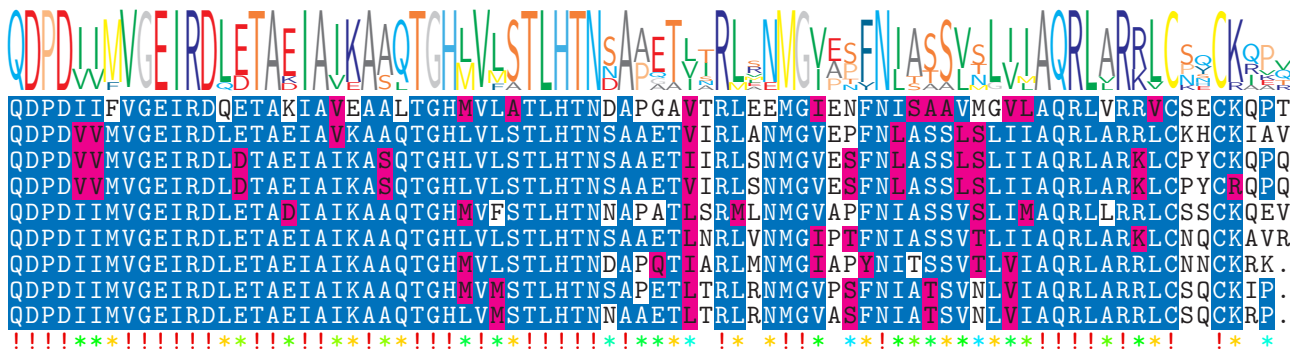
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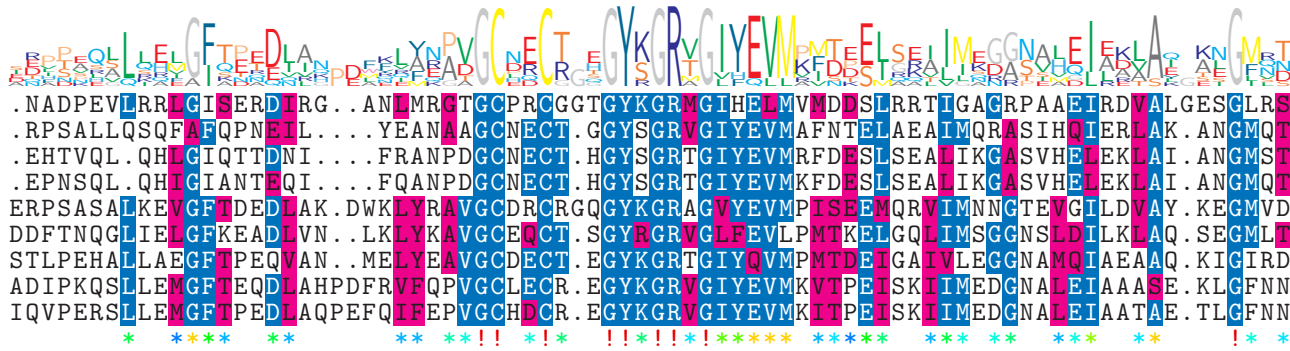
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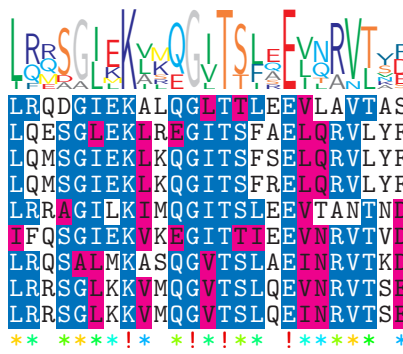
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consensus



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NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



887
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561
561
558
574
577
570
570

 non conserved
 similar
 $\geq 50\%$ conserved