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				MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1028	TT	RS08215	WP 011173991.1		
NTDB id 1306	DR	RS10060	WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAAL	79
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NTDB id 1366	NTHI	RS01950	WP 011271972.1	.....	0
NTDB id 1355	HI	0298 AAC21962.1		.....	0
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NTDB id 1146965	CKW10	RS22255	WP 084104044.1	.....	0
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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
NTDB id 1018	ACIAD	RS01685	WP 004920473.1	.....	0
consensus					

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				ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVVPEYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1306	DR	RS10060	WP 027479822.1	RSIRPQTALNLQAFPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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NTDB id 1018	ACIAD	RS01685	WP 004920473.1	.....	0
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				SGEGQKDLKLGELLQKQWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGFLESTEGIVPDPSSAA	237
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NTDB id 1306	DR	RS10060	WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1058	ABD1	RS01615	WP 001274986.1	.....	0
NTDB id 1018	ACIAD	RS01685	WP 004920473.1	.....	0
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NTDB id 1028	TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
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NTDB id 1058	ABD1 RS01615 WP 001274986.1	.....	0
NTDB id 1018	ACIAD RS01685 WP 004920473.1	.....	0
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NTDB id 1028	TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEIVELGLARPEDVEEAQKQRGGGRLEDTLVQS..GKLRPEATAQA.....VATQL	388
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NTDB id 1410	SGL RS13950 WP 010873519.1	SSSSKKSRAVALRNYFSPFGNKIVAGGHVDAEQLRQAIVQVKKTGRSPPEEKAVTGRELSPELIRQYKKNQLFELKVLV	83
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NTDB id 1401	DSB67 RS12665 WP 010643259.1	.....MLTNLSTVLRQAGILITFSQEESELEQVKASGISMPEALLSS..GFFQSHLLEH.....LSSVF	57
NTDB id 1110	NGFG RS09235 WP 003689817.1	.....MSVGLLRILVQNVVITVEQAEHYH.NESQAGKEVLPMLFSD..GVISPKSLAAL.....LARVF	56
NTDB id 1251	GCO85 RS07725 WP 011946523.1	.....MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYLVKN..KILSAEQIALT.....AAQNF	65
NTDB id 1058	ABD1 RS01615 WP 001274986.1	.....MSALHTSPKFTGFRRLLVEEKHVAATMQTADAACKRAKQDTVAYDIEE..VHLSPSLLAET.....LSAEF	65
NTDB id 1018	ACIAD RS01685 WP 004920473.1	.....MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALKEAKKFKQDVPYLDN..FSISPLTAEI.....LSLEF	65
consensus		.....	65

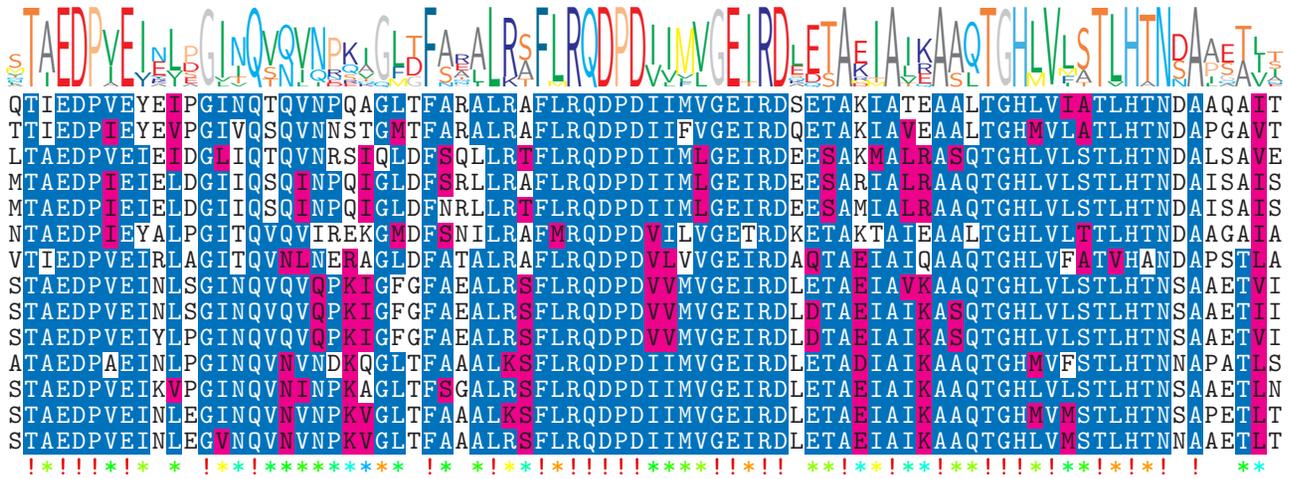
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NTDB id 1384	A4U84 RS08525 WP 010787006.1	.CEQQTERIFDISPSR...WQKNCEEKQLLLRYLAVPVQETE...HKLWLAVDDENNITACEIFA...FMTH..KQEPV	74
NTDB id 1366	NTHI RS01950 WP 011271972.1	RVTAKNGEIFTISPDL...WERNQQQSLLLRYFALPLKEEN...NRLWLGVDLSLSNISACETIA...FITG..KPVPI	79
NTDB id 1355	HI 0298 AAC21962.1	RVTAKNGEIFTISPDL...WERNQQQSLLLRYFALPLKEEN...NRLWLGVDLSLSNISACETIA...FITG..KPVPI	79
NTDB id 1410	SGL RS13950 WP 010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRKFLPLAQQEGDPPSVLVAVDPPDLAAQDELNRIILRVKG...FELRRL	161
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NTDB id 1168	A1552VC RS11070 WP 000957200.1	GLPETLSRYDYAN....LCQQGLRELITRYDALPAAKQG...NLVLLAVSDPTLQAEEFR...FATG..LQVELA	124
NTDB id 1293	VP RS12240 WP 005479695.1	GLSQPELSQYAYAS....LCQQGLRELITRHNAIPHRTP...STLLAVADPTNQAEDDFR...FATG..LQVELV	124
NTDB id 1401	DSB67 RS12665 WP 010643259.1	GLSCTSLNQYAYAS....LCQTLGLRDLITRHNAIPHRTP...STLLAVADPTNQAEDDFR...FATG..LQVELV	124
NTDB id 1110	NGFG RS09235 WP 003689817.1	SYSILDLRHYPRHR....VLMGVLTEEQMVHCVVFRRG...DKVFAVSDPTQMPPIQKTV...SAAG..IAVELV	123
NTDB id 1251	GCO85 RS07725 WP 011946523.1	GVPMLDINCIDVGT....IPVNLVNEKILKRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQ...FHTG..LNTHAI	132
NTDB id 1058	ABD1 RS01615 WP 001274986.1	AEPYFDLDVVDTSQ....IPKDLVDQKLLKHRILPLIQRG...QILYVATSNPSNTEAIDAIR...FNSK..LLVEPV	132
NTDB id 1018	ACIAD RS01685 WP 004920473.1	GEPLLDLGVDPAL....FLKDKIDEKLLIKYRIMPLVHRG...HVLVYVATSNPTNTEAIDAIR...FNSK..LKVEPI	132
consensus		.....	132



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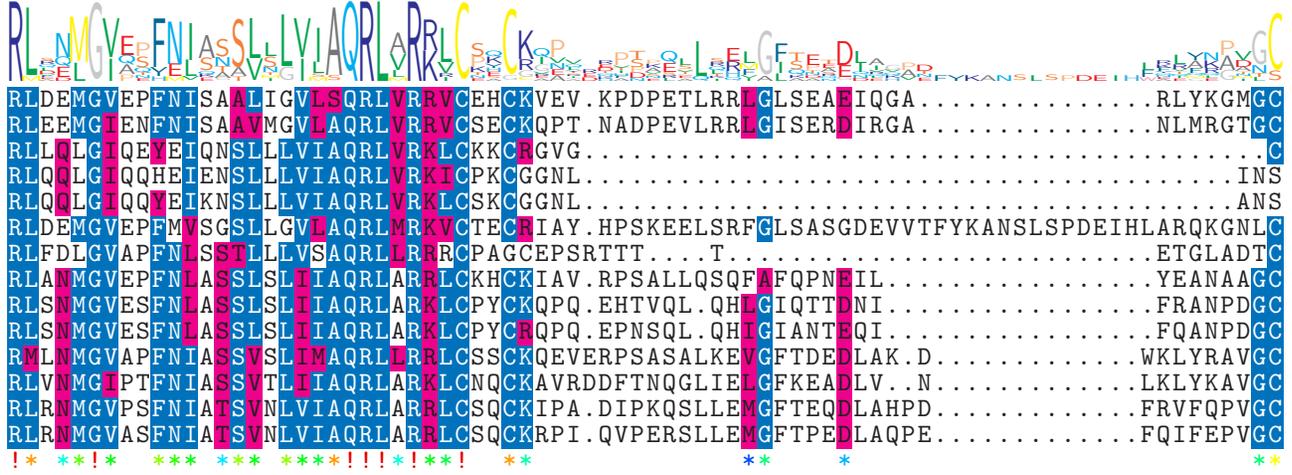
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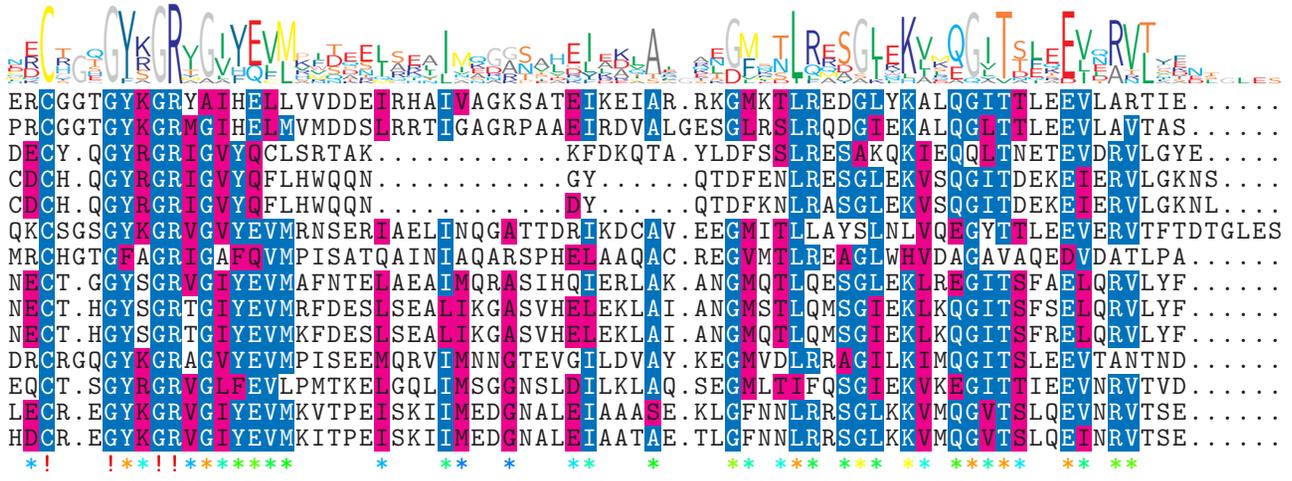
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NTDB id 1028 TT RS08215 WP 011173991.1	EMRAKRKKSALTCRRTCAAELQQEWLDCPYCMTSRFS	889
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consensus		

- ⊠ non conserved
- ⊠ similar
- ⊠ ≥ 50% conserved