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NTDB id	1306	DR	RS10060	WP	027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLDISGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
NTDB id	1028	TT	RS08215	WP	011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id	1384	A4U84	RS08525	WP	010787006.1	0
NTDB id	1123022	EL215	RS00260	WP	126469443.1	0
NTDB id	1366	NTHI	RS01950	WP	011271972.1	0
NTDB id	1355	HI	0298	AAC21962.1	0	
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	GCO85	RS07725	WP	011946523.1	0
NTDB id	1058	ABD1	RS01615	WP	001274986.1	0
NTDB id	1018	ACIAD	RS01685	WP	004920473.1	0
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NTDB id	1306	DR	RS10060	WP	027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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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	1293	VP	RS12240	WP	005479695.1	0
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NTDB id	1110	NGFG	RS09235	WP	003689817.1	0
NTDB id	1251	GCO85	RS07725	WP	011946523.1	0
NTDB id	1058	ABD1	RS01615	WP	001274986.1	0
NTDB id	1018	ACIAD	RS01685	WP	004920473.1	0
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NTDB id	1306	DR	RS10060	WP	027479822.1	SDAGRTGGKLGGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTF LPNPSGFHPGEEVL	237
NTDB id	1028	TT	RS08215	WP	011173991.1	SGEGQKDKLKL GELL LKQGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSPAA	237
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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 GCO85 RS07725 WP 011946523.1	0
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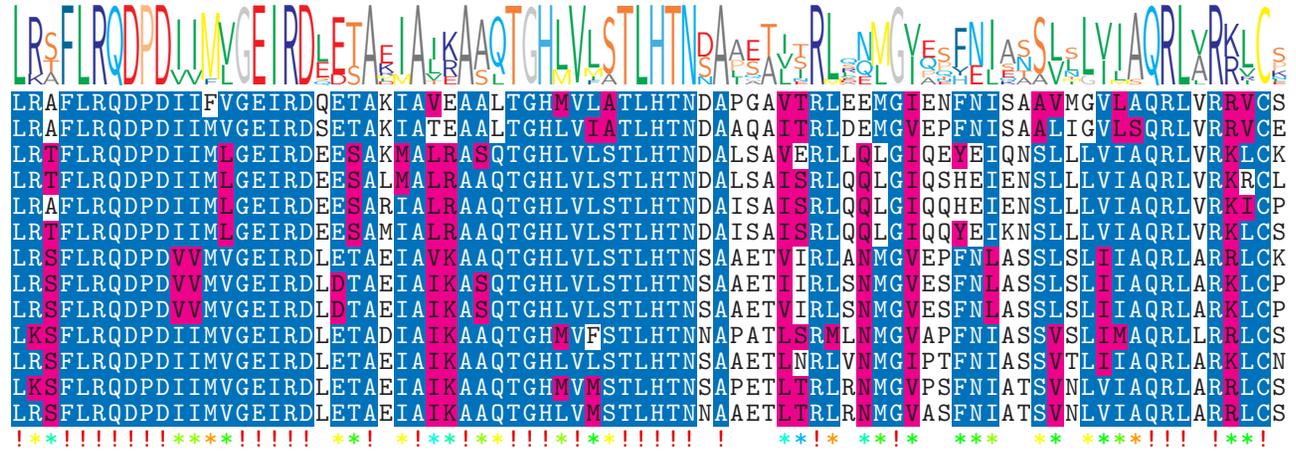
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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEIVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKIRPEALAAQAVATQLGYPVVDPEE	397
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NTDB id 1293 VP RS12240 WP 005479695.1MHSNLSLIRQKGLLTFSSQEEESLIEQVKASGISMPEALSSGFFTSSELAEHLSSIFGLSQPELSQ	66
NTDB id 1401 DSB67 RS12665 WP 010643259.1MLTNLSTVLRQAGILTFSQEEESLLEQVKASGISMPEALSSGFFQSHETEHSSVFGLSCTSLNQ	66
NTDB id 1110 NGFG RS09235 WP 003689817.1MSVGLLRILVQNQVVTVQAEHYY.NESQAGKEVLPMLFSDGVI SPKSLAAL IARVFSYSILDLRH	65
NTDB id 1251 GCO85 RS07725 WP 011946523.1MALATEEYRLQGIGQLVLEKLLDKTKAIELHKLAAAEEKISLQYLVKNKILSAEQIALTAQNFQVPLMDINC	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAAKRAKQDTVAYLDEEVHISPSLLAETISAFAEPYFDLDV	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDVPYLDNFSISPLTIAEILSLEFGEPLLDLGV	74
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NTDB id 1306 DR RS10060 WP 027479822.1	NPPDPKVALIPEATARRVYVVPVRLQGNSLVVAMKDFRNVFALDDLKLTG.....KEILPAVMAEKDIRLIERFYFGE	472
NTDB id 1028 TT RS08215 WP 011173991.1	DPPDPGAPLILPEDTCRRYGVFPHRLEGNRLVLLMKDPRNLLALDDVRLALKRKGLNVEVAPAVATEAAITKLIERFYGK	477
NTDB id 1384 A4U84 RS08525 WP 010787006.1	ISPSRWQKNCEEKQLLLRYLAVPVQETEHKLLAVDDENMLTACEIFAFMTH.....KQTEPVVITASDELYLNAISPE	91
NTDB id 1123022 EL215 RS00260 WP 126469443.1	ISPQYWQQNQKQLLLRYFALPLKEDEHHLVAVDSLNMIAACETFAFLSG.....KLVEPILFETHQLKQLLQSLAPK	89
NTDB id 1366 NTHI RS01950 WP 011271972.1	ISPDLWERNQQQSSLLRYFALPLKEENRNLWLVDSLSNLSACETIAFITG.....KPVEPILLESSQLKELLQQLTPH	96
NTDB id 1355 HI 0298 AAC21962.1	ISPDLWERNQQQSSLLRYFALPLKEENRNLWLVDSLSNLSACETIAFITG.....KPVEPILLESSQLKELLQQLTPN	96
NTDB id 1168 A1552VC RS11070 WP 000957200.1	YDYANLCQQTGLRELI TRYDALPIAKQGNLLVAVSDPTLLQAEEEFRFATG.....LQVELLADHRAALQAARRLYGR	141
NTDB id 1293 VP RS12240 WP 005479695.1	YEYASLCQQTGLRELI TRHNAIPLHRTPTSTLLVAVADPTNQAEDDFRFATG.....LQVELVLADEFRELTAAIRRYGR	141
NTDB id 1401 DSB67 RS12665 WP 010643259.1	YEYASLCQTLGLRDLITRHNALPLNRTSSTLLVAVADPTNQAEDDFRFATG.....LQVELVLADEFRELTAAIRRYGR	141
NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQVVEHCVPVFRRGDKVFAVSDPTQMPQIQKTVSAAQ.....IAVELVIVEDDQLAGLTDWVGR	140
NTDB id 1251 GCO85 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKL SALIDNLLTA	149
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMAIRFNSK.....LKVEPVIVEHDKLERLISEHFVE	149
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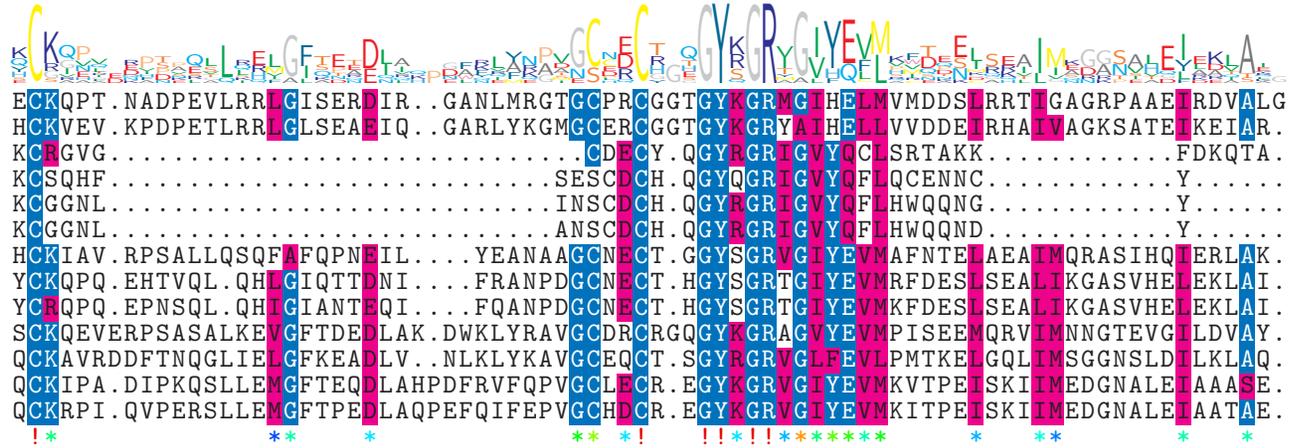


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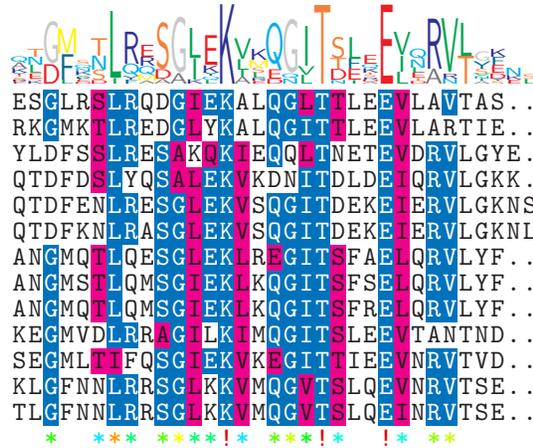


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consensus

 non conserved
 similar
 $\geq 50\%$ conserved