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NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAALLDQGYLGNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIYVPPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	LSMLRSDALRLRLAVPVDETEQGVTVLTSDPRKRDPIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGLGEQLVQEGTLSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGEVITELGFASPDVDSALQKQNVGGRLLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ	397
NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGRLLEDTLVQSGKLRPEALAAQAVATQLGYPPVDPEE	397
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NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSITLRQKGLLTFSQEESLIEQVKASGISMPEALLSSGFFTSSSELAEHLSSIFGLSQPELSQ	66
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NTDB id 112402 A6L30 RS04925 WP 002221967.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMLFSDGVISPKSLAALIARVFSYSILDLRH	65
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NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHLKLA AEKISLLQYIVKNKILSAEQIALTAAQNFGVPMLDINC	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVSAAATMTALDAAKRAKQDVTAYLIEEVHLSPSLLAETISAEFAEYPFDLDV	74
consensus	* * * * *	

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NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
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consensus

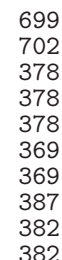
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consensus

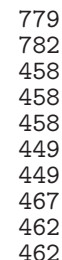
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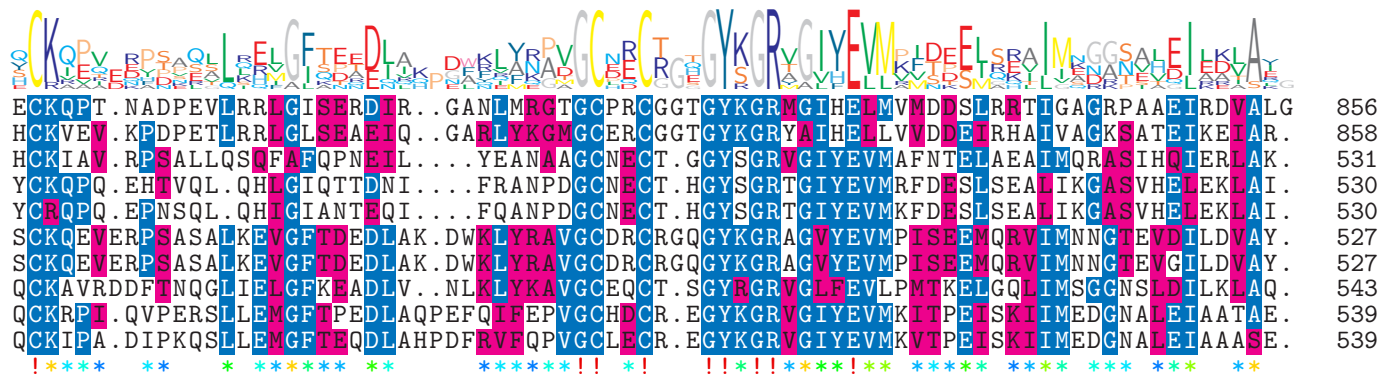
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consensus

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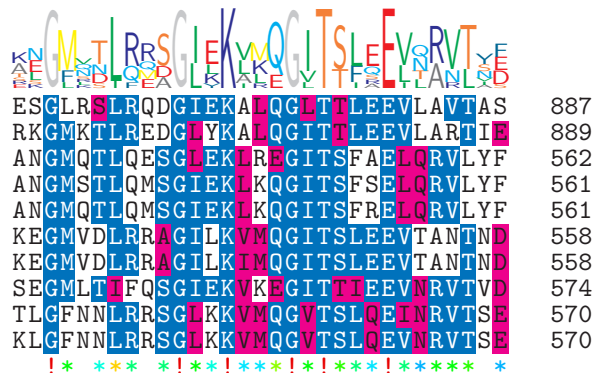
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consensus

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- X non conserved
- X similar
- X ≥ 50% conserved