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		MSXLRIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPPDPAAL	79
NTDB id 1306 DR RS10060 WP 027479822.1		.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1		MSVLTIGDKRRLGAILLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		.....	0
NTDB id 1293 VP RS12240 WP 005479695.1		.....	0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		.....	0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		.....	0
consensus		.....	0

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		RSIRPQTALNLQAPFFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1306 DR RS10060 WP 027479822.1		RSIRPQTALNLQAPFFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1		ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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consensus		.....	0

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NTDB id 1028 TT RS08215 WP 011173991.1		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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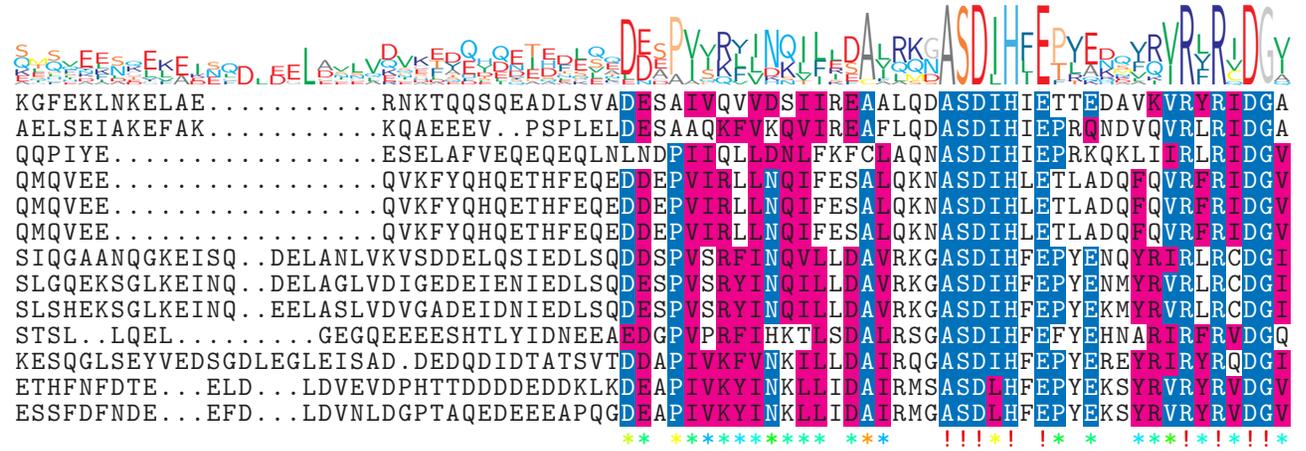
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NTDB id 1251 GC085 RS07725 WP 011946523.1	.....MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNFVGPMLDINC	74
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	.....MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAKRAKQDTVAYLIEEVHLSPSLLAETISAFAEPEYFDLDV	74
consensus	.....*.....**.....*	

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NTDB id 1384 A4U84 RS08525 WP 010787006.1	ISPSRWQKNCEEKQLLLRYLAVPVQETEHKLLAVDDENNLTACEIFAFMTH.....KQTEPVVVIASDELKYLINALSPE	91
NTDB id 119701 NTHI477 RS06655 WP 011271972.1	ISPDLWERNQQQQSLLRYFALPLKEENRNLWLGVDLSNLSACETIAFITG.....KPVEPILLESSQLKELLQQLTPH	96
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NTDB id 1110 NGFG RS09235 WP 003689817.1	YPRHRVLMGVLTEEQMVVEHCVFVFRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDQVGSR	140
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLLIKHRIPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHKKLEKVLGQHFVAE	149
consensus	*.....**.....*!*.....*****.....*.....*	

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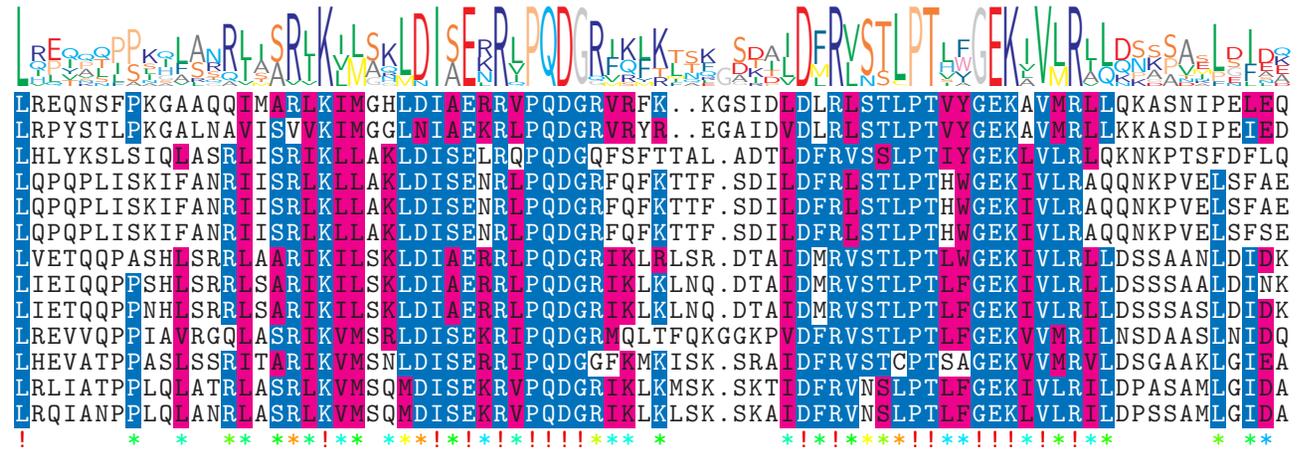
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 consensus



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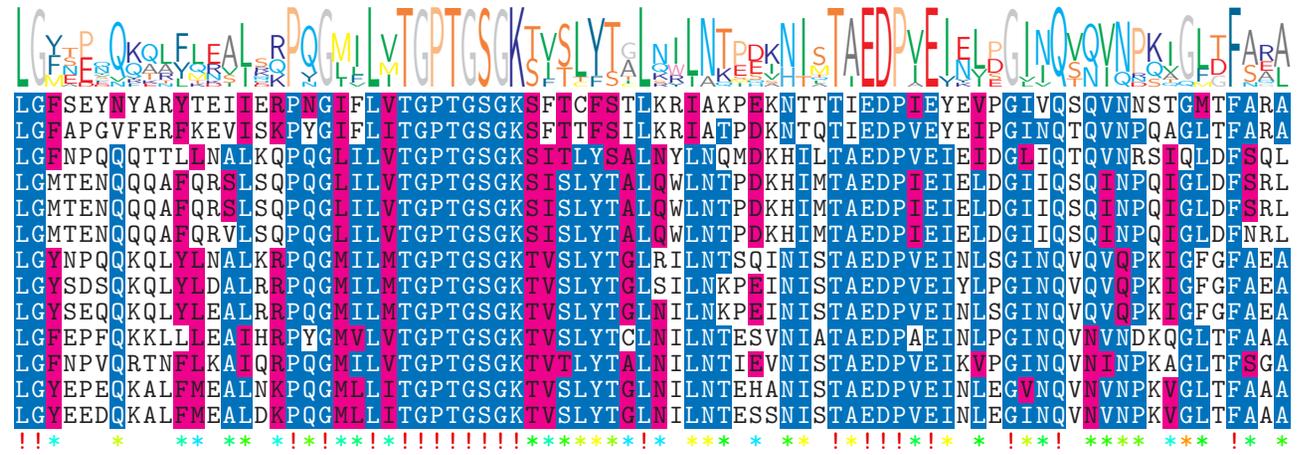
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 consensus



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 consensus



699  
702  
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 non conserved  
 similar  
  $\geq 50\%$  conserved