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NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRRLGAALLDQGYLGDNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
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NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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
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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDLRLVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFGHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKQWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1028 TT RS08215 WP 011173991.1	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
NTDB id 1384 A4U84 RS08525 WP 010787006.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	0
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NTDB id 1028 TT RS08215 WP 011173991.1	EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLIEDTLVQSGKLRPEALAAQAVATQLGYPYVDPEE	397
NTDB id 1384 A4U84 RS08525 WP 010787006.1	MSQYTI.....CEQQTERIFD.....	16
NTDB id 1355 HI 0298 AAC21962.1	MTSYALLHTQRVTAKNGEVFT.....	21
NTDB id 385768 F1537 RS04535 WP 013525533.1	MTSYALLHTQRVTAQNGEIFT.....	21
NTDB id 1366 NTHI RS01950 WP 011271972.1	MTSYALLHTQRVTAQNGEIFT.....	21
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAIILRQAELISATQEQAVVTQVSASGTSVPEALLLSIFHAQELTEQLSHIFGLPETDLSR	66
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NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMFLSDGVISPKSLAALIARVFSYSILDLRH	65
NTDB id 1251 GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEEKISLLQYIVKNKILSAEQIALTAAQNFQVPMMLDINC	74
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEITISLEFCEPLLDLGV	74
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVVEEKHVSAAATMQTALDAAKRAKQDTVAYLIEEVHLSPSLLAETISAEFAEYPFDLDV	74
consensus	*.....*	

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NTDB id 1384 A4U84 RS08525 WP 010787006.1	ISPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTH.....KPVEPILLESSQLKELLQQLTPN	91
NTDB id 1355 HI 0298 AAC21962.1	ISPDWLERNQQQQLLLRYFALPLKEENNRLWLGVDLSNLASACETIAFITG.....KPVEPILLESSQLKELLQQLTPN	96
NTDB id 385768 F1537 RS04535 WP 013525533.1	ISPDWLERNQQQQLLLRYFALPLKEENNRLWLGVDLSNLASACETIAFITG.....KPVEPILLESSQLKELLQQLTPH	96
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NTDB id 1401 DSB67 RS12665 WP 010643259.1	YEYASLCQTLGLRDLITRHNAIPLNRTSSTLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAATIRRLYGR	141
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NTDB id 1251 GC085 RS07725 WP 011946523.1	IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDPPSKQASLKEITQFHTG.....LNTHAIVVETDKLSALIDNLLTA	149
NTDB id 1018 ACIAD RS01685 WP 004920473.1	FDPALFLDKIDKEKLIQKIRIMPLVHRGHVLYATNSPTNIEAMDAIRFNSK.....LKVEPIIVEHDKLIERLLSEHFVE	149
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YDTSQIPKDLVDQKLILKHRIIPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE	149
consensus	* ** * ! * * * * * * * * * * * * * * * * * * *	

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consensus

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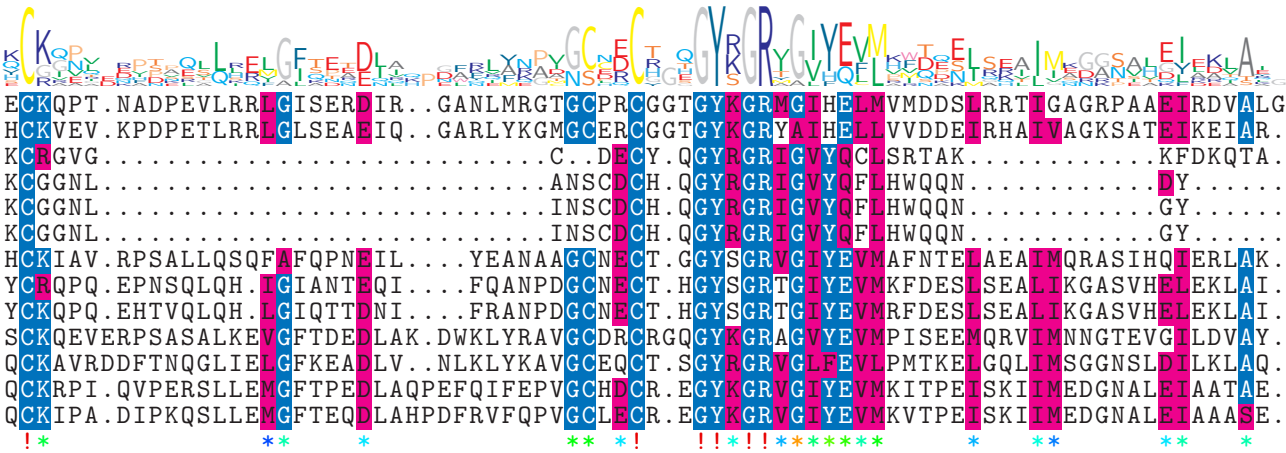
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consensus



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782
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consensus



856
858
429
431
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431
531
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539

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consensus



887
889
461
464
464
464
562
561
561
558
574
570
570

 non conserved
 similar
 $\geq 50\%$ conserved