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NTDB id 1306 DR RS10060 WP 027479822.1	MSXLTIGDRRLGAALLDQGYLGDNDLQRALERHSEVGGRLADVLIIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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NTDB id 43995 K6J58 RS03610 WP 005686724.1		0
NTDB id 1366 NTHI RS01950 WP 011271972.1		0
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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
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAVFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKQWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVDPDSAA	237
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NTDB id 1306 DR RS10060 WP 027479822.1	GSMLRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRGLGEQLVQEGTLSR	317
NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1355 HI 0298 AAC21962.1		0
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Sequence	Position
DQLREALQVQAREGKVKPLGEVITELGFASPDVEVDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDP	1-100
EALKEALEVQKGLPRAKPLGEILVELGLARPEDVEEALQKQRRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEE	1-100
.....MT.....SYALLHTQRVTAKNGEVFTT.....	21-30
.....MT.....SYALLHTQRVTAQNGEIFTT.....	31-40
.....MT.....SYALLHTQRVTAQNGEIFTT.....	41-50
.....MS.....QYT.....ICEQQTERIFDI.....	51-60
.....M.....QYS.....VCDMNSQQVFDI.....	61-70
.....MNIPIQL.....	71-80
.....MLTNLVAIRQAELISATQEAVVTQVSASGTSVPEALLLSIFHAQETLQLSHIFGLPETDLSR	81-90
.....MLTNLSTVLRQAGILTFQSQESLLEQVKASGISMPEALLSSGFFQSHELTLEHLSVFGLSCTSLNQ	91-100
.....MLHNSLSTILRQKGLLTFQSQESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSLQ	101-110
.....MSVGLLRILVQNQVVTVEQAEHYYNESQAGKEVLPMLFSDGVTSPKSLAALIARVFSYSILDLRH	111-120
.....MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNFQVPMLDINC	121-130
.....MSALHTSPKFTGFFRRILVEEKHVSAAATMQTALDAAKRAKQDTVAYLIEEVHSPSLLAETISAEFAEPYFDLDV	131-140
.....MSAFTTPPKFSGFIRRLVEEGYVNAQNMMQALEKAKKFQKQITVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGV	141-150

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NPPDPKVALMIPEATARRYVVVPVRLQGNSLVVAMKDPNRNVFALDDKLITG....KETLPVAVMAEKDIIRLTIERYFGE	472
DPPDPGAPLLLPEDLCRRYGVFPHRLEGNRLVLLMKDPNRNILALDDVRLALKRKGGLNYEVAPAVATEAAITKLTIERFYGK	477
.SPDLWERNQQQQSLILRYFALPLKEENNRLWLGVDLSNLSACETIAFITG....KPVEPILLESSQLKELLQQLTPN	96
.SSDLWARNQQQQSLILRYFALPLKEENNRLWLGVDLSNLSACETISFITG....KPVEPILLESSQLKELLQQLTPH	96
.SPDLWERNQQQQSLILRYFALPLKEENNRLWLGVDLSNLSACETIAFITG....KPVEPILLESSQLKELLQQLTPH	96
.SPSRWQKNCEEKQLLLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTH....KQIEPVVVIASDELYLLNALSPE	91
.SESLWQKNCDEKHILLRYLAIPITQENDDTLWLATDDMNNLSACEIFAFIAH....KTIEPVLITSSDELYLLNQLSPE	90
.....TALCLRYHGVLLDASEEVVHVAVVDAPSHEDDALLHFATT....KRITTCWTRQMEGHA.....	63
YDYANLCQQLGLRELITRYDALPIAKQSNLLLVASDPTLLQAEFEFRFATG....LQVELVLADHRAQLQAATIRRLYGR	141
YEYASLCQTLGLRDLITRHNALPLNRSTSLILAVADPTNLQAEDDFRFATG....LQVELVLADFRELTAAATIRRLYGR	141
YEYASLCQQLGLRELITRHNALPLHRTPTSTLLVADPTNLQAEDDFRFATG....LQVELVLADFRELTAAATIRRLYGR	141
YPRHRVLMGVLTEEQMVFEHCVVFRRGDKVFFAVSDPTQMPQIQKTVSAAG....IAVELVIVEDDQLAGLLDWVGSR	140
IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEITQFHTG....LNTHAIVVETDKLSALIDNLLTA	149
YDTSQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNTEAIDAIRFNSK....LLVEPVIVEHHKLEKVLGQHFAE	149
FDPALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNTEAMDAIRFNSK....LKVEPVIIVEHDKLERLLSEHFVE	149

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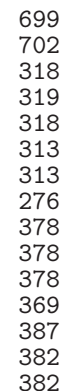
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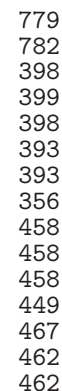
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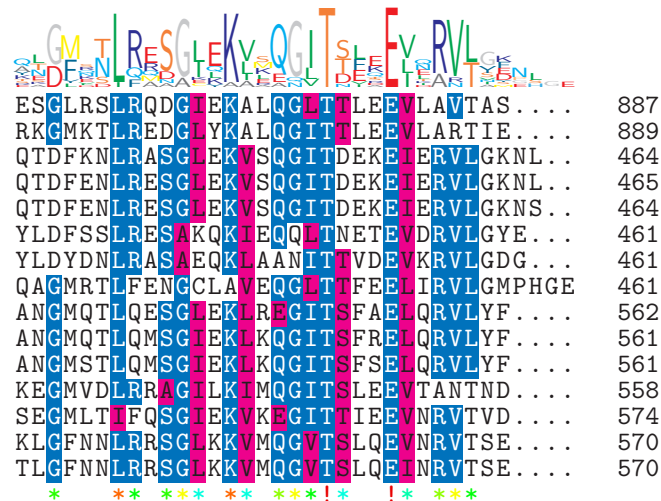
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consensus

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- ☐ non conserved
- ☒ similar
- ☒ > 50% conserved