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NTDB id 1306 DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
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NTDB id 1384 A4U84 RS08525 WP 010787006.1	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 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	SIRPQTALNLQAFPFALEGDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIVVPSGASDA	160
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NTDB id 1058 ABD1 RS01615 WP 001274986.1	0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVLGSM	240
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 consensus

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REALQVQAREGKVKPLGEVITELGFASPDEVDSALQKQNVGGRIEDTLVQSGKLSPEMLARSIAAQLGYEFLDPIQNPP 400
 MSQYTI.....CEQQTERIFD.....ISP 19
 MSQYTI.....CEQQTERIFD.....ISP 19
 MTSYALLHTQRVTAQNGEIFT.....ISP 24
 MTSYALLHTQRVTAQNGEVFT.....ISP 24
 MLTNLVAIIRQAELISATQEAVVTVQSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSTRYDY 69
 MHSNLSTILRQKGLTFSQEESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQY 69
 MLTNLSTVLRQAGILTFSQEESLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFCLSCTSLNQY 69
 MSVGLLRILLVQNQVVTVEQA EHYH.NESQAGKEVLPMLFSDGVTSPKSLAALIAARVFSYSILDRLRHY 68
 ...MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFVGPMLDINCIDV 77
 ...MSAFTTPPKFSGFIRRLVVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEITISLEFGEPLLDLVDFDP 77
 ...MSALHTSPKFTGFRRLLVEEKHVSAAATMQTALDAAKRAKQDVTVAYLIEEVHLSPLSLAETISAEFAEYPFDLDVYDT 77

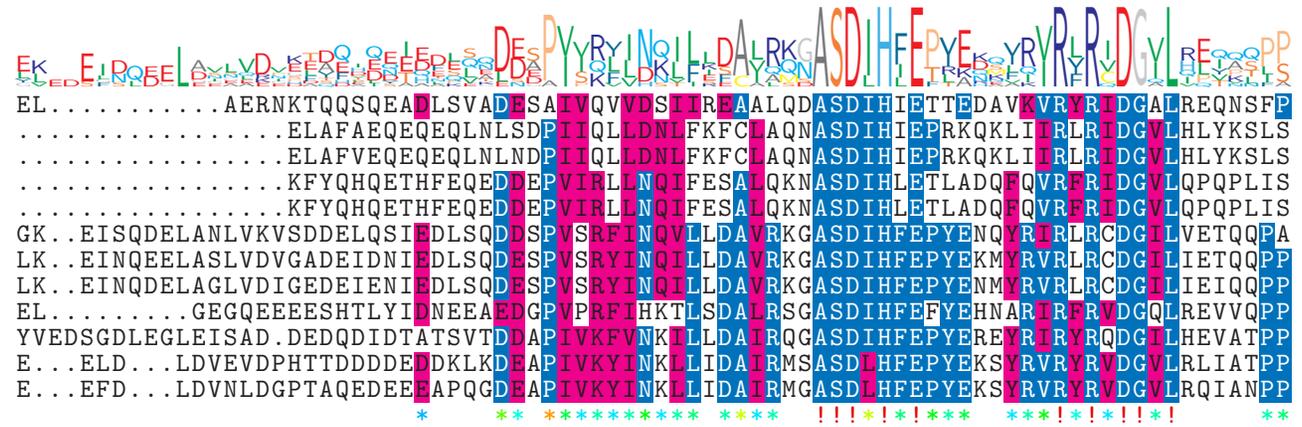
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 consensus

DPKVALMIP EATARRVYVVPVRLQGNSLVVAMKDPNRVFDLDDLKLTITGKETLPAVMAEKDITIRLTIERYFGEKGF EKLNK 480
 SRWQKNCEEKQLLLRRLAVPVQETEHKLLVAVDDENNLTA CEIFAFMTHKQIEPVVIASDELKYLNLNALSPEQQPFY EES 99
 SRWQKNCEEKQLLLRRLAVPVQETEHKLLVAVDDENNLTA CEIFAFMTHKQIEPVVIASDELKYLNLNALSPEQQPIY EES 99
 DLWERNQQQQSLLIRYFALPLKEENRLLVGVDSL SNLSACETIAFITGKPV EPILESSQLKELLQQLTPHQMQV EEQV 104
 DLWERNQQQQSLLIRYFALPLKEENRLLVGVDSL SNLSACETIAFITGKPV EPILESSQLKELLQQLTPNQMQV EEQV 104
 ANLCQQLGLRELITRYDALPIAKQGNL LLLAVSDPTLLQAE EEFRFATGLQVELALADHRALQAAITRRLYGRS IQGAANQ 149
 ASLCQQLGLRELITRHNALPLHRT PSTLLLAVADPTNQAEDDFRFATGLQVELV LADDFRELSTAIRRLYGRSL S S H E K S G 149
 ASLCQTLGLRDLITRHNALPLNRTSSTLILAVADPTNLQAEEDDFRFATGLQVELV LADDFRELSTAIRRLYGRSL G Q E K S G 149
 HRVLMGVLTEEQMV E F H C V P V F R R G D K V F F A V S D P T Q M P Q I Q K T V S A A G I A V E L V I V E D D Q L A G L L D W V G S R S T S L . L Q 146
 GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALTDNLLTAKESQGLSE 157
 ALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATS NPTNIEAMD AIRFNSKLLKVEPIIVEHDKLERLLSEHFVEETHFNFD T 157
 SQIPKDLVDQKLLIKHRIPLIQRGQILYVATS NPSNIEAIDAIRFNSKLLV E P V I V E H H K L E K V L G Q H F A E E S S F D F N D 157

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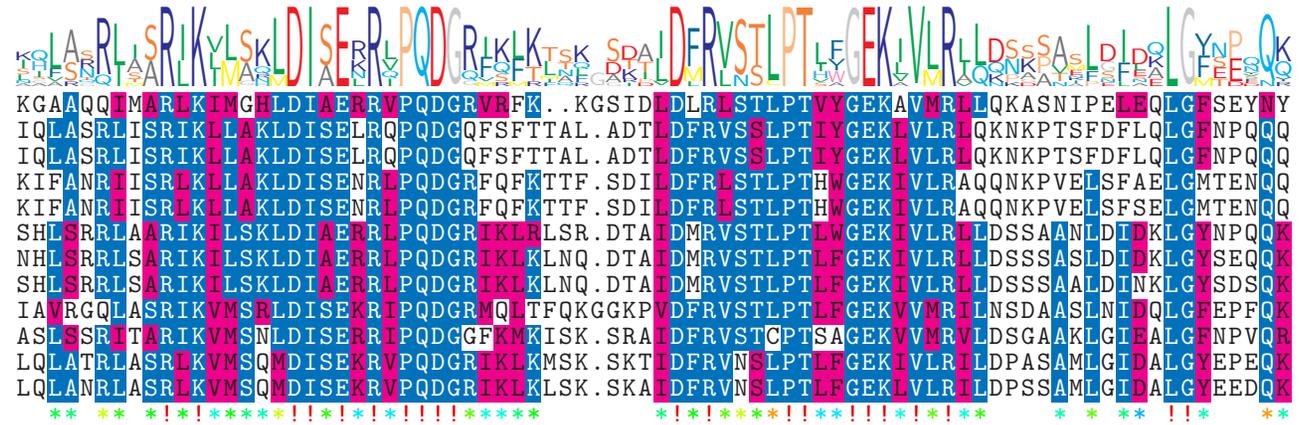
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 consensus



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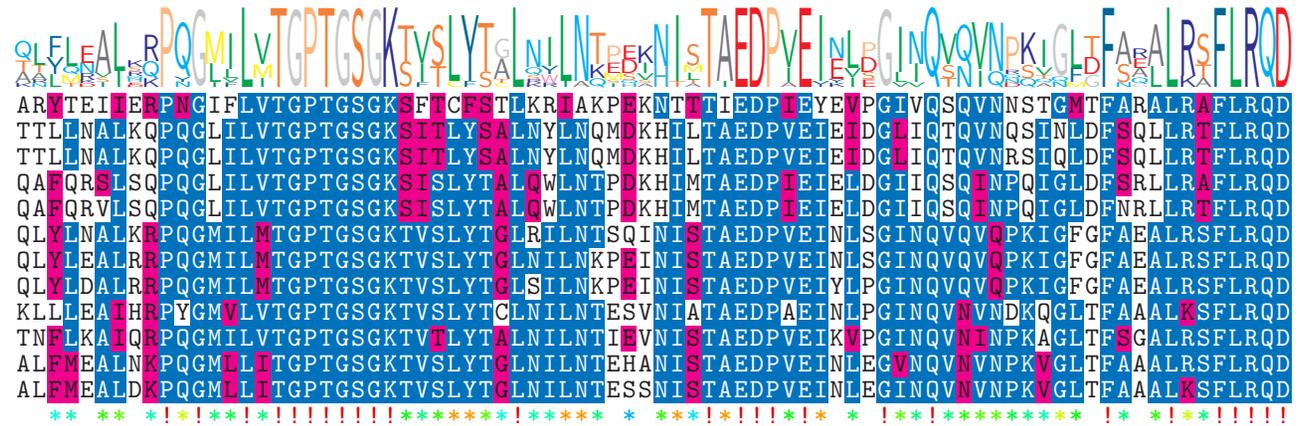
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 consensus



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