

logo

		MSXLSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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 1251	GCO85 RS07725 WP 011946523.1	0
NTDB id 1110	NGFG RS09235 WP 003689817.1	0
NTDB id 151082	ADJ79 RS09925 WP 050715822.1	0
NTDB id 1058	ABD1 RS01615 WP 001274986.1	0
NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
consensus			0

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		RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAVFLNPLDTLSEEEVDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVP...P	158
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NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
consensus			0

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		SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1028	TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKQWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVDPDSAA	237
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NTDB id 151082	ADJ79 RS09925 WP 050715822.1	0
NTDB id 1058	ABD1 RS01615 WP 001274986.1	0
NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
consensus			0

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 LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALPQAWHEELFRRAYPQKNRNLGEVLVQEGKLSR 317
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DQLREALQVQAREGKVKPLGEVITELGFASPDEVDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQ 397
 EALKEALEVQKGLPRAKPLGETLVELGLARPEDVEALQKQRGGGRLEDTLVQSGKLRPEALAQAVATQLGYPYVDPEE 397
MLTNLVAILRQAEILISATGEQAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSR 66
MLTNLSTVLRQAGILTFSSQEESSLIEQVKASGISMPEALLSSGFFQSHLTELHLSVVFGLSCTSLNQ 66
MHSNLSLILRQKGLLTFSSQEESSLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQ 66
MALATEEYRIQGIQGLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFQVPMIDINC 74
MSVGLLRILVQNVVTVVEQAHHY.NESQAGKEVLPMLFSDGVI SPKSLAALITARVFSYSILDLRH 65
 ...MATVESPAQAAPLPGLAHTLVMTGKLGQAADLYKKAQQSNKNFIAELTGSGAVSAFDLAHTISAFAAPLIDAAA 77
 ...MSAL...HTSPKFTGFFRRLVVEEKHVSAAATMTALDAAKRAKQDTVAYLITEEVHLSPSLLAETISAFAEPYFDLDV 74
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 consensus

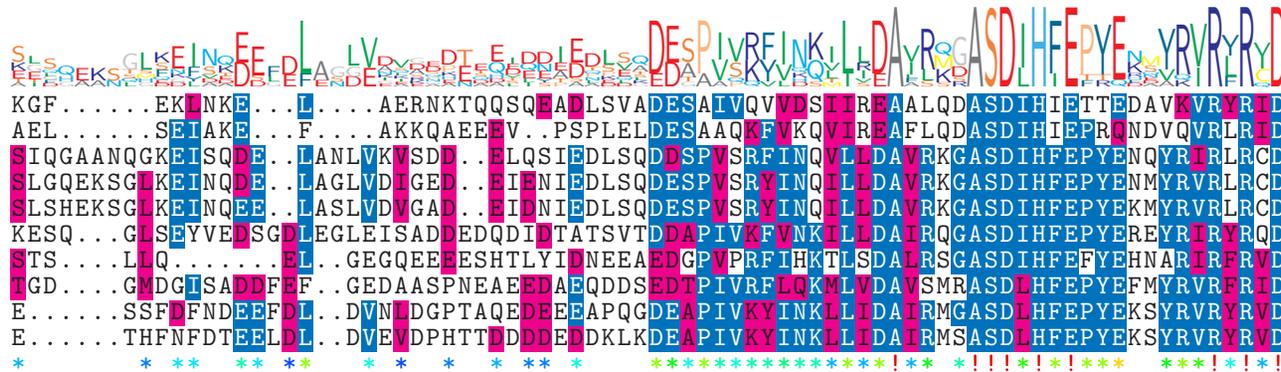
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 DPPDPGAPLLIPEDLCRRYGVFPHRLEGNRLVLLMKDPRNILALDDVRLALKRKGLNYEVAPAVATEAAITKLIERYFGK 477
 YDYANLCQQLGLRELITRYDALPIAKQGNLLLLAVSDPTLLQAEFFRFATG.....LQVELALADHRALQAAIRRLYGR 141
 YEYASLCQTLGLRDLITRHNALPLNRTSSLLILAVADPTNLQAEDDFRFATG.....LQVELVLADFRELTAAIRRLYGR 141
 YEYASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQAEDDFRFATG.....LQVELVLADFRELSTAIRRLYGR 141
 IDVGTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTA 149
 YPRHRVLMGVLTEEQMVEFHCVFVFRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDWVGSF 140
 IDPNRLPQDLIDRKLIVKYRILPLSKRGNRLIATADPTDNEAAEKVKFATQ.....MGVEWVIAEYDKLSHLIETATRG 152
 YDTSQIPKDLVDQKLLKHRILPLIQRQILYVATSNPSNIEATDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAE 149
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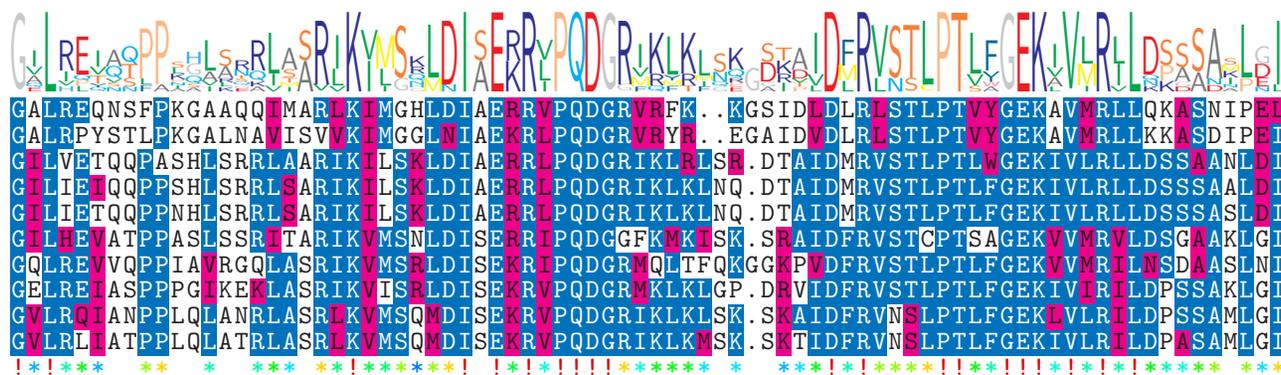
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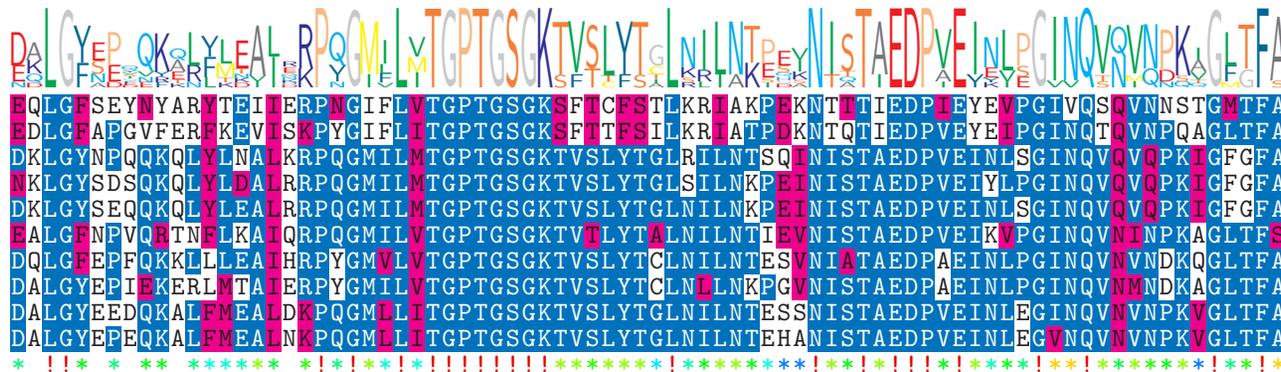
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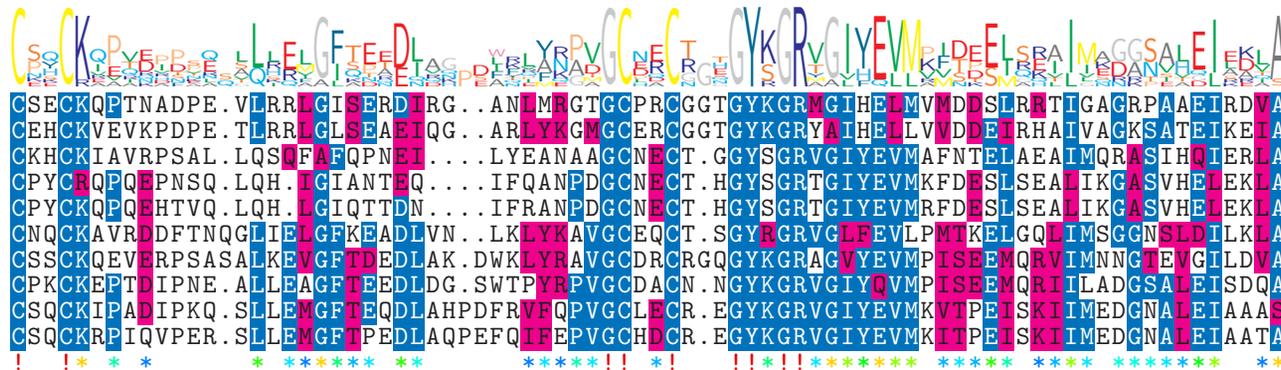
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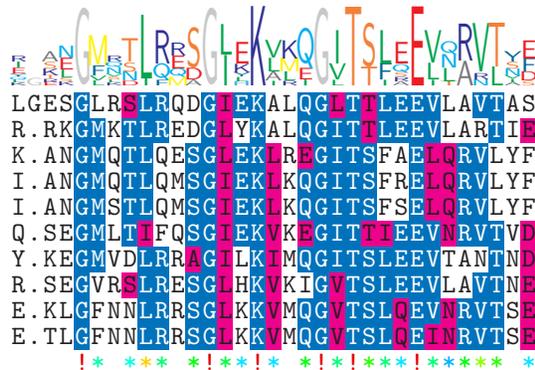
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non conserved
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