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NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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NTDB id 1468 ASU2 RS05090 WP 014991734.1		0
NTDB id 63191 AABJ68 RS18950 WP 001025193.1		0
NTDB id 1436 BW25113 RS00530 WP 001025145.1		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 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
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NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTDGDLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
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consensus		

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NTDB id 1028	TT RS08215 WP 011173991.1	LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	320
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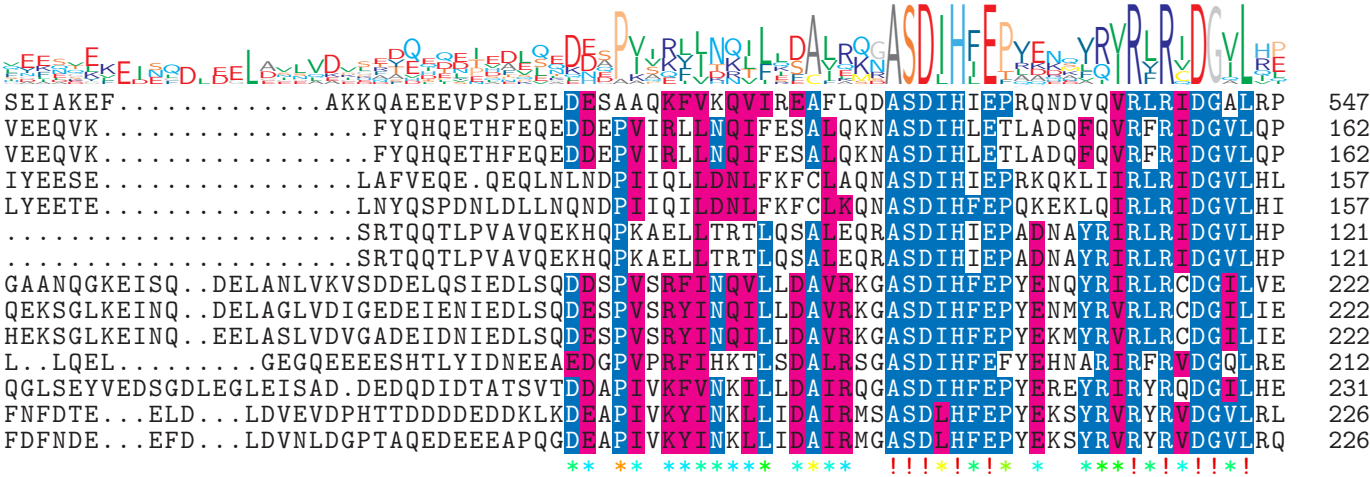
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NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMFLSDGVISPKSALAALIARVFSYSILDLRHYPR	68
NTDB id 1251	GC085 RS07725 WP 011946523.1	...MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFVPMPLDINCIDV	77
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NTDB id 1384	A4U84 RS08525 WP 010787006.1	SRWQKNCEEKQLLRLYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTHK....QTEPVVVIASDELKYLNLALSPEQ	94
NTDB id 1468	ASU2 RS05090 WP 014991734.1	SLWQKNCDEKHLILRYLAIPIQENDDTLWLATDDMNNLSACEIFAFIAHK....TIEPVLLISSDELKYLNLALSPEQ	93
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NTDB id 1436	BW25113 RS00530 WP 001025145.1	TALCLRYHGVLLDASEEVVHVAVVDAPSHELLDALHFATTK....RIEITCWTRQQMEGHA.....	63
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NTDB id 1401	DSB67 RS12665 WP 010643259.1	ASLCQTLGLRLDITRHNALPLNRTSSTLILAVADPTNLQAEDDFRFATGL....QVELVLADFRELTAATIRRLYGR	144
NTDB id 1293	VP RS12240 WP 005479695.1	ASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNLQAEDDFRFATGL....QVELVLADFRELSTAIRRLYGR	144
NTDB id 1110	NGFG RS09235 WP 003689817.1	HRVLMGVLTEEQMVFEHCVPVFRRGDKVFFAVSDPTQMPQIKTQVSAAGI....AVELVIVEDDQLAGLLDWVGR	143
NTDB id 1251	GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKETQFHTGL....NTHAIVVETDKLSALIDNLTAKES	152
NTDB id 1018	ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNTEAMDAIRFNSKL....KVEPIIVEHDKLERLLSEHFVEETH	152
NTDB id 1058	ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSKL....LVEPVIVEHHKLEKVLGQHFAEES	152
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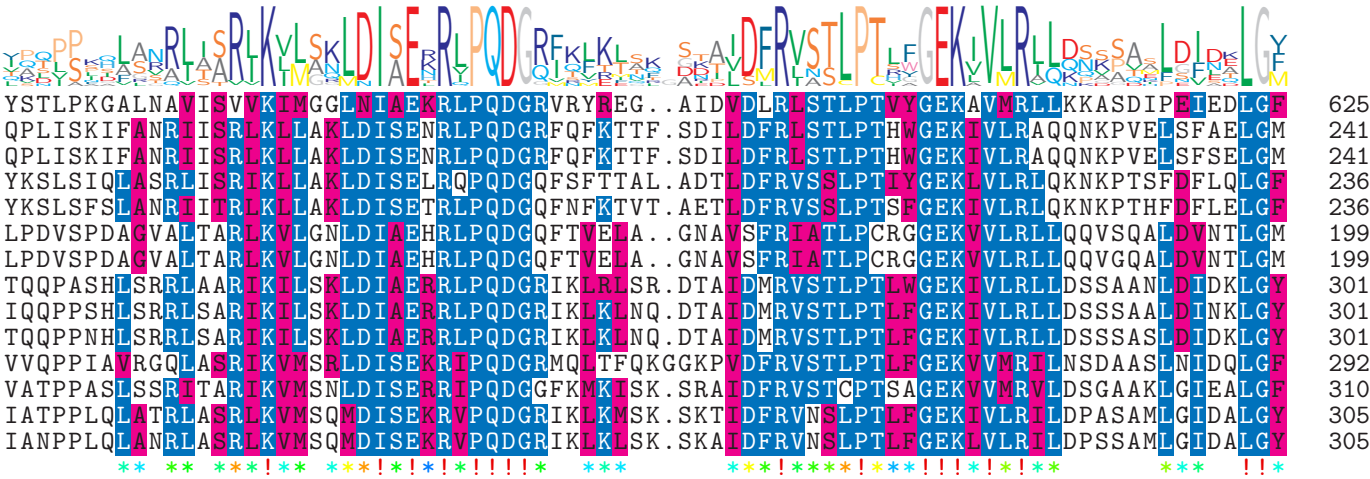
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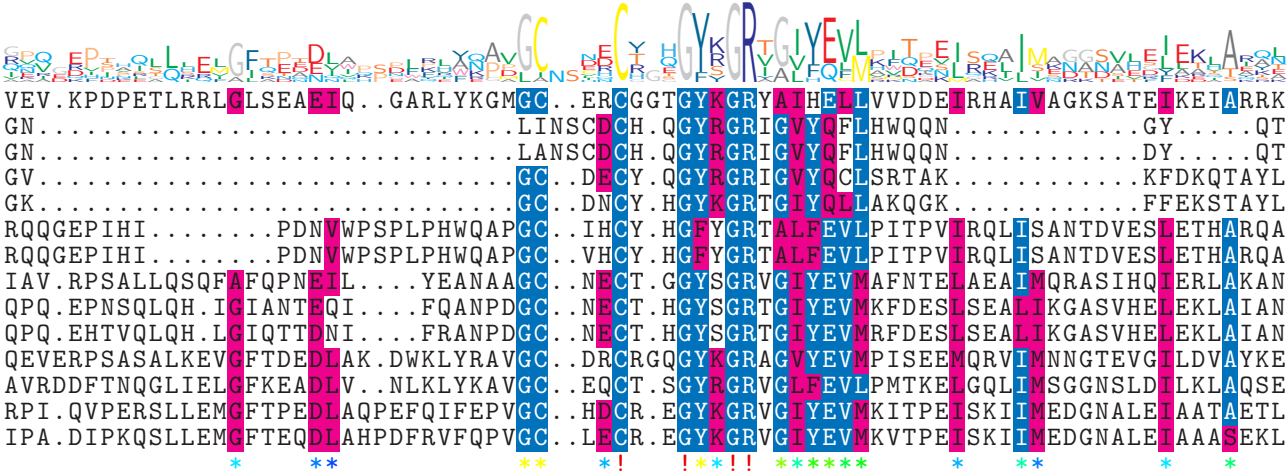
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consensus					



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 non conserved
 similar
 $\geq 50\%$ conserved