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NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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NTDB id 1293 VP RS12240 WP 005479695.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 242258 CJ086 RS02970 WP 075463376.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
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NTDB id 1251 GC085 RS07725 WP 011946523.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
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consensus	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0

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NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
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NTDB id 242258 CJ086 RS02970 WP 075463376.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
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consensus	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0

logo

NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
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NTDB id 242258 CJ086 RS02970 WP 075463376.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
NTDB id 1110 NGFG RS09235 WP 003689817.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
NTDB id 1251 GC085 RS07725 WP 011946523.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	0
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logo

NTDB id 1028 TT RS08215 WP 011173991.1	LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	320
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consensus	LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	0

logo

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NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLVAILRQAELISATQEQAQVITQVSASGTSVPEALLSIFHAQELTEQLSHIFGLPETDLSRYDY	69
NTDB id 1293	VP RS12240 WP 005479695.1	MLTNLSTVLRQAGILTFSQEESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQYDY	69
NTDB id 242258	CJ086 RS02970 WP 075463376.1	MHSNLSTILRQKGLLTFSQEESLIEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQYDY	67
NTDB id 1110	NGFG RS09235 WP 003689817.1	...MTLGLAL...AQSRRITAPTL.LTQLEQ....SAREKRTQLIDELVSSGIMSAHDLAVFVAGKYQMPLLDLAQYKL	68
NTDB id 1251	GC085 RS07725 WP 011946523.1	...MSVGLLR....IL....VQNNQ.VVTVEQAEHYYNESQAGKEVLPMFLSDGVISPKSLAALIARVFSYSILDLRHYPR	77
NTDB id 1058	ABD1 RS01615 WP 001274986.1	...MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNFVGPMLDINCIDV	77
NTDB id 1018	ACIAD RS01685 WP 004920473.1	...MSALHTSPKFTIGFFRRLVEEKHVSAAATMQTALDAAKRAKQDITVAYLIEEVHLSPLSLAETISAEFAEYFDDLVDVDT	77
consensus		...MSAFTTPPKFSGFIRRLVEEYGVNAQNMQALEKAKKFKQDITVPYLLIDNFSISPLTIAETISLEFGEPLLDLVGFD	77

logo

NTDB id 1028	TT RS08215 WP 011173991.1	DPGAPLLIPEDLCRRYGVFPHRLGEGNRIIVILMKDPRNIALDDVRLALKRKGLNVEVAPAVATEAAITKLIERFYGKAEL	480
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NTDB id 1110	NGFG RS09235 WP 003689817.1	HRVLMGVLTIEQMVEFHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVEDDQLAGLLDWVGSRTS	143
NTDB id 1251	GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGNTLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVETDKLSALIDNLLTAKES	152
NTDB id 1058	ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVEHHKLEKVLGQHFAEES	152
NTDB id 1018	ACIAD RS01685 WP 004920473.1	ALFLDKKIDELKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDAIRFNSK.....LKVEPVIVEHDKLERLLSEHFVEETH	152
consensus		LQVELVIVEHDKLVLRQLSLANEAPTE.....LNTHAIVVETDKLSALIDNLLTAKES.....LLVEPVIVEHHKLEKVLGQHFAEES	152

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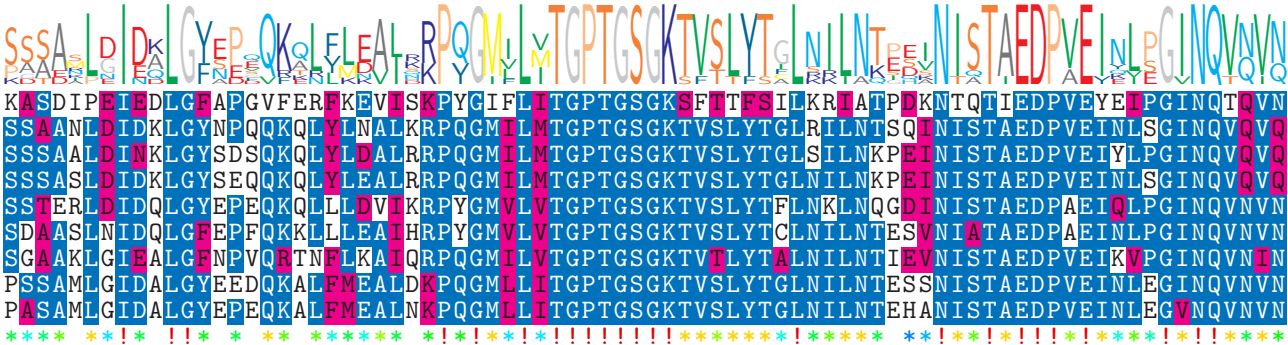
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NTDB id 1168	A1552VC RS11070 WP 000957200.1	GAANQGK...EISQDELANLVKV.SDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGILV	221
NTDB id 1401	DSB67 RS12665 WP 010643259.1	QEKSGLK...EINQDELAGLVDI.GEDEIENIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYENMYRVRRLCDGILI	221
NTDB id 1293	VP RS12240 WP 005479695.1	HEKSGLK...EINQDELASLVV.GADEINIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYENMYRVRRLCDGILI	221
NTDB id 242258	CJ086 RS02970 WP 075463376.1	I...KSLIP...KQEAQIEYDPGAAAVRRTTTDGIIDDAVPVVRFLQKLFTALLRGTSDLHFEPFETFYRVRFRIDGILA	217
NTDB id 1110	NGFG RS09235 WP 003689817.1	L..LQELG...E...GQEE...EESHTLYIDNEEAEDGPVPRFIHKTLSDALRSGASDIHFEPYEHNAIRIRFRVDGQLR	211
NTDB id 1251	GC085 RS07725 WP 011946523.1	QGLSEYVEDSGDLGLEISAD..DEDQDIDTATSVTDDAPIVKFVNKILLDAIRQGASDIHFEPYEREYRIRYRQDGILH	230
NTDB id 1058	ABD1 RS01615 WP 001274986.1	FDFNDE...EFD...LDVNLDG.PTAQEDDEEAPQGDDEAPIVKYINKLLIDAIRMGASDLHFEPYEKSYRVRVRVDGVLR	225
NTDB id 1018	ACIAD RS01685 WP 004920473.1	FNFDTE...ELD...LDVEVDP.HTTDDDDDDDKLKDDEAPIVKYINKLLIDAIRMSASDLHFEPYEKSYRVRVRVDGVLR	225
consensus		KQAEFEEVPSPLELDESAAQKFVKQVIREAFLQDASDIHIEPRQNDVQVRLRIDGALR.....EISQDELANLVKV.SDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGILV	225

logo

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NTDB id 1168	A1552VC RS11070 WP 000957200.1	ETQQPASHLSRRLAARIKILSKLDIAERRLPQDGRIKLRLSR.....DTAIDMRVSTLPTLWGEKIVLRLLD	288
NTDB id 1401	DSB67 RS12665 WP 010643259.1	EIQQPPSHLSRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.....DTAIDMRVSTLPTLFGKIVLRLLD	288
NTDB id 1293	VP RS12240 WP 005479695.1	ETQQPPNHLRRLSARIKILSKLDIAERRLPQDGRIKLKLNQ.....DTAIDMRVSTLPTLFGKIVLRLLD	288
NTDB id 242258	CJ086 RS02970 WP 075463376.1	QVAQPPLDIRDKIATRIKVLRLDISEKRVPPQDGRMKLLITVPKDKNDKDNKETIERAIDFRVSTLPTLFGKIVLRILE	297
NTDB id 1110	NGFG RS09235 WP 003689817.1	EVVQPPPIAVRGQLASRIKIVMSRLDISEKRIPQDGRMQLTFQK.....GGKPVDFRVSTLPTLFGKIVMRLILN	279
NTDB id 1251	GC085 RS07725 WP 011946523.1	EVATPPASLSSRITARIKIVMSNLDISEKRIPQDGGFKMKISK.....SRAIDFRVSTCPTSAGEKIVMRLVLD	297
NTDB id 1058	ABD1 RS01615 WP 001274986.1	QIANPPLQLANRLASRLKIVMSQMDISEKRVPQDGRIKLKLKSK.....SKAIDFRVNSLPTLFGKIVLRILD	292
NTDB id 1018	ACIAD RS01685 WP 004920473.1	LIATPPLQLATRLASRLKIVMSQMDISEKRVPQDGRIKLKLKSK.....SKTIDFRVNSLPTLFGKIVLRILD	292
consensus		AIDVDLRLSTLPTVYGEKAVMRLK.....DTAIDMRVSTLPTLWGEKIVLRLLD.....DTAIDMRVSTLPTLFGKIVLRLLD	292

logo

NTDB id	1028	TT	RS08215	WP	011173991.1
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NTDB id	1058	ABD1	RS01615	WP	001274986.1
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consensus					



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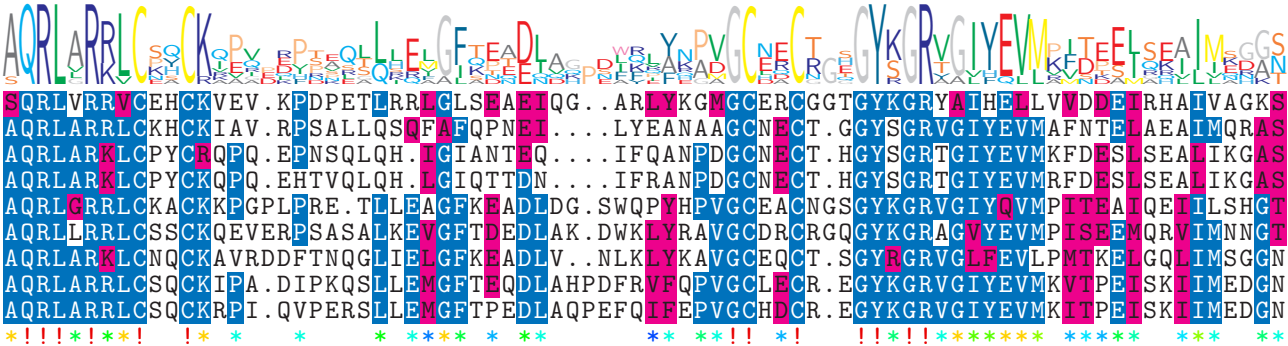
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consensus					



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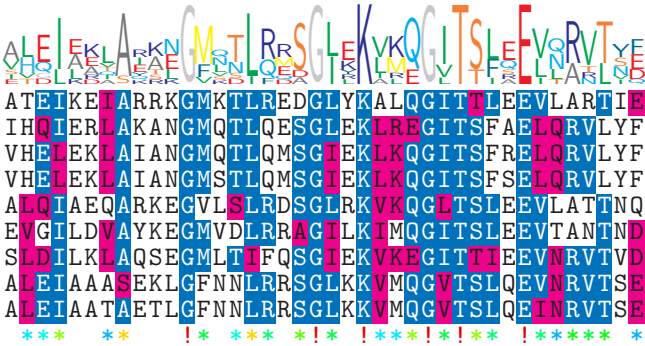
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consensus					



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NTDB id	1028	TT	RS08215	WP	011173991.1
NTDB id	1168	A1552VC	RS11070	WP	000957200.1
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NTDB id	1058	ABD1	RS01615	WP	001274986.1
NTDB id	1018	ACIAD	RS01685	WP	004920473.1
consensus					



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 non conserved
 similar
 $\geq 50\%$ conserved