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NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTITGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTTIEDRFGIPLVELHRVEIPPKVK	0
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NTDB id 1062733 ACG4IU RS10835 WP 000957200.1		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 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1410 SGL RS13950 WP 010873519.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTSKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTSKSAFLYALAKHYPELGLPVPPPPSG	160
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1410 SGL RS13950 WP 010873519.1	EGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	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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consensus		

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NTDB id 1410 SGL RS13950 WP 010873519.1	LRSDALRYGAVPIIGFQNGEVEVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	6
NTDB id 1028 TT RS08215 WP 011173991.1	LRSDALRYGAVPIGIFQNGEVEVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	320
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consensus		

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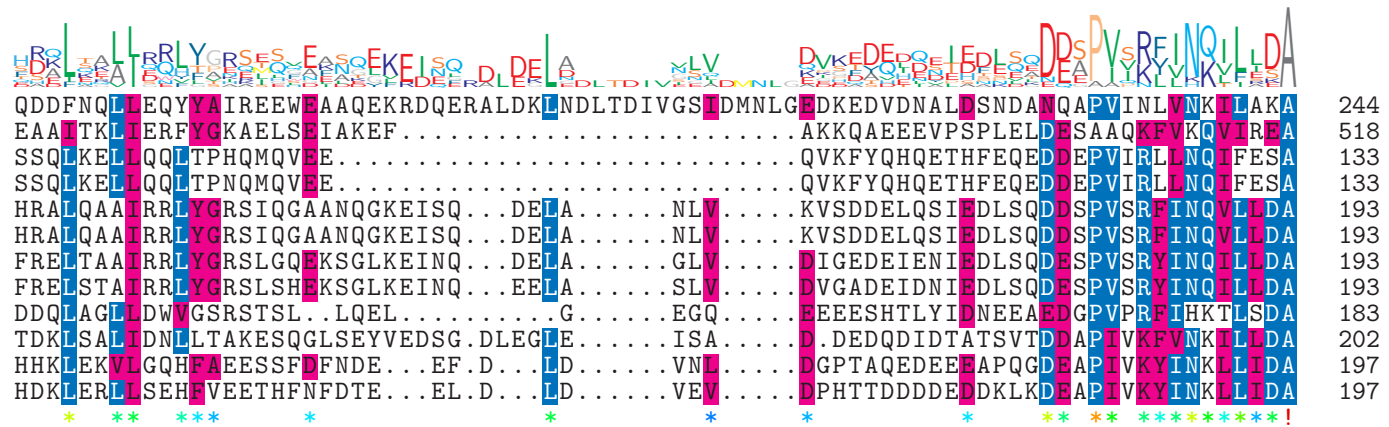
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NTDB id 1355 HI 0298 AAC21962.1	MTSY..ALLHTQRTVTAQ.....NGEIFT..	21
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NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAAILRQAEELISATREQAVVTQVSASGTSVPEALLLEL..SIFHAQELTEQ.....LSHIFGLP	60
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NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSLILRQKGLLTFQSQEESLLEQVKASGISMPEALLSS..GFFTSSELAEH.....LSSIFGLS	60
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNVVTVTEQAHEHY..NESQAGKEVLPMLFSD..GVISPKSLAAL.....IARVFSYS	59
NTDB id 1251 GC085 RS07725 WP 011946523.1	..MALATEEYRLQGIQGLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKN..KILSAEQIALT.....AAQNFQVP	68
NTDB id 1058 ABD1 RS01615 WP 001274986.1	..MSALHTSPKFTIGFFRRLLVEEKHVSAAATMQTALDAAKRAKQDVTAYLIEE..VHLSPSLLAET.....ISAFAEP	68
NTDB id 1018 ACIAD RS01685 WP 004920473.1	..MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDITVPLYIDN..FSISPLTLAEI.....ISLEFGEF	68
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NTDB id 1355 HI 0298 AAC21962.1	ISPDL.....WERNQQQSSLLRYFALPLKEEN...NRLWLGVDLSNLSACETIAFITG.....KPVEPILLE	82
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NTDB id 1401 DSB67 RS12665 WP 010643259.1	CTSLNQYAYAS....LCQTLGLRDLITRHNALPLNRTS...STLILAVADPTNLQAEDDFRFATG.....LQVELVLAD	127
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NTDB id 1110 NGFG RS09235 WP 003689817.1	ILDRLHYPRHR....VLMGVLTEEQMVFEHCVVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG.....IAVELVIVE	126
NTDB id 1251 GC085 RS07725 WP 011946523.1	MLDINCIDVGT....IPVNLVNEKLIKRRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAIVVE	135
NTDB id 1058 ABD1 RS01615 WP 001274986.1	YFDLDVYDTSQ....IPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNSK.....LLVEPVIVE	135
NTDB id 1018 ACIAD RS01685 WP 004920473.1	LLDLGVFDPAL....FLKDKIDEKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDIAIRFNSK.....LKVEPIIVE	135
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consensus

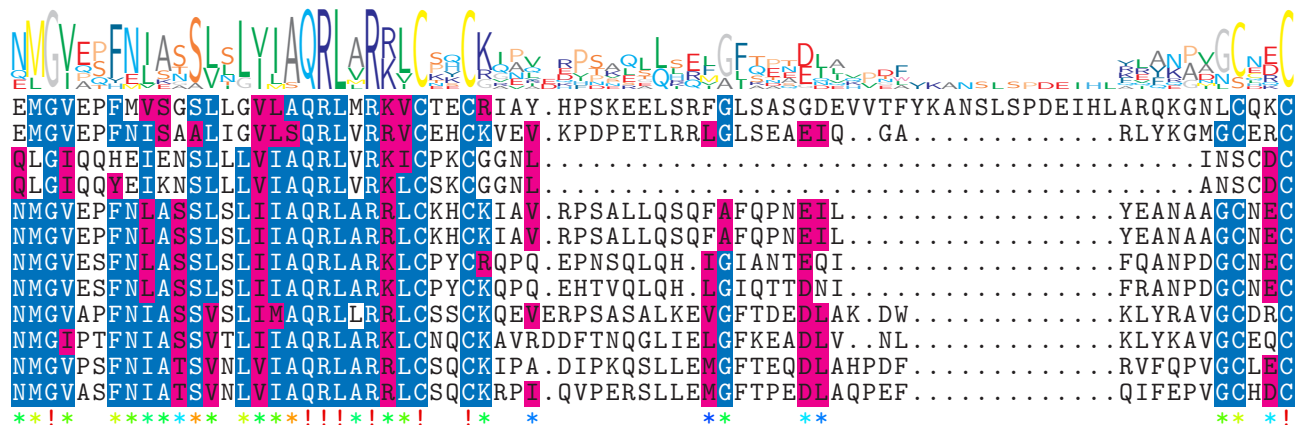


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consensus



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consensus



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889
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464
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NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved