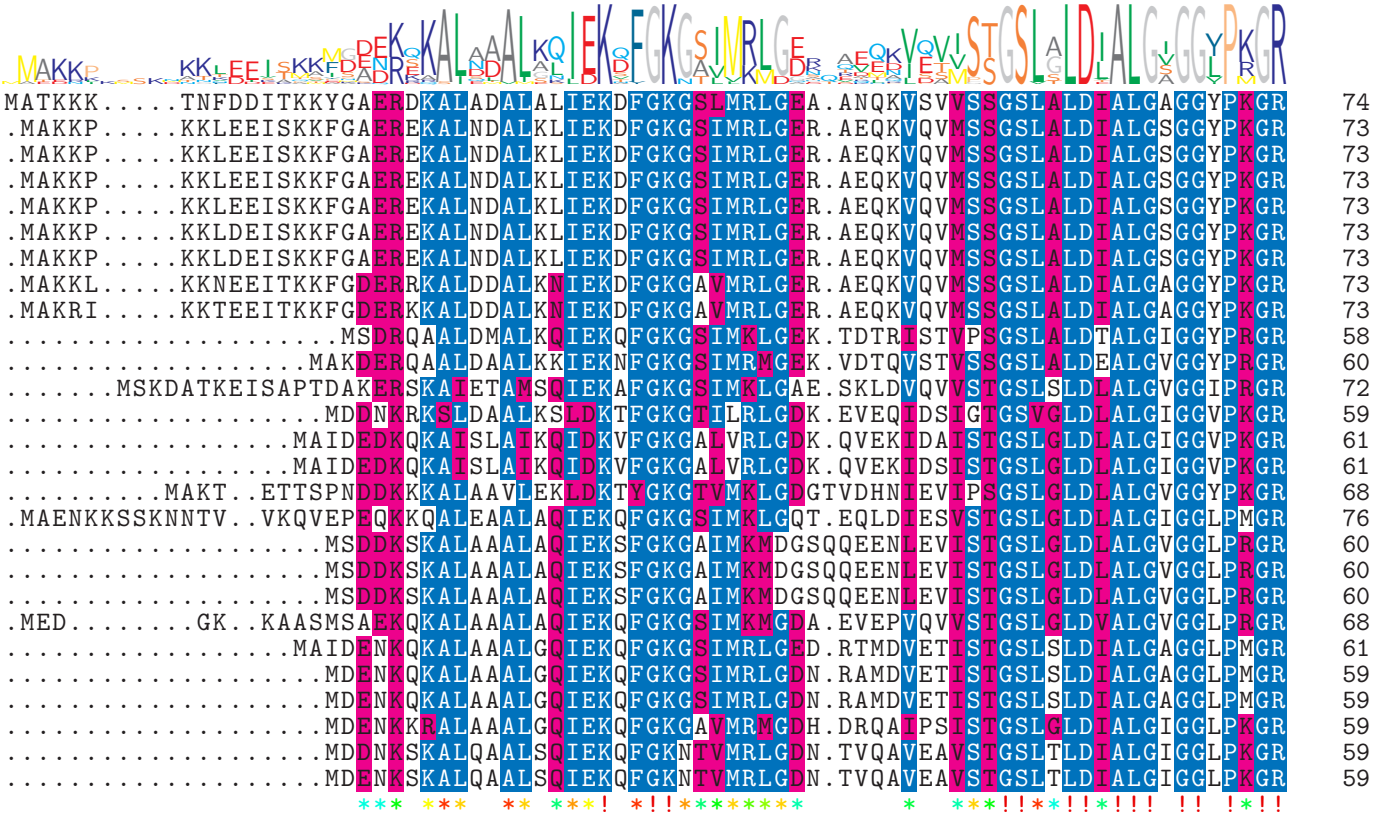


logo

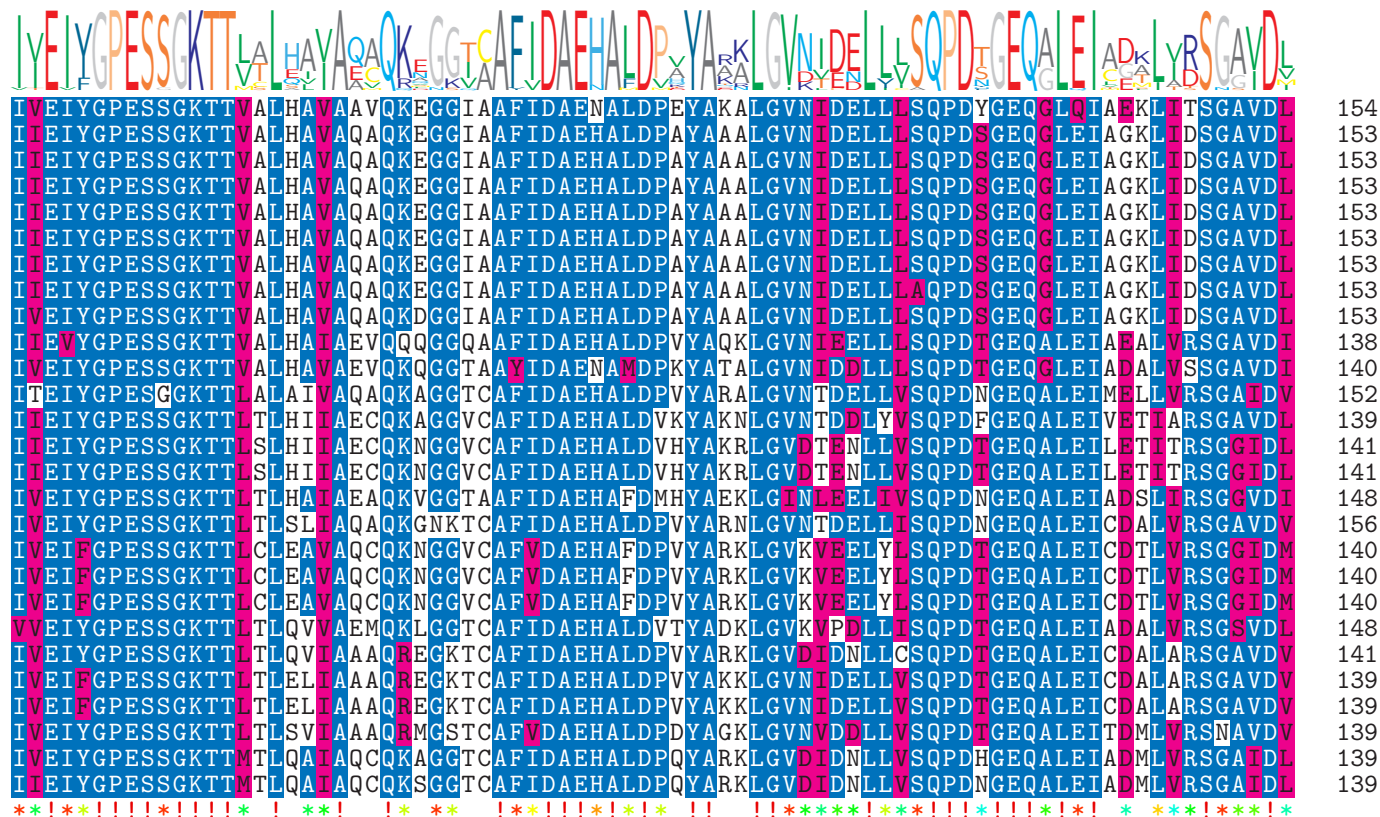
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NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
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NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1214 NCTC11637 00359 SQJ03206.1
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NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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Sequence	Score
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DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
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GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGQGR ENAKQFLKENKDIMLMIQE QIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGR ENAKNYLADHEDVEDEVRLKVR AAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGQGEKTIATIAERPMEQETIDRVM AAIRAGNAGEAPALAPAPAA . PEAEEA	363
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DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
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GAKIGQGDKNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
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GERIGQGRDNCREFLR ENAE LAREIENKVR EHLGVTPMGAVTLAAE . . VE . ED	352
GDKIGQGGKANAITWLKENPAAAEIEKKVRELLNNQDAKPD . . FV . . VD . GND AEETE QDF	352
GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLN PENMQLI . . AE TSSAAD DVEFGAVPEEF	354
GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLN PENMQLI . . AE TSSAAD DVEFGAVPEEF	354
GSKIGQGGKANAAKYLEENPEIGQETIEQQIRAKLLVTSANTKA . . TP . . VA . EDLADADI	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLT KASDQTA . . A . . HD . ETEEEPDLLES	349
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logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved