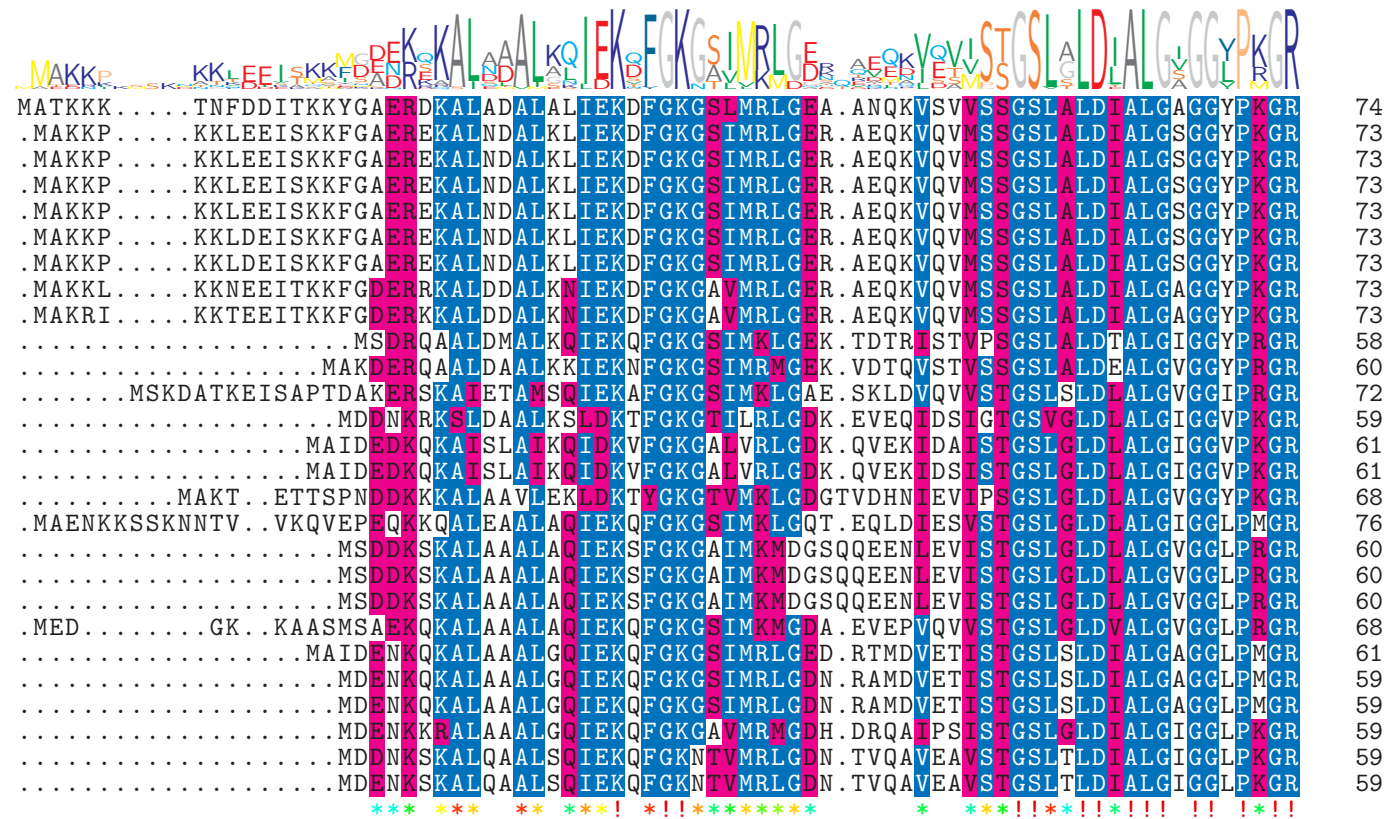


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NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 0004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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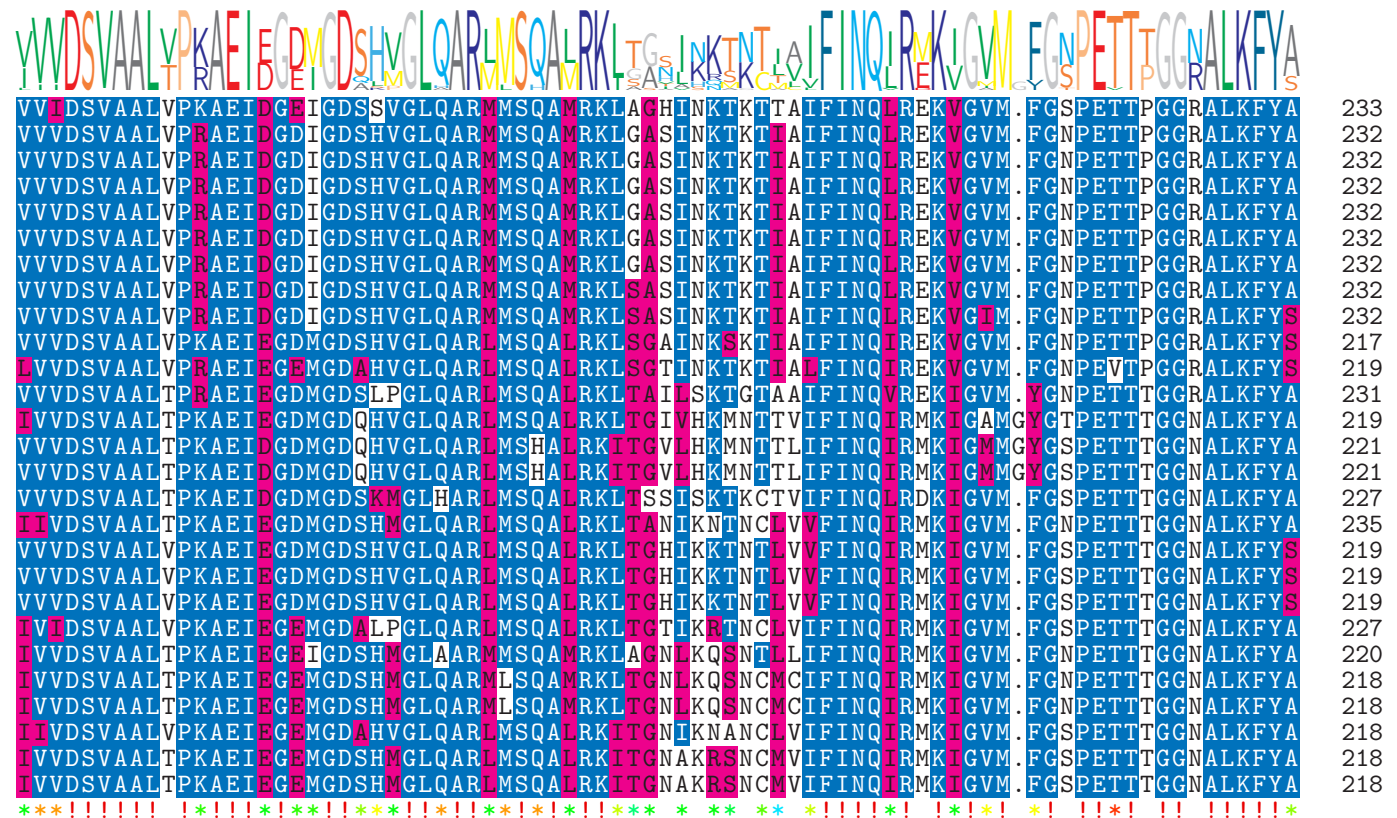
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE . . . SKKDE . . . VAQVDS . VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE . . . SKKDE . . . AAQVDS . VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGQKEKTIAYIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAA . PEAEEA	363
DKKLGQGRNSKAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDE . . GE . E	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
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GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAE . . VE . ED	352
GDKIGQGKANAITWLKENPAAAEIEKKVRELLNNQDAKPD . . FV . . VD . GNDAAETEQDF	352
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNMQLI . . AE TSSAADDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNMQLI . . AE TSSAADDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSANTKA . . TP . . VA . EDLADADI	347
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GNKIGGQKNNVIRYFENNQIAEIERNIREQLLTGTNGAV . . Q . . I . . EDEEEPDLLES	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349

consensus

 non conserved
 similar
 ≥ 50% conserved