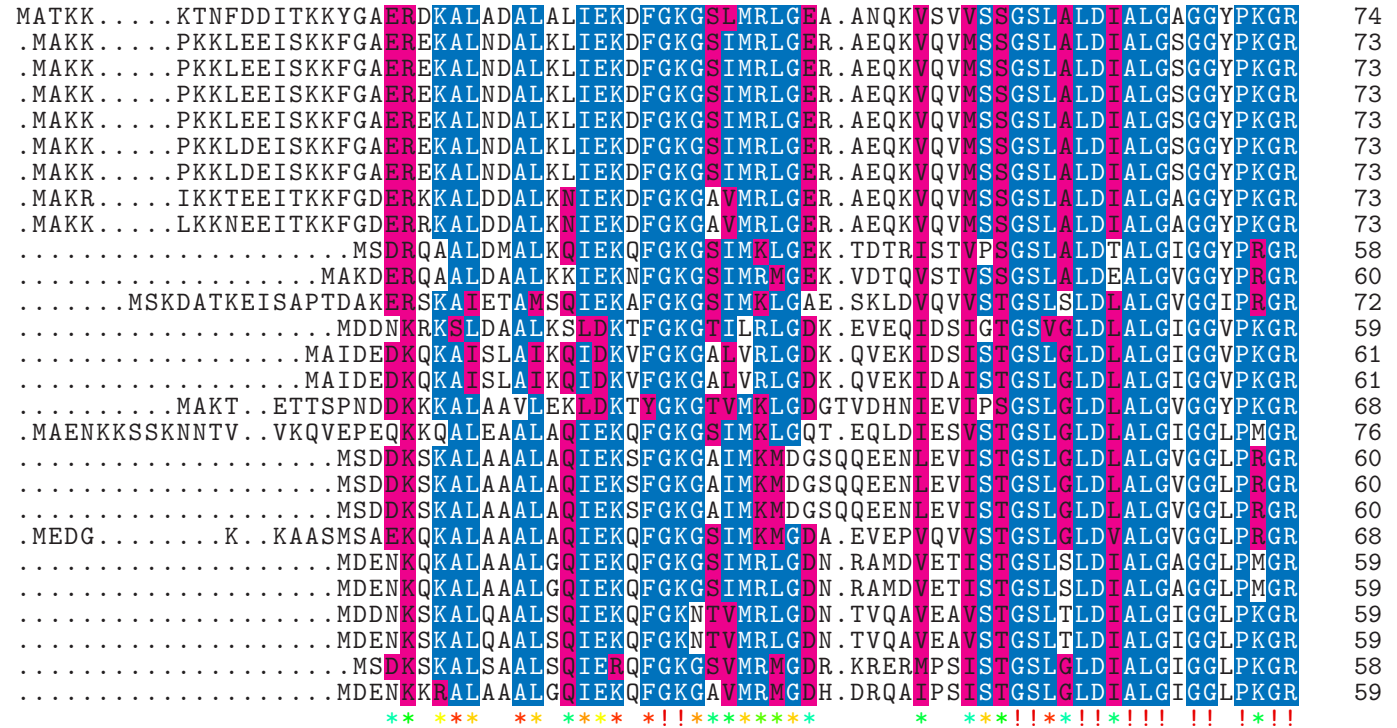


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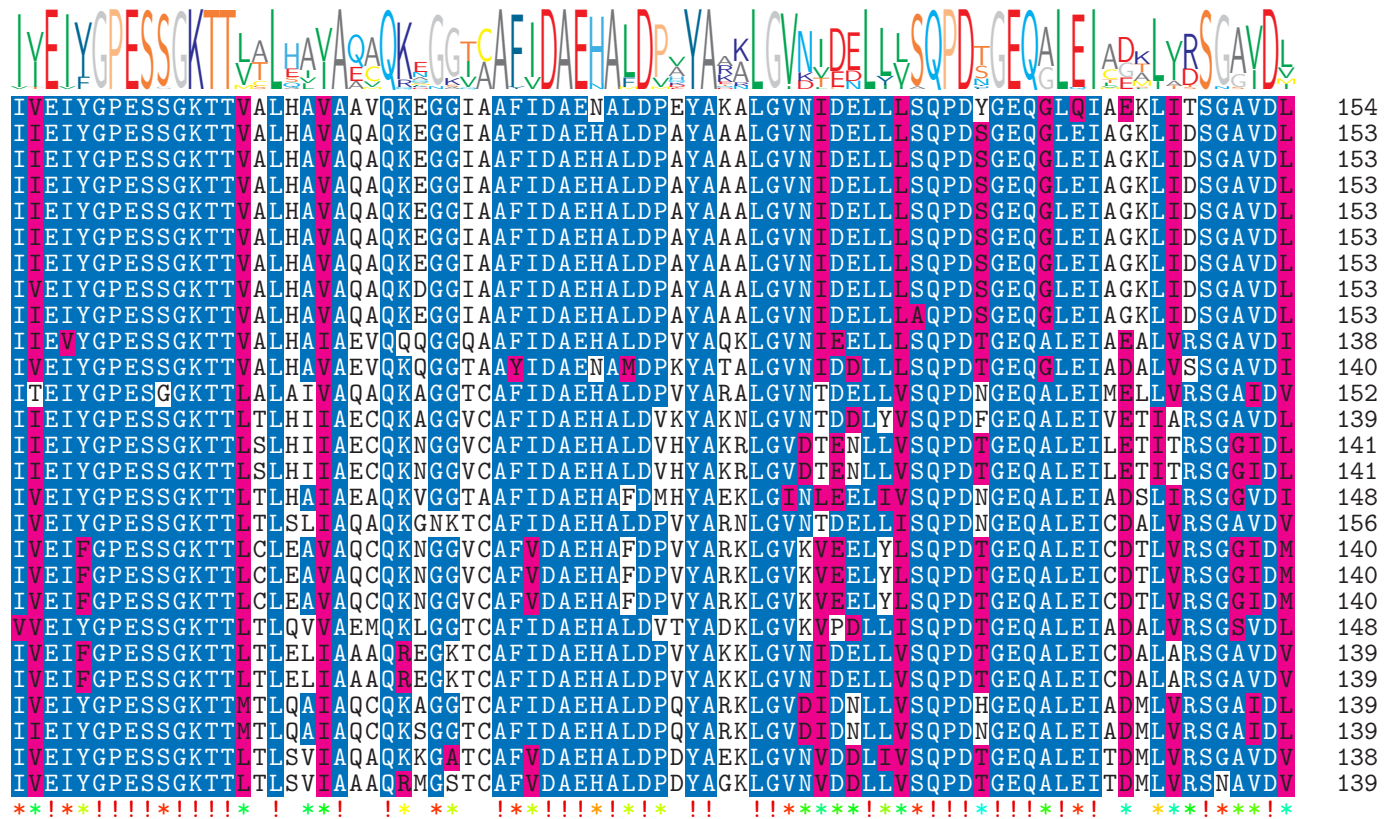
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consensus

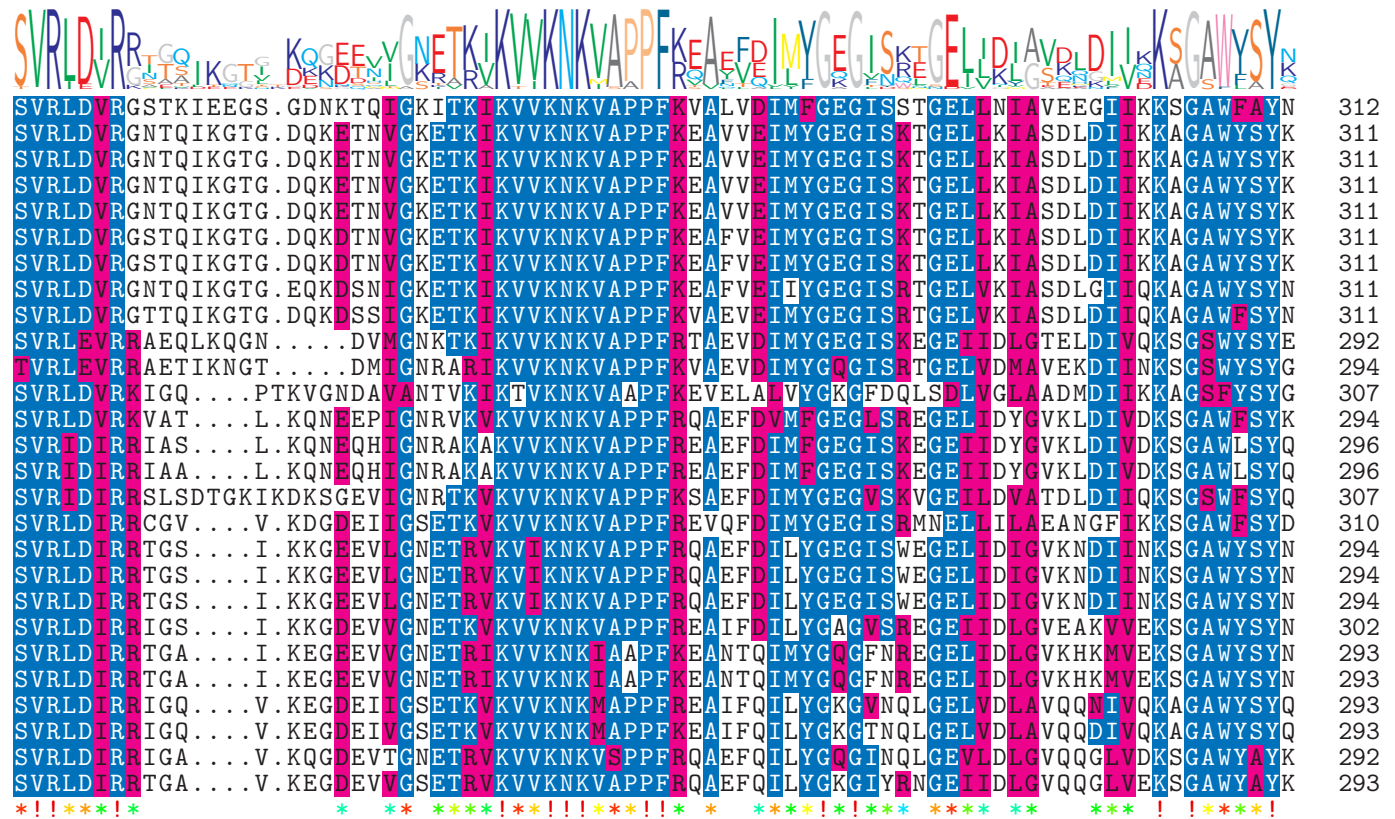
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consensus

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Sequence	Score
DEKIGQGA EKAKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED	387
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEVFAEIDHQRVVRVQFLIDGEEAAE . . . SKKDE . . . VAQVDS . . VNEEVPLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEIFDEIDHQRVVRVQFLIDGEEAAE . . . SKKDE . . . AAQVDS . . VNEEVPLDLGDELEIE	381
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GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE E TDDLALDLNNGIEIE	377
EERLGQGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
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GERIGQGRDNCREFLRENAELAREIENKVRHLGVTPM GAVTLAEV . EED	352
GDKIGQKANKACKYLKENPEIAKTLDKKLREMLLPEN MQLIAETSSA . . ADDVEFGAVPE . EF	354
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logo

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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved