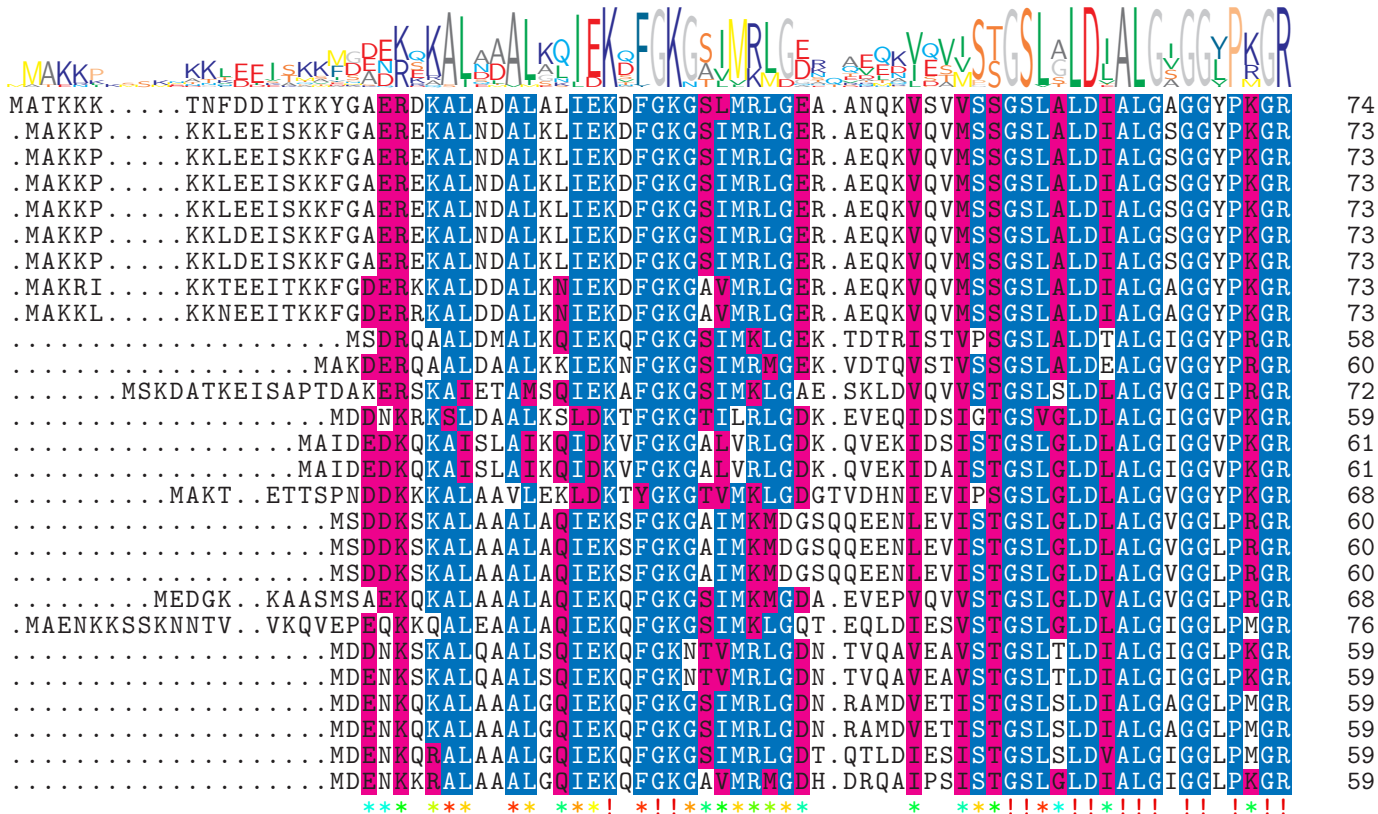


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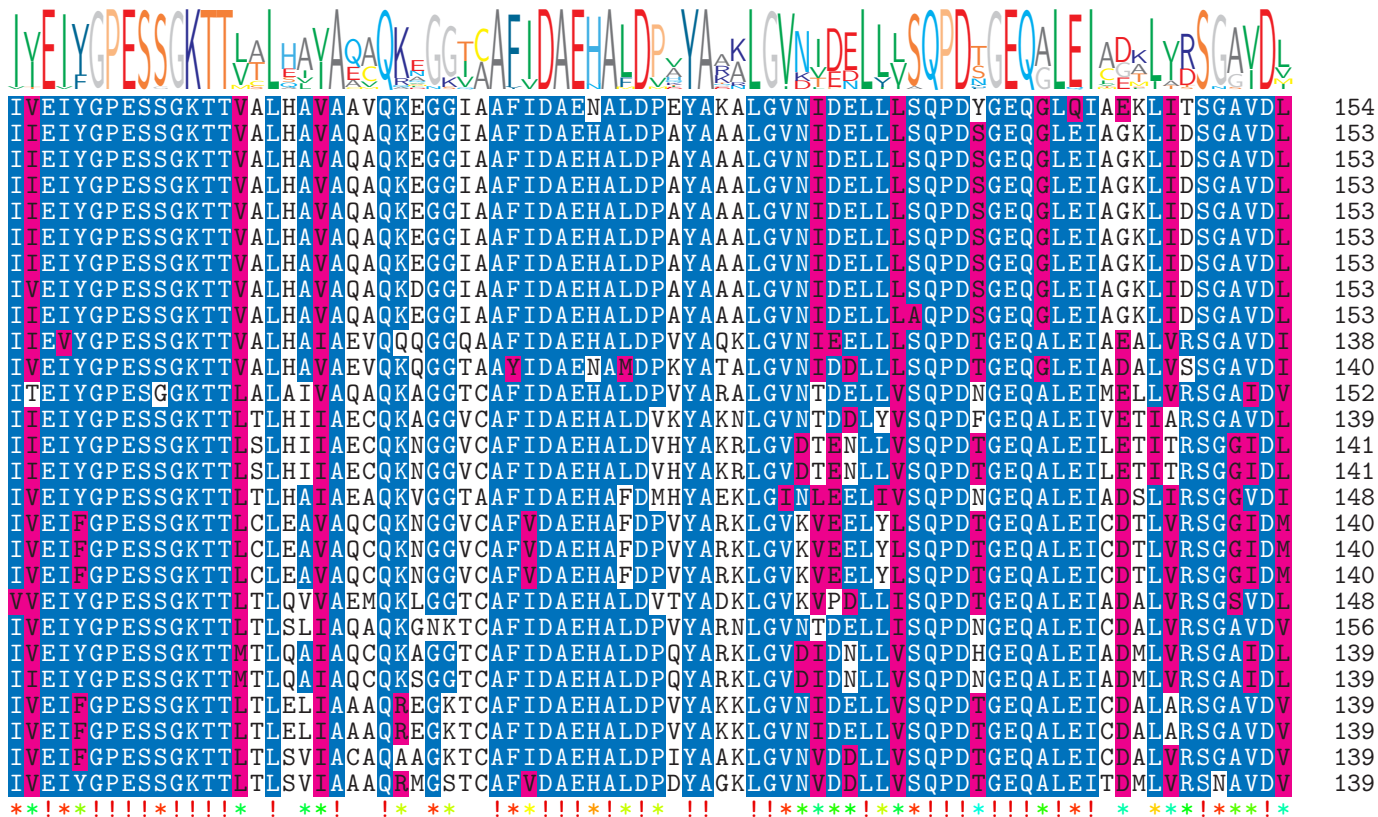
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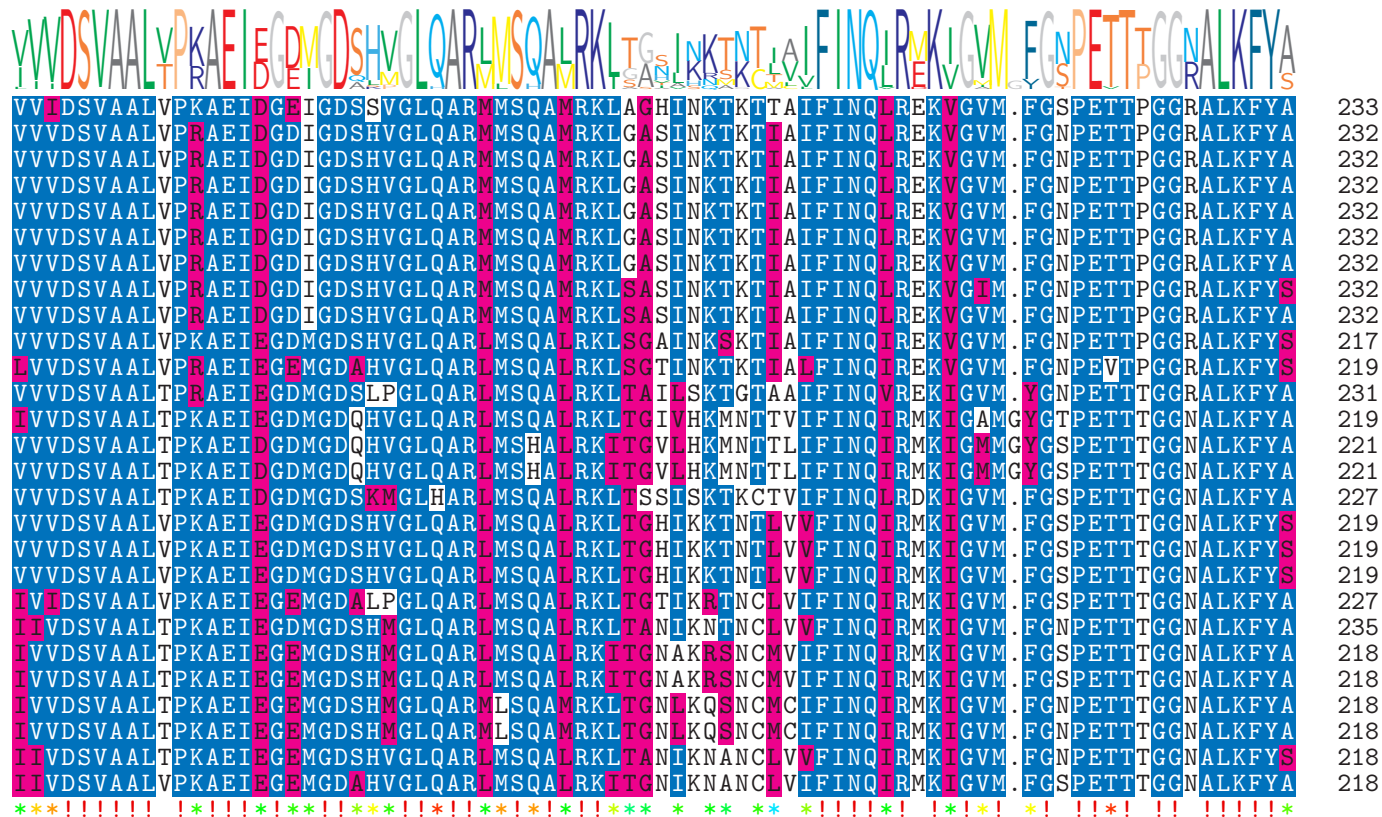
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consensus

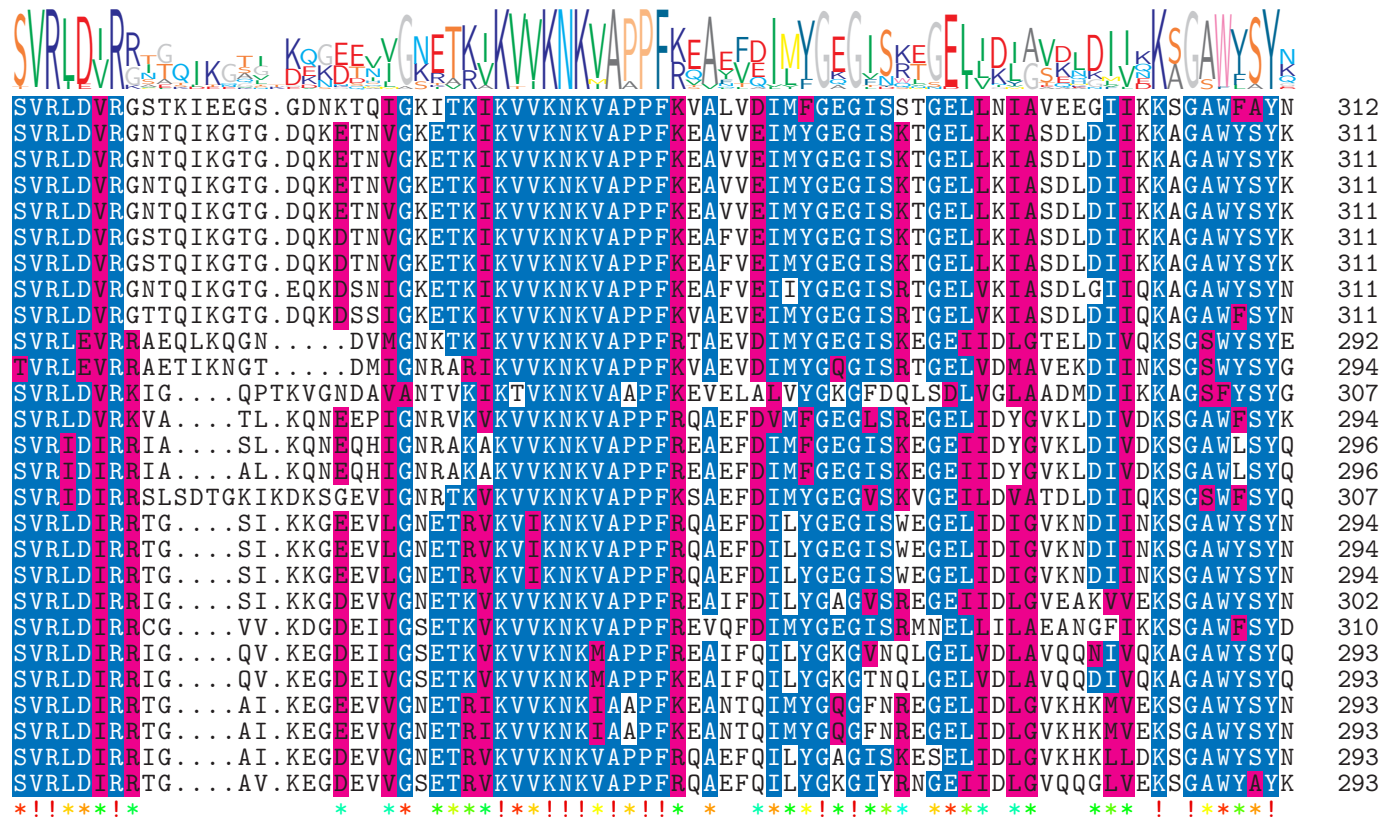
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLADNPVFAEIDHKVVRVQFLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLADNPVFEIDHQVVRVQFLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKKFLADNPVFEIDDHKVRVQYGLIEDNTEEEKQSKEK.....ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNNGVVQQAEETQEEL.EFE.E.....DNNNGV...V	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVQYGLSDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQGEKKTIAITAEERPMEQEIHDRVMAAIRAGNAGEAPALAPAPAPE..A.AEA.....	363
DKKLGGGRENSKAFLENPEAIDEITKAIQNSMGTGEMISGSEDDEGEE.....	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLEEME.....	347
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GERIGQGRDNCREFLRENAELAREIENKVVREHLGVTPMGAVTLAAEEVEE.D.....VEEFSEE..EL.....	352
GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNSVLKATASDSNDES..D...VEEFSEE..EL.....	372
GNKIGQGGKNNVIRYLEENPQISTEIAVIREQLLTQASDQTAAHDETEEPD..LLES.....	349
GKIGQGGKNNVIRYFEENNQIAFEIERNIREQLLTGTGTGAVQI.EDEEEDP..LLES.....	349
GDKIGQGGKANACKYLLKENPEIAKTLDKKLREMLLNPNMQLIAE.....TS..SAADDVEFGAVPEEF.....	354
GDKIGQGGKANACKYLLKENPEIAKTLDKKLREMLLNPNMQLIAE.....TS..SAADDVEFGAVPEEF.....	354
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GSKIGQGGKANAAKYLEENPEIAGQIEQQIRAKLLVTSANTKATPVAEDLADA..DI.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved