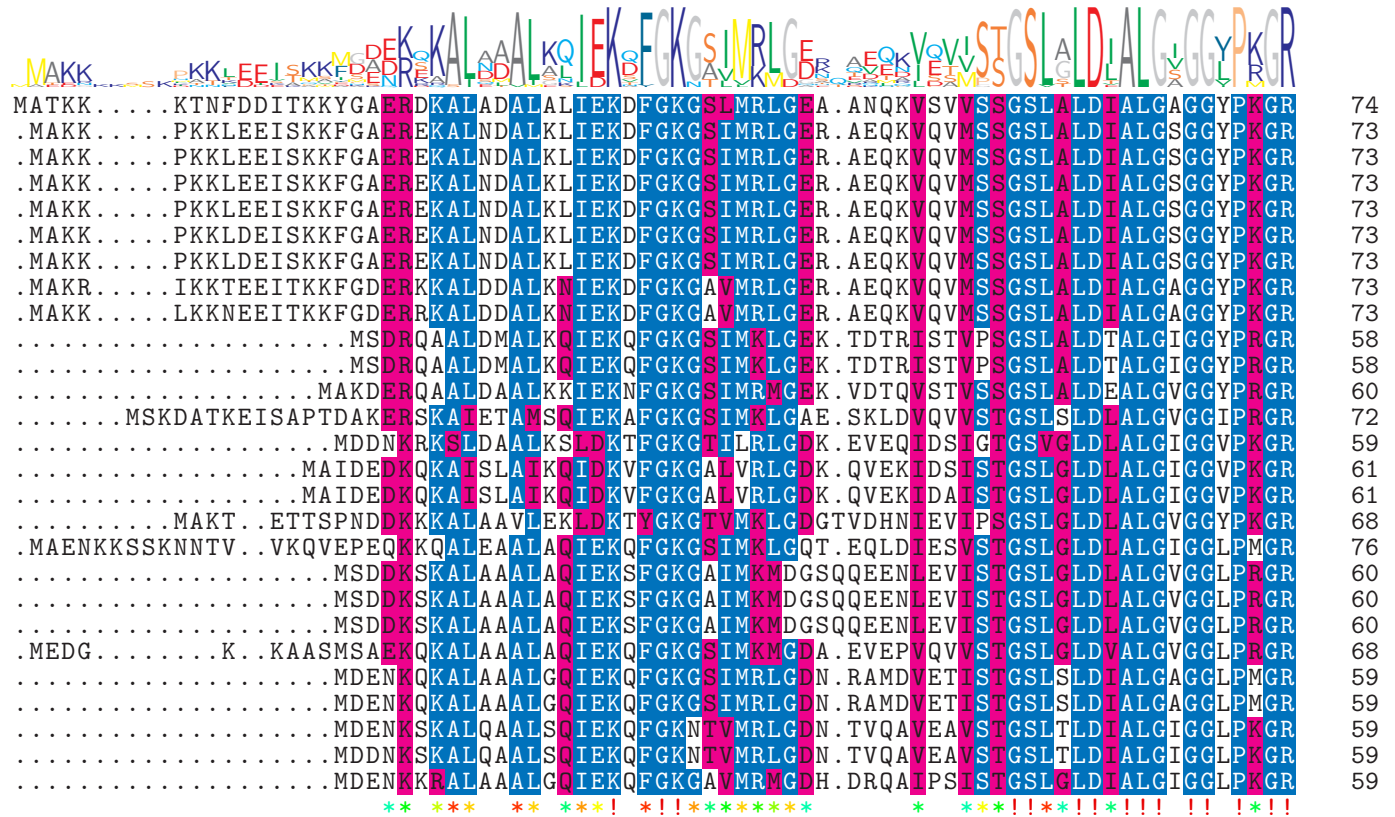


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consensus

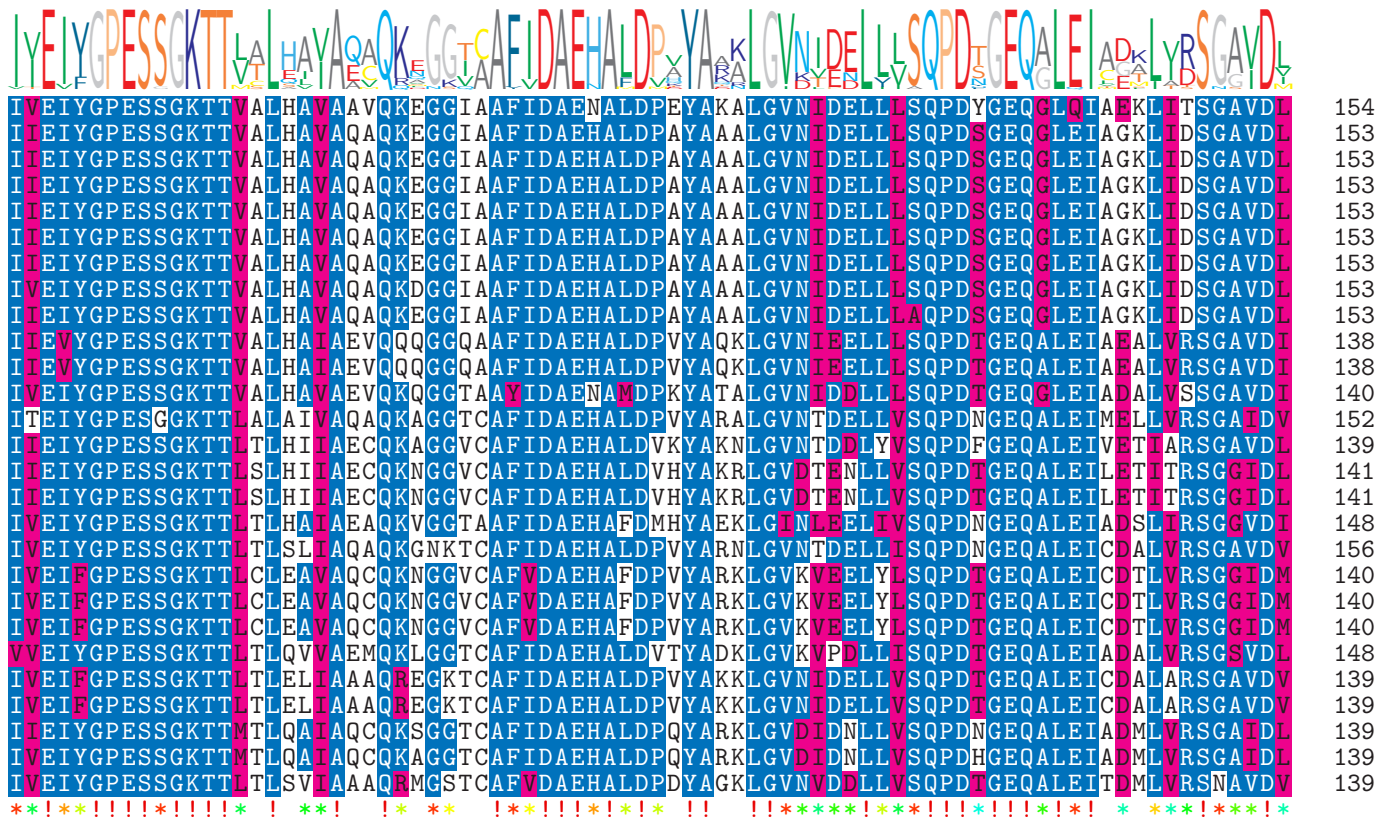
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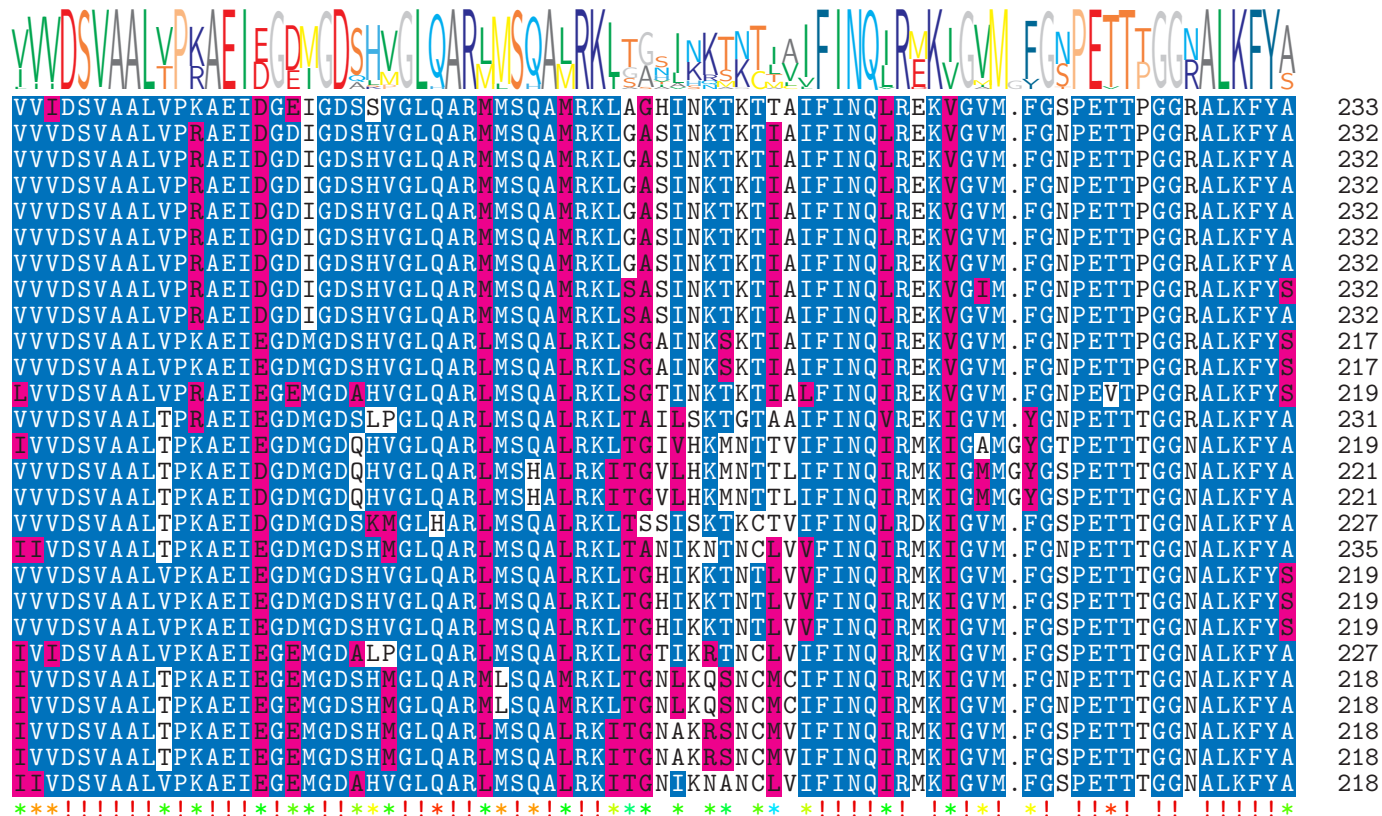
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consensus

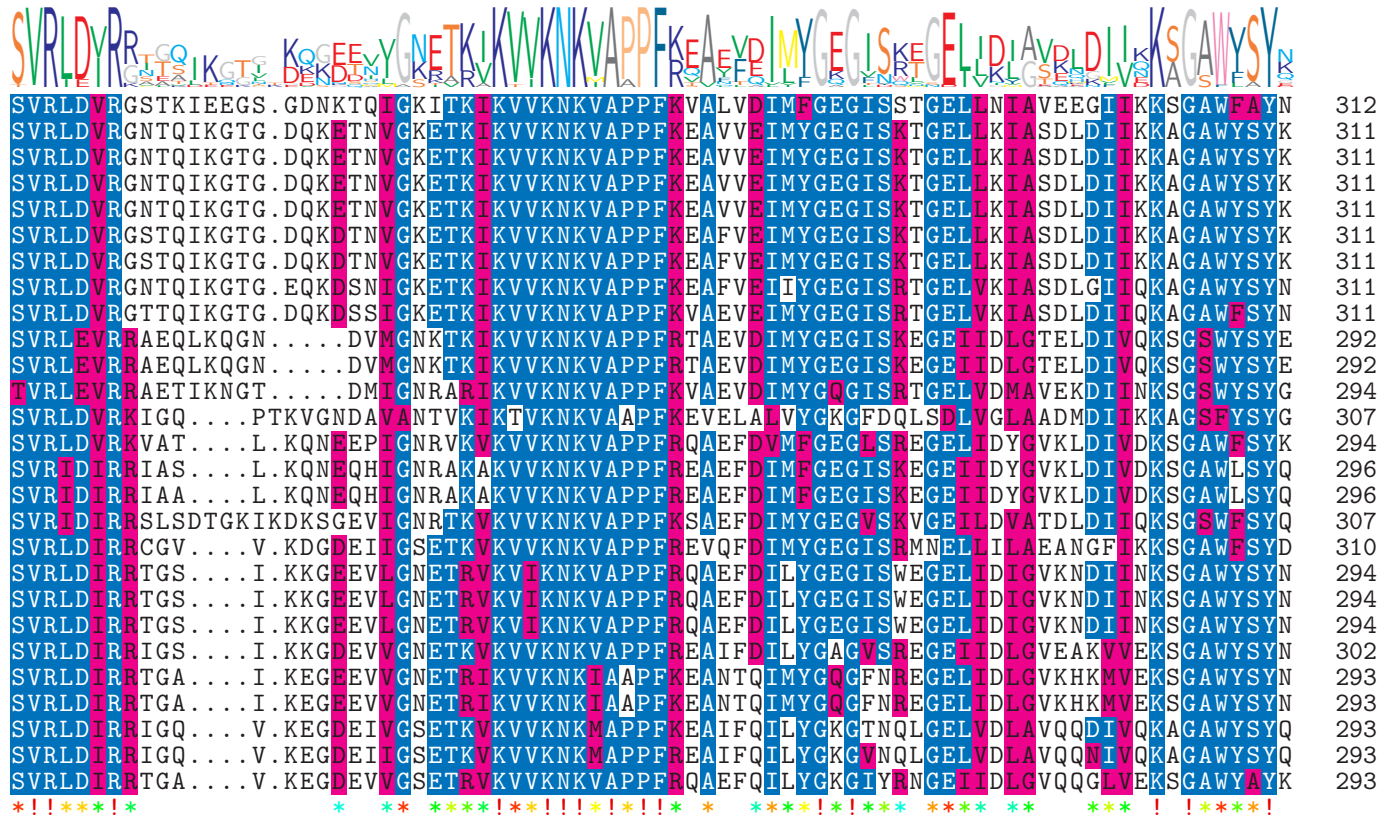
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consensus

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGQGS E NA K KYLAEHPEIF D DEID K QVRSKFG L IDGEEVSEQD T ENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLAEHPEIF D DEID K QVRSKFG L IDGEEVSEQD T ENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLAEHPEIF D DEID K QVRSKFG L IDGEEVSEQD T ENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA D NPEVFAEID H QVVRVQF G LIDGEEAAE....SKKDE....VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGS E NA K KYLA D NPEIF D DEID H QVVRVQF G LIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGS E NA K KFLADNPEIF D DDID H KVRVQY G LIEDNTEEEKQSSEK.....ETDEK..ADKNLVLEDDTIEIE	382
GEKIGQGS E NA K KRYLADHPQLF D DEID R KVRVKF G LLEESEEEESAMAVASE.....E.....TDDLALDLDNNGIEIE	377
EERLGGGREN A KQFLKENK D IMLMIQEQIREHY G L D NNGVVQQQAETQEEL.EFE.E.....	348
EERLGGGREN A KQFLKENK D IMLMIQEQIREHY G L D NNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGRENA K NYLADHEDVEVLRKVR A AYG I SDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGGKEKTIAYIAERP E MEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGGREN S KAF L KENPEIA D EITKAIQNSMG I EGMI....SGSEDDE..GEE.....	343
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DTKLGGGRD T VKELIKDNPELAELEAKIREKLQAK.....	343
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GDKIGGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GDKIGGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGGGKNNVIRYFEENNQIA E EIERNIREQLLTGTN....GAVQ.I.EDEEEDPD....LLES.....	349
GNKIGGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEEEEDPD....LLES.....	349
GSKIGGGKANAAKYLEENPEIGQEIERAKLLVTSAN....TKATPVAEDLADAD....I.....	347

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved