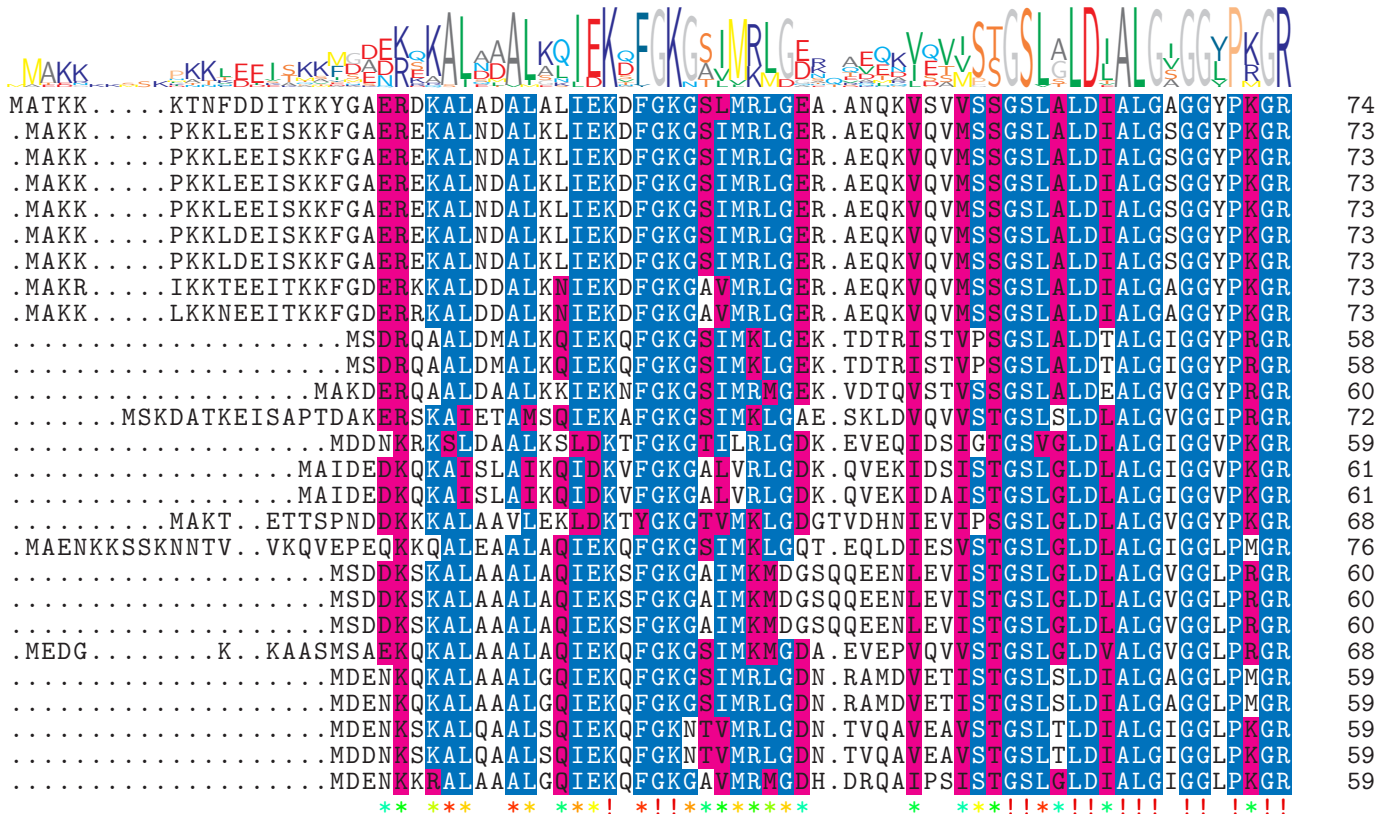


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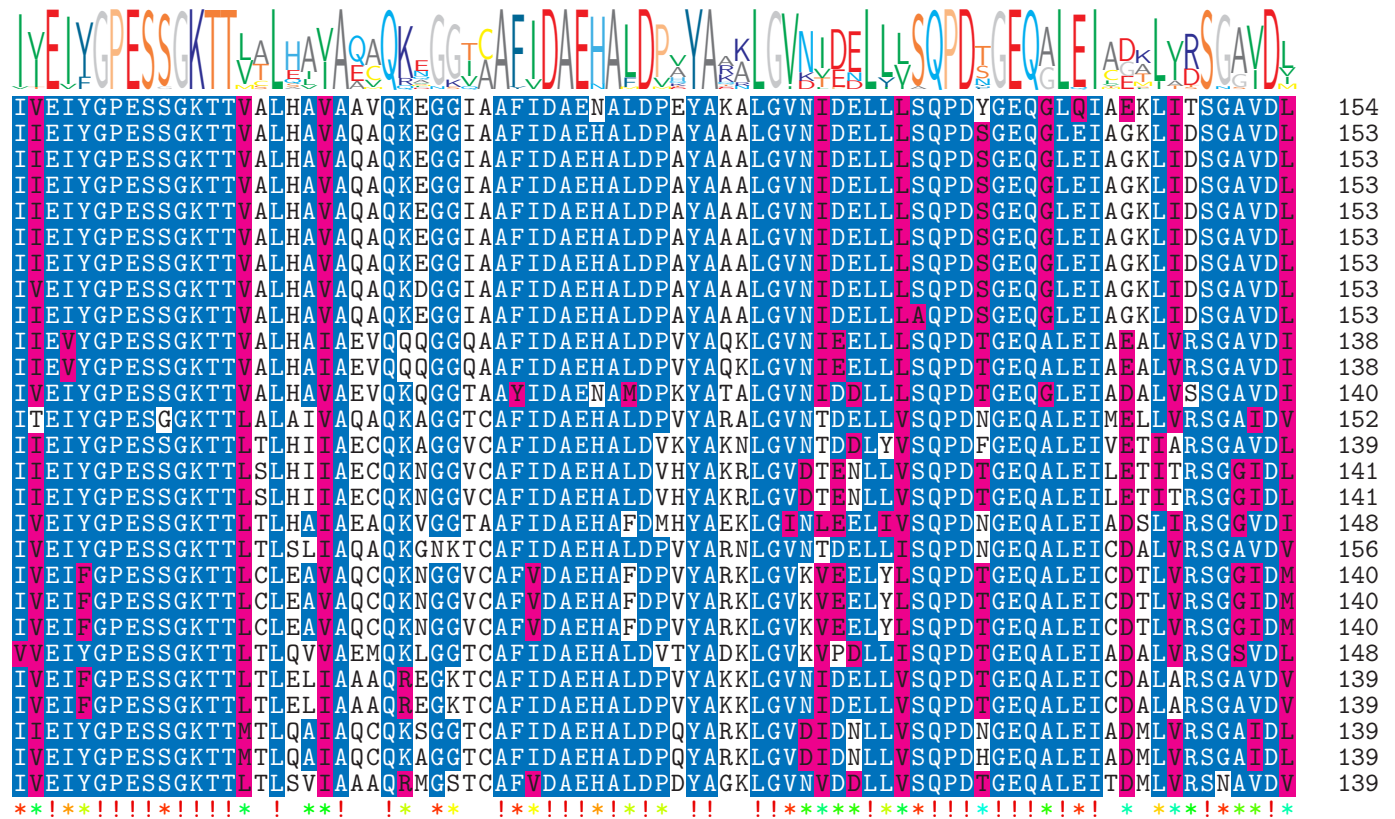
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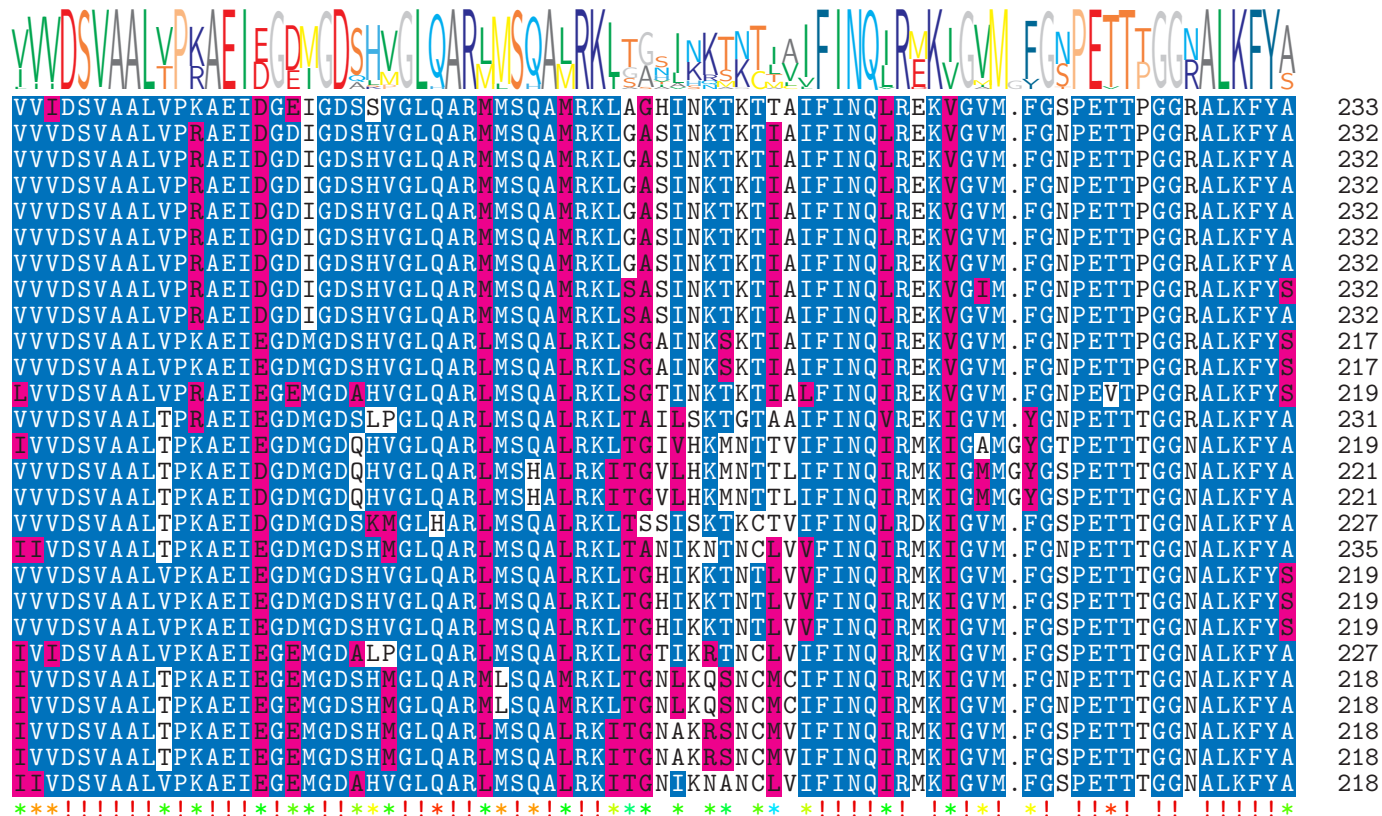
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consensus

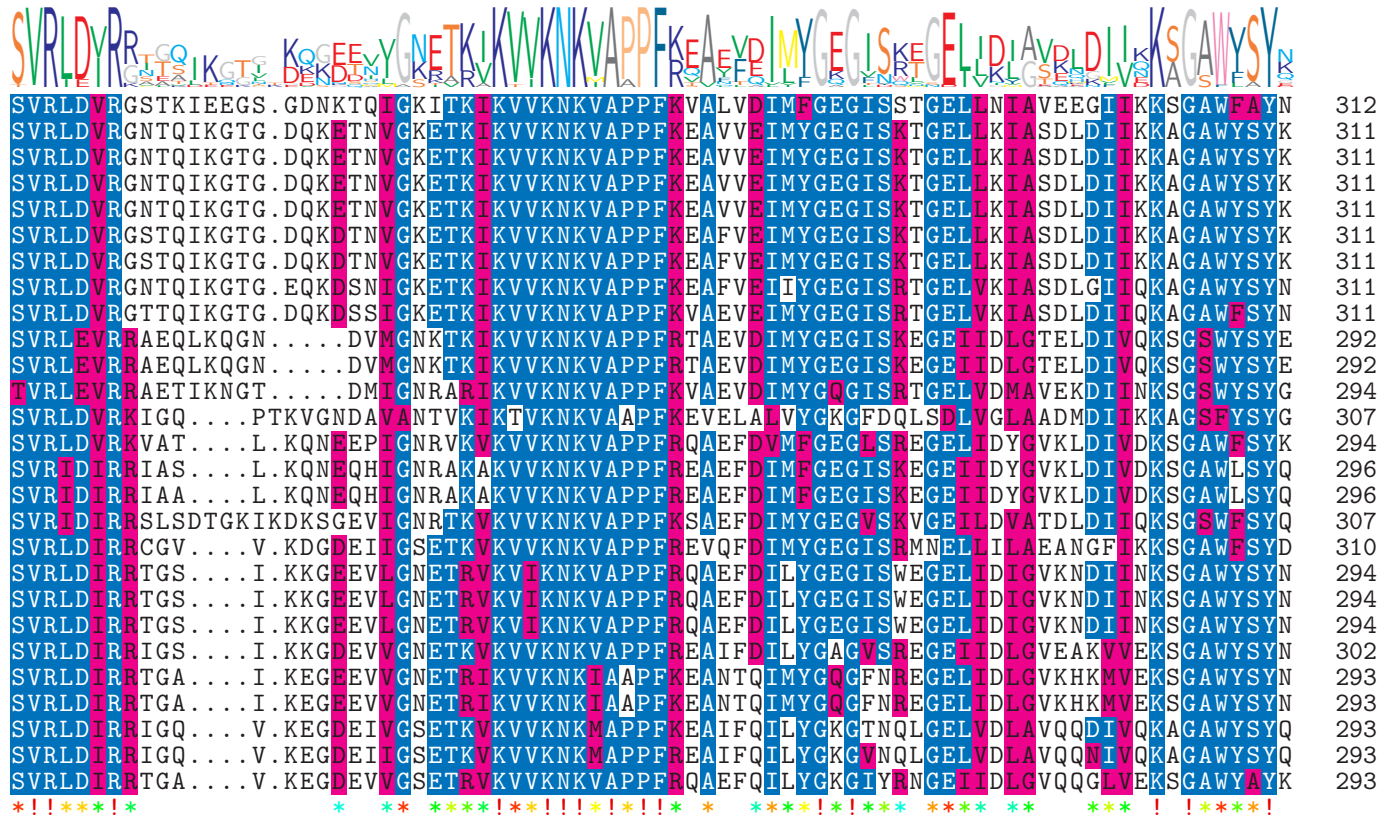
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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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 KYLA E HP E IF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS E NA K KYLA D NPEIF F DEID H QVRVQFGLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS E NA K KFLADNPEIF F DDID H KVRVQYGLIEEDNTEEEKQSKEK.....ETDEK..ADKNLVLEDDTIEIE	382
GEKIGQGS E NA K KRYLADHPQLF F DEID R KVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLDNNGIEIE	377
EERLGGGREN A KQFLKENKDIMLMIQE Q IREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
EERLGGGREN A KQFLKENKDIMLMIQE Q IREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
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DERIGGGKEKTIAYIAERP E MEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
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DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
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GNKIGGGKNNVIRYFEENNQIAFEIERNIREQLLTGTN....GAVQ.I.EDEEEDPD....LLES.....	349
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GSKIGGGKANAAKYLEENPEIQGEIEQQIRAKLLVTSAN....TKATPVAEDLADAD....I.....	347

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved