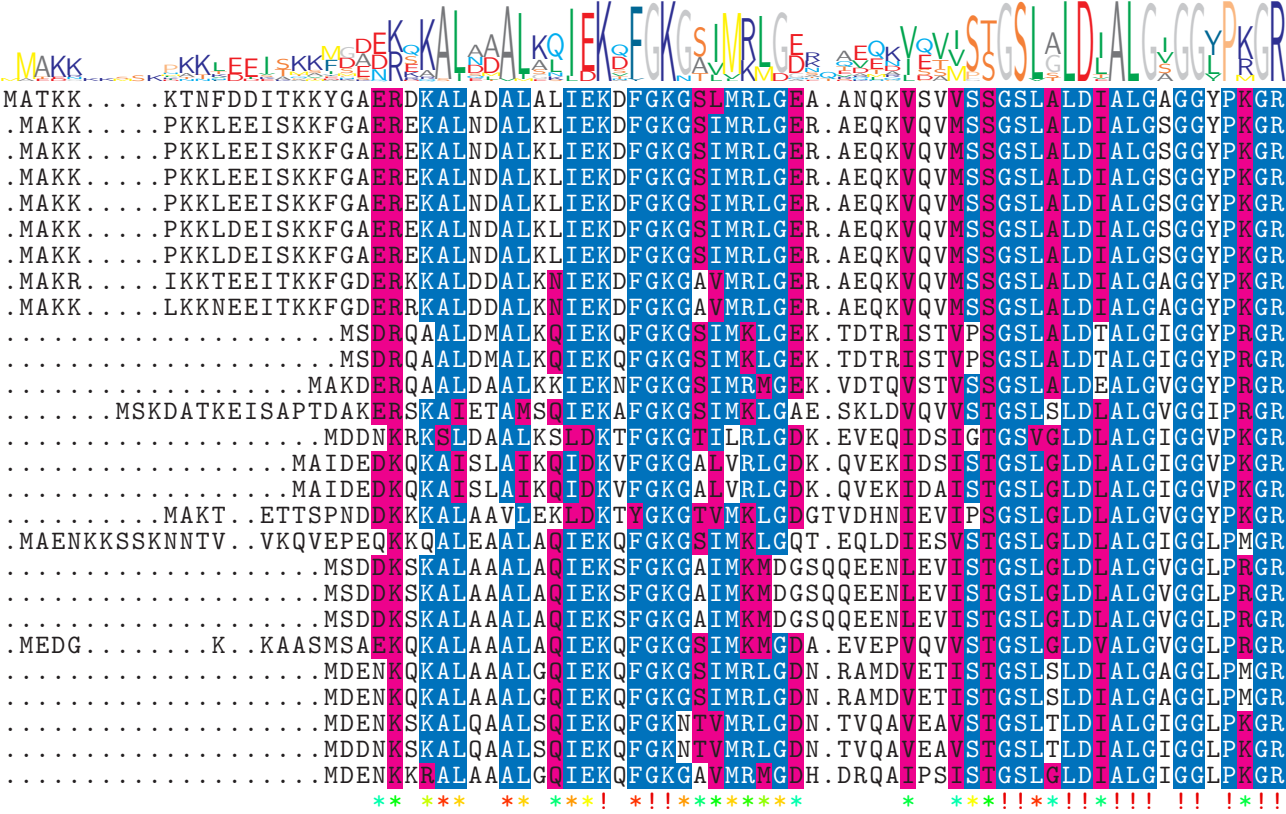


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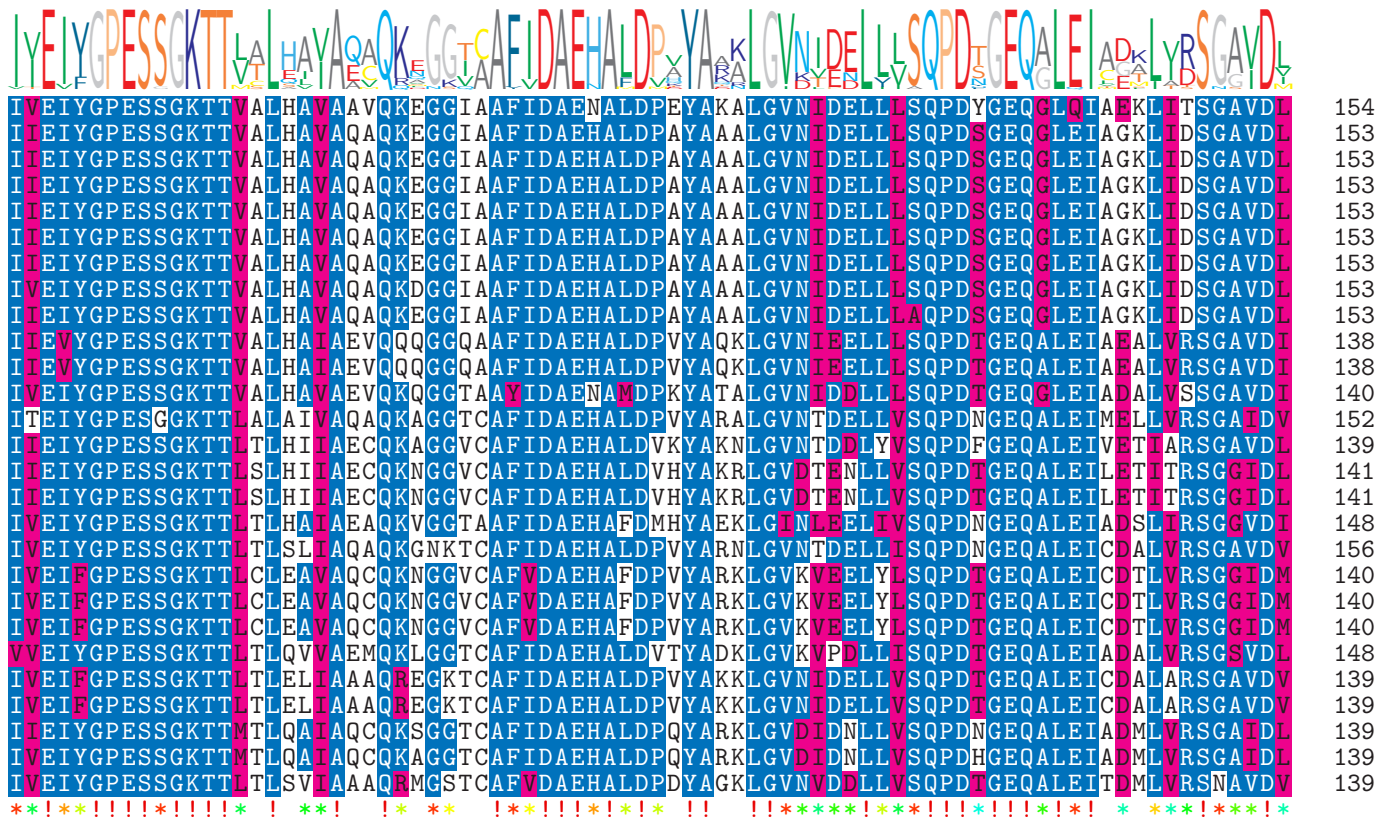


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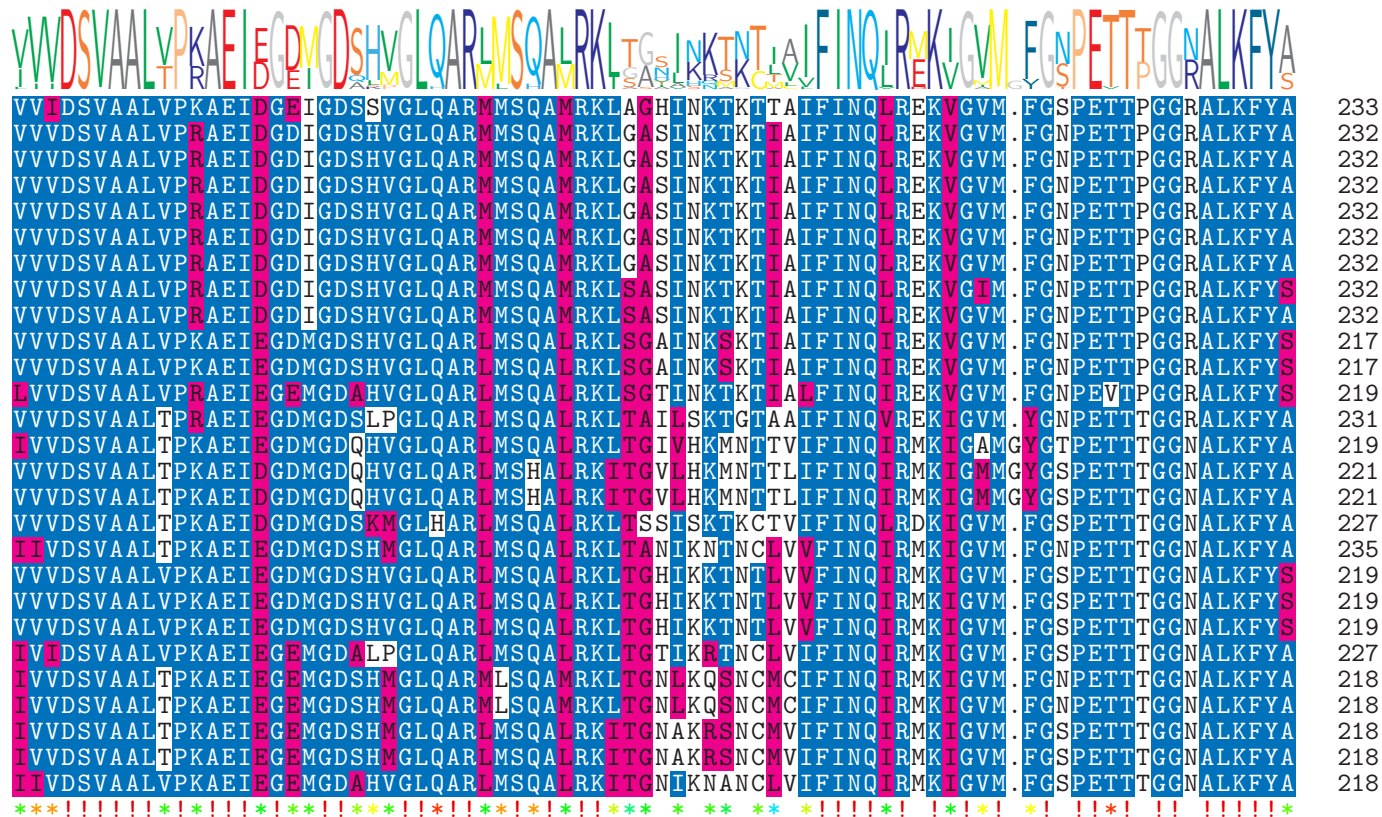
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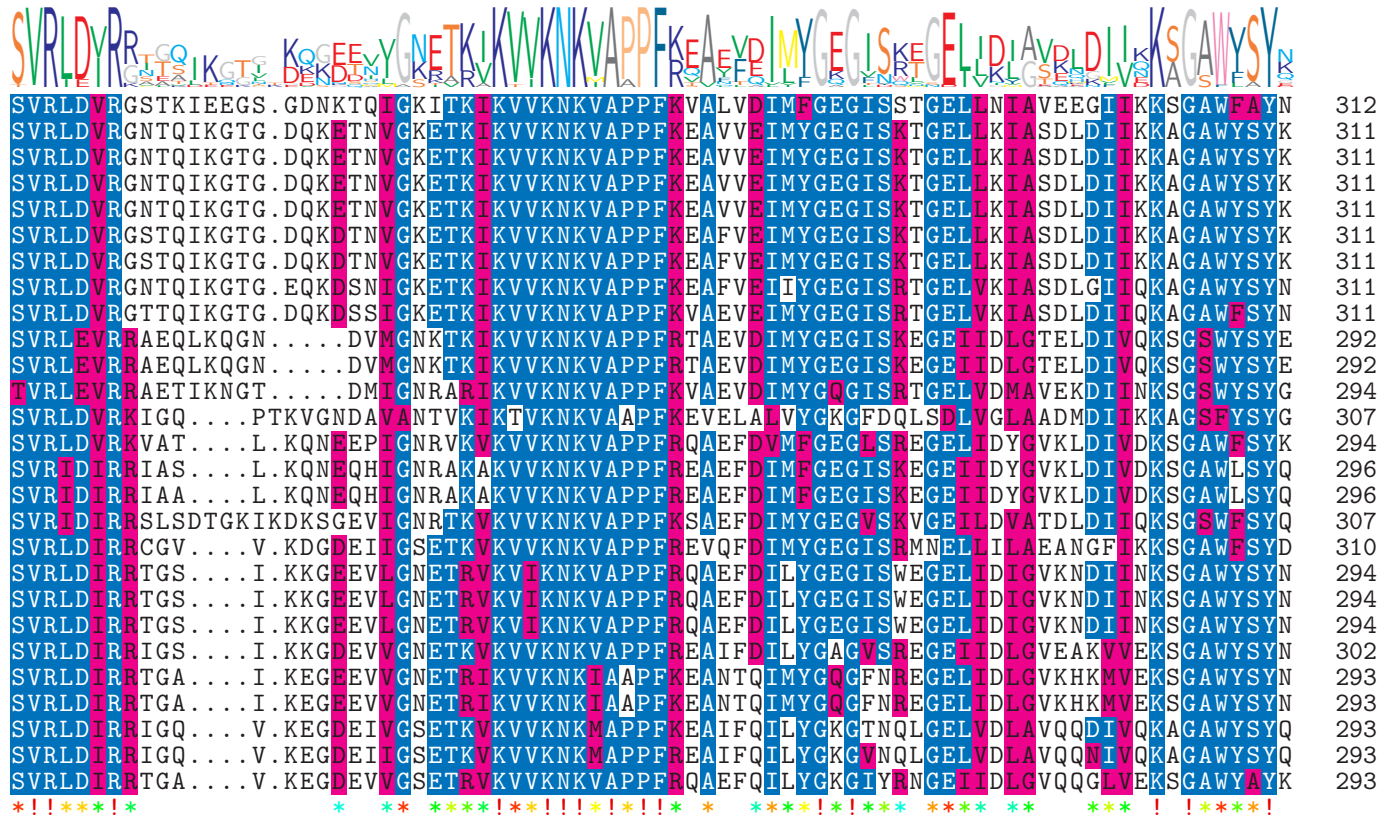
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consensus

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Sequence	Score
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DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS E NA K KYLA E HP E IF F DEID K QVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA D NPEVFA E ID H QVRVQF G LIDGEEAAE....SKKDE....VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGS E NA K KYLA D NPEIF F DEID H QVRVQF G LIDGEEIAE....SKKDE....AAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGS E NA K KFLA D NPEIF F DDID H KVRVQY G LIEDNTEEEKQSSKE....ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGS E NA K KRYLA D HPQL F DEID R KVRVKF G LLEESEEEESAMAVASE.....E.....TDDLALDLDNNGIEIE	377
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EERLGGGREN A KQFLKENKD I MLMIQE Q IREHY G LDNNGVVQQAEETQEEL.EFE.E.....	348
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DERIGGGKEKTIAYIA R PEMEQE I RDRVMAA I RAGNAGEAPALAPAPAAPEAAEA.....	363
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved