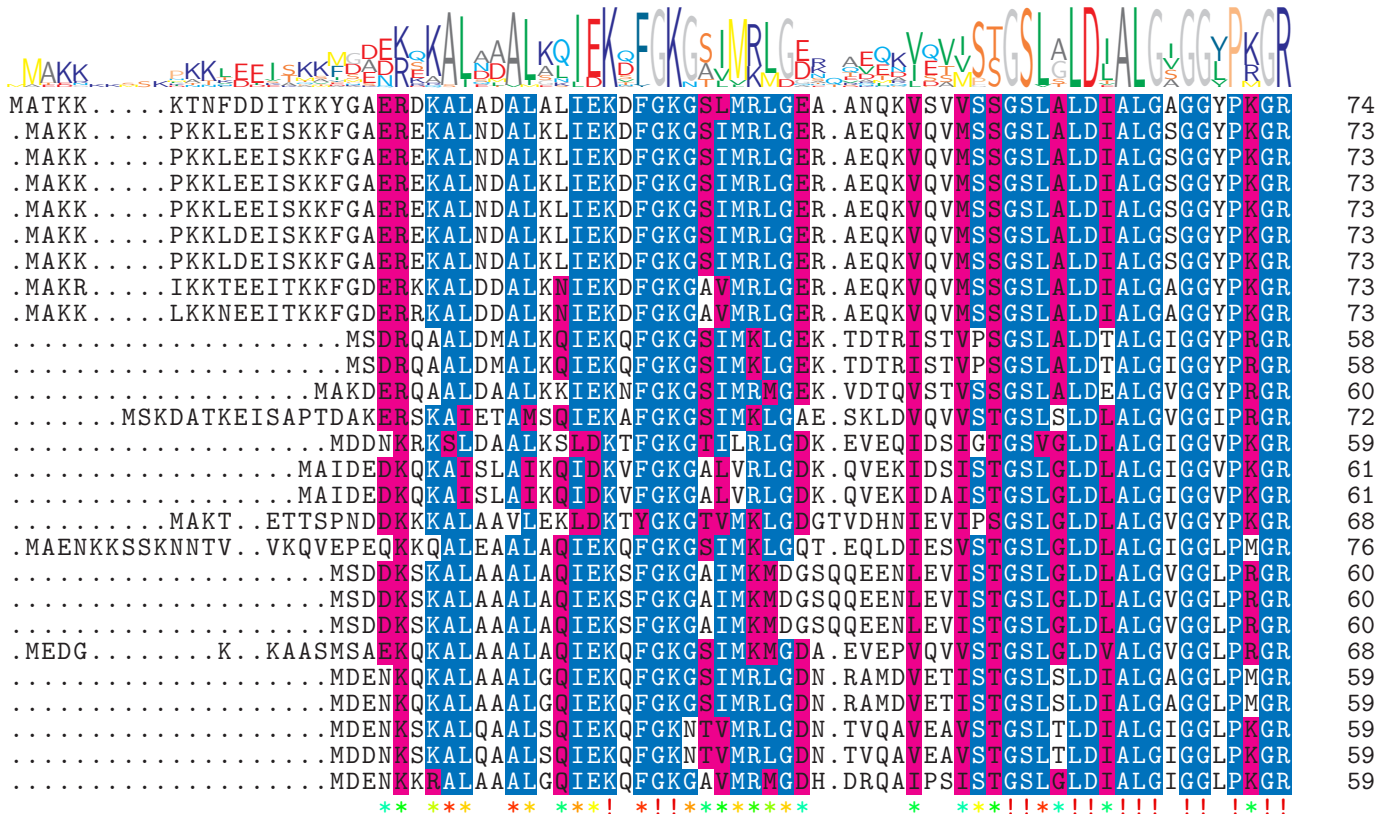


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consensus

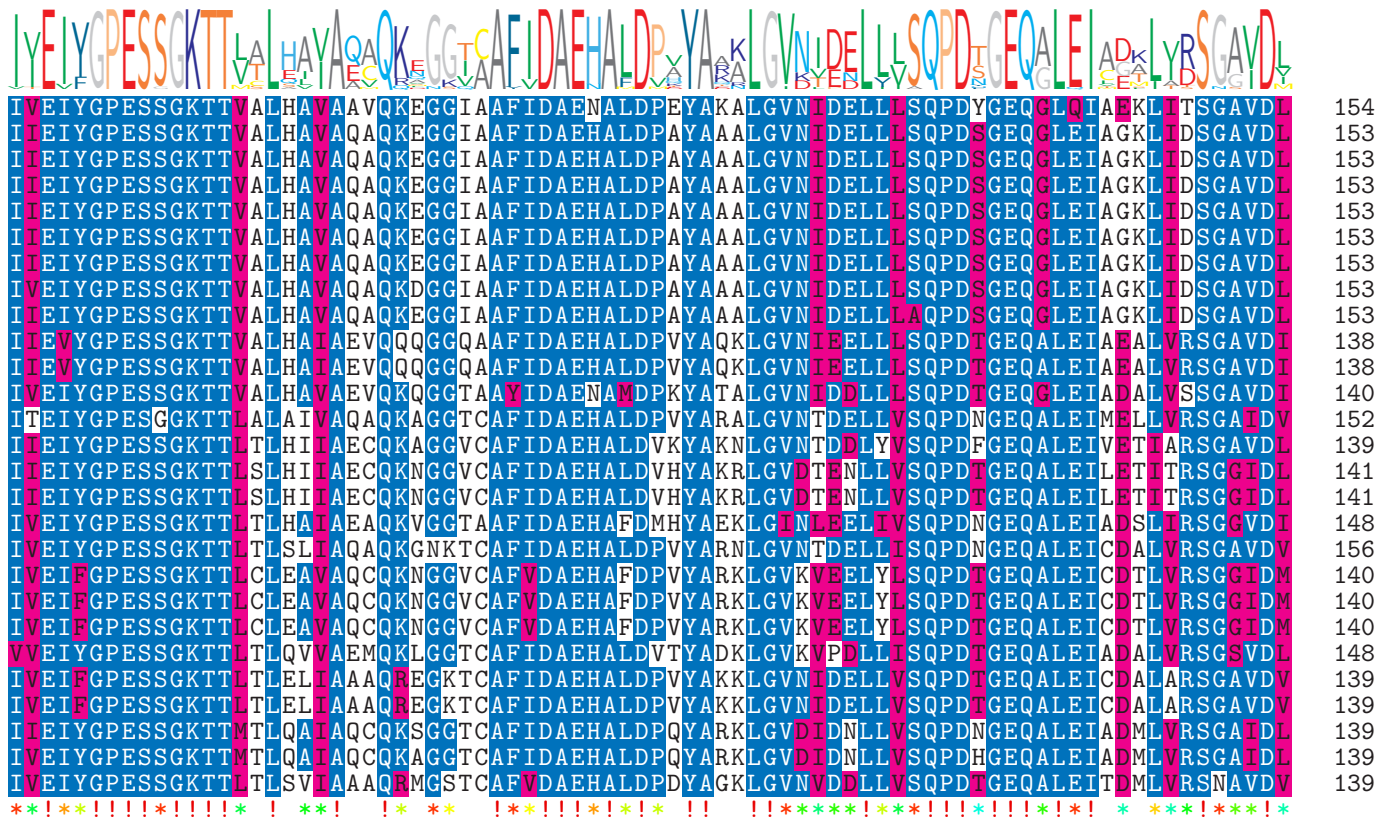
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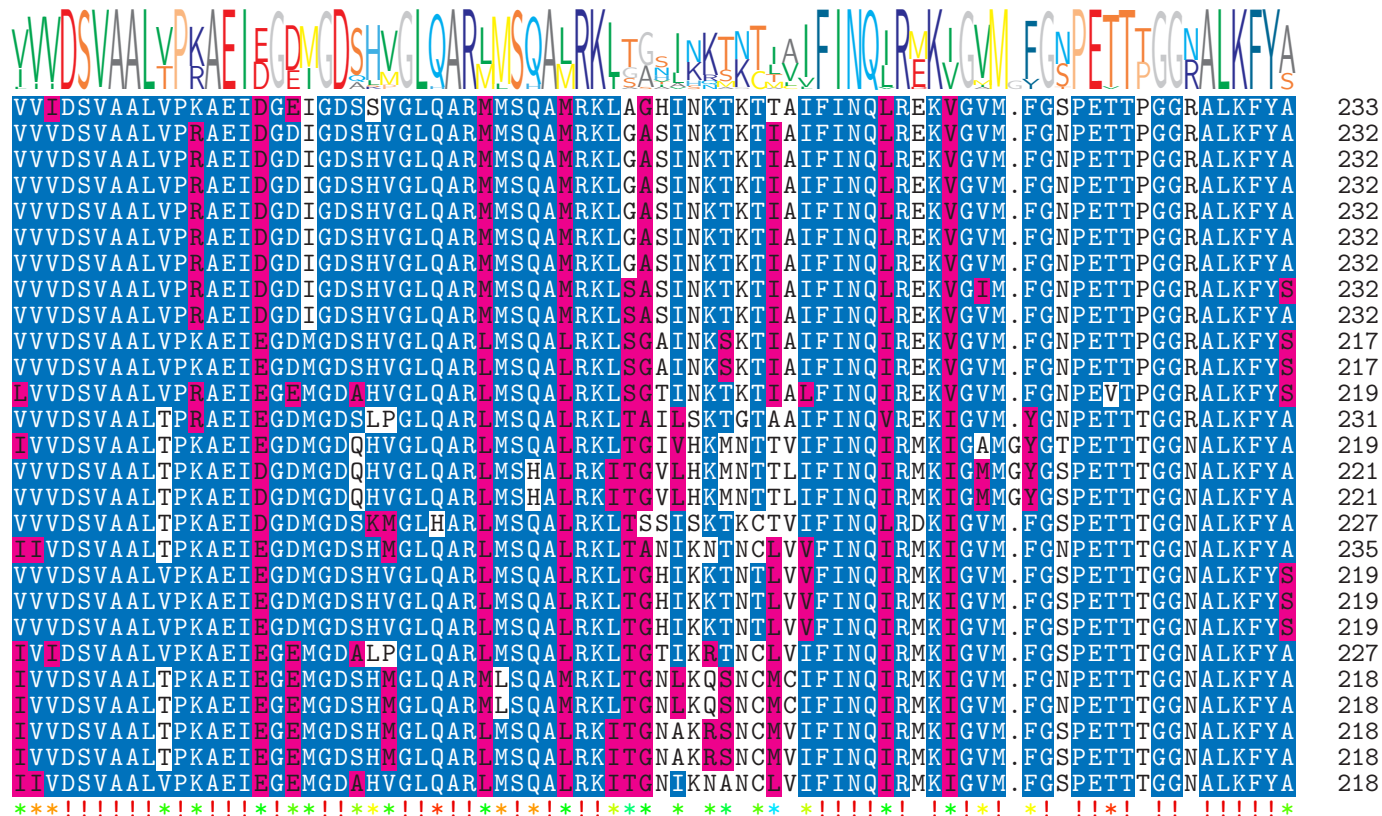
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consensus

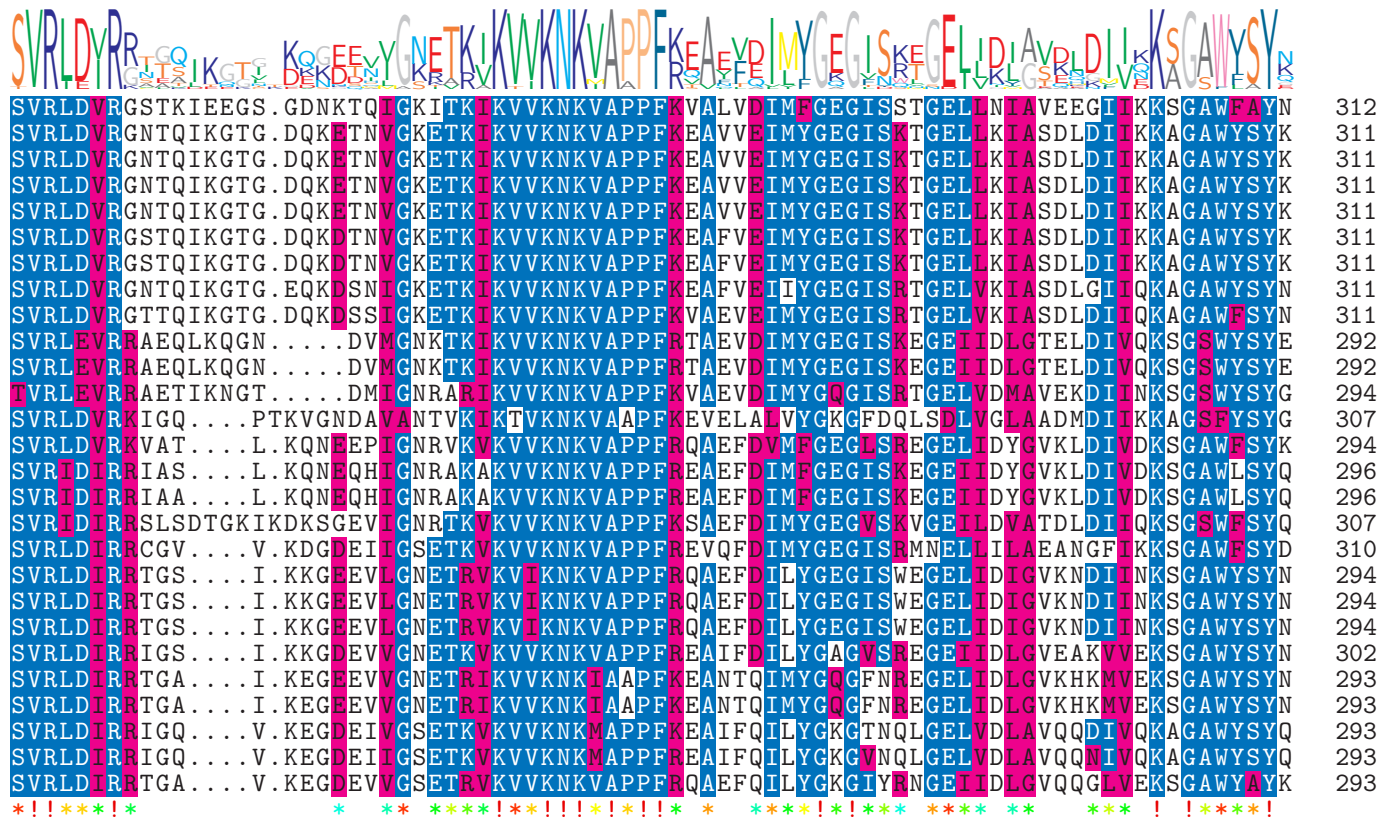
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGSENAKKYLADNPEIFDEIDHQVRVQFGLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKE...ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYCLDNNGVVQQAEETQEEL.EFE.E.....	348
EERLGGGRENAAKFLADNPKDIMLMIQEQUIREHYCLDNNGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDVRLEKVRRAAYGTSVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGGEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DTKLGGGRDTPVKELTKDNPELAEELAKIREKLQAK.....	343
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GDKIGGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GDKIGGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEEEDPD....LLES.....	349
GNKIGGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEEEDPD....LLES.....	349
GSKIGGGKANAAKYLENPEIQGEIEQQIRAKLVTSAN....TKATPVAEDLADAD....I.....	347

logo

		LEE	
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

- non conserved
- similar
- ≥ 50% conserved