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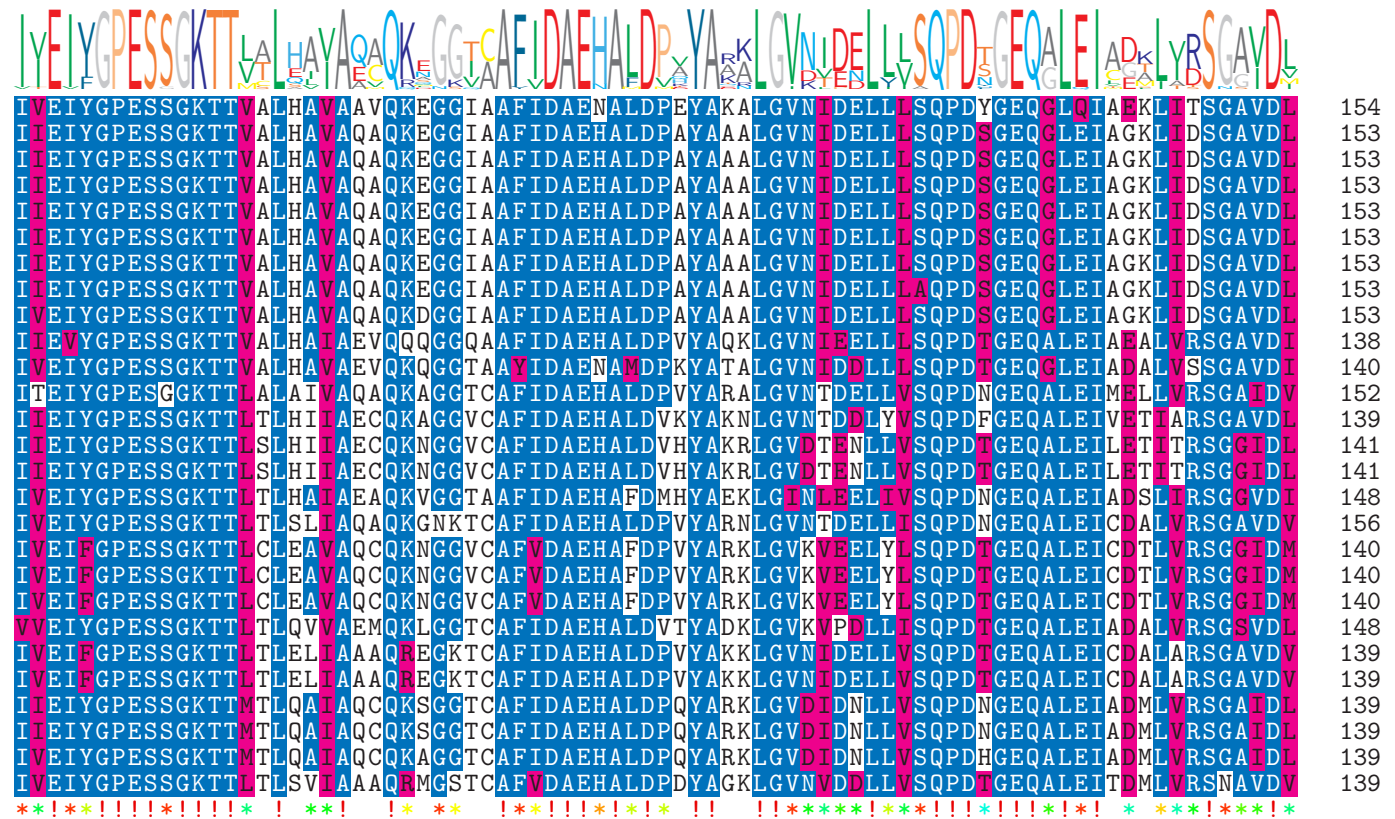
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consensus

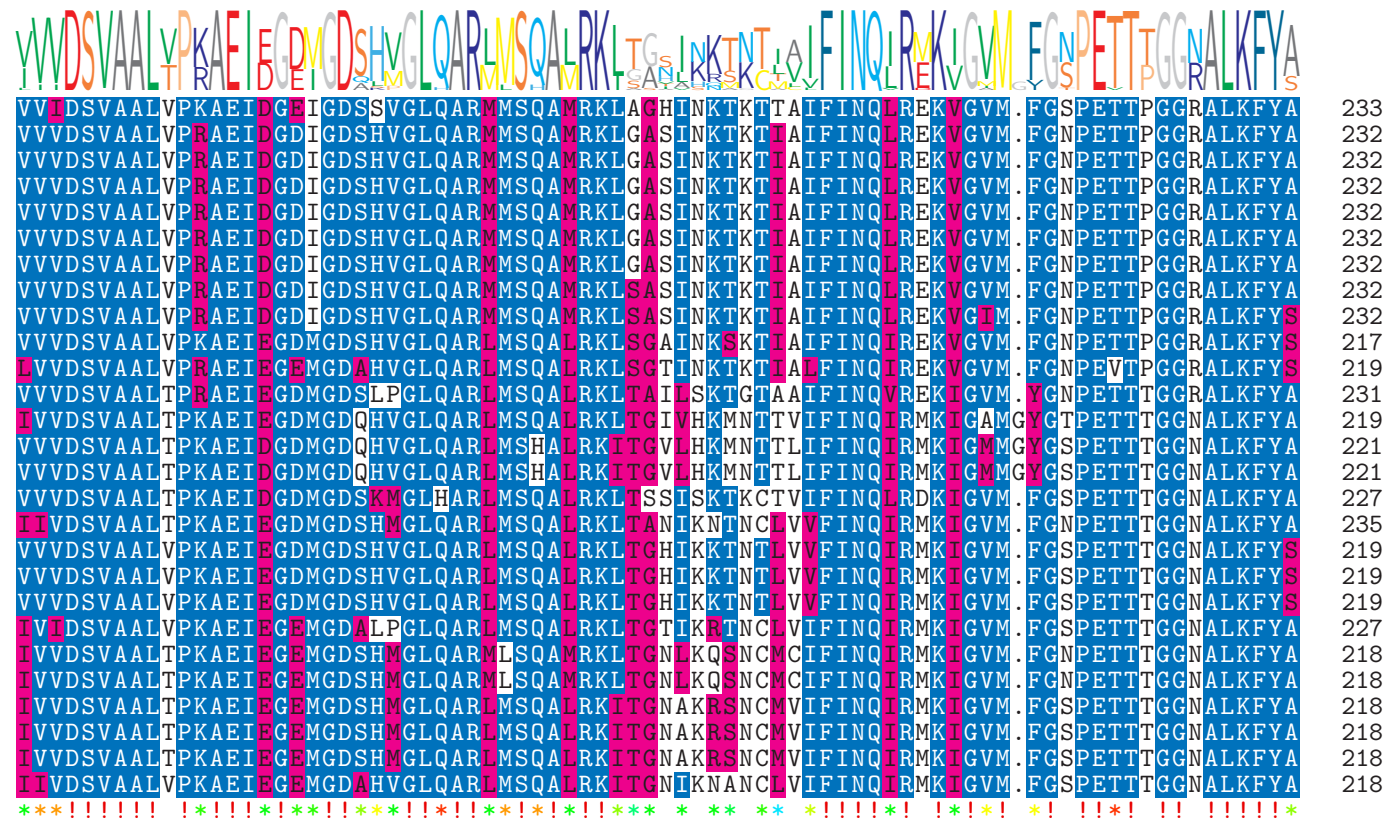
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

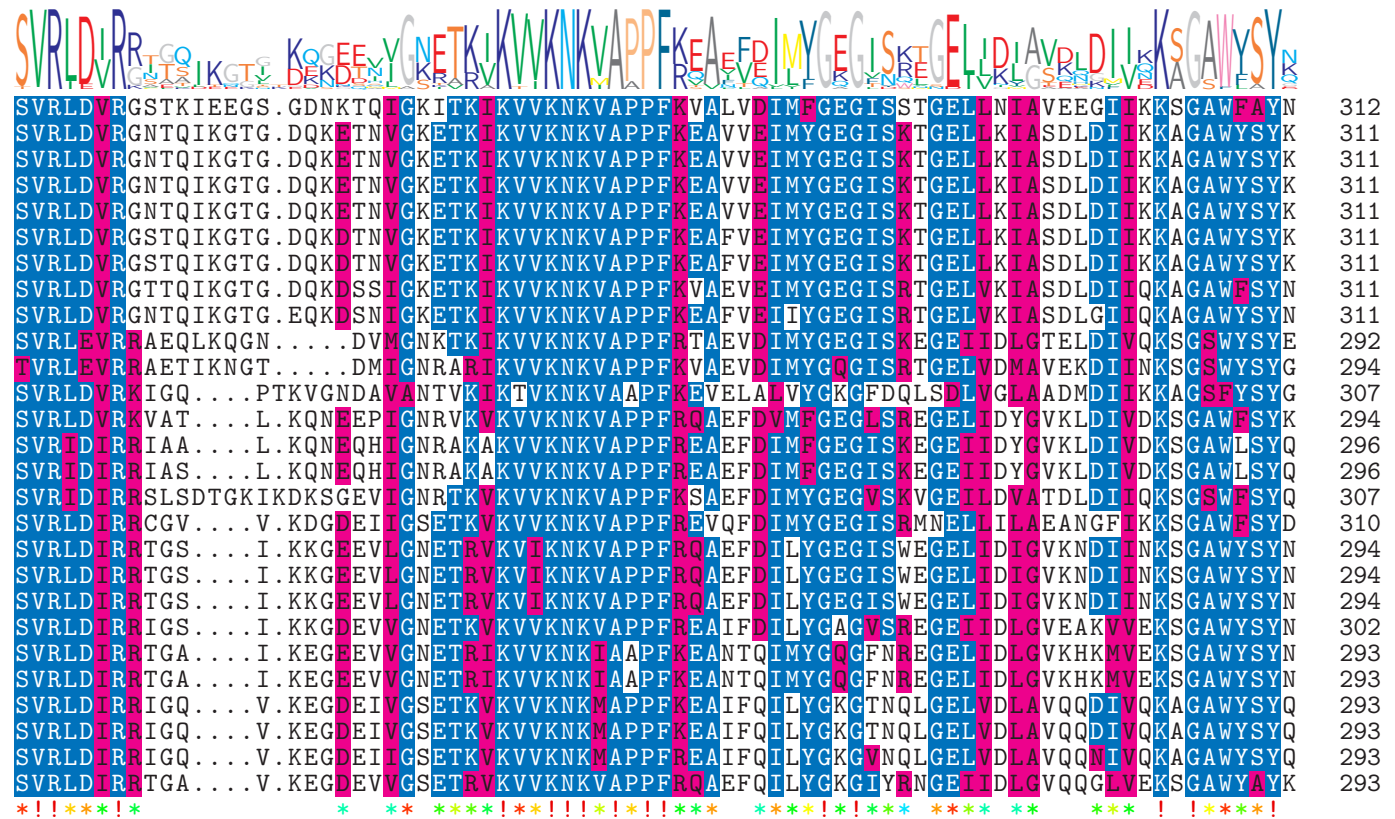
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consensus

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NTDB id 1205 PSJM300 05545 AFN77183.1

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAADNPVFAEIDHQVRVQFGLIDGEEAAE.....SKKDE.....VAQVDS..VNEEVPLDLGDEL	378
DEKIGQGS ENAKKYLAADNPVFEIDHQVRVQFGLIDGEEIAE.....SKKDE.....AAQVDS..VNEEVPLDLGDEL	378
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGS ENAKKFLADNPVFEIDHKVVRVQGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGREN AKQFLKENKDIMLMIQE QIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGGGREN AKNYLADHEDVEDEVRLKVR AAYGISDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA	363
DKKLGGGREN SKAFLKENPEIADEITKAIQNSMGI EGMISGS..EDDEGE..E.....	343
DKKLGGGREN AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGREN AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGGGRDNCREFLRENAELAREIENKVR EHLGVTPMGAV..TLAEEVEED.....	352
GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVFEFGAVPE.....EF.....	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVFEFGAVPE.....EF.....	354
GNKIGGQKNNVIRYFEENTQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..A.HDETEEPPD..LLES.....	349
GSKIGGQKANA AKYLENPEIQEIEQQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

			E	I	E	E	
NTDB id 600 KW2 RS01765 WP 011675413.1		387					
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE	388					
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NTDB id 1205 PSJM300 05545 AFN77183.1		347					
consensus							

-  non conserved
-  similar
-  ≥ 50% conserved