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consensus

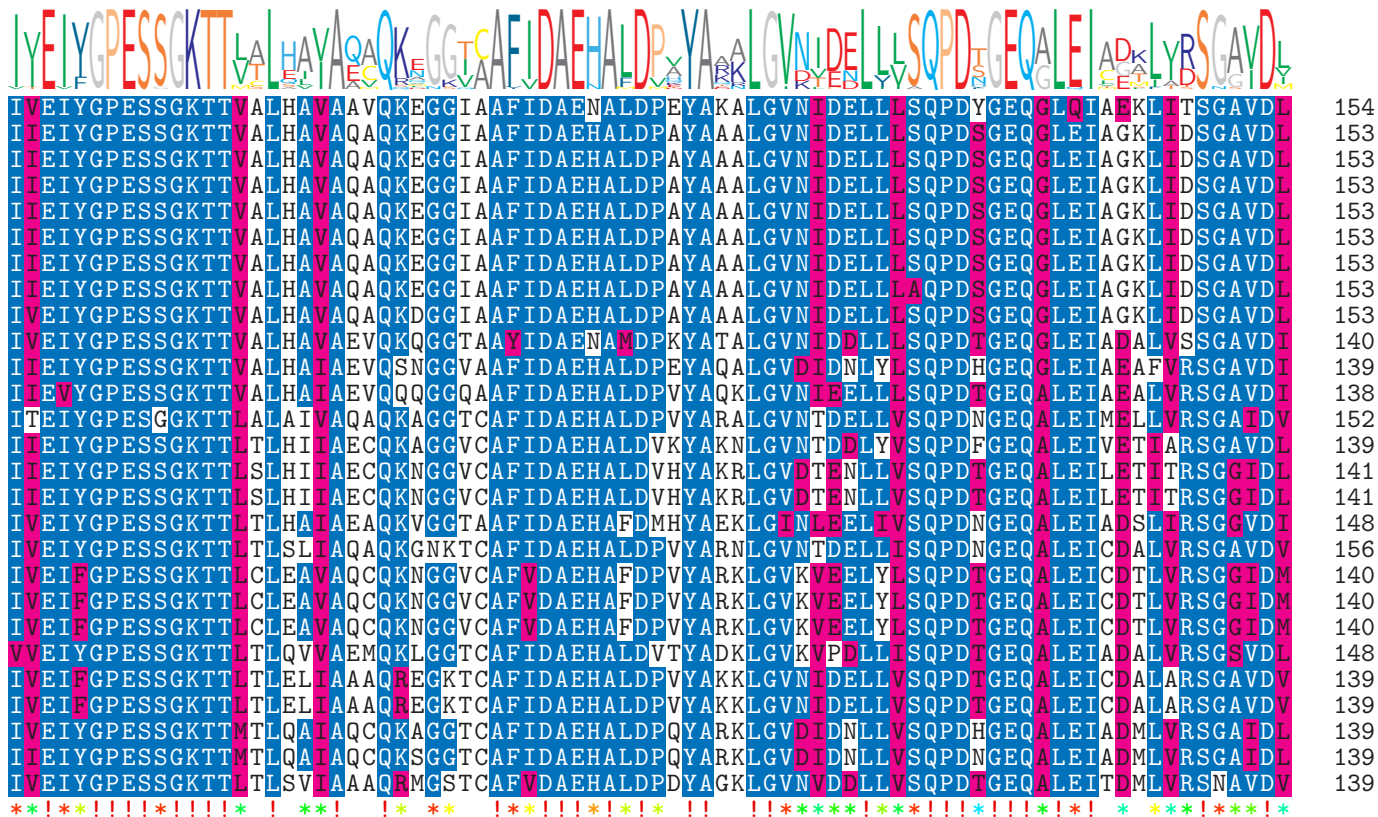
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consensus

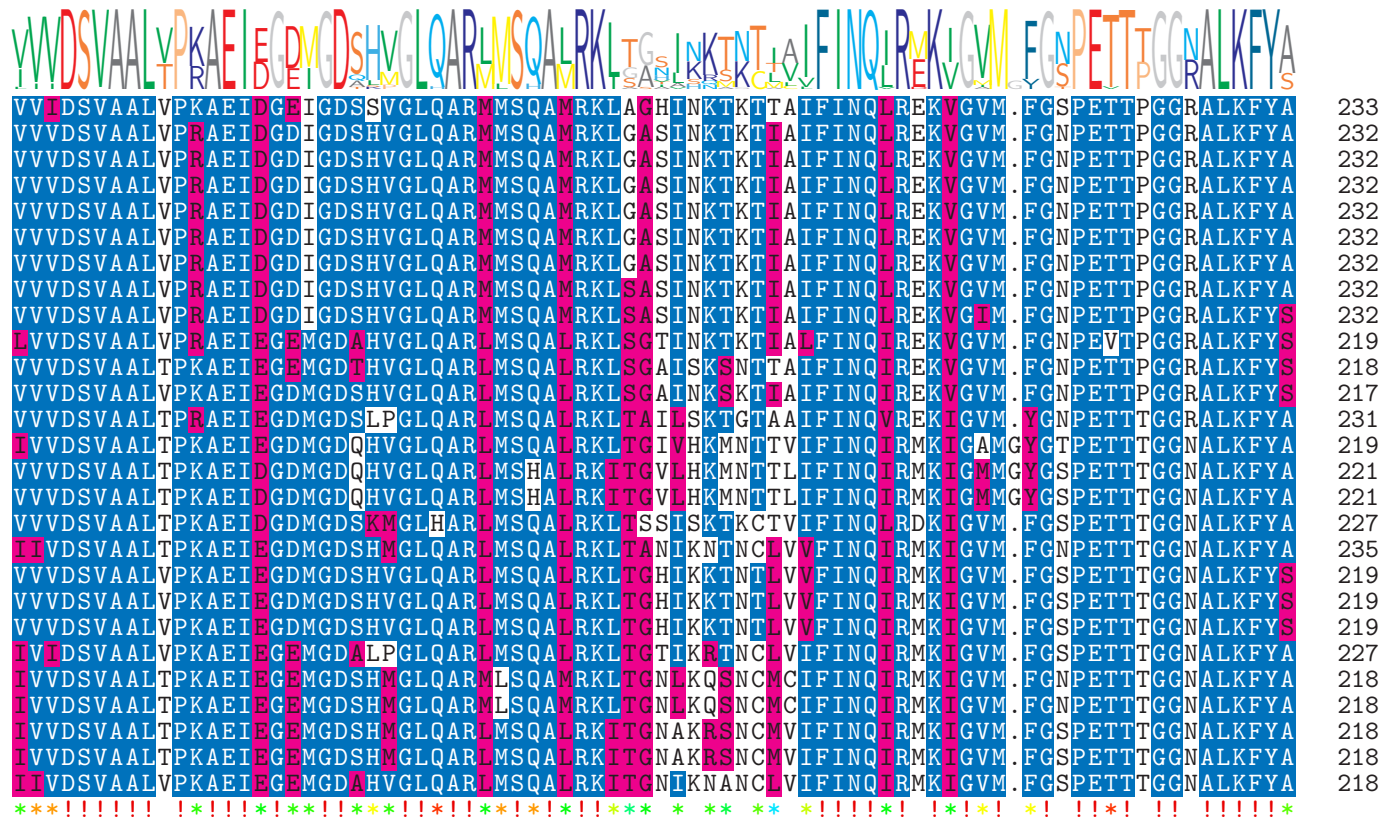
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consensus

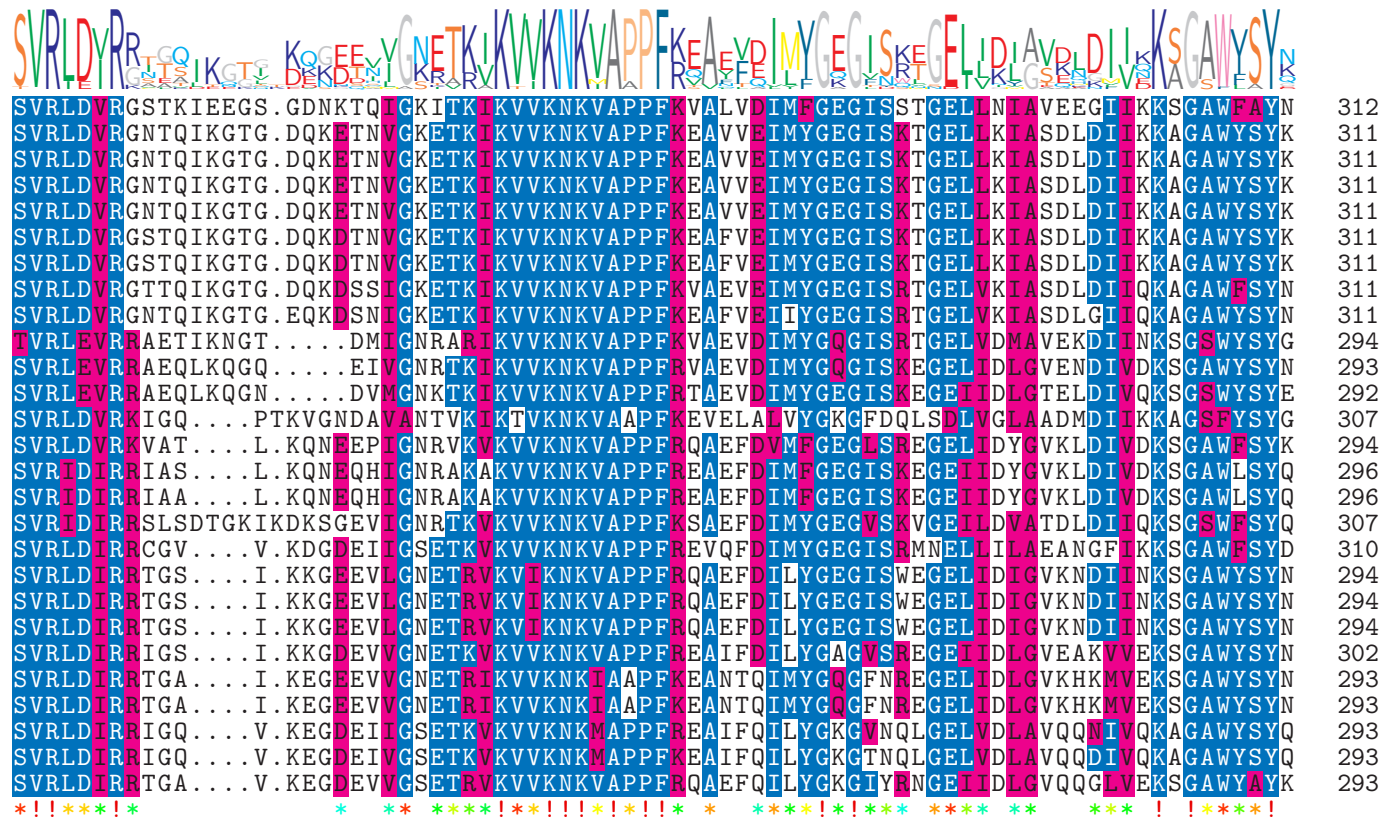
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consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ENAKKYLANPEVFAEIDHQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
SERIGQGR ENAKKNYLADHEDVEDEVRLKVR AAYGISDVPEEDLPTTEDEQINILPDDSTEE.....	355
GERMGQG KENVKMYLKENPQIKEEIDRKLRKELGISDGDVEETEDA...PKSLFDEE.....	347
EERLGGQREN AKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQQAEEETQEELEFEE.....	348
DERIGQG KEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
DKKLGGQREN SKAFLKENPEIADEITKAIQNSMGTIEGMI....SGSEDD..EGEE.....	343
DKKLGGQREN AKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLEEME.....	347
DKKLGGQREN AKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLEEME.....	347
DTKLGGQRD TVKELIKDNPEIAEELEAKIREKLQAK.....	343
GKIGGGKNN AVKWLKENPEIAADKLEQEIINTLASNPNS....VLKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET DGER.....PEE.....	348
GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET DGER.....PEE.....	348
GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET DGER.....PEE.....	348
GERIGGGRDNCREFLRENAELAREIENKVRHLGVTPMG.....AVTLA.EEVEED.....	352
GDKIGGGKANACKY LKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GDKIGGGKANACKY LKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEEEP D..LL..ES.....	349
GNKIGGGKNNVIRYFEENNQIAEEIERNIREQLLTTGTN....GAVQ..I.EDEEEEP D..LL..LES.....	349
GSKIGGGKANAAKYLEENPEI GQIEQQIRAKLLVTSAN....TKATPVAEDLADAD..I.....	347

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
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consensus			

- non conserved
- similar
- ≥ 50% conserved