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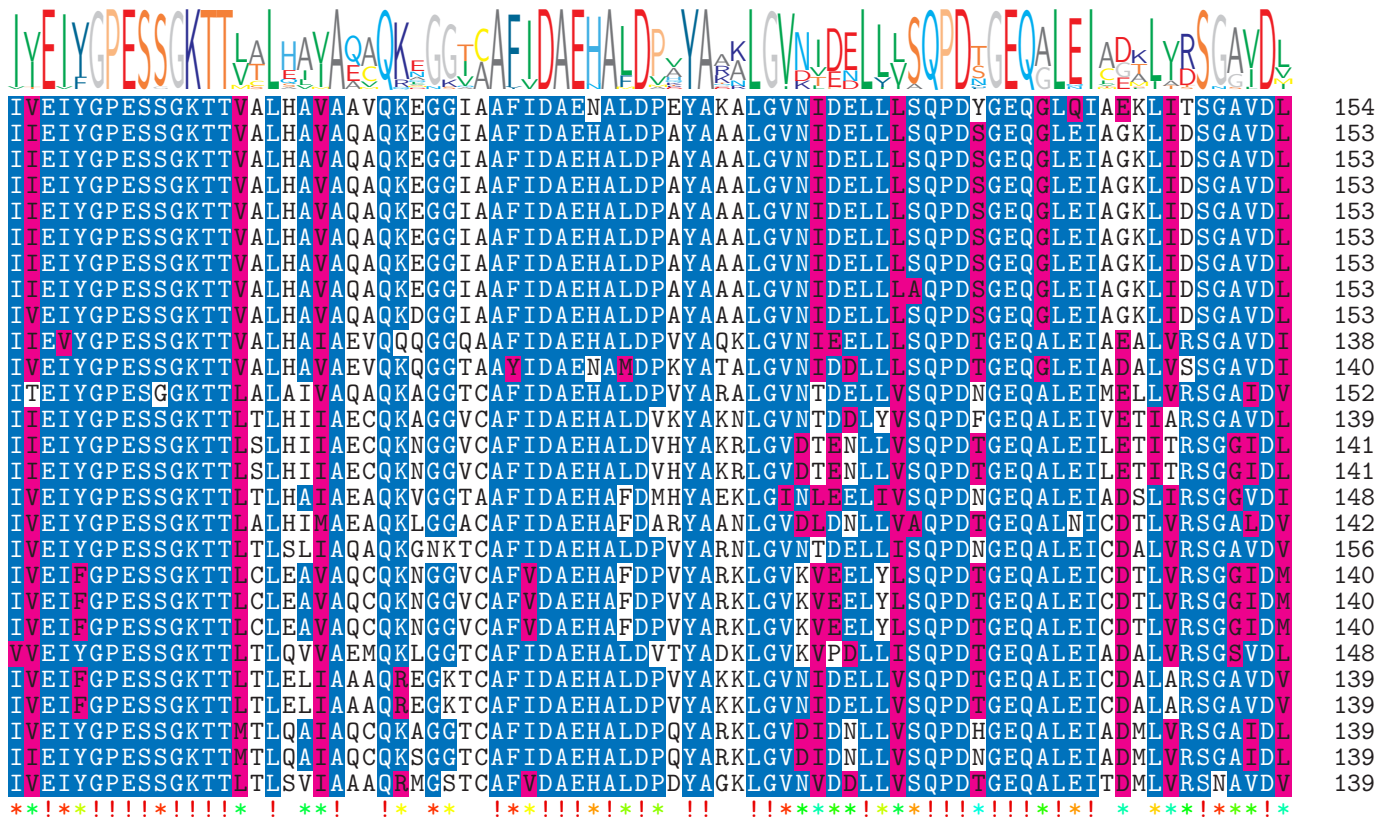
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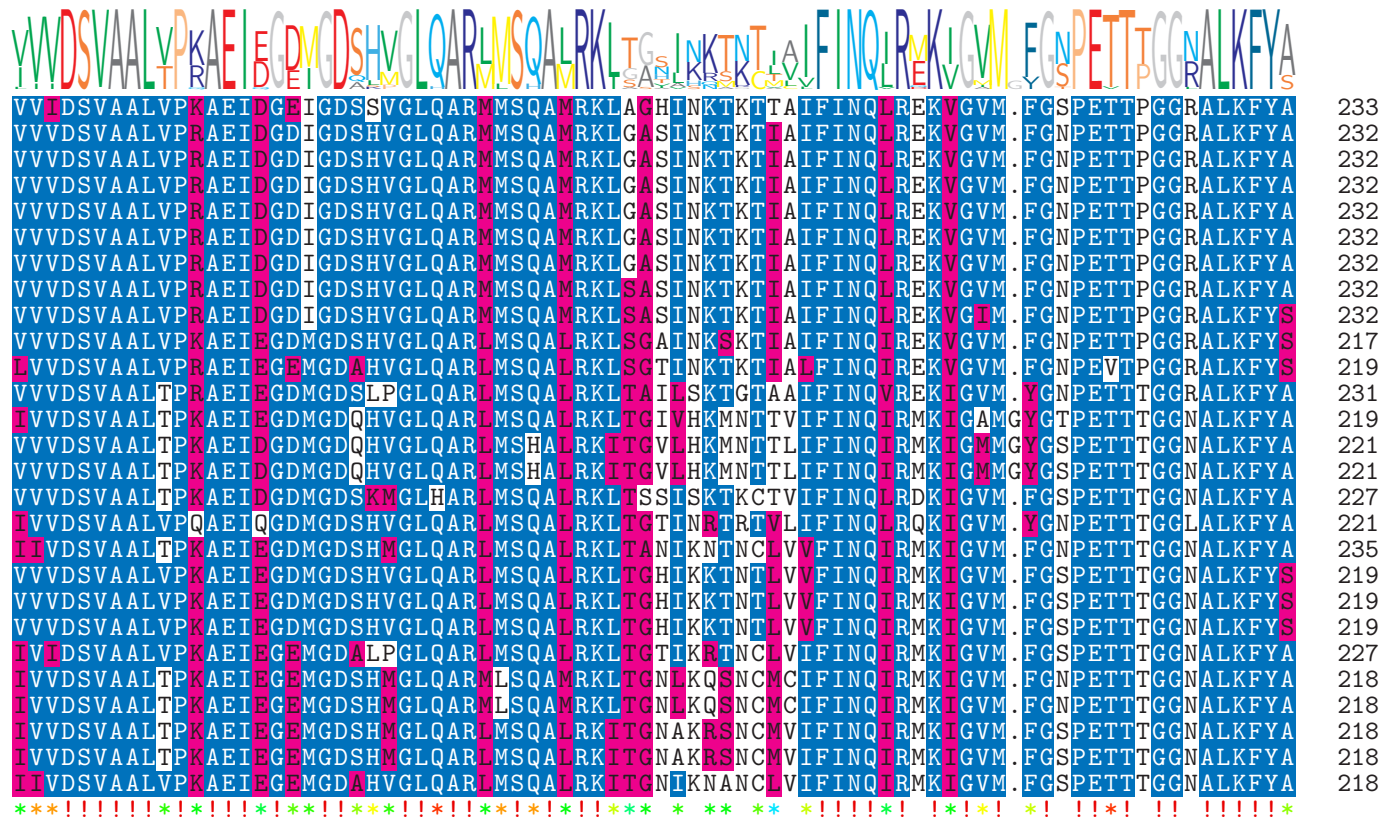
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consensus

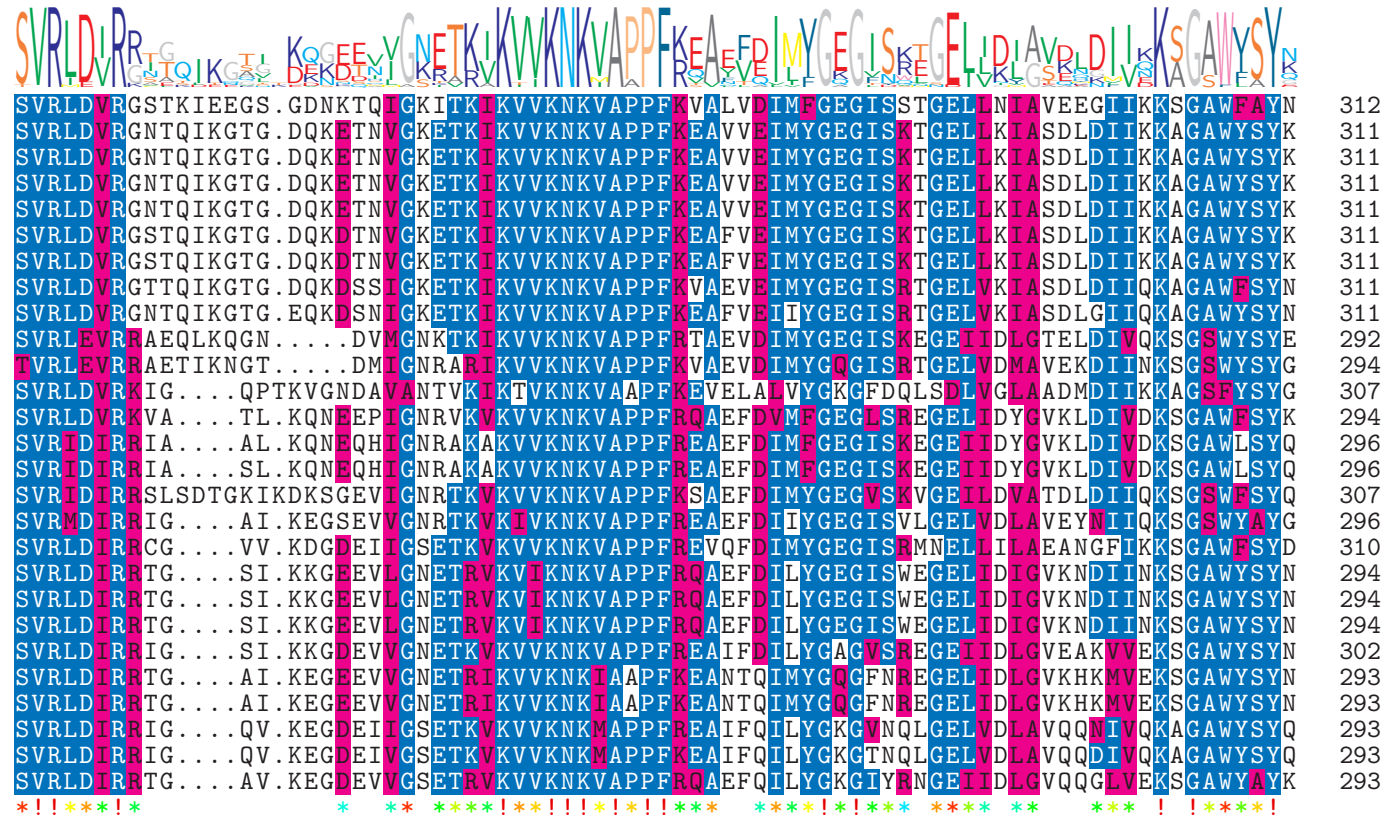
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLADNPEIFDEIDHQRVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVAAAYGISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
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DKKLGQGRNSKAFLENPEIAIDETIKATQNSMCTEGM....ISGSDEDE..GE..E.....	343
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EEIRIGQGREAAKAWLRERPELQEEIRRVQKEAMGVQPP....RSRAEMDEVYLE..E.....	347
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNCVEMH....ITEGTQDETDGE..R.....PEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNCVEMH....ITEGTQDETDGE..R.....PEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNCVEMH....ITEGTQDETDGE..R.....PEE.....	348
GERIGQRDNCREFLRENAELAREIENKVRHLGVTPM....GAVTLA.EEEVE..D.....	352
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GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETEE..EPDLL..ES.....	349
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved