

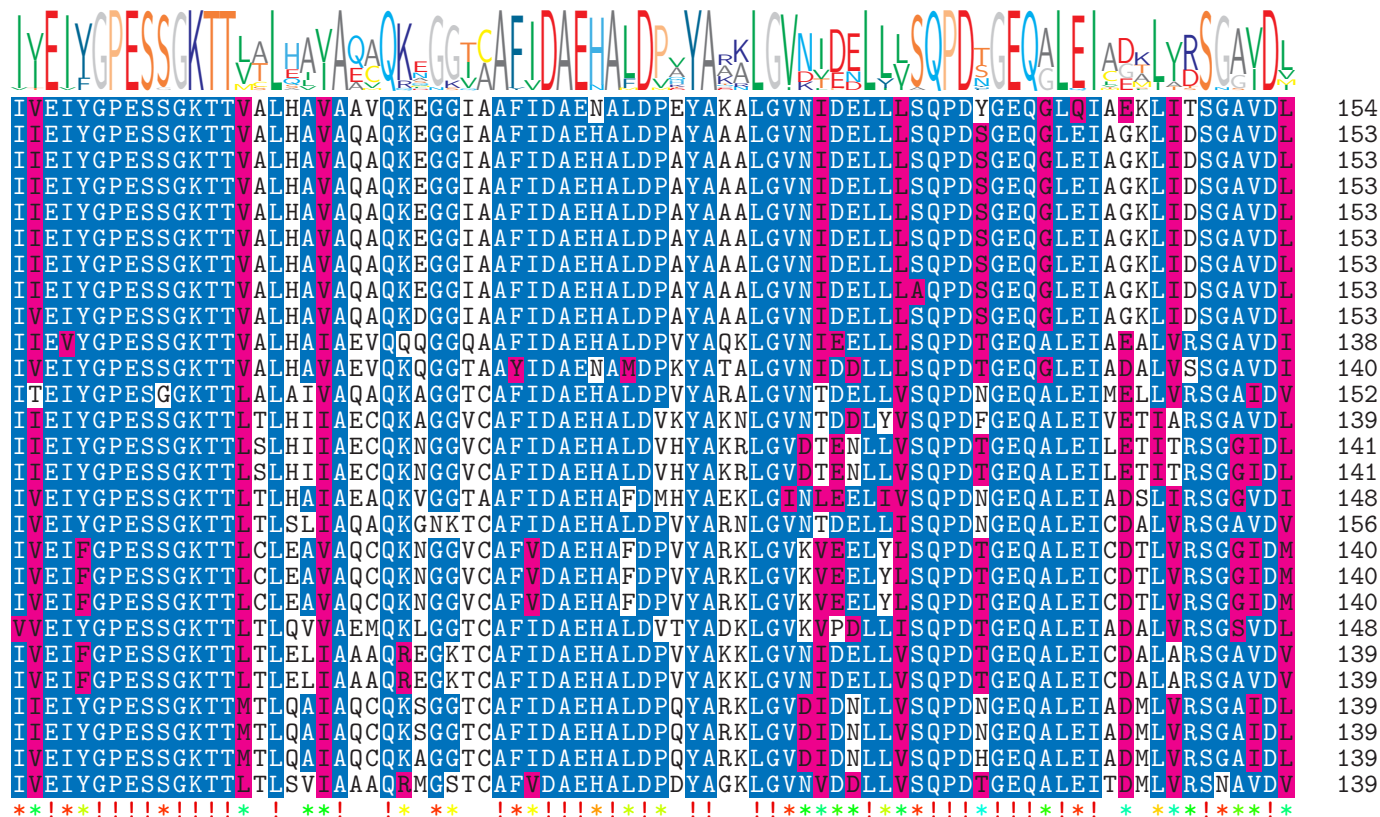
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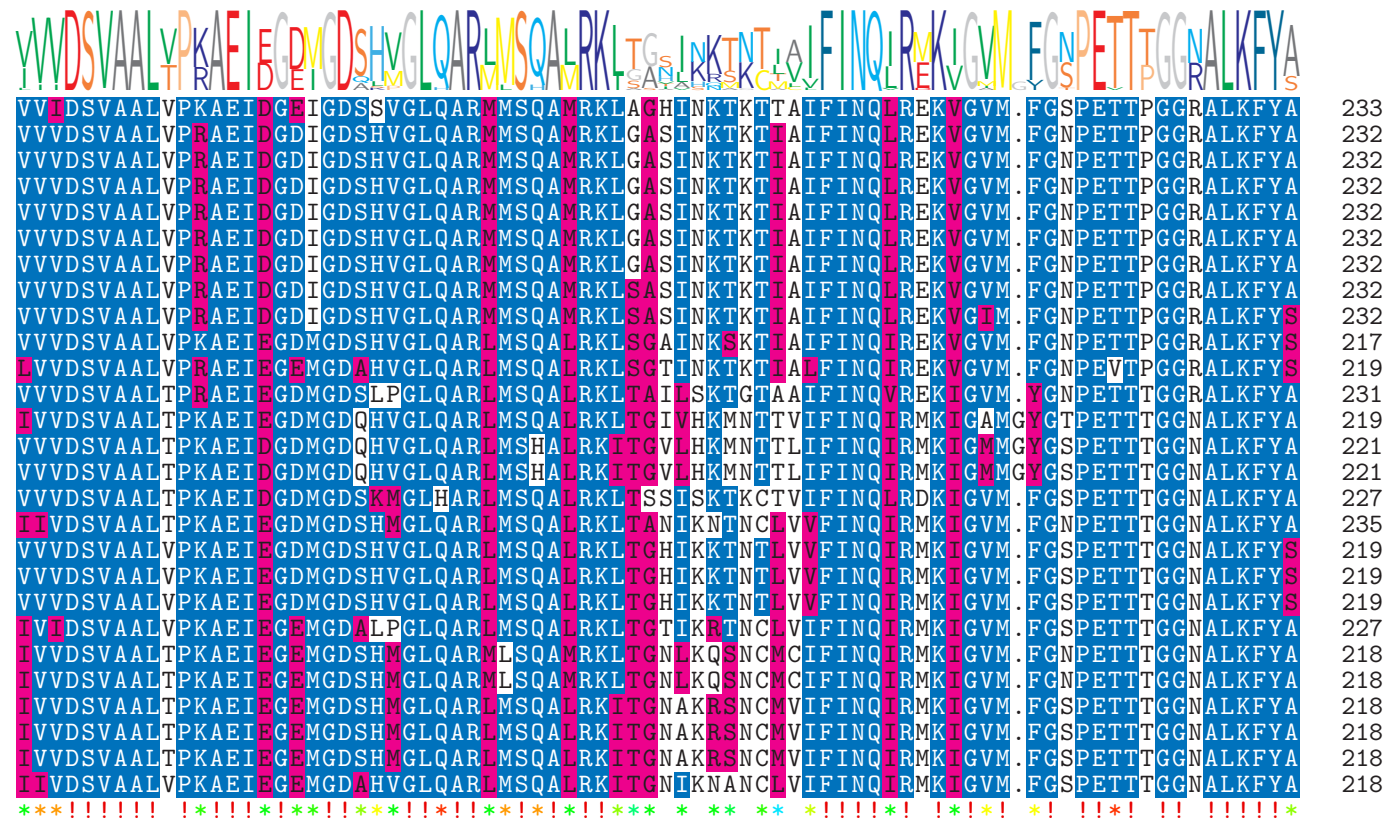
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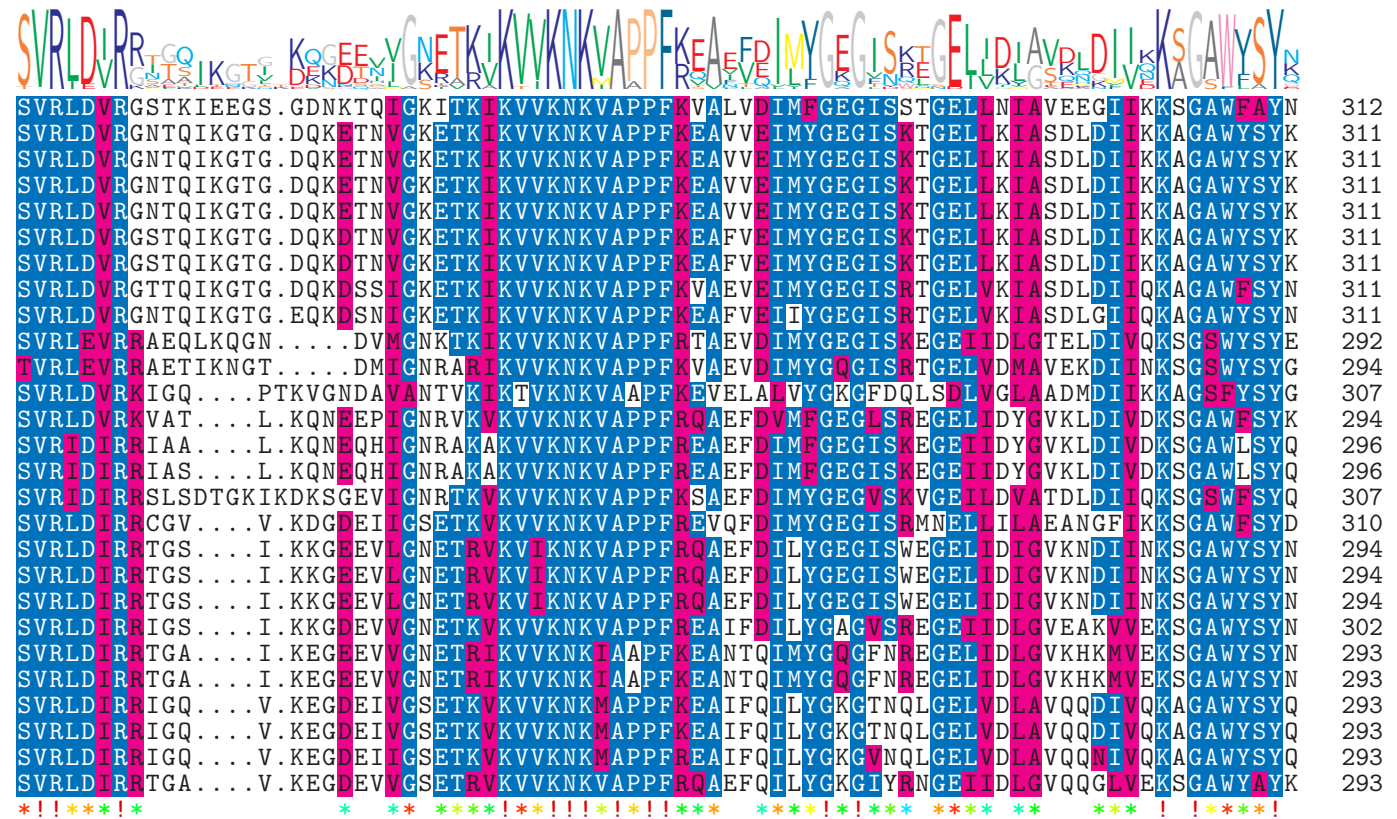
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Sequence	Score
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DEKIGQGSEN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGSEN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGSEN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGSEN ⁺ AKKYLA ⁺ DNPEVFA ⁺ EID ⁺ HQVRVQFGLIDGEEAAE.....SKKD ⁺ E.....VAQVDS..VNEEVTLDLGDEL	378
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GEKIGQGSEN ⁺ AKRYLADHPQLF ⁺ DEID ⁺ RKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGSEN ⁺ AKKFLADNPEIF ⁺ DDID ⁺ HKVRVQYGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGREN ⁺ AKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAAEE.TQEEL.E..FE.E.....	348
SERIGGGREN ⁺ AKNYLADHEDVEDEVRLK ⁺ VRAAYG ⁺ ISDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE	355
DERIGGGKEKTIA ⁺ YIAERP ⁺ MEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA	363
DKKLGGGREN ⁺ SKAFLKENPEIA ⁺ DEITKAIQNSMGIEGMISGS..EDDEGE. ⁺ E.....	343
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD ⁺ TVKELIKDNPELAE ⁺ ELEAKIREKLQAK	343
GTKIGQGKNN ⁺ AVKWLKENPEIA ⁺ DKLEQEI ⁺ RNTLASNPNSVLK..ATASDSND ⁺ ESDVEEFSE.....EEL	372
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GAKIGGQKDN ⁺ VRVWLKENPEIS ⁺ DEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E	348
GAKIGGQKDN ⁺ VRVWLKENPEIS ⁺ DEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E	348
GERIGGGRDN ⁺ CREFLRENAELAREIENK ⁺ VREHLGVTPMGAV..TLAEEVEED ⁺	352
GDKIGGQKAN ⁺ ACKYLKENPEIA ⁺ KTLDKKLREMLLNPNMQLI..AETSSAAD ⁺ VEFGAVPE.....EF	354
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GNKIGGQKNN ⁺ VIRYFEENTQIAE ⁺ EIERNIREQLLTGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S	349
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GSKIGGQKANA ⁺ KYLEENPEI ⁺ GQIE ⁺ EQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

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consensus								

-  non conserved
-  similar
-  ≥ 50% conserved