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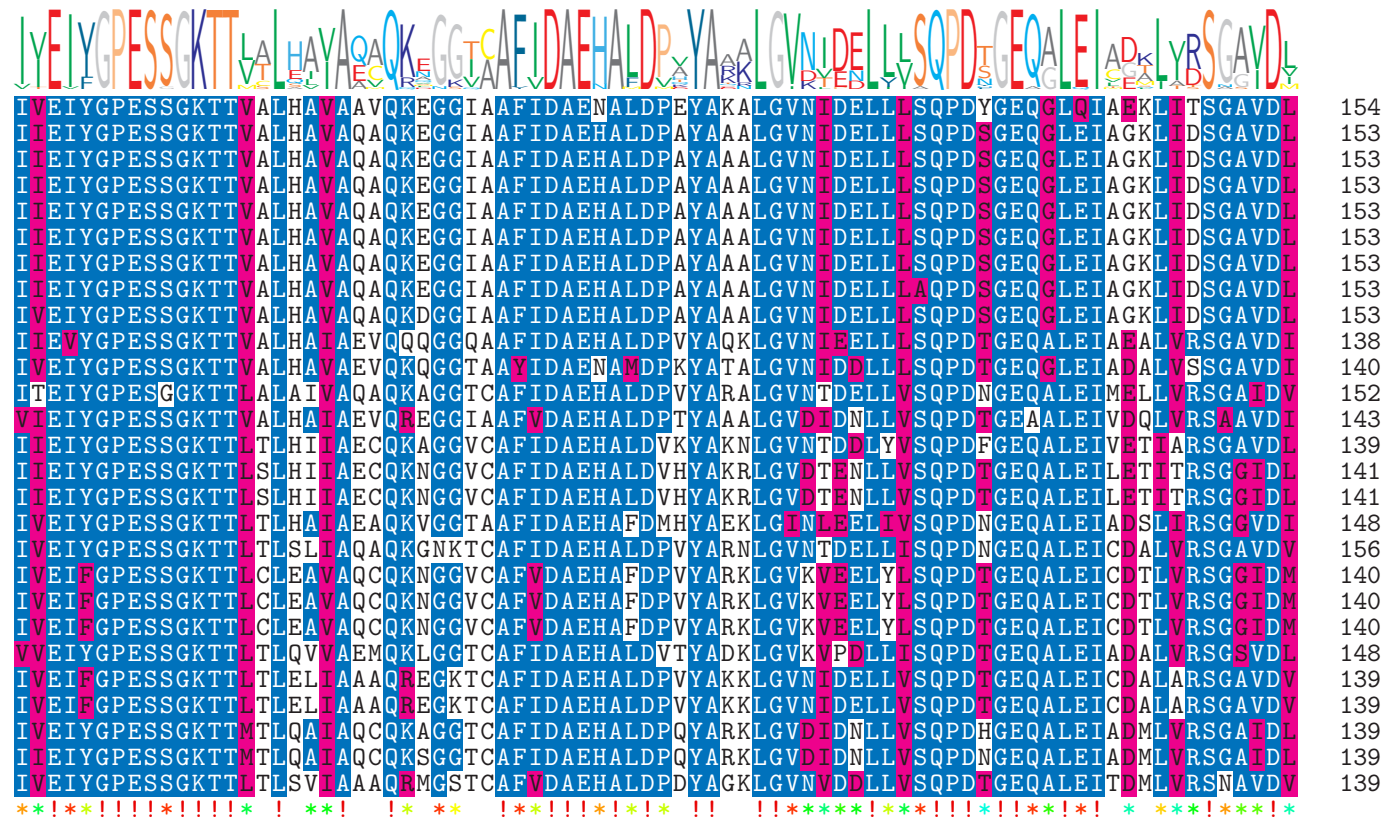
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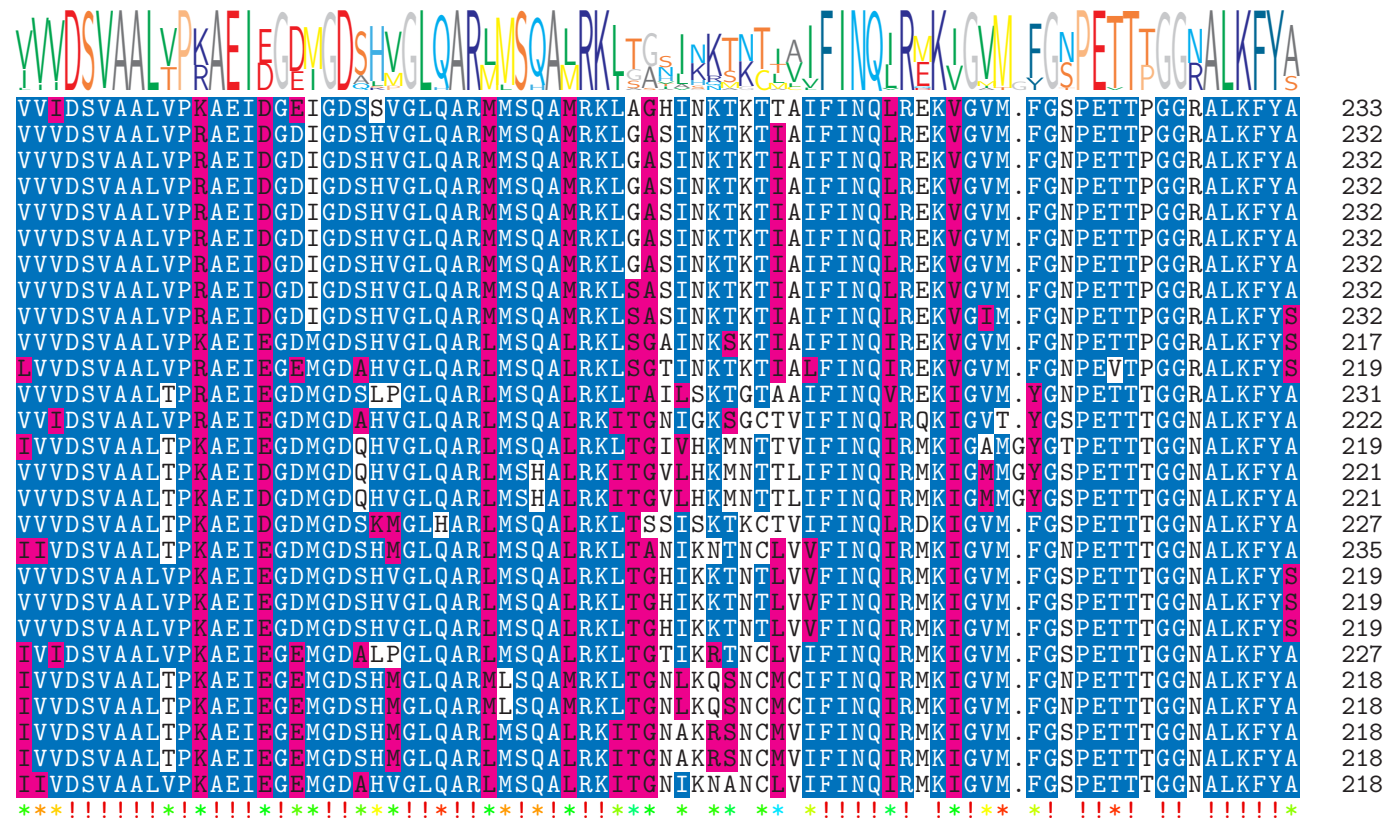
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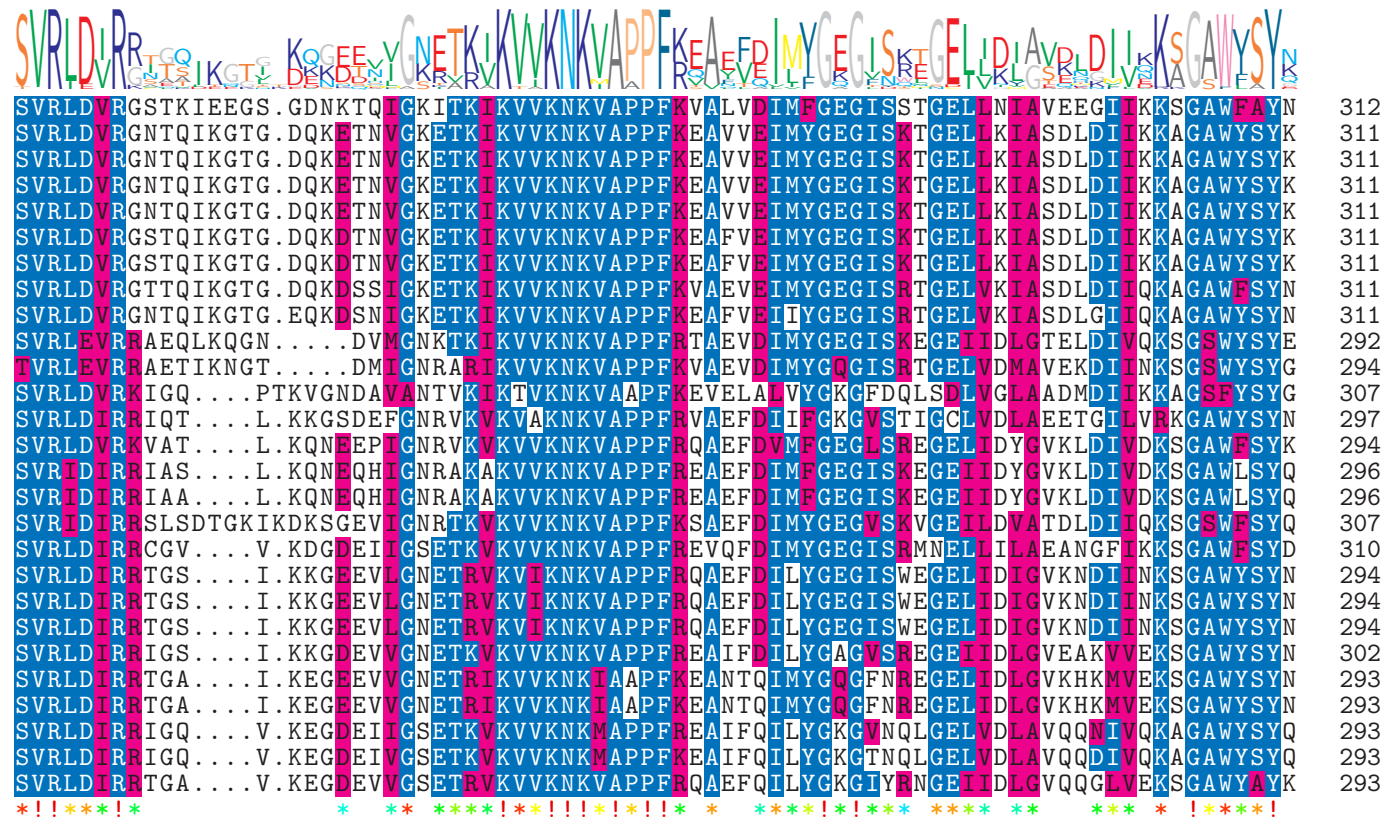
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Sequence	Score
DEKIGQGA ⁶ AKAK ¹ NYL ¹ KEHQ ¹ DV ¹ FDEID ¹ HKV ¹ RAAH ¹ GL ¹ LD ¹ DDSEVAETEEETTA...SKTKAKAKKEEKAVETEEIELELED..	387
DEKIGQGS ⁶ ENAK ¹ KYLA ¹ EHPEIF ¹ DEID ¹ KQV ¹ RSKF ¹ GL ¹ IDGEEVSEQD ¹ TENKK...DE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁶ ENAK ¹ KYLA ¹ EHPEIF ¹ DEID ¹ KQV ¹ RSKF ¹ GL ¹ IDGEEVSEQD ¹ TENKK...DE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁶ ENAK ¹ KYLA ¹ EHPEIF ¹ DEID ¹ KQV ¹ RSKF ¹ GL ¹ IDGEEVSEQD ¹ TENKK...DE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁶ ENAK ¹ KYLA ¹ DNPEVFA ¹ EID ¹ HQV ¹ RVQF ¹ GL ¹ IDGEEAAE...SKK...DE...VAQVDS..VNEEVTLDLGDEL	378
DEKIGQGS ⁶ ENAK ¹ KYLA ¹ DNPEIF ¹ EID ¹ HQV ¹ RVQF ¹ GL ¹ IDGEEIAE...SKK...DE...AAQVDS..VNEEVTLDLGDEL	378
GEKIGQGS ⁶ ENAK ¹ RYLADHPQLF ¹ DEID ¹ RKV ¹ RVKF ¹ GL ¹ LEESEESAMAVASE...E.....TDDLALDLNGI	374
GEKIGQGS ⁶ ENAK ¹ KFLADNPEIF ¹ DDID ¹ HKV ¹ RVQY ¹ GL ¹ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTI	379
EE ⁶ RLGQGREN ¹ AKQFL ¹ KEN ¹ KDIMLMIQE ¹ QIREHY ¹ GLD ¹ NNGVVQQQAETQE...EL.EFE.E.....	348
SERIGQGREN ¹ AK ¹ NYLADHEDVE ¹ DEV ¹ RLKV ¹ RAAY ¹ GIS ¹ SDVPEEDLPTTEDE...QI.NILPDDST....EE.....	355
DERIGQGKE ¹ KTIA ¹ YIAERPE ¹ MEQE ¹ IKDR ¹ MAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
GDNISQGRD ¹ NAIKY ¹ LEEKPEFTE ¹ QIKKL ¹ REKLDKGAVVSANSVSKVNEDDEDEDVDLEE.....	358
DKKLGGGREN ¹ SKAFL ¹ KENPEIA ¹ DEITKAIQNSMG ¹ IEGMISGSED....D..EGEE.....	343
DKKLGGGREN ¹ AKALLKEDKALADEIT ¹ TLKIKESIG ¹ SNEEIMPLPD...E..PLEEME.....	347
DKKLGGGREN ¹ AKALLKEDKALADEIT ¹ TLKIKESIG ¹ SNEEIMPLPD...E..PLEEME.....	347
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GTKIGQGKNN ¹ AVKWLKENPEIAD ¹ KLQEIRNTLASNPNSVLKAT....ASDSNDES ¹ DVEEFSE...EEL.....	372
GAKIGQGKDN ¹ VRVWLKENPEIS ¹ DEIDAKIRALNGVEMHITEGTQ...DETDGER.....PE.....E.....	348
GAKIGQGKDN ¹ VRVWLKENPEIS ¹ DEIDAKIRALNGVEMHITEGTQ...DETDGER.....PE.....E.....	348
GAKIGQGKDN ¹ VRVWLKENPEIS ¹ DEIDAKIRALNGVEMHITEGTQ...DETDGER.....PE.....E.....	348
GERIGQGRD ¹ NCREFLRENAELAR ¹ EIENK ¹ VREHLGVTPMGAVTLA....EEVEED.....	352
GDKIGGKAN ¹ ACKYLKENPEIAKTLD ¹ KKLREMLLNPNENMLIAE...TSSAADDVEFGAVPE...EF.....	354
GDKIGGKAN ¹ ACKYLKENPEIAKTLD ¹ KKLREMLLNPNENMLIAE...TSSAADDVEFGAVPE...EF.....	354
GNKIGQGKNN ¹ VIRYLEENPQISTEIE ¹ EA ¹ IREQLLT ¹ TKASDQTAA....HDETEEEP ¹ DLL..ES.....	349
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GSKIGGKAN ¹ ACKYLEENPEIG ¹ QIEEQ ¹ IRAKLLVTSANTKATP...VAEDLADADI.....	347

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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved