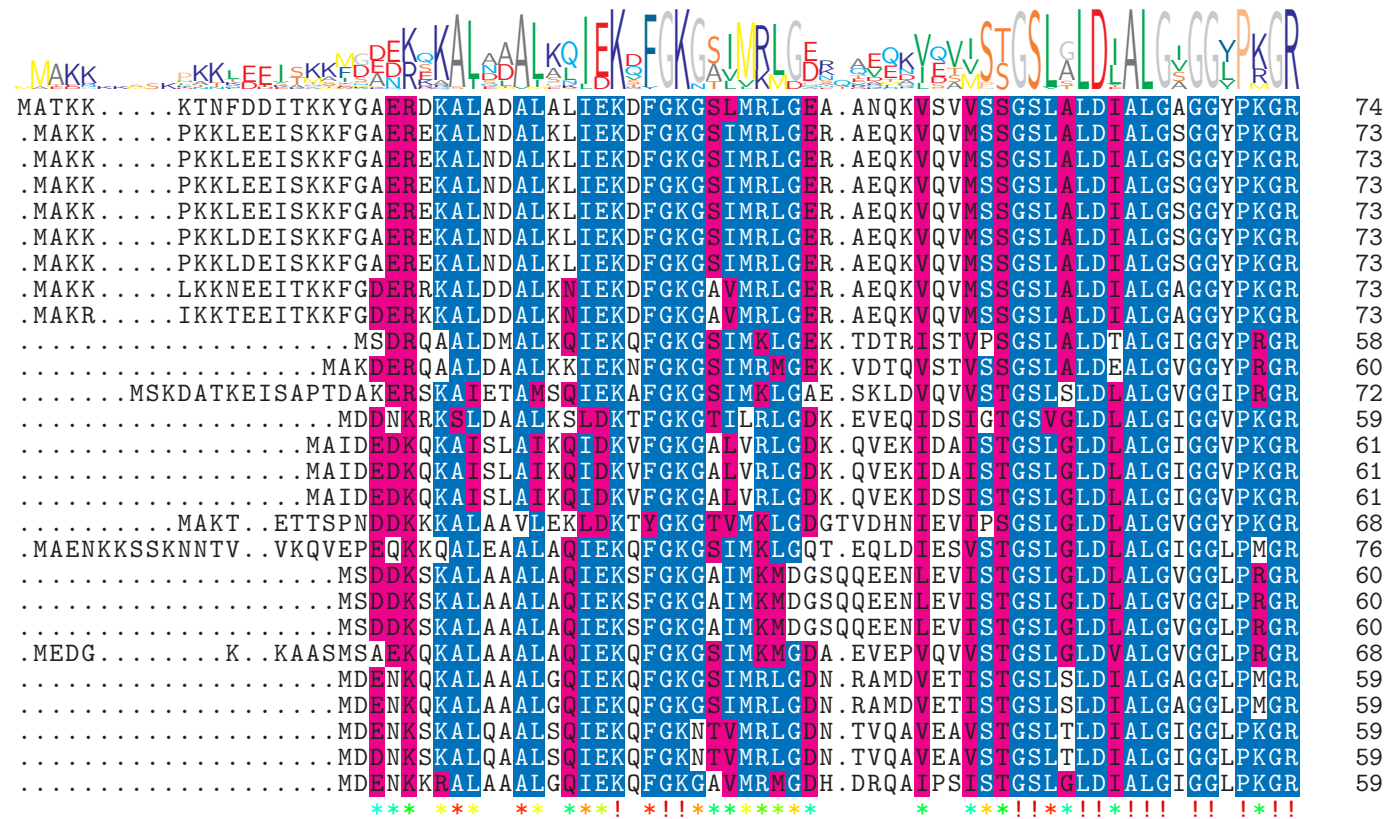


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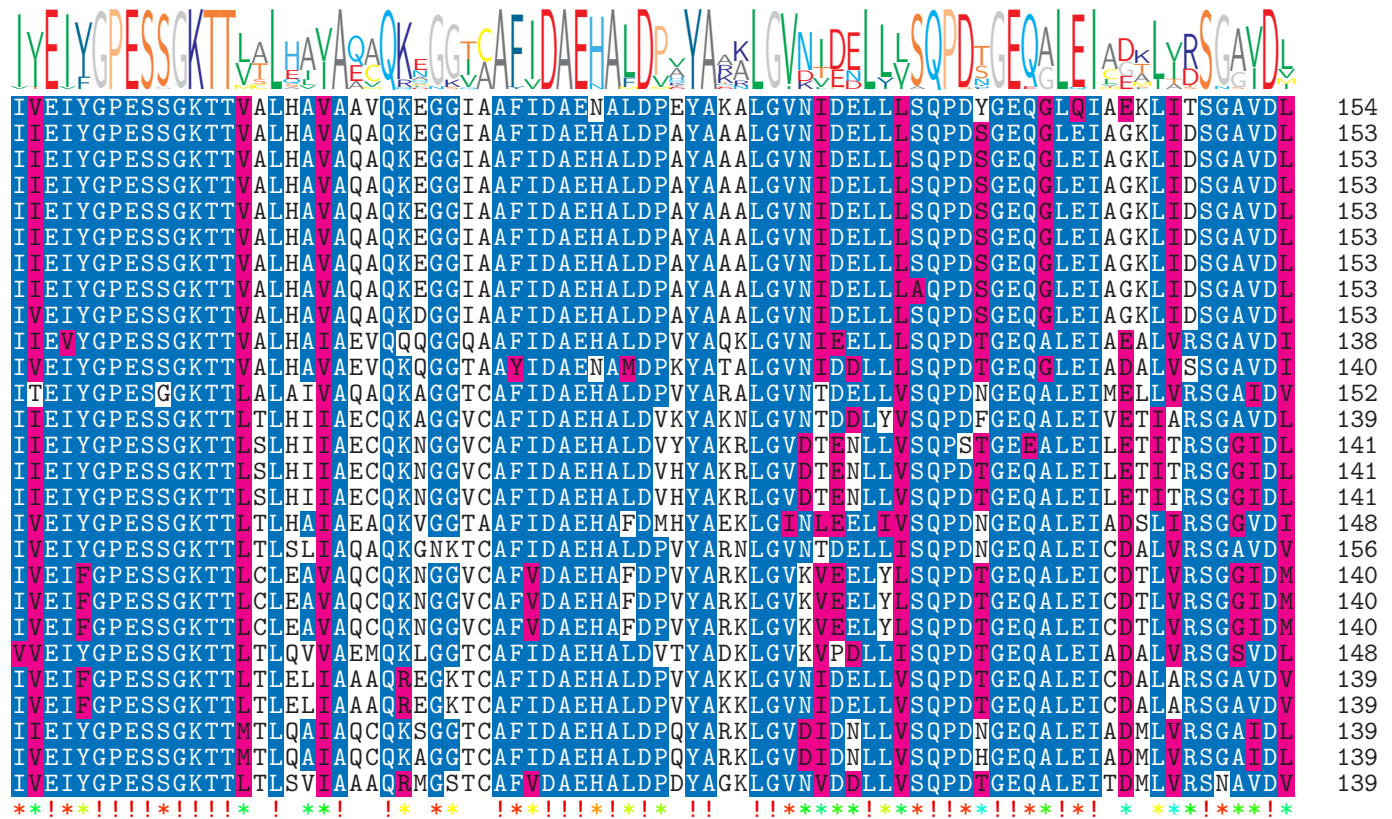
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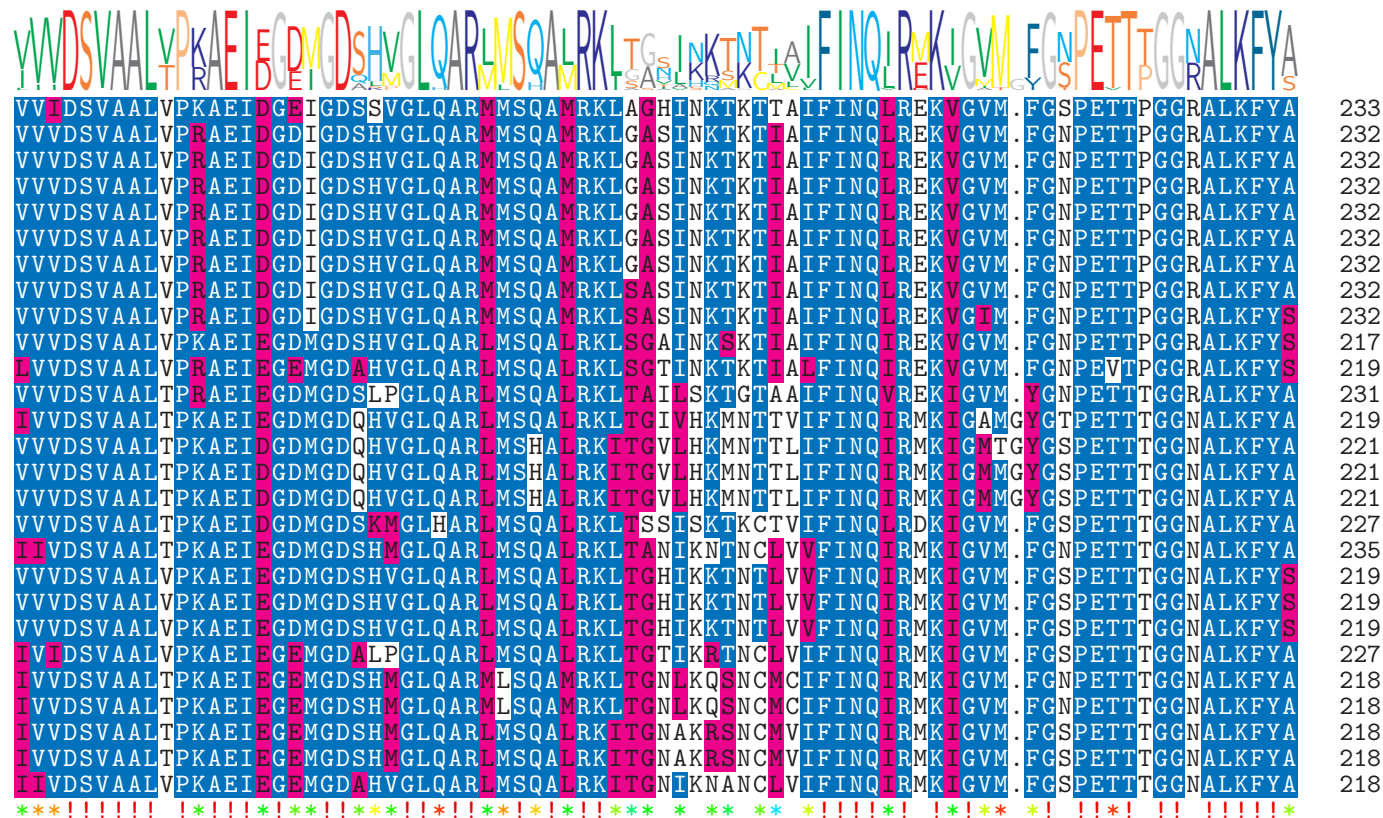
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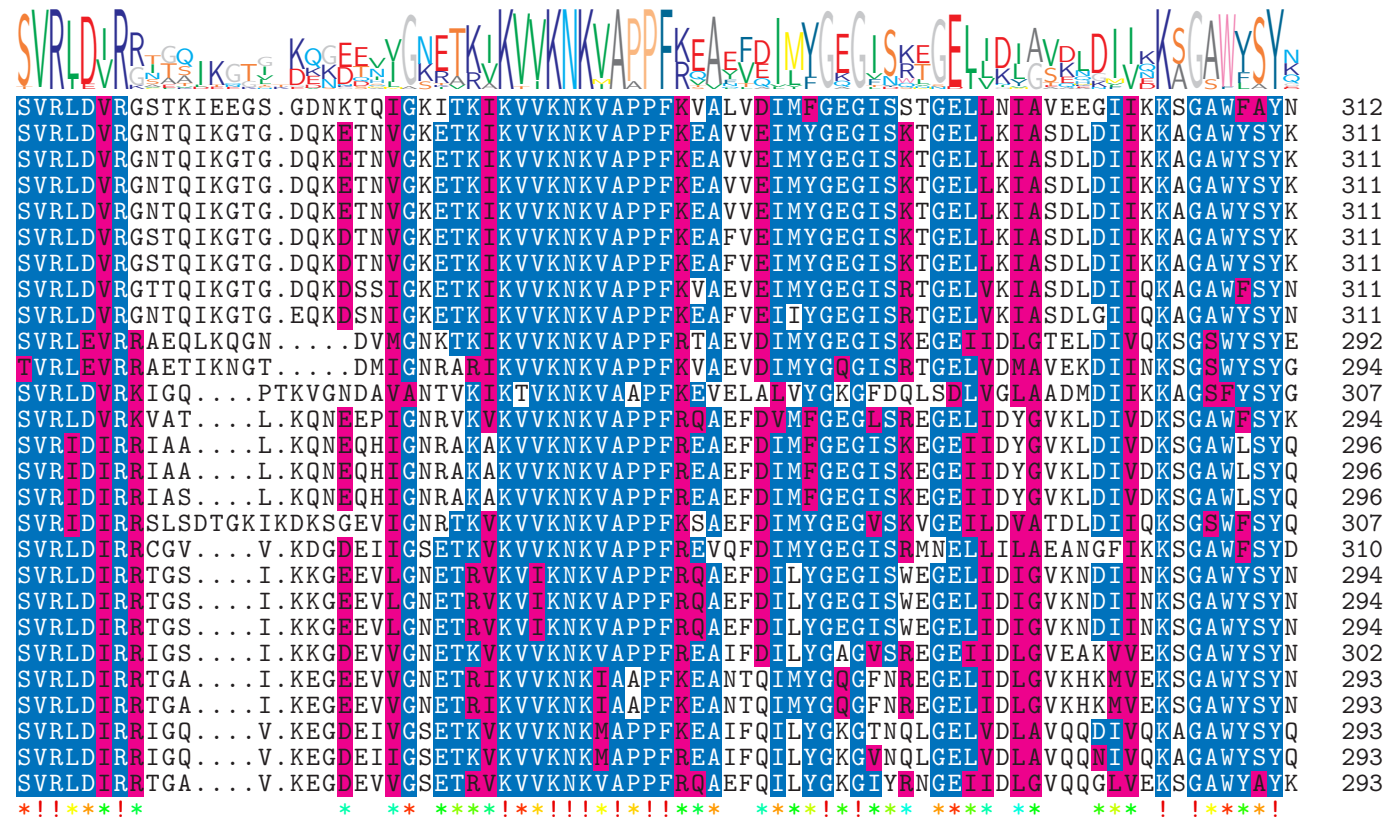
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consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ ADNPE ⁺ IF ⁺ DEID ⁺ DHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ ADNPE ⁺ IF ⁺ DEID ⁺ DHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ RYLA ⁺ DHP ⁺ QL ⁺ FD ⁺ EID ⁺ DRK ⁺ VR ⁺ VKF ⁺ CLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLADN ⁺ PE ⁺ IF ⁺ DD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERL ⁺ GGGREN ⁺ AKQ ⁺ FLKEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DEV ⁺ RLK ⁺ V ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGG ⁺ KEKTIAY ⁺ IA ⁺ ERPE ⁺ MEQE ⁺ IRDR ⁺ MAA ⁺ IRAGNAGEAPALAPAAPEAAEA.....	363
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PE ⁺ IA ⁺ DEIT ⁺ KA ⁺ ITQNSM ⁺ CI ⁺ EGMIS....GSEDD..EGEE.....	343
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALANE ⁺ ITL ⁺ KI ⁺ KESIG ⁺ SNEEIM....PLPDE..PLEEME.....	347
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KI ⁺ KESIG ⁺ SNEEIM....PLPDE..PLEEME.....	347
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KI ⁺ KESIG ⁺ SNEEIM....PLPDE..PLEEME.....	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IKDN ⁺ PE ⁺ LA ⁺ EEL ⁺ EAK ⁺ IREKLQAK.....	343
GTKIGG ⁺ KNNA ⁺ VK ⁺ WLKEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QEI ⁺ RNTLA ⁺ SNPNSV....LKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGG ⁺ GKDN ⁺ VRV ⁺ WLKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RALN ⁺ GVEMHIT....EGTQDETD.....GERPEE.....	348
GAKIGG ⁺ GKDN ⁺ VRV ⁺ WLKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RALN ⁺ GVEMHIT....EGTQDETD.....GERPEE.....	348
GAKIGG ⁺ GKDN ⁺ VRV ⁺ WLKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RALN ⁺ GVEMHIT....EGTQDETD.....GERPEE.....	348
GERIGG ⁺ GRDNC ⁺ REFLREN ⁺ AE ⁺ LARE ⁺ IE ⁺ DN ⁺ KV ⁺ REHL ⁺ CVTPMGA....V.TLAEVEEED.....	352
GDKIGG ⁺ GKAN ⁺ ACKYL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PENMQ....LIAETSSAADDVE..FGAVPEEF.....	354
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GNKIGG ⁺ GKNN ⁺ VIRY ⁺ FEENN ⁺ QIA ⁺ EIE ⁺ ERN ⁺ IREQLLT ⁺ TGTNG....AVQ.I.EDEEEPD....LLES.....	349
GNKIGG ⁺ GKNN ⁺ VIRY ⁺ LEEN ⁺ PQISTE ⁺ IE ⁺ AV ⁺ IREQLLT ⁺ TASDQ....TAA.HDETEEEDPD....LLES.....	349
GSKIGG ⁺ GKAN ⁺ AKYLEEN ⁺ PE ⁺ IG ⁺ EIE ⁺ EQQ ⁺ IRAK ⁺ LLV ⁺ TSA ⁺ NT.....KATPVAEDLADAD....I.....	347

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved