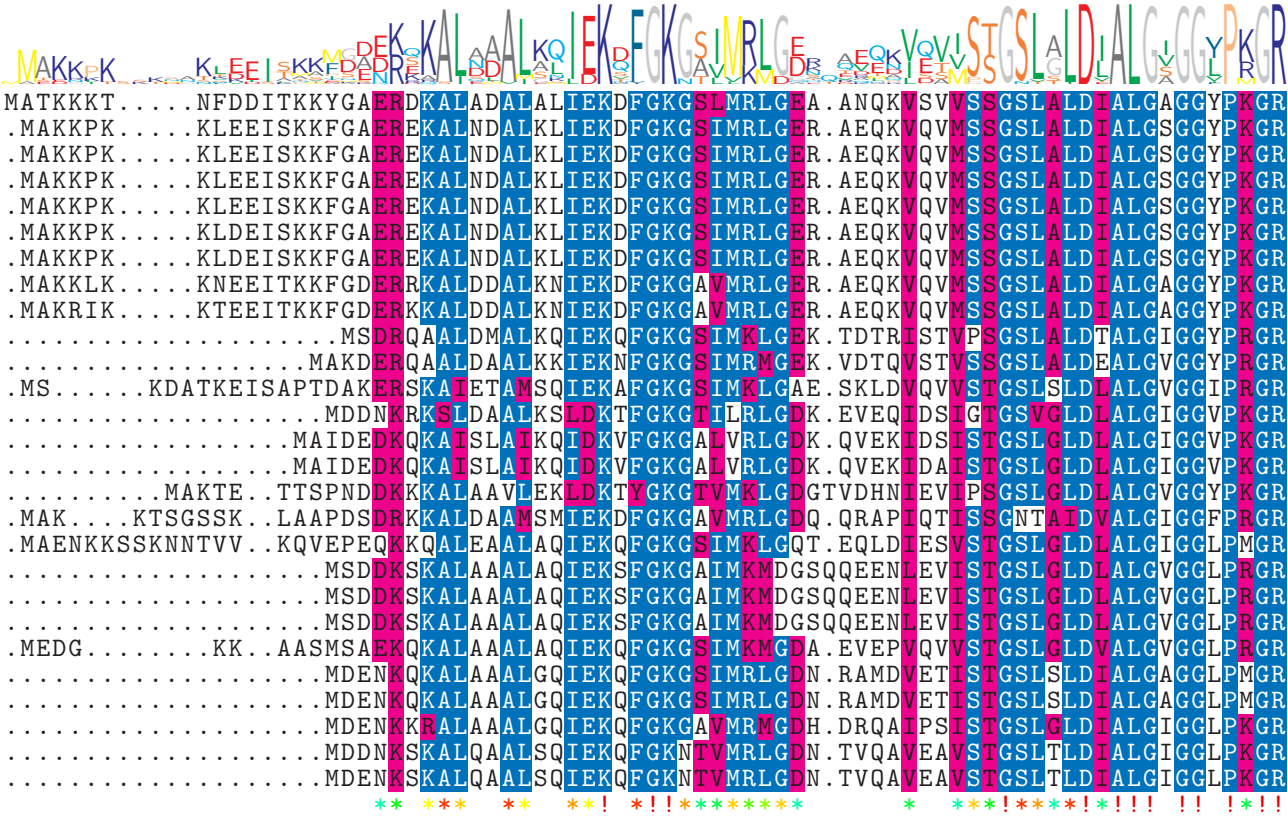


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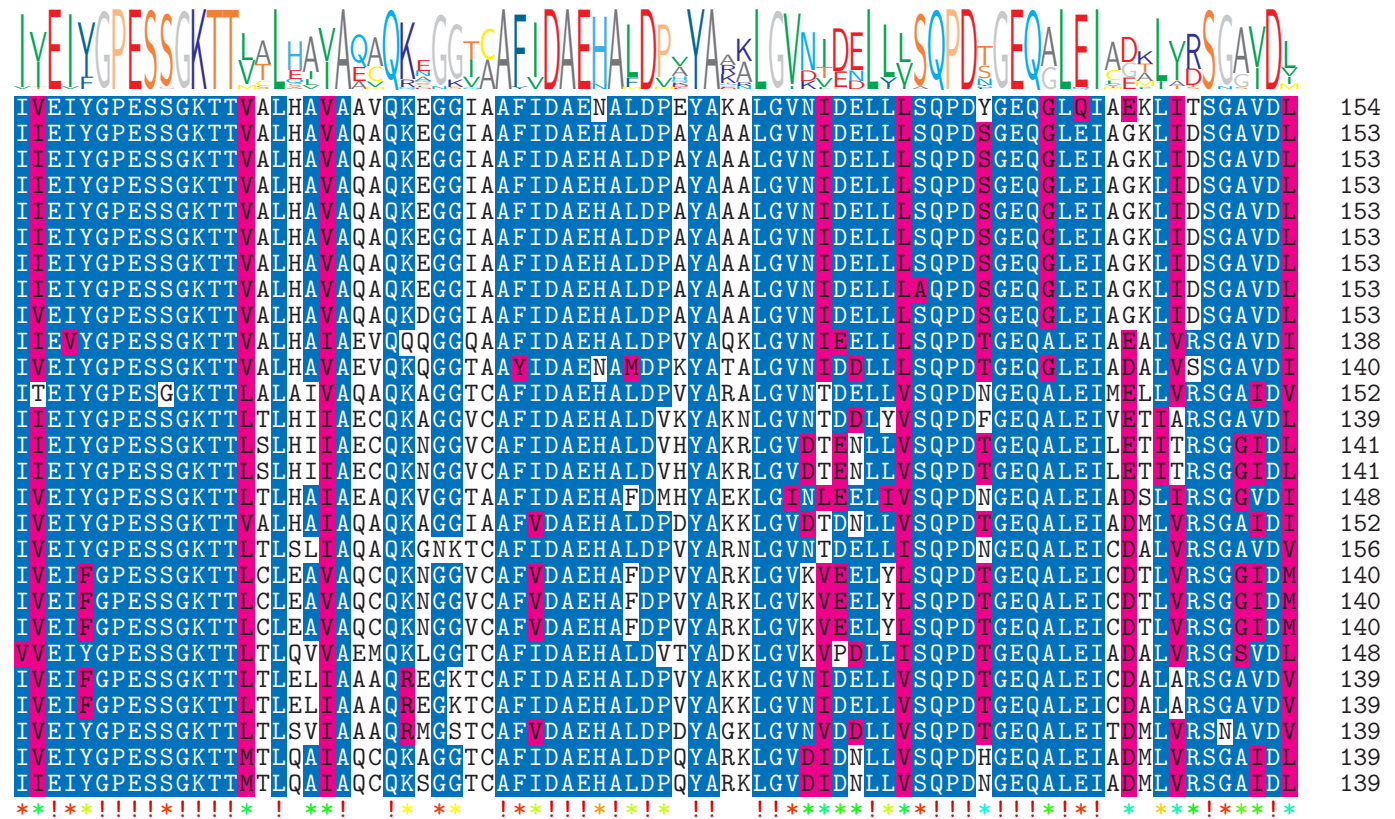


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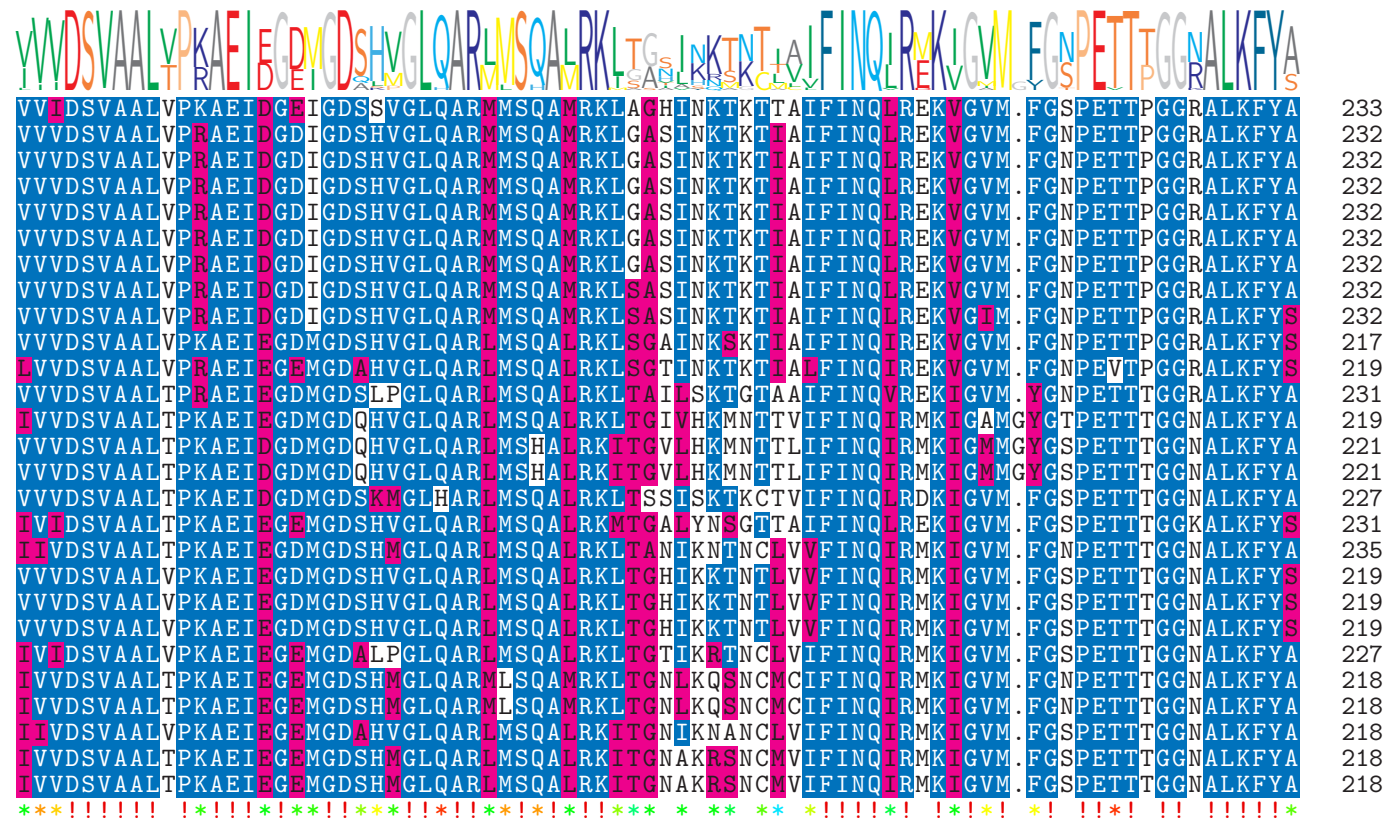
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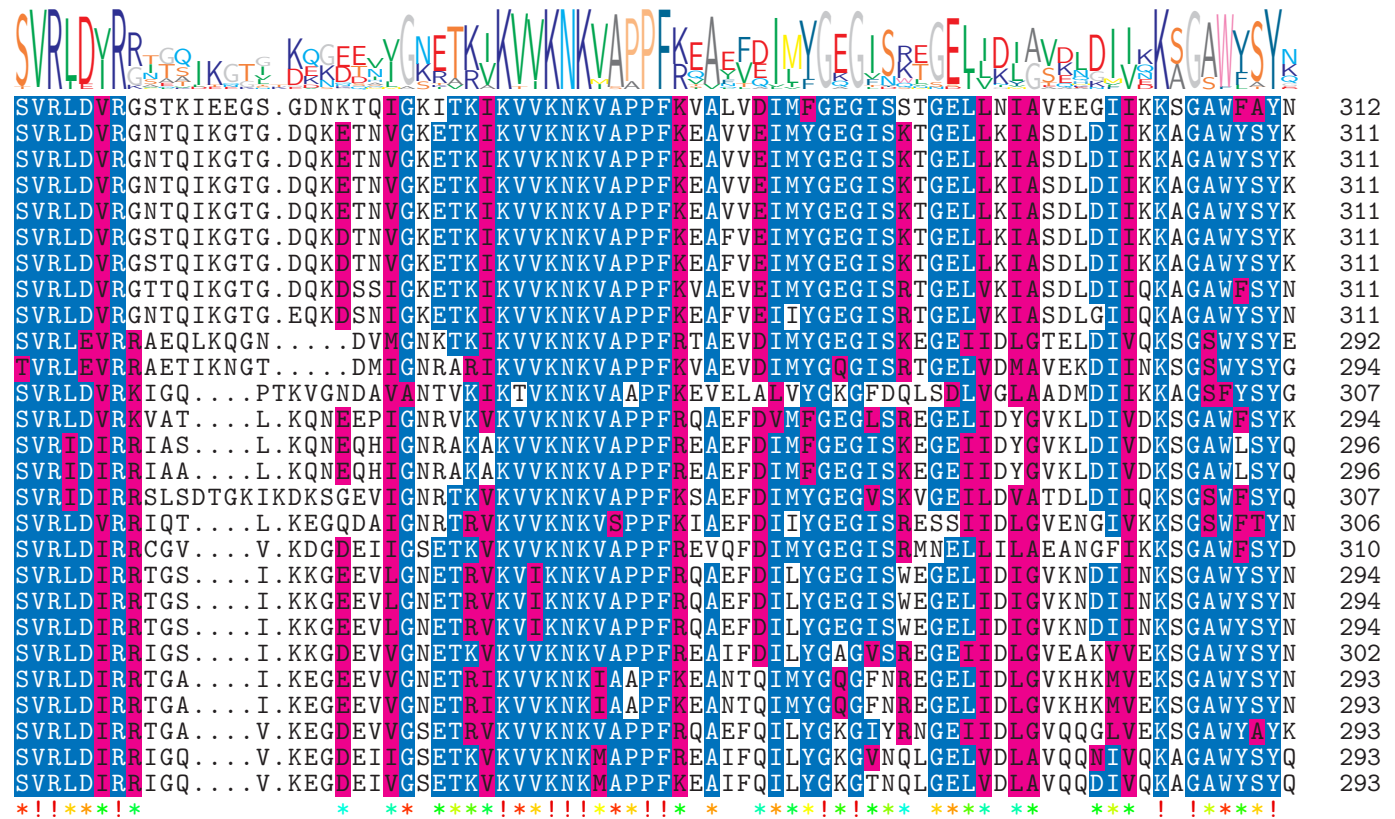
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consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ DK ⁺ V ⁺ RSK ⁺ FC ⁺ LIDGEEVSEQD ⁺ TENKK ⁺ DE....PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ FE ⁺ ID ⁺ ID ⁺ DK ⁺ RV ⁺ VK ⁺ FC ⁺ LLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
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EERL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQE ⁺ EL ⁺ .EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DEV ⁺ RLK ⁺ V ⁺ RAAY ⁺ CS ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQG ⁺ KEKT ⁺ IAY ⁺ IA ⁺ ERP ⁺ MEQE ⁺ IRDRV ⁺ MAA ⁺ IRAGNAGEAPALAPA.PAAP.....EAAE.A.....	363
DKKL ⁺ GGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IQNSM ⁺ CTEGMISGSEDDEGEE.....	343
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALAD ⁺ EIT ⁺ TLK ⁺ IKES ⁺ IGSNEEIMPLPDEPLEEME.....	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALAD ⁺ EIT ⁺ TLK ⁺ IKES ⁺ IGSNEEIMPLPDEPLEEME.....	347
DTKL ⁺ GGGRD ⁺ TVKEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ LE ⁺ AK ⁺ IREKLQAK.....	343
GDQL ⁺ GGQKE ⁺ KAR ⁺ IFL ⁺ KEN ⁺ PD ⁺ LAE ⁺ IERL ⁺ IFEKL ⁺ CTGEFAAKAGEENQDMAVP.....GVGD.DL..SDDPVMVNPVDFD	378
GTKIGGQK ⁺ ANAVK ⁺ WL ⁺ KEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QE ⁺ IRNTLASNPNSVLKATASDSNDES....DVEE.....FSEEEL	372
GAKIGGQK ⁺ DNVRV ⁺ WL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHITEGT.....QDE....TDGE.....RPEE...	348
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GDKIGGQK ⁺ ANACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TL ⁺ DKKL ⁺ REMLLN ⁺ PENMQLIAETSSAADV....EFGA.....VPEEF..	354
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GSKIGGQK ⁺ ANAAK ⁺ YLEN ⁺ PE ⁺ IGQE ⁺ IEQQ ⁺ IRAKLL ⁺ VT ⁺ SANTKATPVAEDLADA....DI.....	347
GNKIGGQK ⁺ NNVIR ⁺ YLEN ⁺ PE ⁺ IQ ⁺ ISTE ⁺ IEAV ⁺ IREQLLT ⁺ KASDQTAA.HDETEEEP.....DLL.....ES....	349
GNKIGGQK ⁺ NNVIR ⁺ YFEN ⁺ NQ ⁺ IAE ⁺ IEIR ⁺ NI ⁺ REQLLT ⁺ TGTNGAVQ.I.EDEEEP.....DLL.....LES....	349

logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved