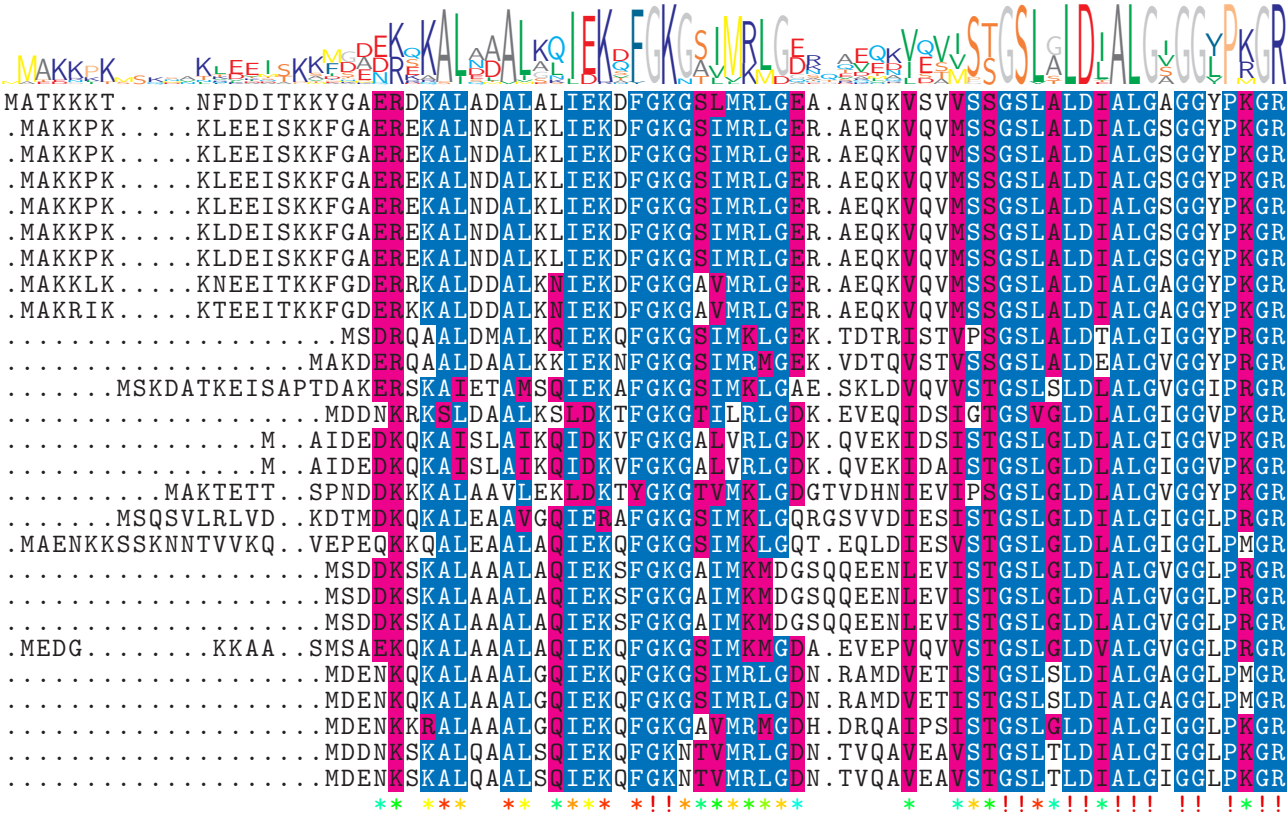


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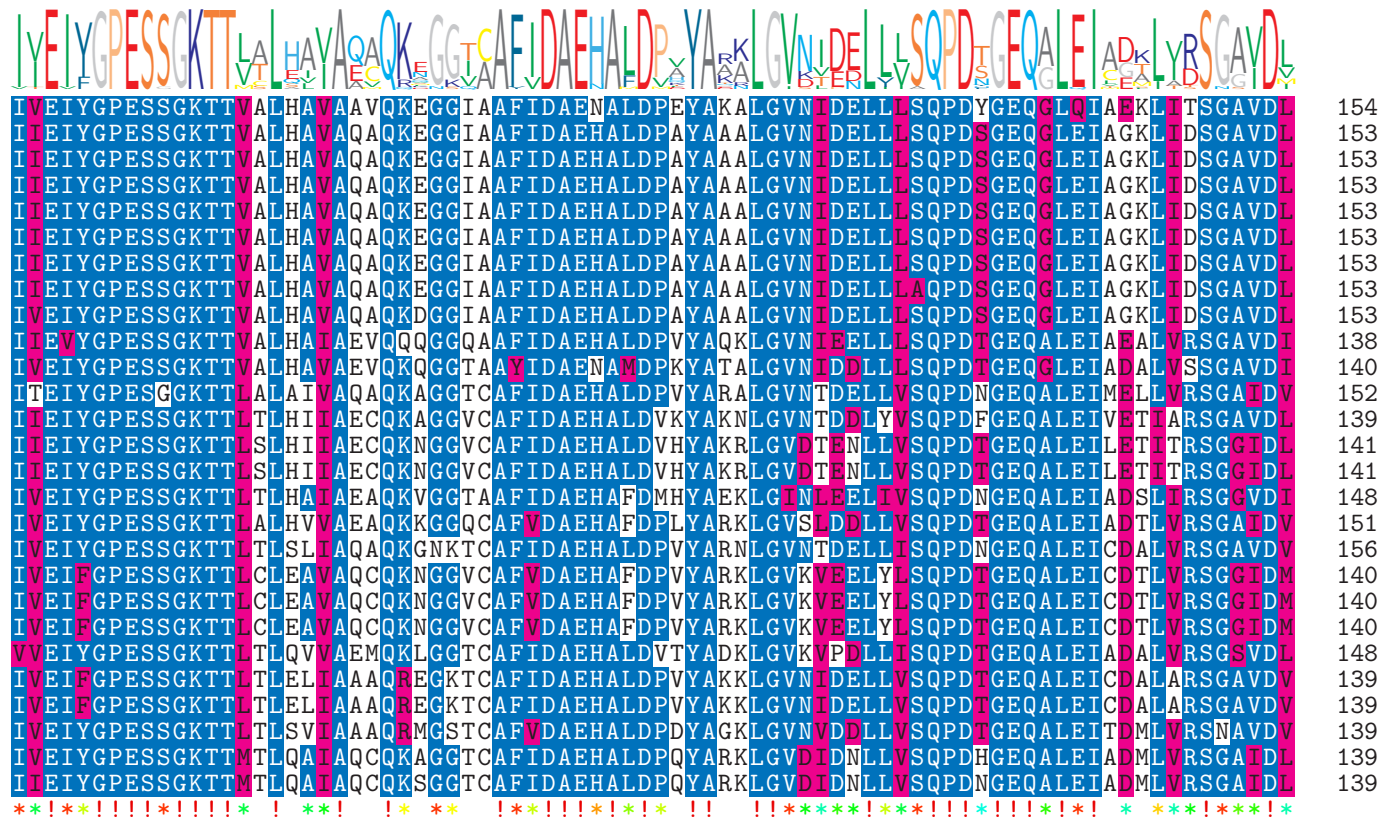


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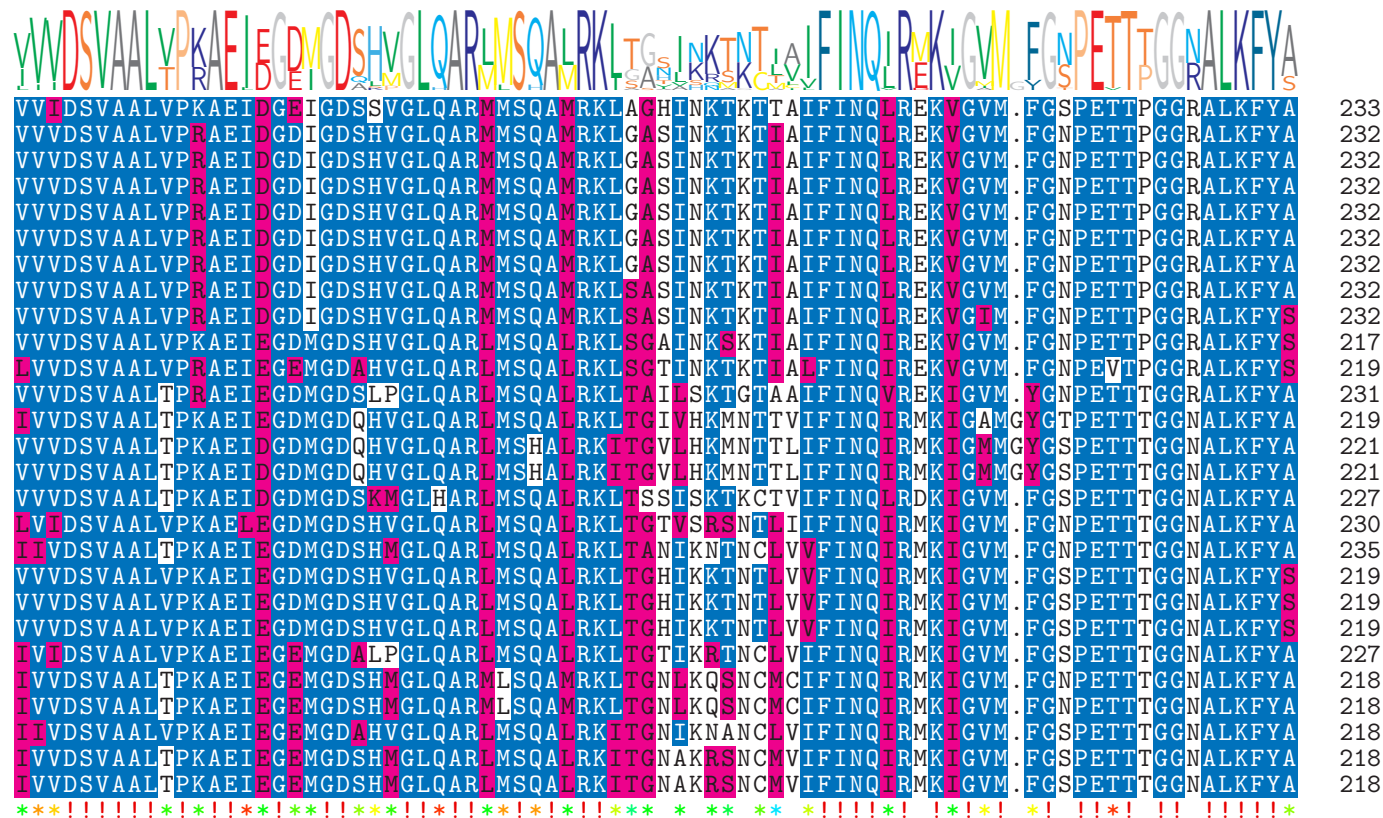
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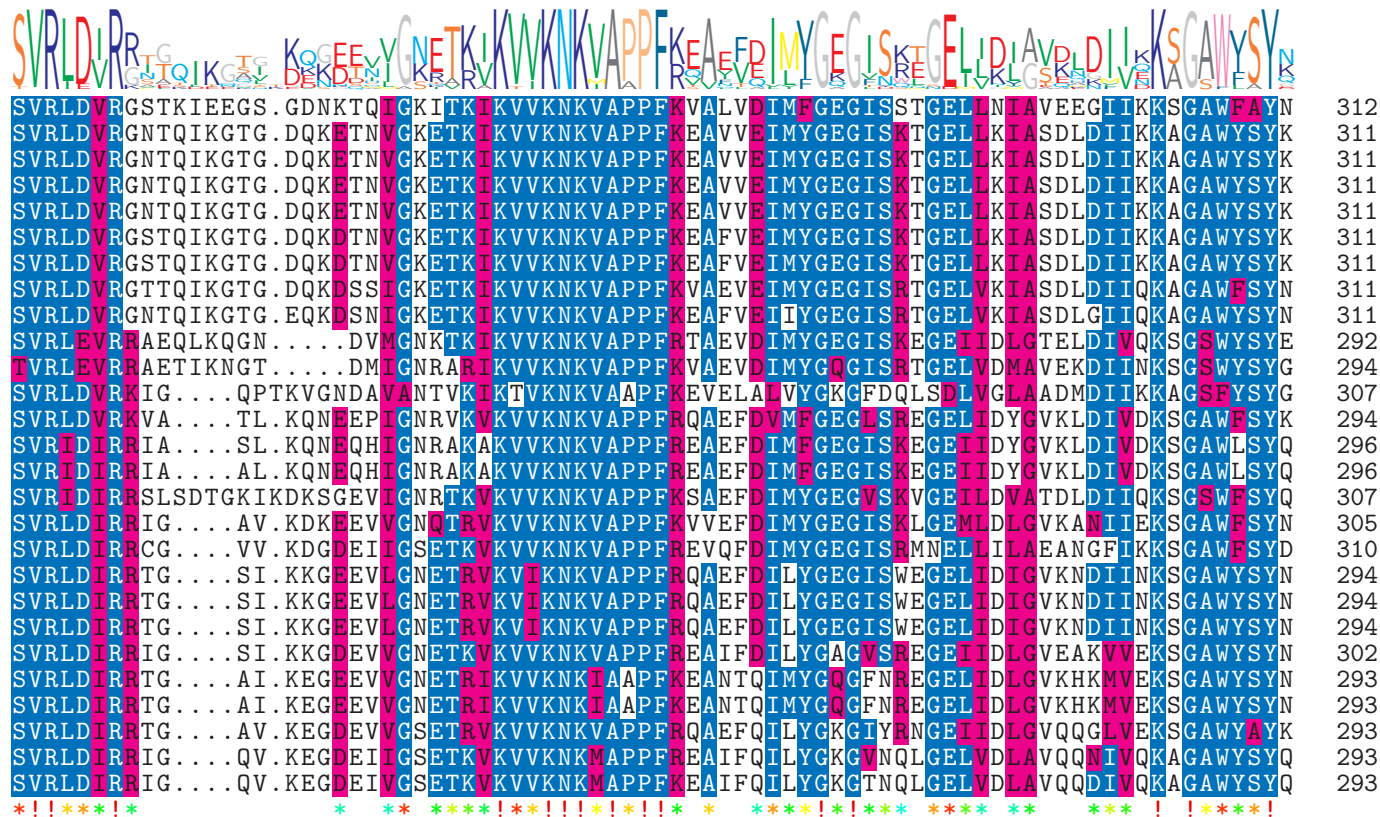
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consensus

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Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EID ⁺ QV ⁺ RSK ⁺ FL ⁺ IDGEEVSEQD..TENKK ⁺ DE....PKKEEA..VNEEVPLDLGDELE	383
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EID ⁺ QV ⁺ RSK ⁺ FL ⁺ IDGEEVSEQD..TENKK ⁺ DE....PKKEEA..VNEEVPLDLGDELE	383
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GEKIGGGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPEI ⁺ FD ⁺ DI ⁺ DHK ⁺ VR ⁺ VQ ⁺ YCL ⁺ IEEDNTEEKQ..SSKEK.....ETDEK..ADKNLVLELDDTIE	380
EE ⁺ RL ⁺ LGGS ⁺ RE ⁺ NA ⁺ KQ ⁺ FL ⁺ KE ⁺ NKD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQA..EETQE ⁺ EL ⁺ .EFE.E.....	348
SERIGGGS ⁺ RE ⁺ NA ⁺ KNYL ⁺ AD ⁺ HED ⁺ VED ⁺ EVRL ⁺ KV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPT..TEDE.QI.NILPDDST....EE.....	355
DERIGGQ ⁺ KE ⁺ KT ⁺ IAY ⁺ IA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VMA ⁺ IRAGNAGEAPALAPAPAPEAA.EA.....	363
DKKL ⁺ GGGREN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PEI ⁺ AD ⁺ EITKA ⁺ IQNSM ⁺ CI ⁺ EGMIS..GSEDDE..GE.....	343
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADEI ⁺ TLK ⁺ IKES ⁺ IGSNEEIM..PLPDEP..LEEM.E.....	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADEI ⁺ TLK ⁺ IKES ⁺ IGSNEEIM..PLPDEP..LEEM.E.....	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPEL ⁺ AEEL ⁺ EAK ⁺ IREKLQAK.....	343
STRIGGGS ⁺ RE ⁺ NA ⁺ KQ ⁺ FLRD ⁺ NP ⁺ AAE ⁺ EEN ⁺ AV ⁺ ANAG ⁺ IAEEM..IGGPGGEDDDAG.GAA.....GVGDEA.....	366
GTKIGGQ ⁺ KNN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQE ⁺ IRNTL ⁺ ASNPN ⁺ SV..LKATASDSND ⁺ ES.DVE.....EFSEEEL.....	372
GAKIGGQ ⁺ KD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMHIT..EGT.....QDE.TDG.....ERPEE.....	348
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GDKIGGQ ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEMQ..LIAETSSAAD ⁺ V.EFG.....AVPEEF.....	354
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GSKIGGQ ⁺ KANA ⁺ AK ⁺ YLE ⁺ EN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ IRAKLL ⁺ YTSANT..KATPVAEDLDA.DI.....	347
GNKIGGQ ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ QISTE ⁺ IEA ⁺ VIREQLL ⁺ TKASDQ..TAA.HDETEEEP.DLL.....ES.....	349
GNKIGGQ ⁺ KNN ⁺ VIR ⁺ YLE ⁺ FEEN ⁺ QIAE ⁺ IE ⁺ ERN ⁺ IREQLL ⁺ TTGTNG..AVQ.I.EDEEEP.DLL.....LES.....	349

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved