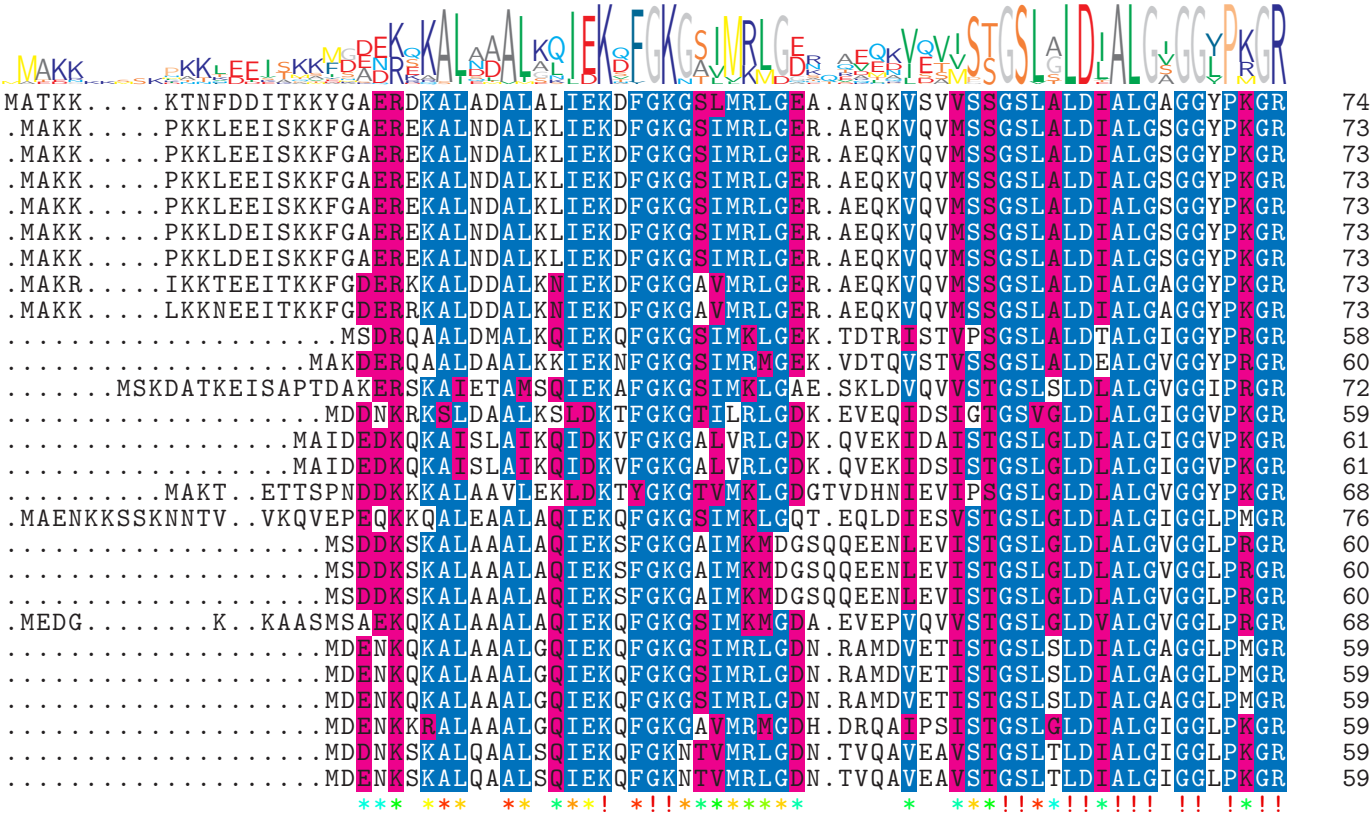


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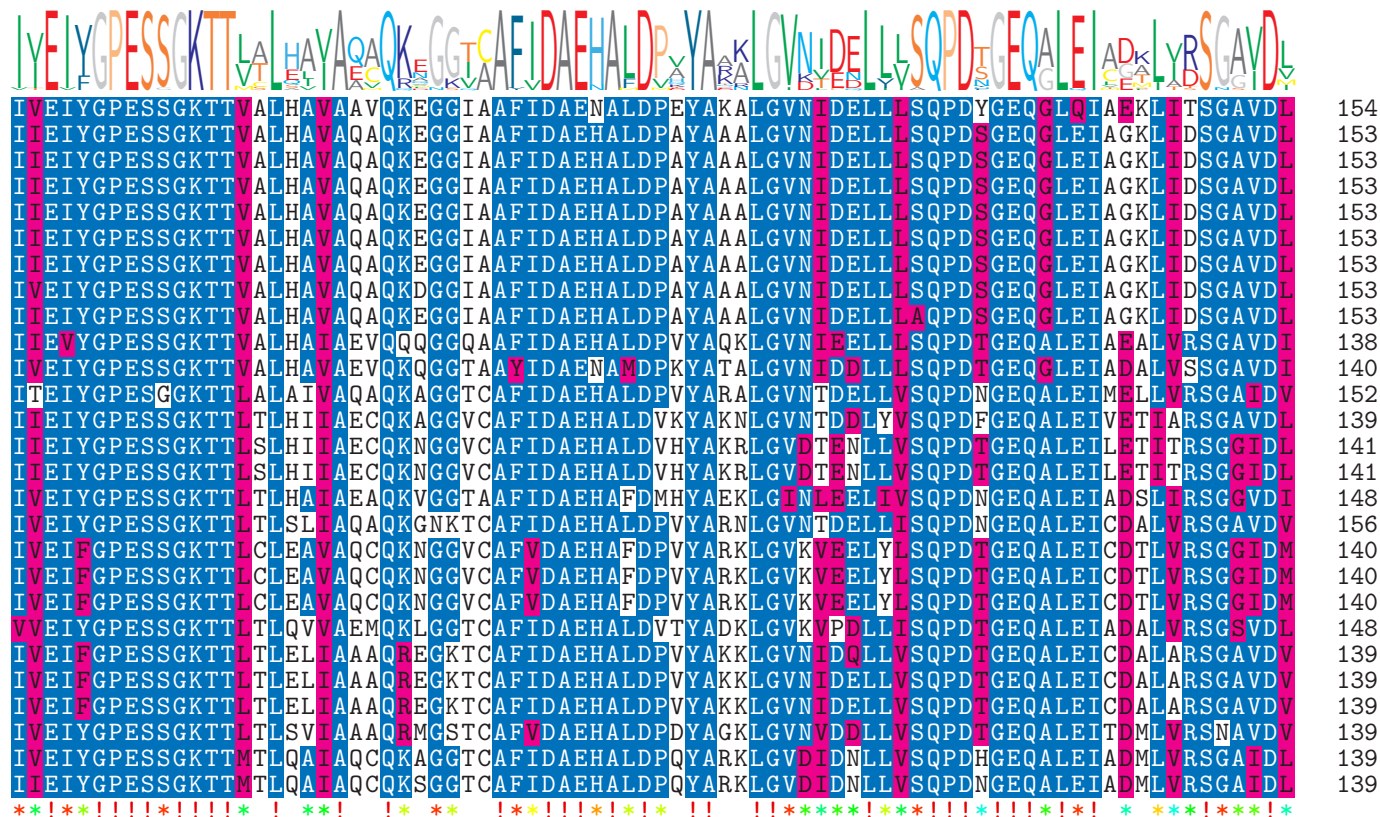
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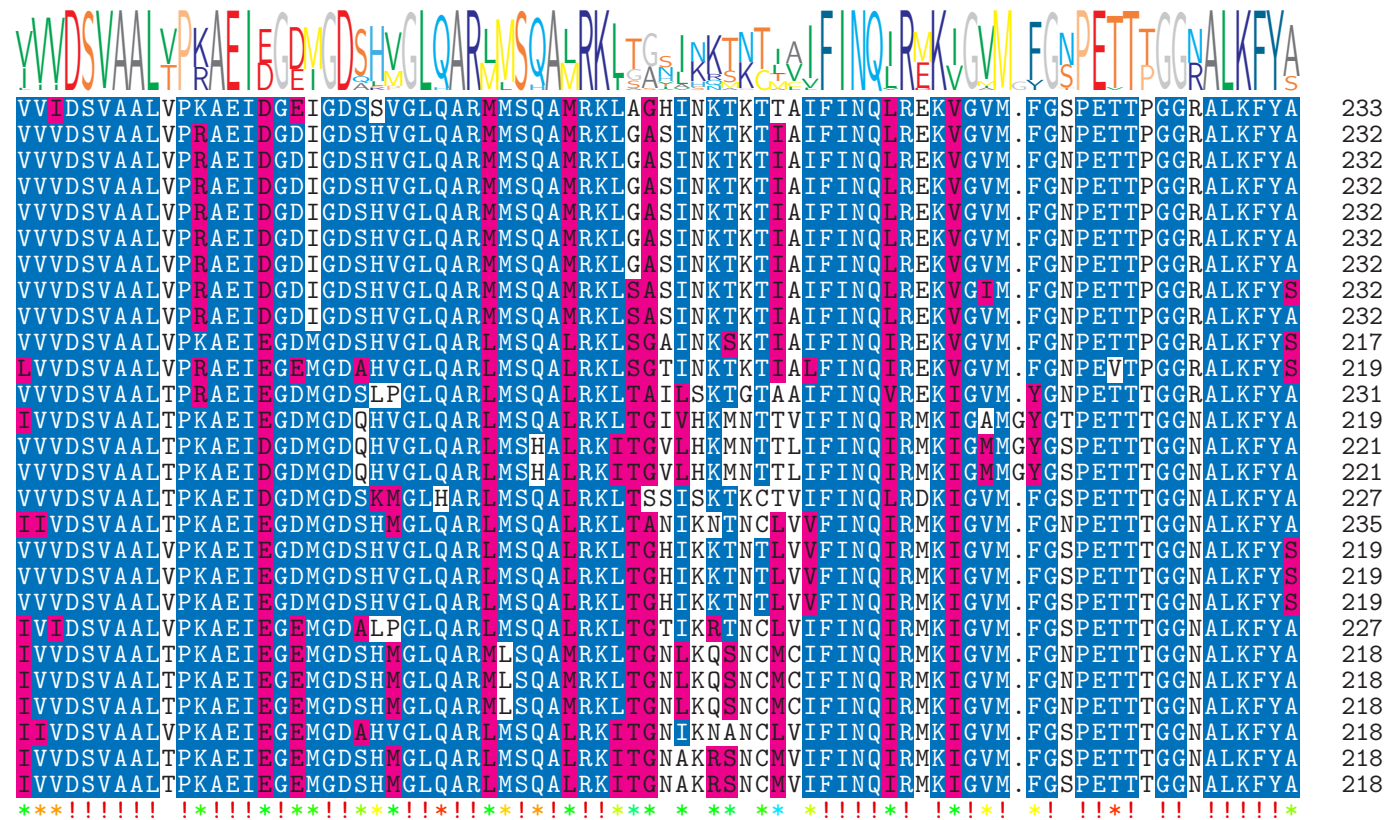
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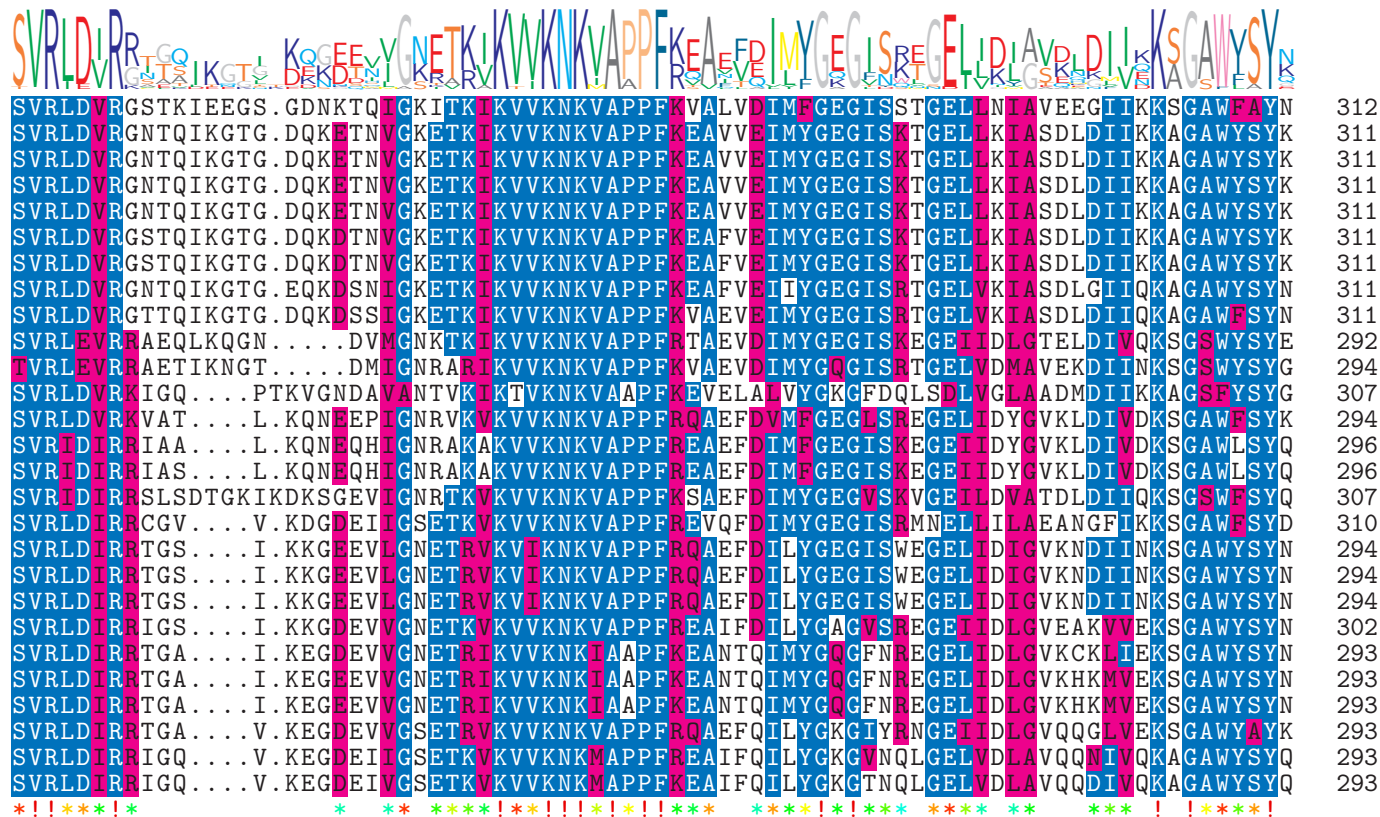
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consensus

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Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ GLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ DEID ⁺ HQ ⁺ V ⁺ RVQF ⁺ GLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
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SERIGGGREN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ VRAAY ⁺ CTSDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGKE ⁺ KTI ⁺ AYIA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VMAAIRAGNAGEAPALAPAAA.PEAAEA.....	363
DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEIA ⁺ DEIT ⁺ KAT ⁺ IQNSM ⁺ TEGMIS....GSEDD..EGEE.....	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEIM....PLPDE..PLEEME.....	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEIM....PLPDE..PLEEME.....	347
DTKLGGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
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GAKIGGGK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMHIT....EGTQ.....DET ⁺ DGERPEE.....	348
GAKIGGGK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMHIT....EGTQ.....DET ⁺ DGERPEE.....	348
GERIGGGRD ⁺ NCRE ⁺ FLRE ⁺ NA ⁺ E ⁺ LARE ⁺ IE ⁺ EN ⁺ KV ⁺ REHL ⁺ GVTPMGA....VTL..AEEVEED.....	352
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved