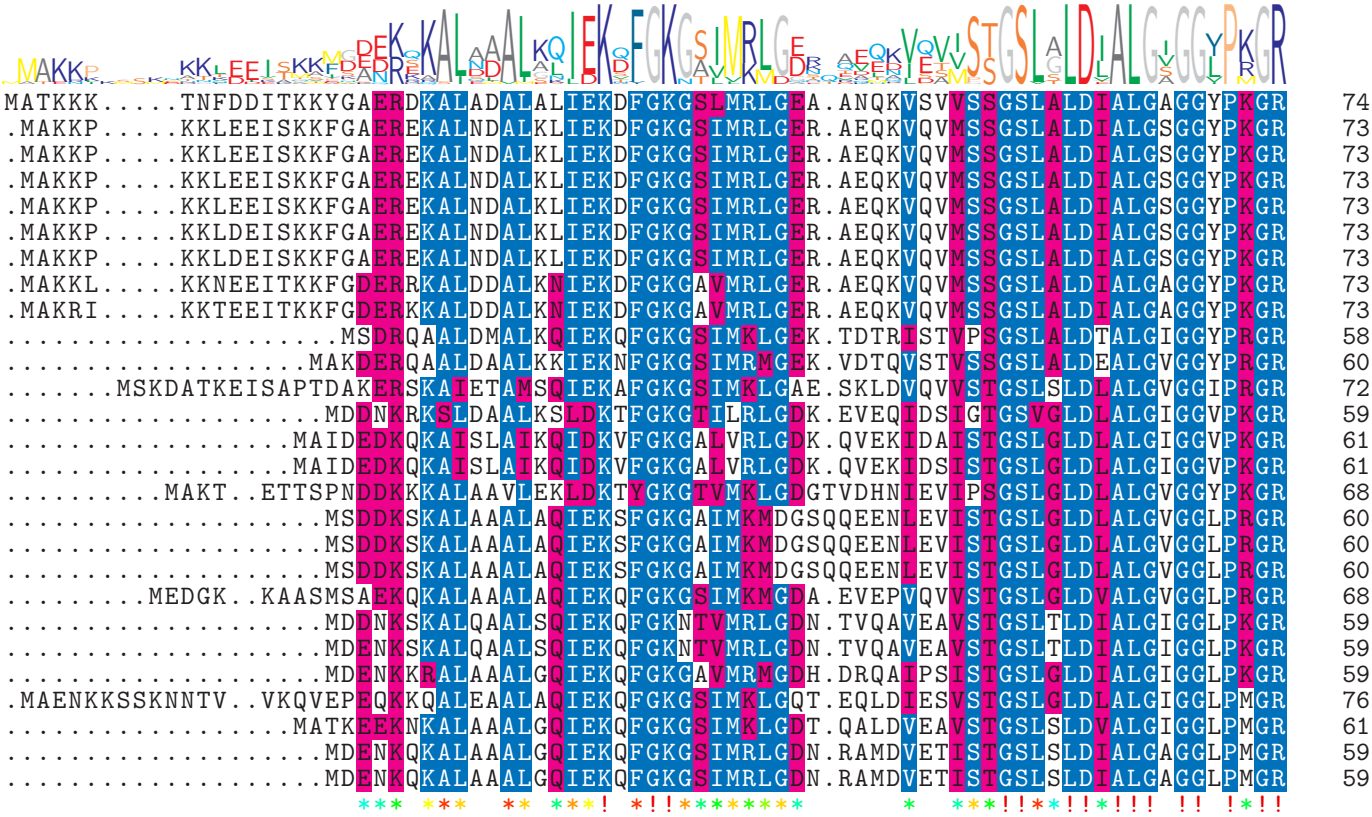


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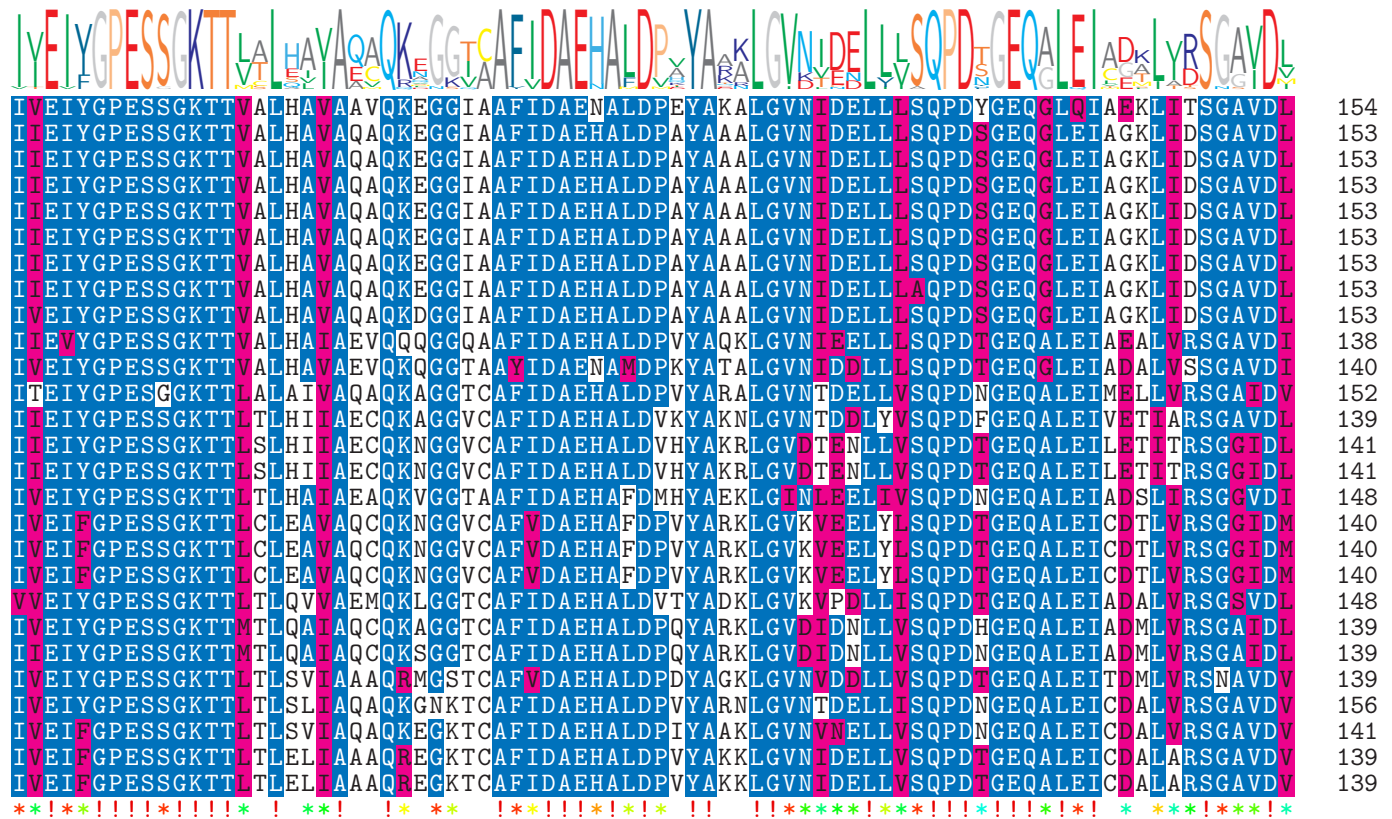
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consensus



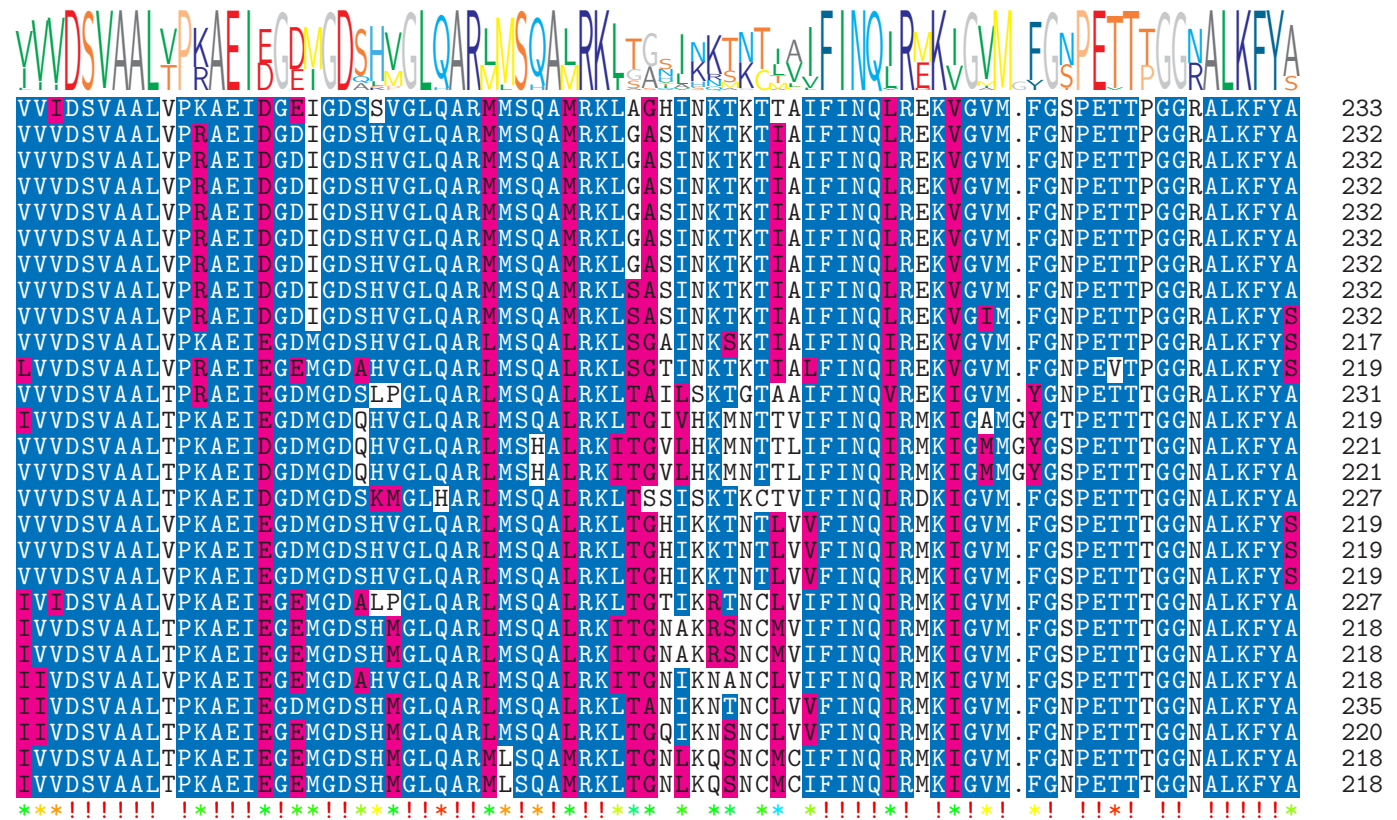
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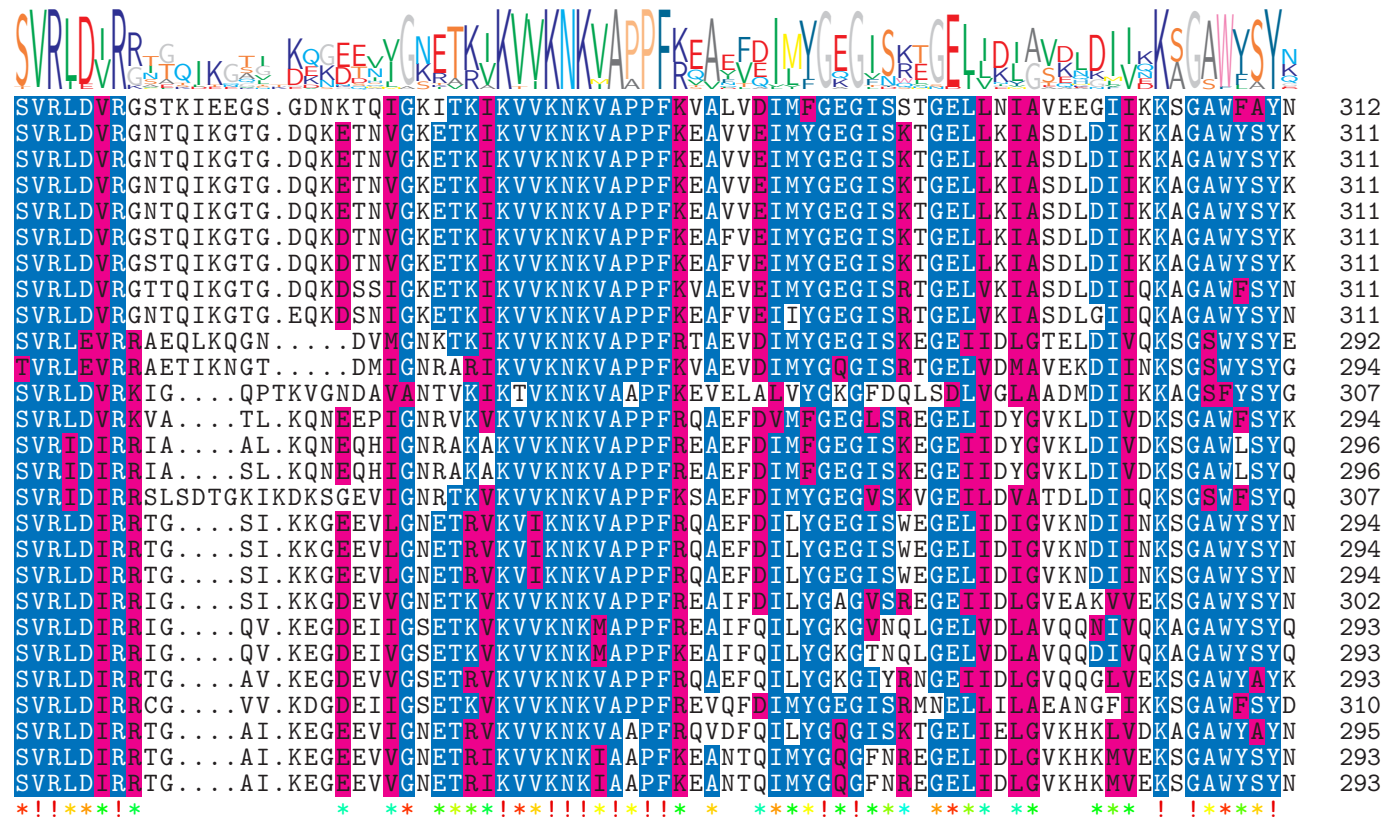
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Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ V ¹² RAAH ¹³ CI ¹⁴ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ¹ ENAK ² KYLA ³ EHPE ⁴ IF ⁵ DEID ⁶ DKQ ⁷ VR ⁸ SKF ⁹ CLIDGEEVSEQD ¹⁰ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAK ² KYLA ³ EHPE ⁴ IF ⁵ DEID ⁶ DKQ ⁷ VR ⁸ SKF ⁹ CLIDGEEVSEQD ¹⁰ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAK ² KYLA ³ EHPE ⁴ IF ⁵ DEID ⁶ DKQ ⁷ VR ⁸ SKF ⁹ CLIDGEEVSEQD ¹⁰ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAK ² KYLA ³ ADNP ⁴ EVFA ⁵ EID ⁶ HQ ⁷ VR ⁸ VQF ⁹ CLIDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ¹ ENAK ² KYLA ³ ADNP ⁴ IF ⁵ DEID ⁶ HQ ⁷ VR ⁸ VQF ⁹ CLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ¹ ENAK ² RYLAD ³ HP ⁴ QI ⁵ FD ⁶ EID ⁷ RK ⁸ VR ⁹ VKF ¹⁰ CLLEESEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGQGS ¹ ENAK ² KFLAD ³ NPE ⁴ IF ⁵ DD ⁶ ID ⁷ HK ⁸ VR ⁹ VQY ¹⁰ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ¹ RL ² LGQGR ³ ENAK ⁴ QFL ⁵ KEN ⁶ KD ⁷ IMLM ⁸ IQEQ ⁹ IREHY ¹⁰ CLDNNGVVQQQA ¹¹ EETQEEL.EFE.E.....	348
SERIGQGR ¹ ENAK ² NYLAD ³ HED ⁴ VED ⁵ EVRL ⁶ KV ⁷ RAAY ⁸ CI ⁹ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQG ¹ KEK ² TIAY ³ IA ⁴ ERP ⁵ EME ⁶ QE ⁷ IRDR ⁸ VMAAIRAGNAGEAPALAPAAPEAA.EA.....	363
DKKL ¹ GGQGR ² ENSKA ³ FL ⁴ KNPE ⁵ IA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ TEGMI....SGSEDDGE...E.....	343
DKKL ¹ GGQGR ² ENAK ³ ALL ⁴ KED ⁵ KALADEIT ⁶ TLK ⁷ IKES ⁸ ISG ⁹ SNEEI....MPLPDEPLEEME.....	347
DKKL ¹ GGQGR ² ENAK ³ ALL ⁴ KED ⁵ KALADEIT ⁶ TLK ⁷ IKES ⁸ ISG ⁹ SNEEI....MPLPDEPLEEME.....	347
DTKL ¹ GGQGRD ² TVKEL ³ IKDN ⁴ PE ⁵ LAE ⁶ ELEAK ⁷ IREKLQAK.....	343
GAKIGQGKD ¹ NVRV ² WLKEN ³ PEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHI....TEGTQDET ⁸ DGE.....RPEE.....	348
GAKIGQGKD ¹ NVRV ² WLKEN ³ PEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHI....TEGTQDET ⁸ DGE.....RPEE.....	348
GAKIGQGKD ¹ NVRV ² WLKEN ³ PEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHI....TEGTQDET ⁸ DGE.....RPEE.....	348
GERIGQGRD ¹ NCRE ² FLIRE ³ NAELARE ⁴ IE ⁵ ENK ⁶ VREHL ⁷ CVTPMG....AVTLAAEEVEED.....	352
GNKIGQGK ¹ NNVIR ² YLEEN ³ PQISTE ⁴ IE ⁵ AVIREQLLTKASD....QTAAHDET.EEEPDL....LES.....	349
GNKIGQGK ¹ NNVIR ² YFEEN ³ QIAE ⁴ IE ⁵ ERNIREQLLTGTN....GAVQI.ED.EEEPDL....LLES.....	349
GSKIGQGKANAA ¹ AKY ² LEEN ³ PEIG ⁴ EQE ⁵ IQ ⁶ IRAKLL ⁷ VTAN....TKATPVAEDLADADI.....	347
GTKIGQGKNNA ¹ VKWLKEN ² PEIAD ³ KL ⁴ EQE ⁵ IRNTL ⁶ ASNPNS....VLKATASDSNDES ⁷ DV...EEFSEEL.....	372
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved