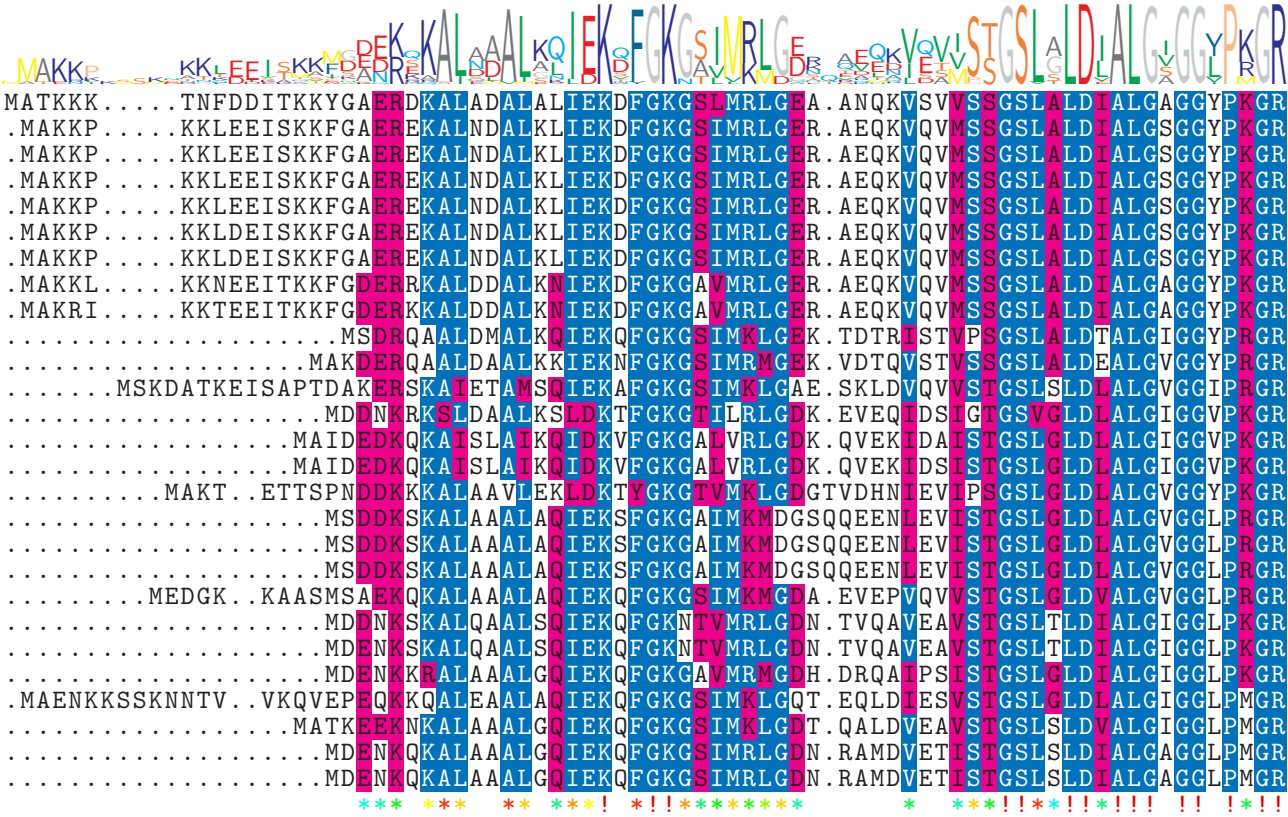


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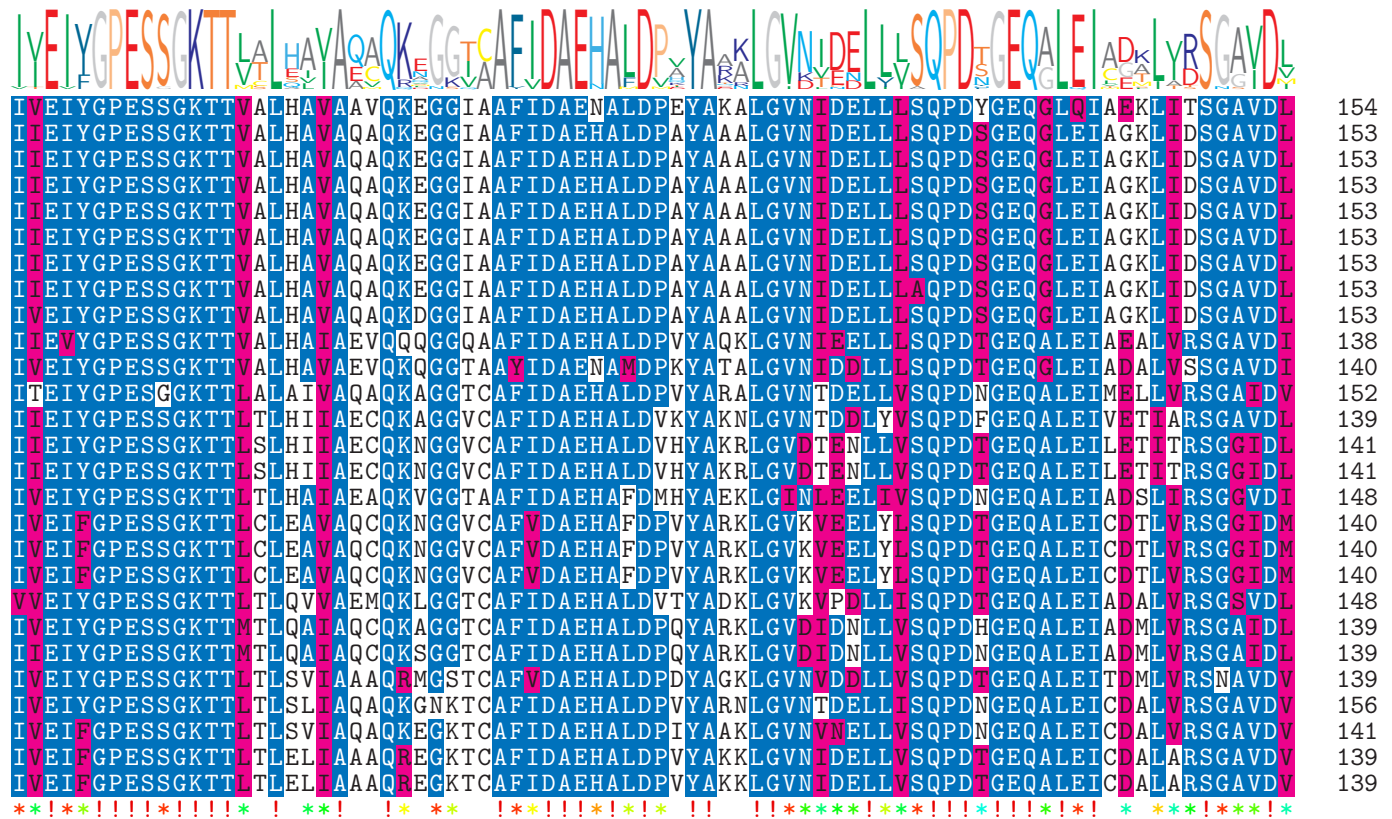


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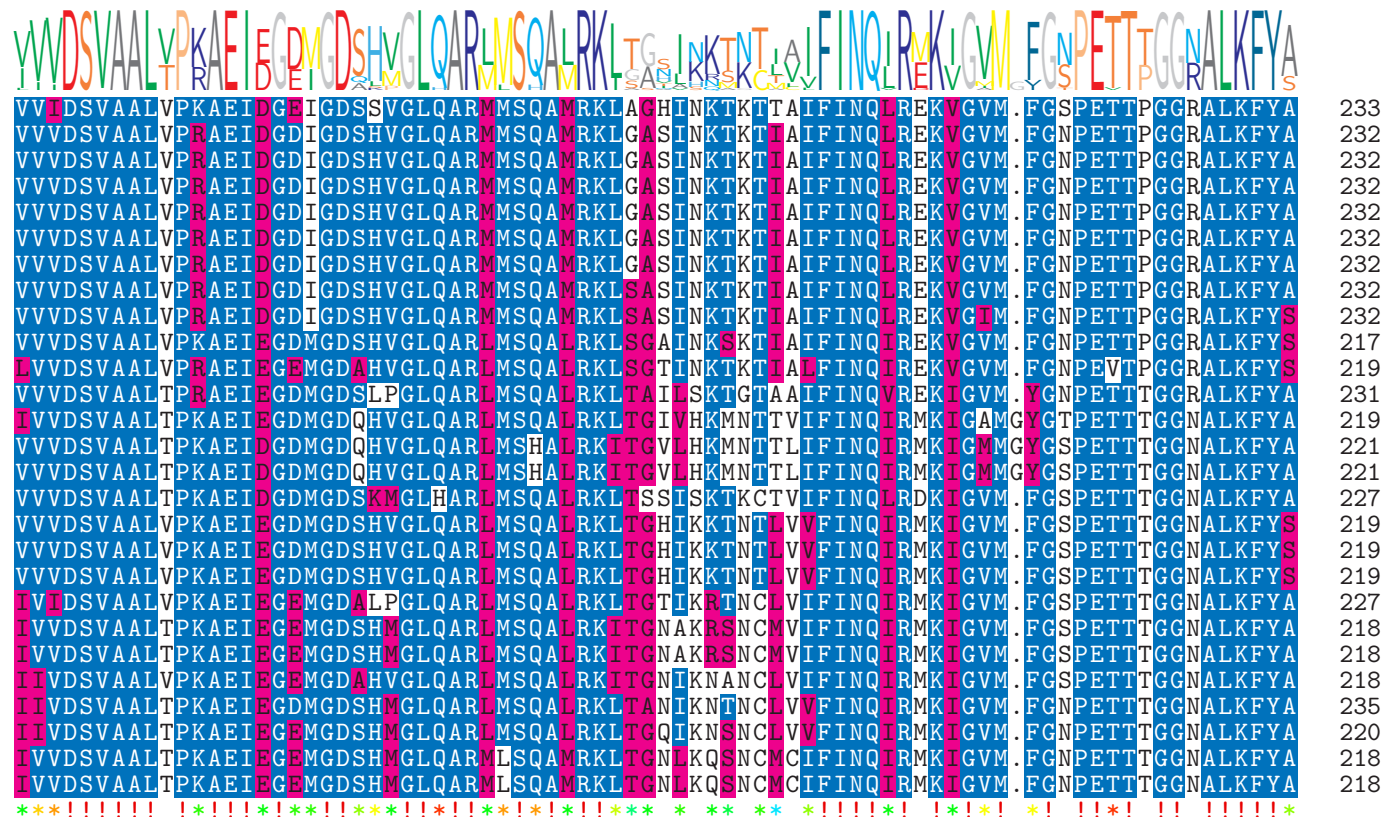
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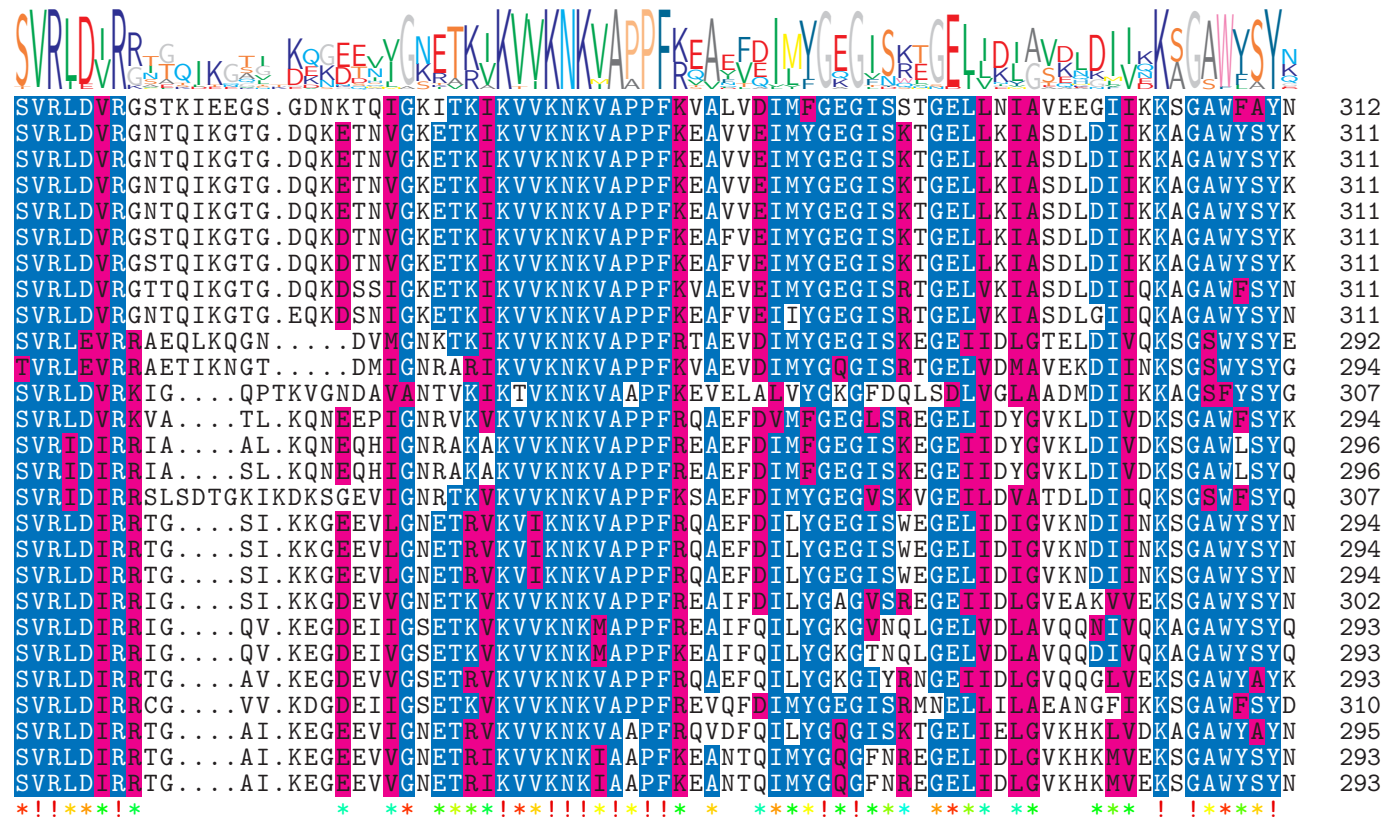
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consensus

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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.....TDDLALDLNGIEIE	377
GEKIGQGS ¹ ENAK ² KFLAD ³ NP 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 VE ⁵ D ⁶ VR ⁷ LK ⁸ VRAAY ⁹ CI ¹⁰ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQG ¹ KEK ² TIAY ³ IA ⁴ ERP ⁵ EME ⁶ QE ⁷ ID ⁸ DRVMAAIRAGNAGEAPALAPAAPEAA.EA.....	363
DKKL ¹ GGQGR ² ENSKA ³ FL ⁴ KN ⁵ PEIA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ TEGMI....SGSEDDGEEE.....	343
DKKL ¹ GGQGR ² ENAK ³ ALL ⁴ KED ⁵ KALADEIT ⁶ TLK ⁷ IKESIG ⁸ SNEEI....MPLPDEPLEEME.....	347
DKKL ¹ GGQGR ² ENAK ³ ALL ⁴ KED ⁵ KALADEIT ⁶ TLK ⁷ IKESIG ⁸ SNEEI....MPLPDEPLEEME.....	347
DTKL ¹ GGQGRD ² TVKEL ³ IKDN ⁴ PELA ⁵ EEL ⁶ EAK 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
GSKIGQGKANAAK ¹ YLEEN ² PEIG ³ QIE ⁴ EQ ⁵ IRAKLL ⁶ VTSAN....TKATPVAEDLADADI.....	347
GTKIGQGKNNAVK ¹ WLKEN ² PEIA ³ DK ⁴ LE ⁵ QEI ⁶ IRNTL ⁷ ASNPNS....VLKATASDSNDES ⁸ VDV...EEFSEEL.....	372
GEKIGQGKANAMK ¹ WLEE ² HP ³ EALALE ⁴ TK ⁵ IRNELLANPEK....VLAADIAEKN.ESST...GLEADY.....	354
GDKIGQGKANACKY ¹ LKEN ² PEIA ³ AKTLD ⁴ KKL ⁵ REMLLN ⁶ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354
GDKIGQGKANACKY ¹ LKEN ² PEIA ³ AKTLD ⁴ KKL ⁵ REMLLN ⁶ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved