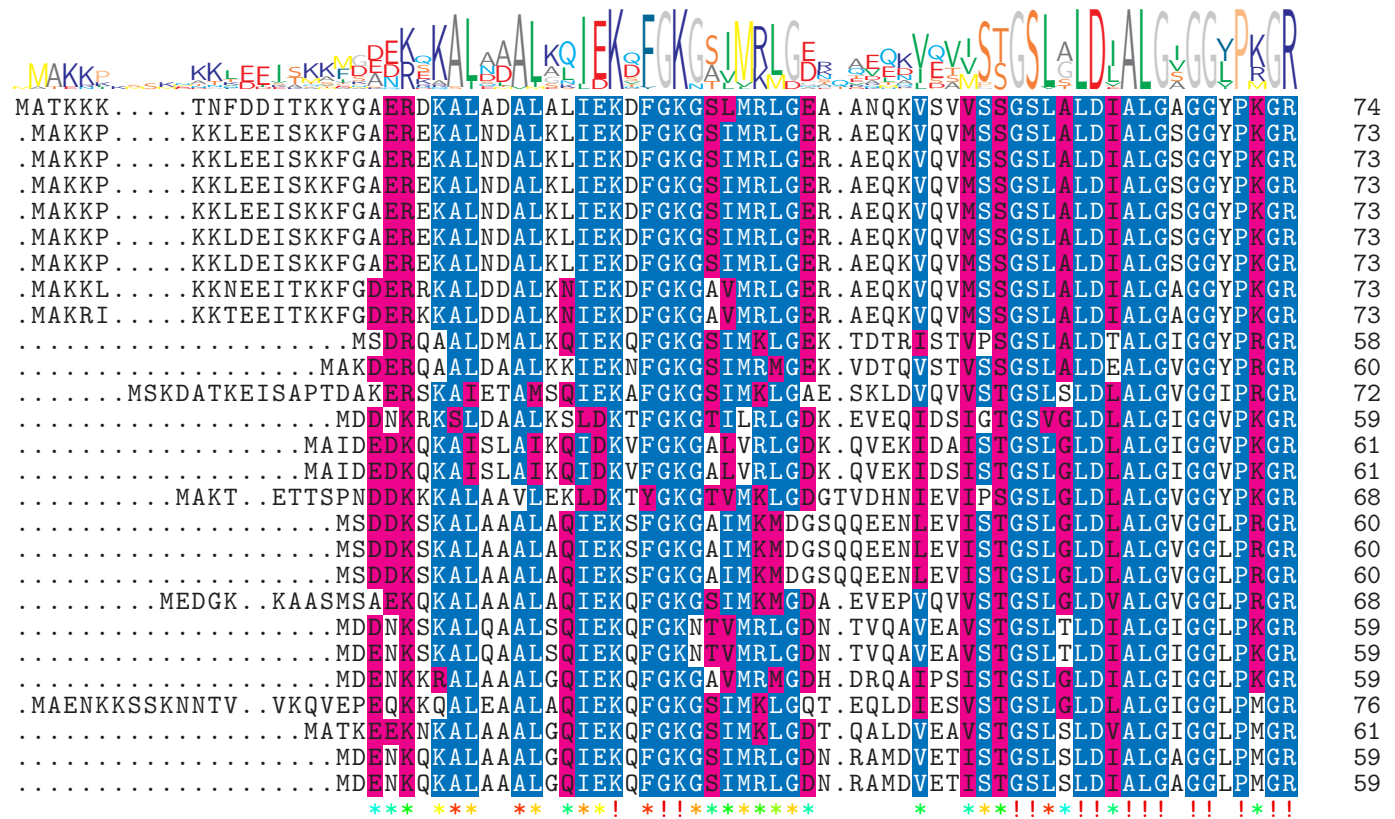


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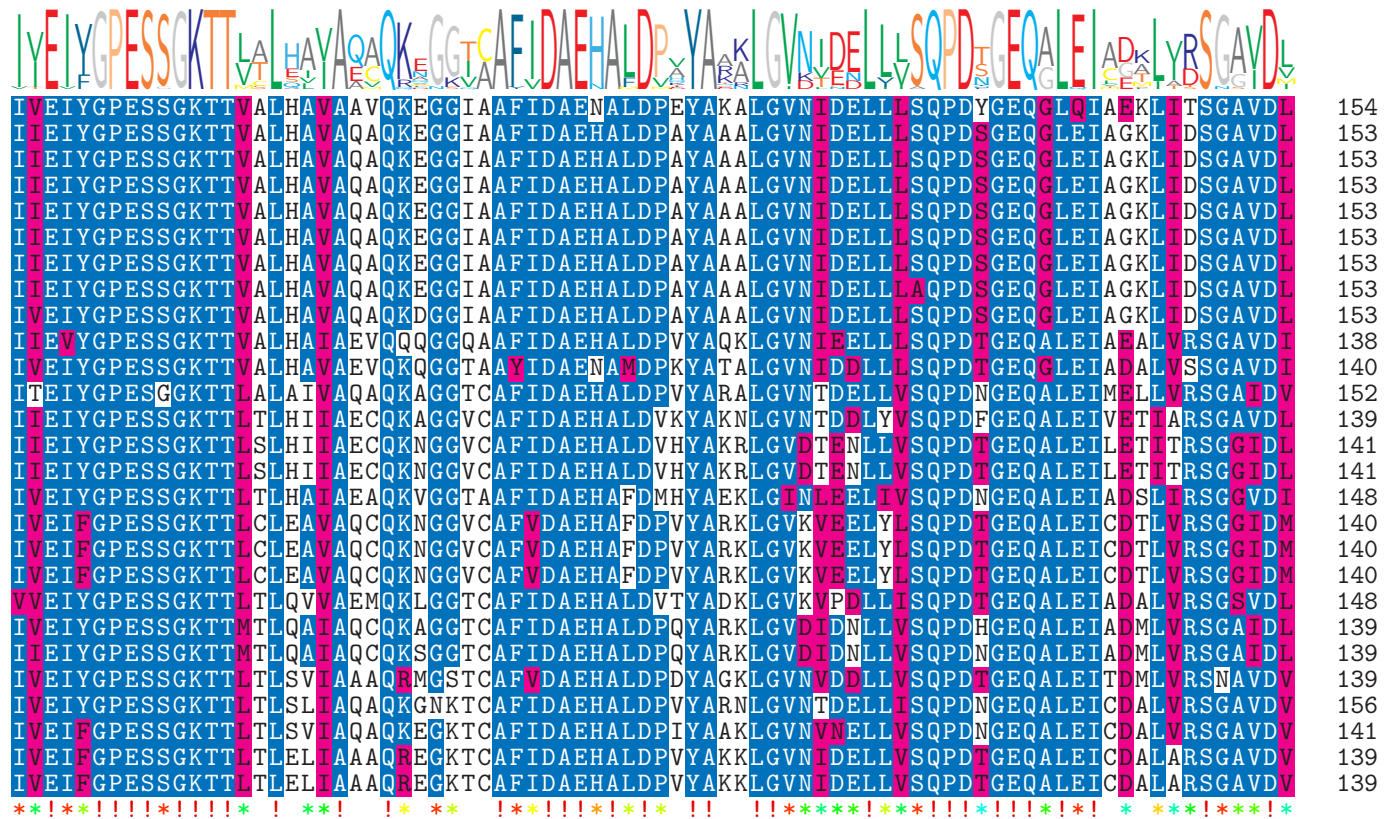
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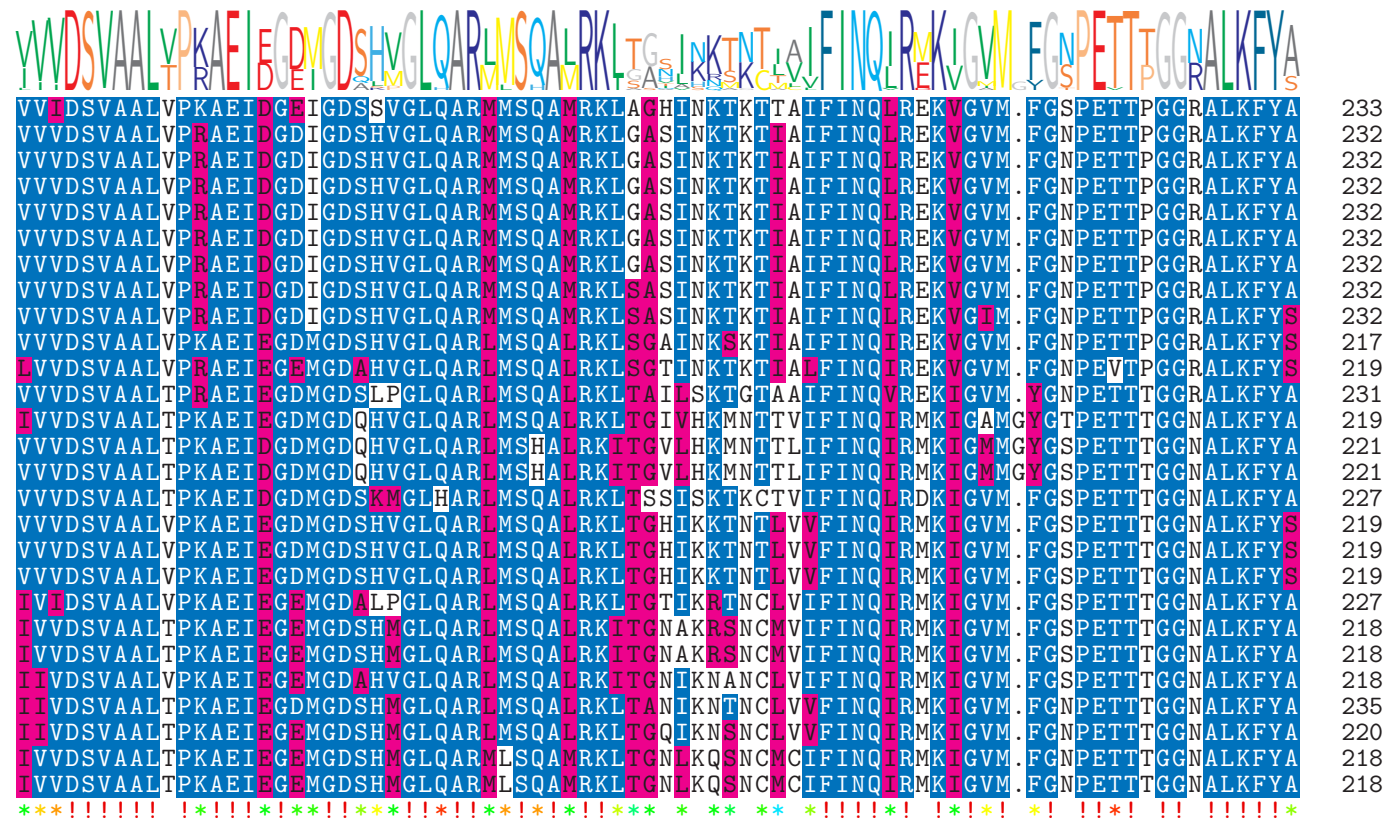
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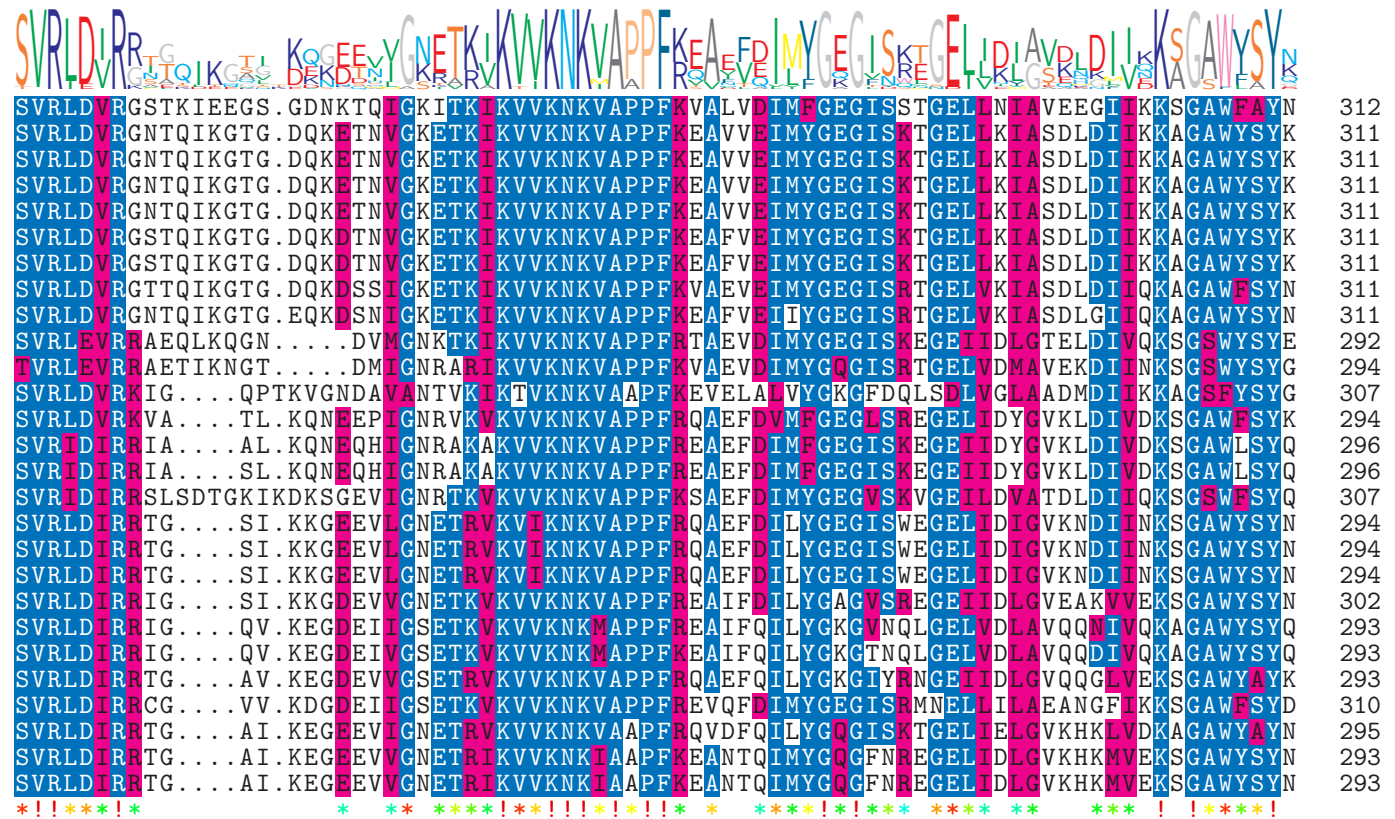
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consensus

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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.....TDDLALDLNNGIEIE	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 V ⁹ RAAY ¹⁰ CI ¹¹ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQG ¹ KEK ² TIAY ³ IA ⁴ ERP ⁵ EME ⁶ QE ⁷ ID ⁸ DRV ⁹ MAAIRAGNAGEAPALAPAAPEAA.EA.....	363
DKKL ¹ GGQGR ² ENSKA ³ FL ⁴ KN ⁵ PEIA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ CI ¹⁰ EGMI....SGSEDDGE...E.....	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 IKD ⁴ NP ⁵ ELAE ⁶ ELEAK ⁷ IREKLQAK.....	343
GAKIGQGKD ¹ NVR ² VWL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHI....TEGTQDET ⁹ DGE.....RPEE.....	348
GAKIGQGKD ¹ NVR ² VWL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHI....TEGTQDET ⁹ DGE.....RPEE.....	348
GAKIGQGKD ¹ NVR ² VWL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALN ⁸ GVEMHI....TEGTQDET ⁹ DGE.....RPEE.....	348
GERIGQGRD ¹ NCRE ² FL ³ IRENA ⁴ ELARE ⁵ IE ⁶ ENK ⁷ VREHL ⁸ CVTPMG....AVTLAAEEVEED.....	352
GNKIGQGK ¹ NNVIR ² YLEEN ³ PQ ⁴ ISTE ⁵ IE ⁶ AVIREQLLTKASD....QTAAHDET.EEEPDL....LES.....	349
GNKIGQGK ¹ NNVIR ² YFEEN ³ QIA ⁴ EIE ⁵ ERNIREQLLTGTN....GAVQI.ED.EEEPDL....LLES.....	349
GSKIGQGKANAAK ¹ YLEEN ² PEIG ³ QEI ⁴ EQ ⁵ IRAKLL ⁶ VTAN....TKATPVAEDLADADI.....	347
GTKIGQGK ¹ NNAVK ² WL ³ KN ⁴ PEIA ⁵ DK ⁶ LE ⁷ QEI ⁸ IRNTL ⁹ ASNPNS....VLKATASDSNDES ¹⁰ VDV...EEFSEEL.....	372
GEKIGQGKANAMK ¹ WLEE ² HP ³ EALALE ⁴ TK ⁵ IRNELLANPEK....VLAADIAEKN.ESST...GLEADY.....	354
GDKIGQGKANACKY ¹ LKN ² PEIA ³ AKTLD ⁴ KKL ⁵ REMLLN ⁶ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354
GDKIGQGKANACKY ¹ LKN ² PEIA ³ AKTLD ⁴ KKL ⁵ REMLLN ⁶ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved