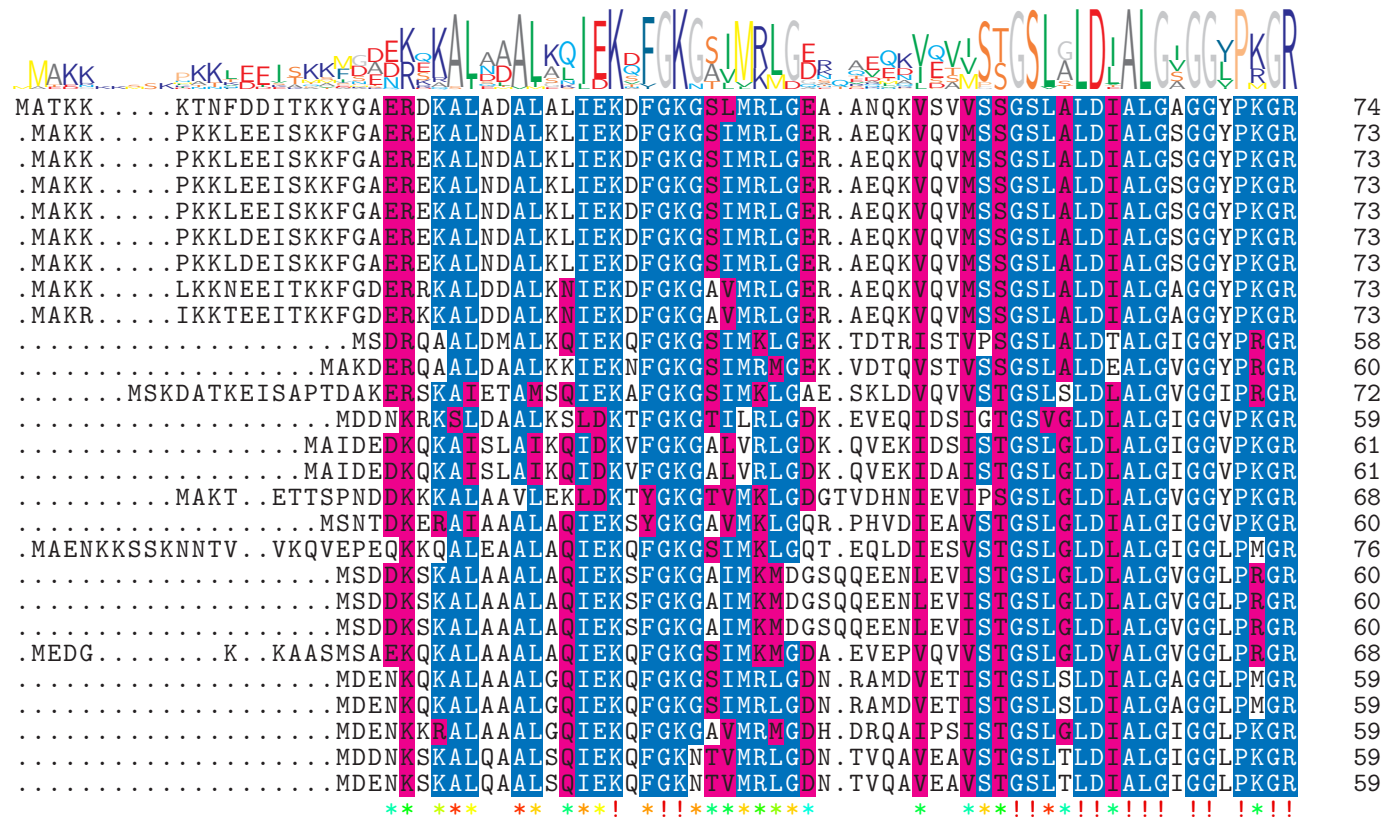


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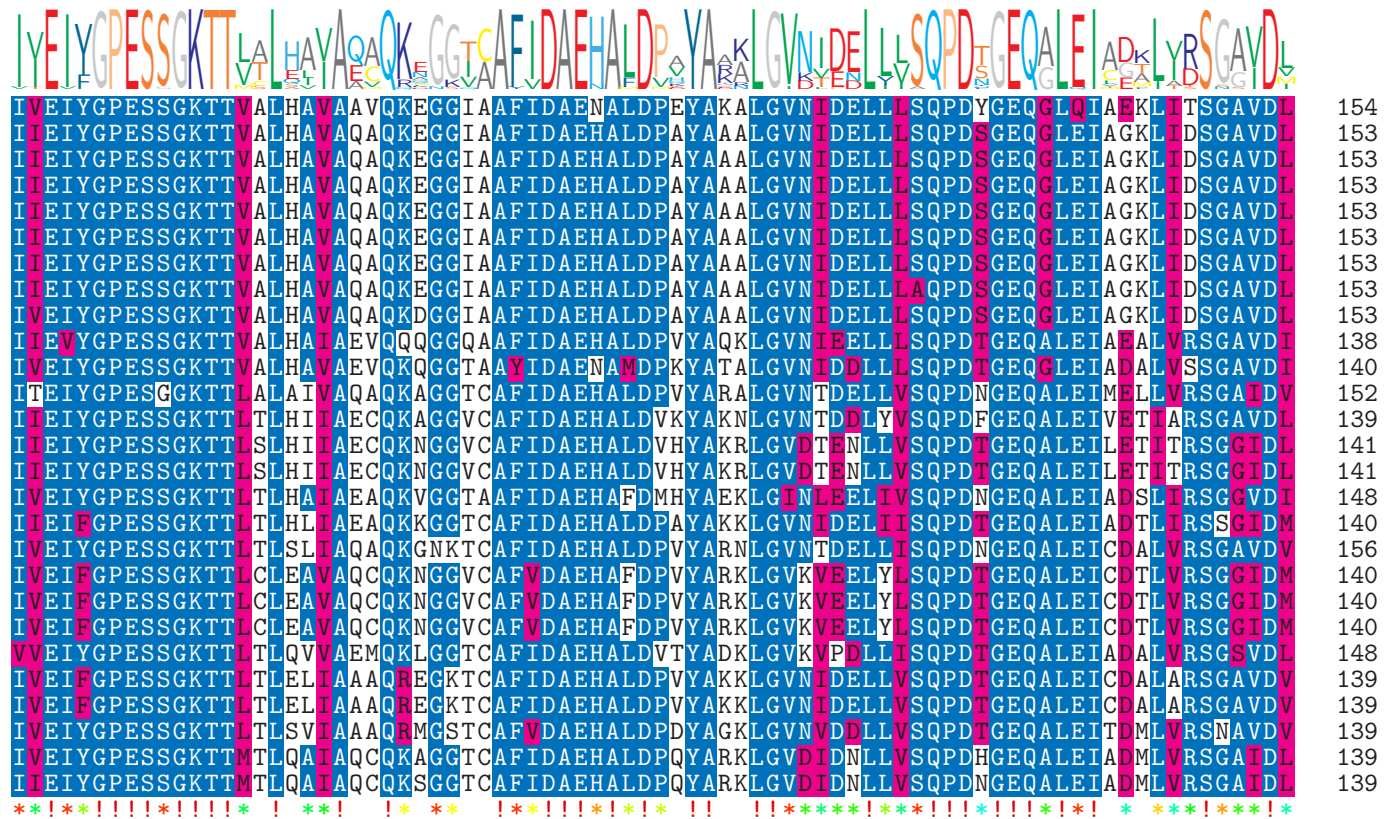
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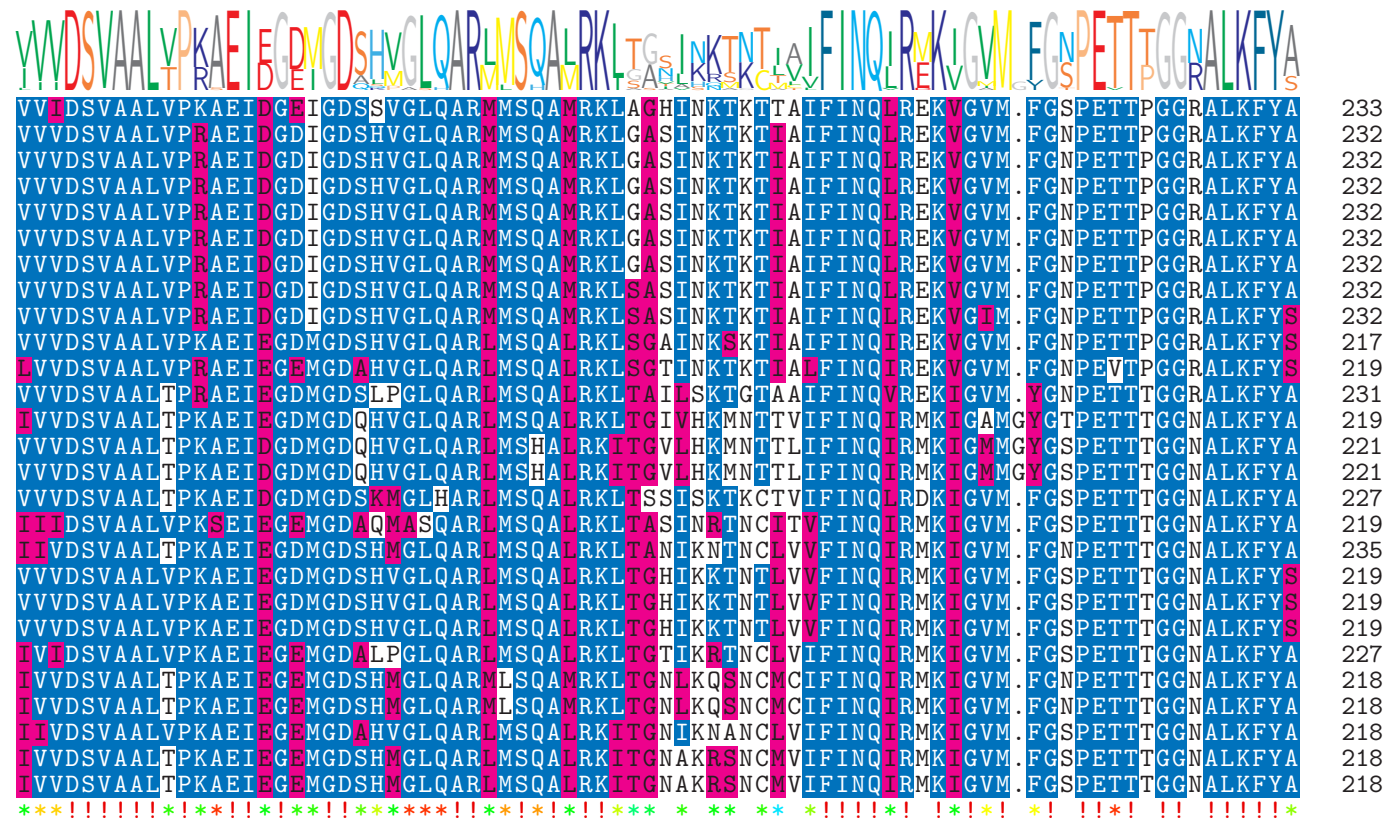
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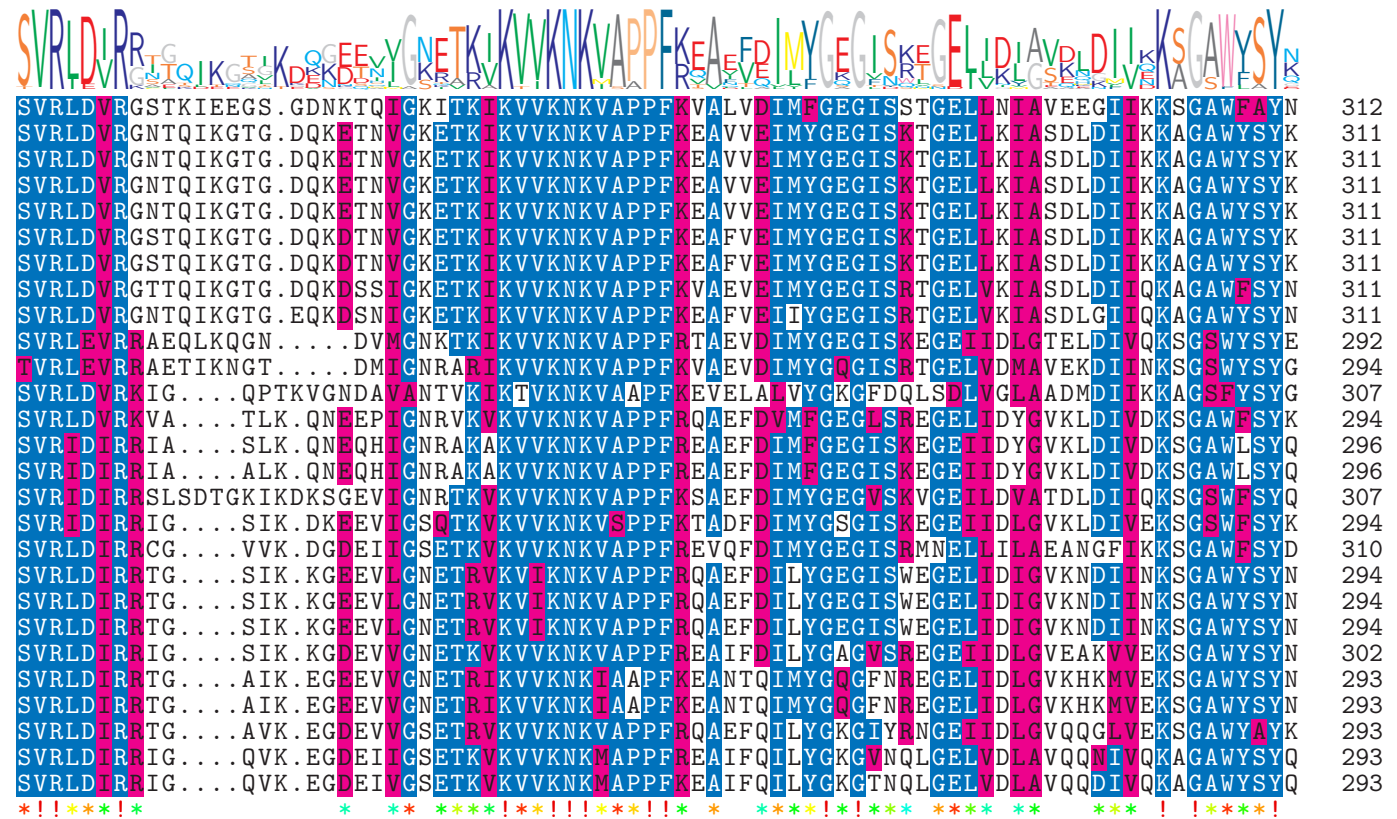
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consensus

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Sequence	Score
DEKIGGGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ NPE ⁷ IF ⁸ DE ⁹ ID ¹⁰ HK ¹¹ VR ¹² AAH ¹³ CI ¹⁴ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AEHP ⁵ EIF ⁶ DE ⁷ ID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ CLIDGEEVSEQD ¹² TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AEHP ⁵ EIF ⁶ DE ⁷ ID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ CLIDGEEVSEQD ¹² TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AEHP ⁵ EIF ⁶ DE ⁷ ID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ CLIDGEEVSEQD ¹² TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ ADNP ⁵ EIF ⁶ DE ⁷ ID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ CLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIE	381
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ ADNP ⁵ EF ⁶ FA ⁷ IE ⁸ DH ⁹ QV ¹⁰ RV ¹¹ QF ¹² CLIDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEIE	381
GEKIGGGS ¹ EN ² AK ³ RYL ⁴ ADHP ⁵ QIF ⁶ DE ⁷ ID ⁸ RK ⁹ VR ¹⁰ VKF ¹¹ CLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGGGS ¹ EN ² AK ³ KFL ⁴ ADNP ⁵ EIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQY ¹¹ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ¹ RL ² GGGREN ³ AK ⁴ QFL ⁵ KEN ⁶ KD ⁷ IMLM ⁸ IQEQ ⁹ IREHY ¹⁰ CLDNNGVVQQQA ¹¹ EETQEEL.EFE.E.....	348
SERIGGGREN ¹ AK ² NYL ³ ADH ⁴ ED ⁵ VE ⁶ EV ⁷ RL ⁸ KV ⁹ RAAY ¹⁰ CTSDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEK ¹ TIAY ² IA ³ ERP ⁴ EME ⁵ QE ⁶ IRDR ⁷ MAAIRAGNAGEAPALAPAAPEAAEA.....	363
DKKLGGGREN ¹ SKA ² FL ³ KEN ⁴ PEIA ⁵ DEIT ⁶ KA ⁷ IQNSM ⁸ TEGMI....SGSEDDGE..EE.....	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALADEIT ⁵ TLK ⁶ IKESIG ⁷ SNEEI....MPLPDEPL..EEME.....	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALADEIT ⁵ TLK ⁶ IKESIG ⁷ SNEEI....MPLPDEPL..EEME.....	347
DTKLGGGRD ¹ TVK ² ELI ³ KDN ⁴ PELAE ⁵ ELEAK ⁶ IREKLQAK.....	343
NV ¹ RIGGGREN ² VVK ³ YL ⁴ KEHP ⁵ QIS ⁶ NE ⁷ EIK ⁸ IREKSLKITNI....NLDQTEEEND.....	343
GTKIGGKNN ¹ AVK ² WL ³ KEN ⁴ PEIA ⁵ DK ⁶ LQE ⁷ URNTLA ⁸ SNPNS....VLKATASDSNDES ⁹ DVE..EFSEEEEL.....	372
GAKIGGQK ¹ DNVR ² VL ³ KEN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VEMHI....TEGT.....QDET ⁹ DG..ERPEE.....	348
GAKIGGQK ¹ DNVR ² VL ³ KEN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VEMHI....TEGT.....QDET ⁹ DG..ERPEE.....	348
GAKIGGQK ¹ DNVR ² VL ³ KEN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VEMHI....TEGT.....QDET ⁹ DG..ERPEE.....	348
GE ¹ RIGGGRDNC ² REFL ³ RNAEL ⁴ LARE ⁵ IN ⁶ KKV ⁷ REHL ⁸ CVTPMG....AV.TLAEVEEED.....	352
GDKIGGQKAN ¹ ACKYL ² KEN ³ PEIA ⁴ AKT ⁵ LD ⁶ KKL ⁷ REMLLN ⁸ PNEM....QLIAETSSAADDVEFG..AVPEEF.....	354
GD ¹ KIGGQKAN ² ACKYL ³ KEN ⁴ PEIA ⁵ AKT ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PNEM....QLIAETSSAADDVEFG..AVPEEF.....	354
GSKIGGQKAN ¹ AAKY ² LEEN ³ PEIG ⁴ QIE ⁵ QQI ⁶ IRAKLL ⁷ YTSAN....TKATPVAEDLADADI.....	347
GN ¹ KIGGQKNN ² VIRY ³ LEEN ⁴ PEI ⁵ STE ⁶ IE ⁷ EA ⁸ VIRE ⁹ QLLT ¹⁰ KASD....QTAA.HDETEEEEPDLL....ES.....	349
GN ¹ KIGGQKNN ² VIRY ³ FEEN ⁴ NO ⁵ IAE ⁶ IE ⁷ ERN ⁸ IRE ⁹ QLLT ¹⁰ TGTN....GAVQ.I.EDEEEEPDLL....LES.....	349

logo

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved