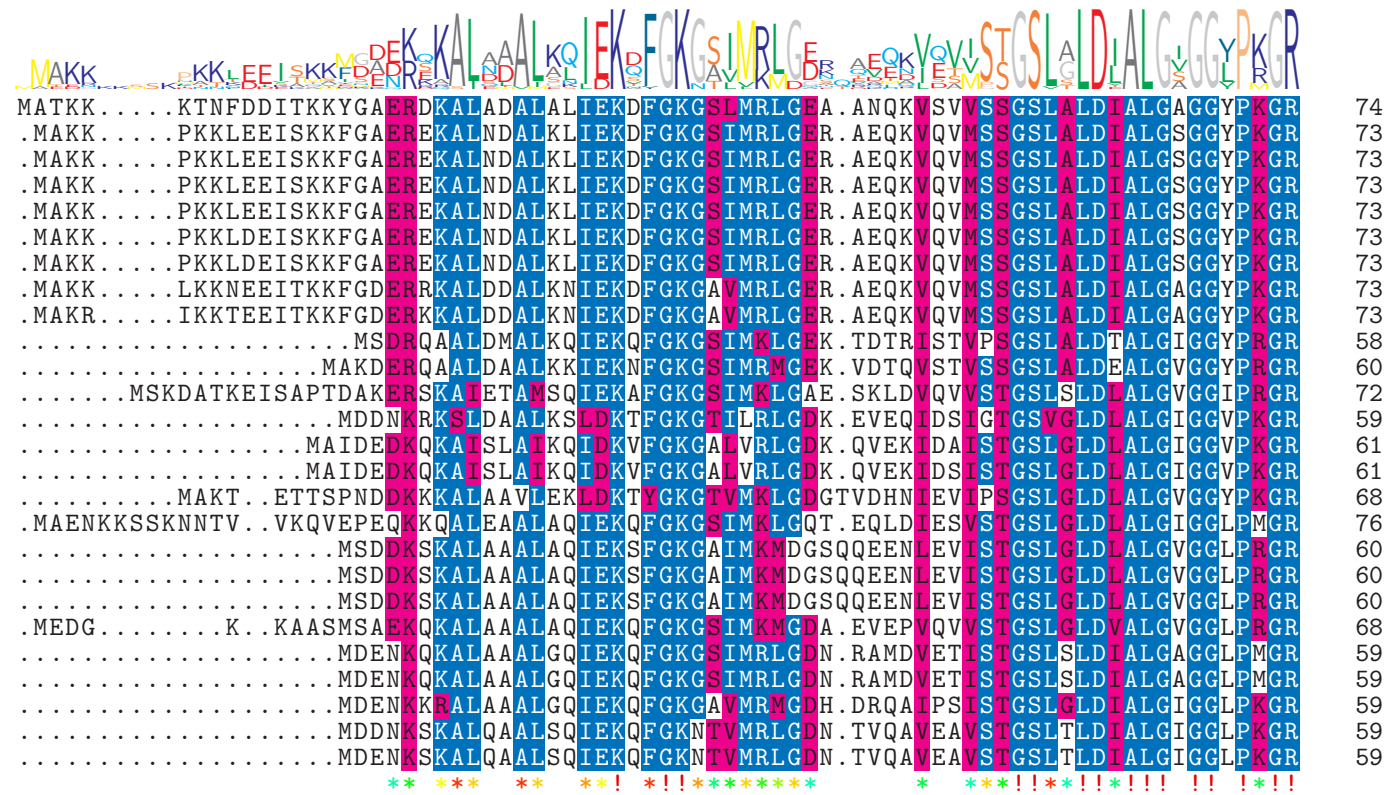


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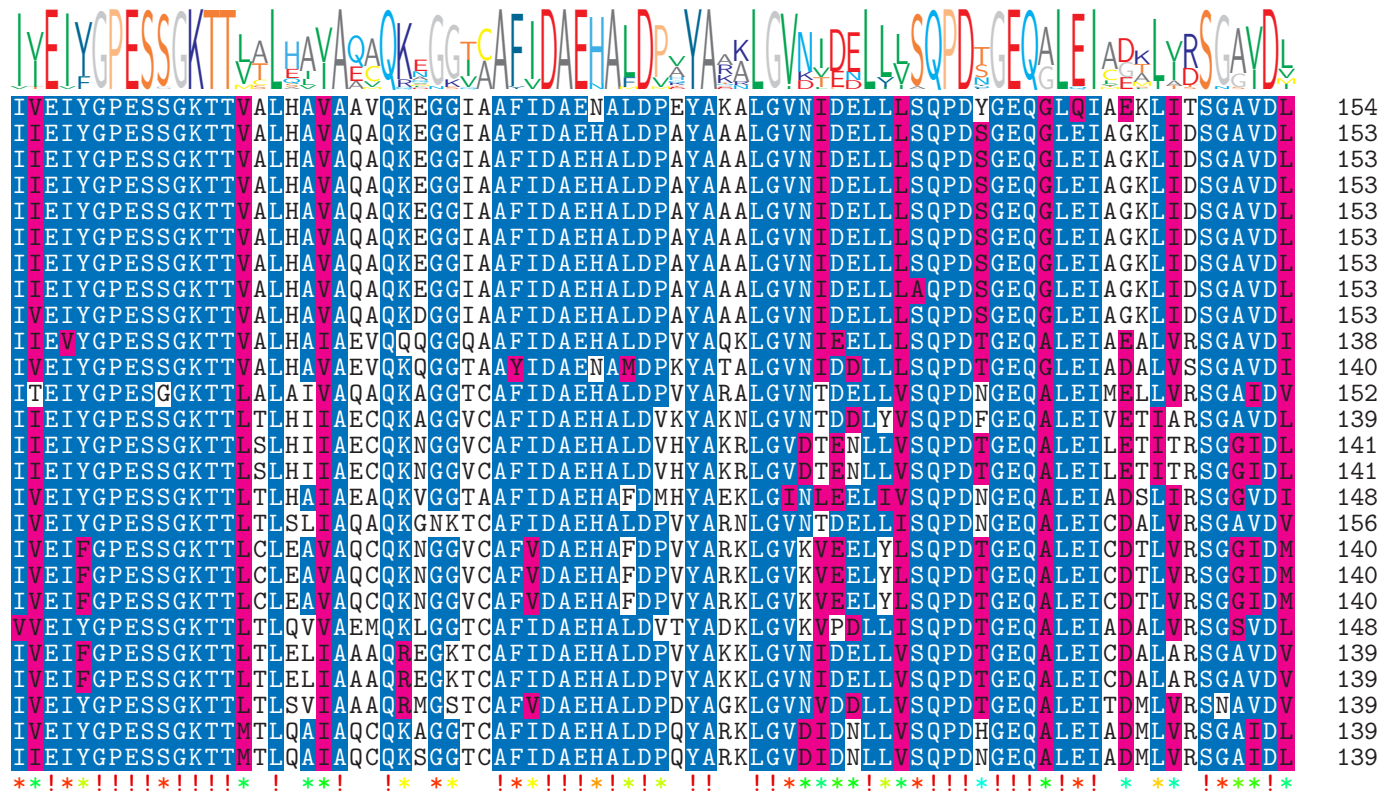
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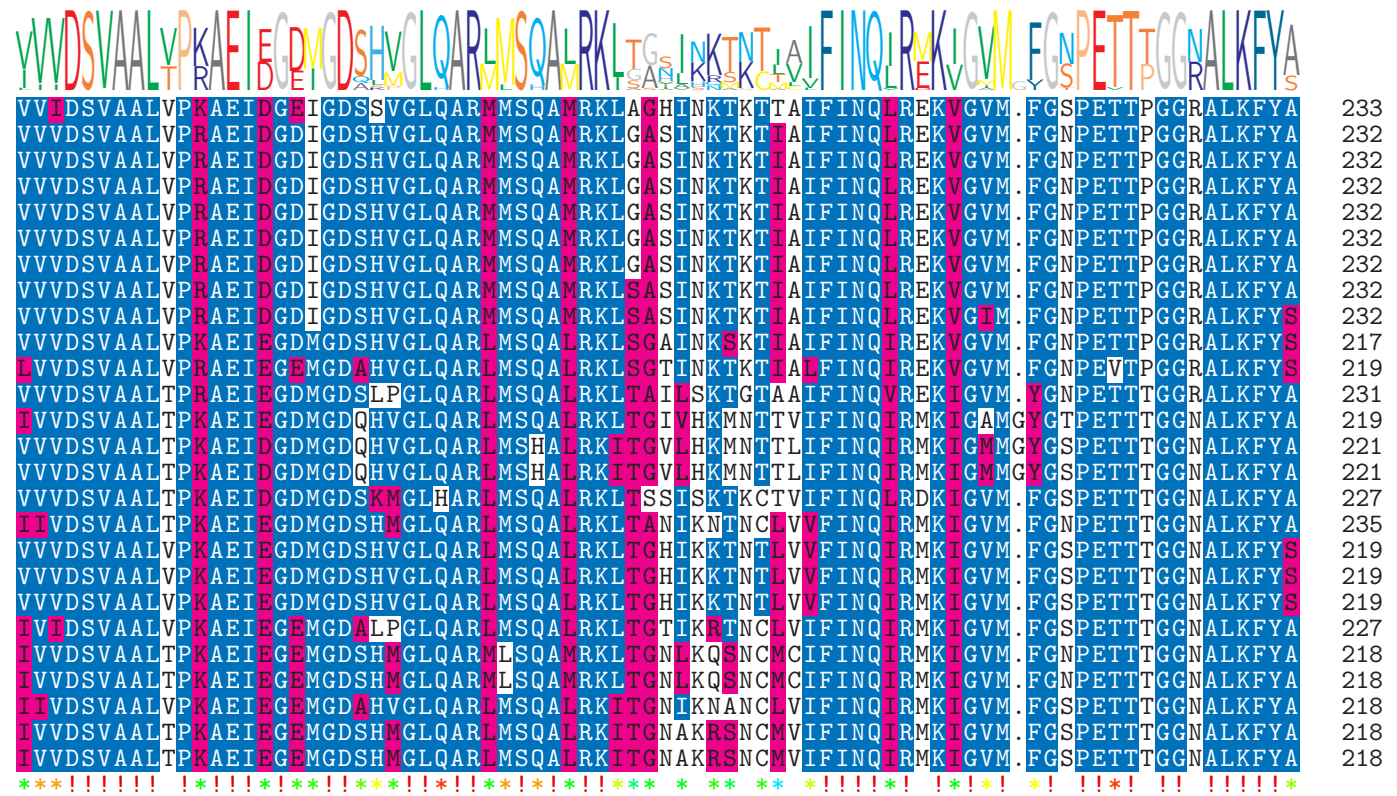
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consensus

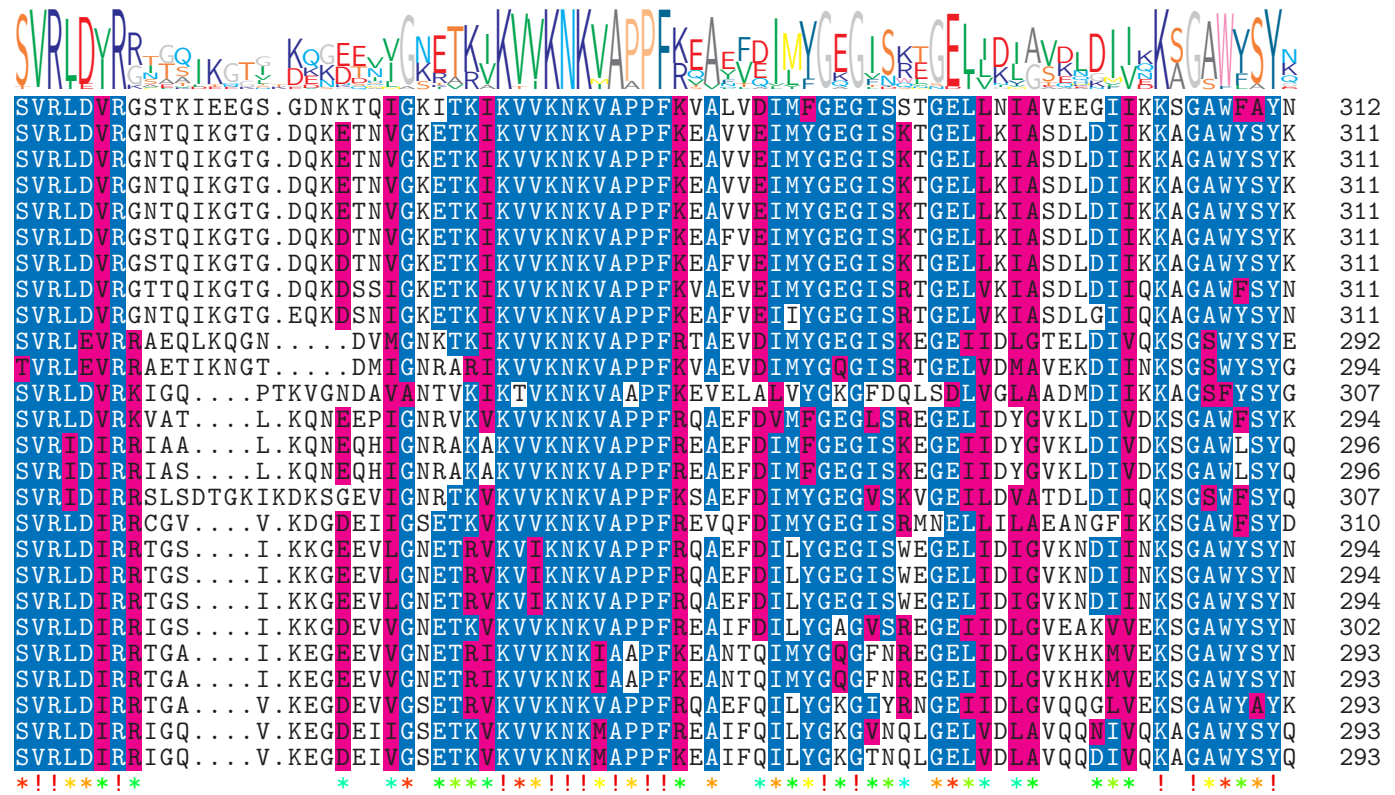
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consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ ADNP ⁺ EI ⁺ FD ⁺ ED ⁺ DK ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ ADNP ⁺ EVFA ⁺ ED ⁺ ED ⁺ HQ ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEAAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ FD ⁺ ED ⁺ DK ⁺ VR ⁺ VKF ⁺ GL ⁺ LEESEEAESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NP ⁺ EI ⁺ FD ⁺ DD ⁺ ED ⁺ DK ⁺ VR ⁺ VQY ⁺ GL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EER ⁺ LGQGR ⁺ ENAK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQ ⁺ REHY ⁺ GL ⁺ DNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ KNYLAD ⁺ HED ⁺ VE ⁺ DE ⁺ VR ⁺ LVRAAY ⁺ GIS ⁺ SDVPEEDLPTTEDE.QI.NILP ⁺ DST.....EE.....	355
DERIGQGEK ⁺ TIAY ⁺ IA ⁺ ERP ⁺ PEME ⁺ Q ⁺ IRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ AD ⁺ EIT ⁺ KAI ⁺ QNSM ⁺ CT ⁺ EGMI....SGSEDDE..GE..E.....	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EIT ⁺ LK ⁺ IKES ⁺ IS ⁺ SNEEI....MPLPDEP..LE..E.....	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EIT ⁺ LK ⁺ IKES ⁺ IS ⁺ SNEEI....MPLPDEP..LE..E.....	347
DTKLGGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NP ⁺ ELAE ⁺ LEAK ⁺ IREKLQAK.....	343
GTKIGQGN ⁺ NAV ⁺ KL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KE ⁺ IEIR ⁺ NTLAS ⁺ NPNS....VLKATASDSND..ESDVEEFSEEEEL.....	372
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KIRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KIRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KIRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GERIGQGRD ⁺ KN ⁺ REF ⁺ LN ⁺ AE ⁺ LARE ⁺ EI ⁺ EN ⁺ KVR ⁺ REHL ⁺ GVTPMG....AV.TLAEVEVE..D.....	352
GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGGQKANA ⁺ AK ⁺ YLE ⁺ EN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ RAKLL ⁺ VT ⁺ SA.....TKATPVAEDLA..DADI.....	347
GNKIGQGN ⁺ NN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ QI ⁺ STE ⁺ EI ⁺ EA ⁺ VIRE ⁺ QLLT ⁺ KASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGGQKN ⁺ NN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ QI ⁺ STE ⁺ EI ⁺ EA ⁺ VIRE ⁺ QLLT ⁺ TG ⁺ TN....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

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NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384
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consensus

 non conserved
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 ≥ 50% conserved