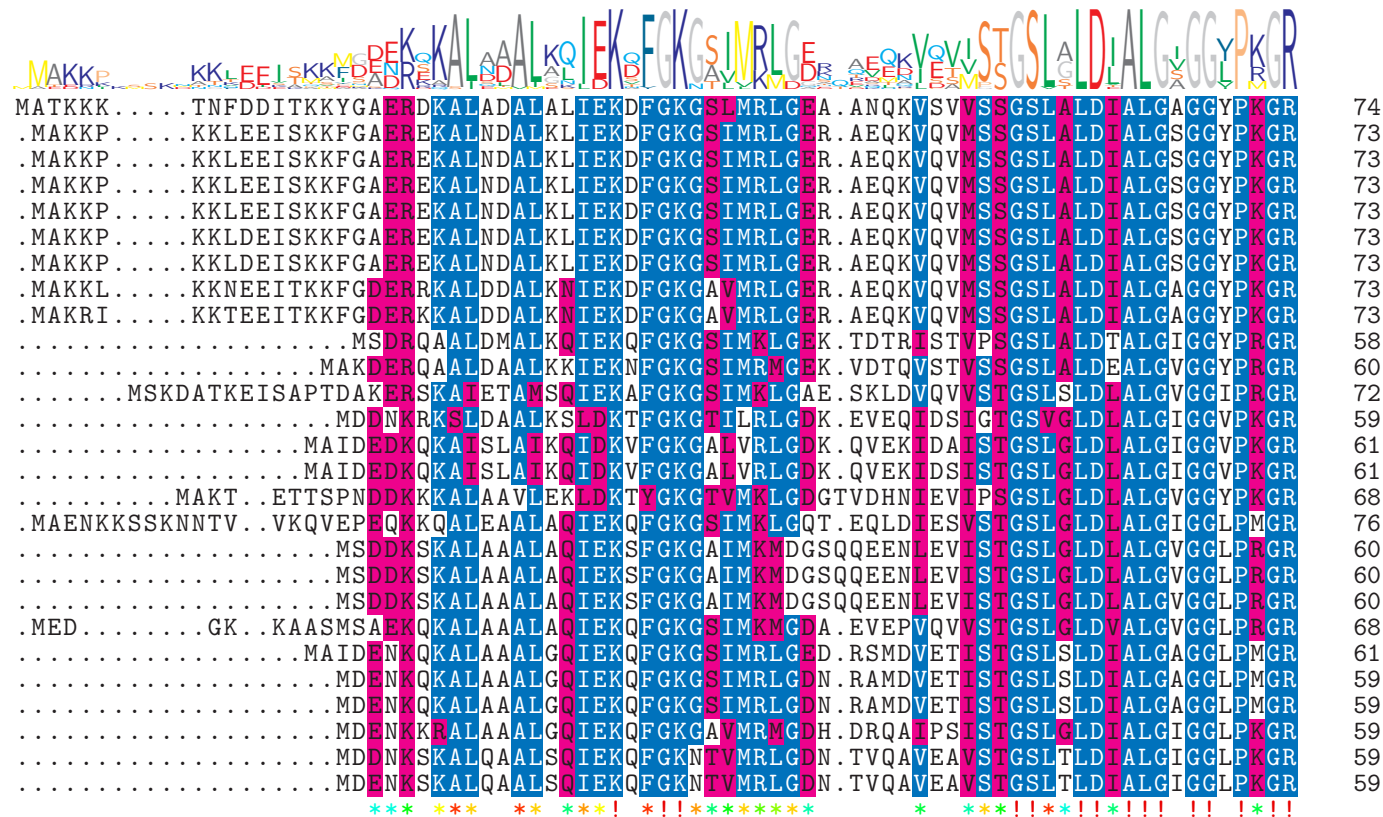


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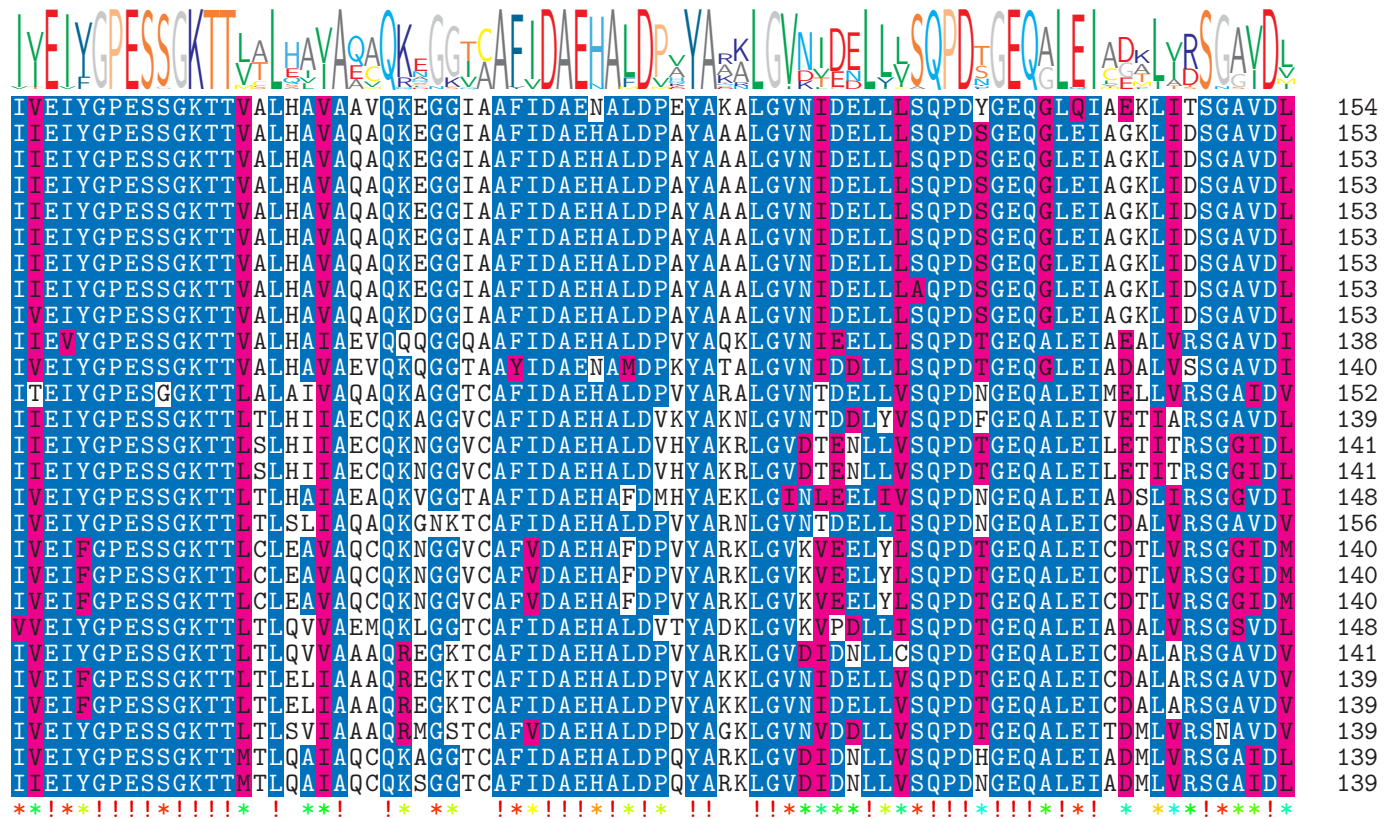
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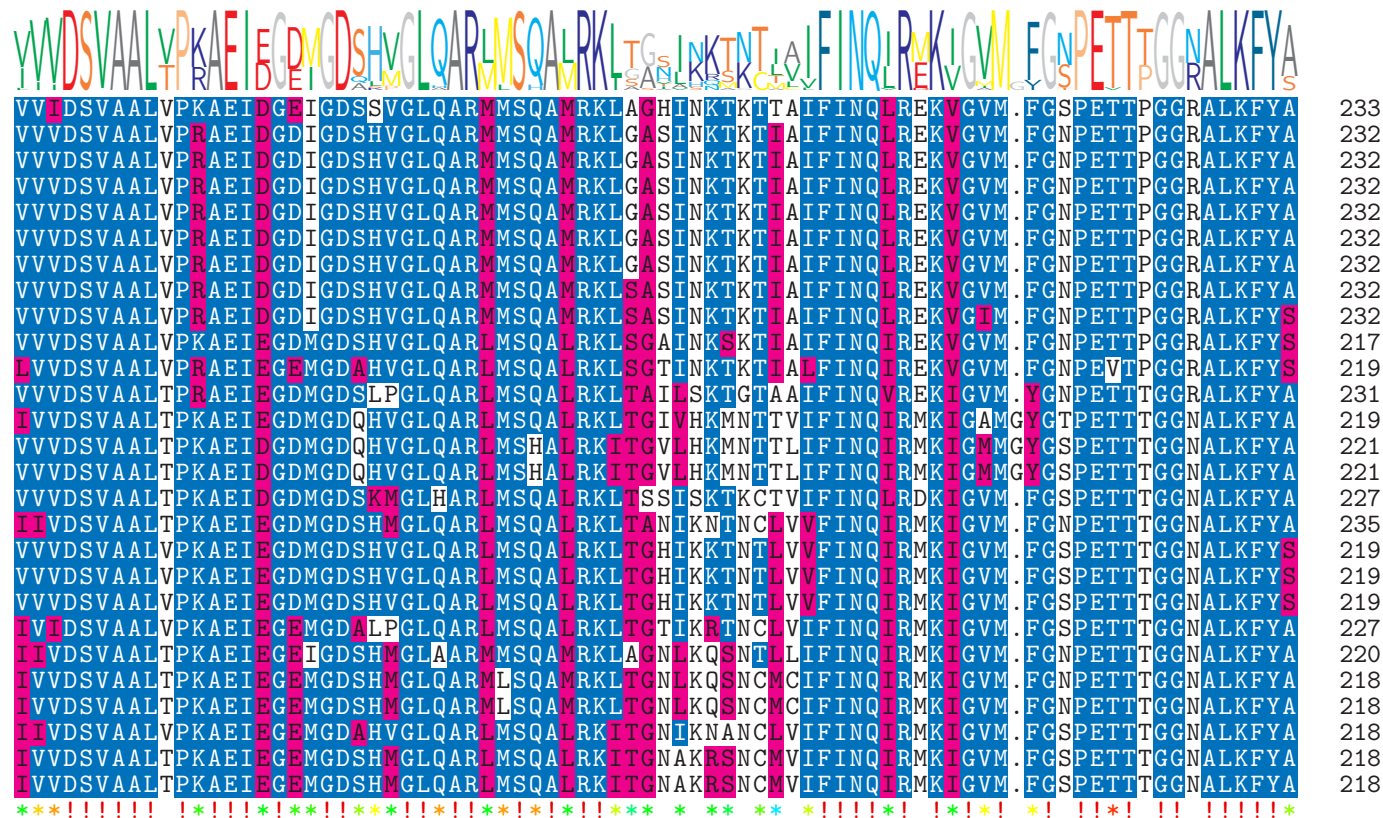
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consensus

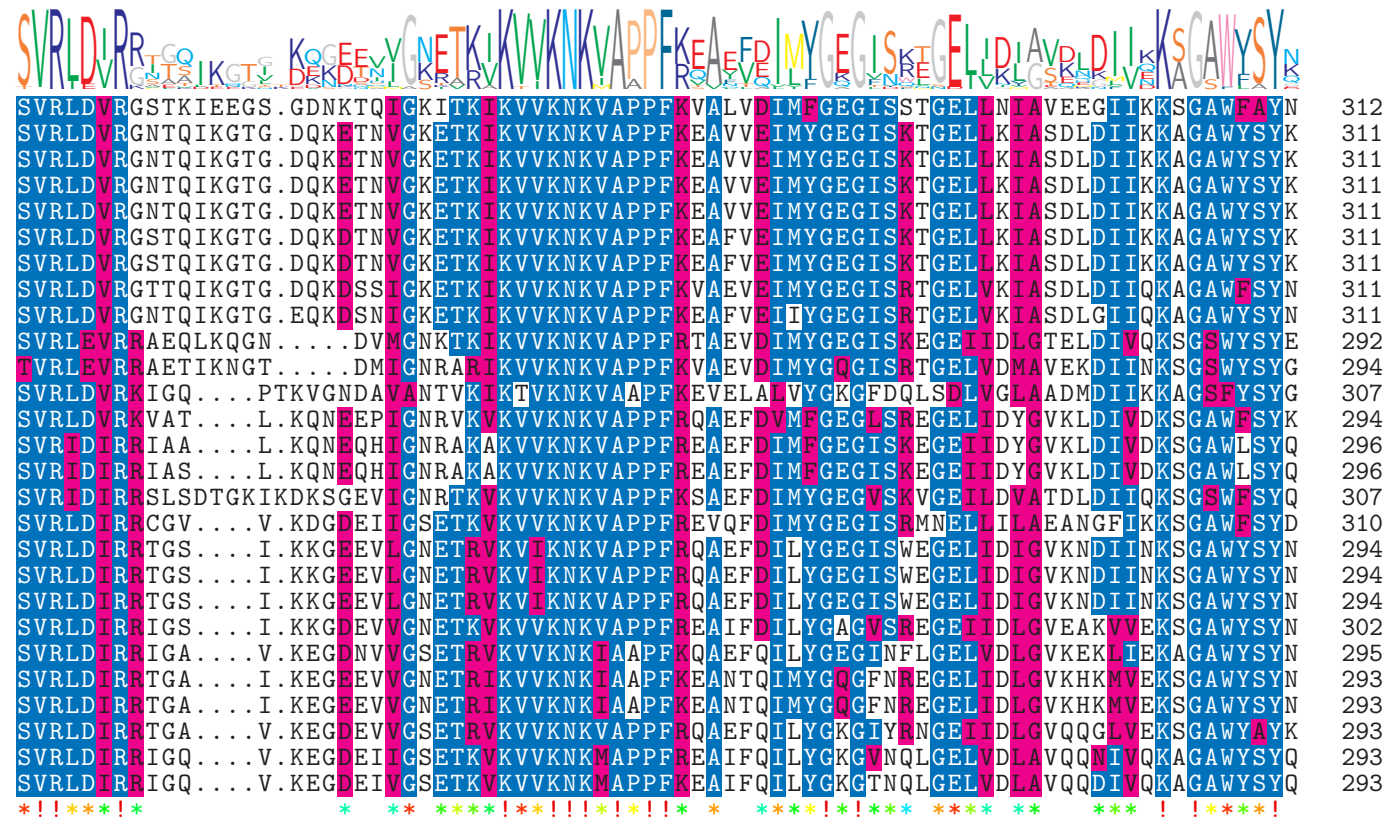
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consensus

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Sequence	Score
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DEKIGQGSEN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTENKKDE....PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE	385
DEKIGQGSEN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTENKKDE....PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE	385
DEKIGQGSEN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQDTENKKDE....PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE	385
DEKIGQGSEN ⁺ AK ⁺ KYL ⁺ ADNP ⁺ EVFA ⁺ ED ⁺ DH ⁺ QV ⁺ RVQF ⁺ GL ⁺ IDGEEAAE....SKKDE....VAQVDS ⁺ .VNEEVTLDLGDELEIE	381
DEKIGQGSEN ⁺ AK ⁺ KYL ⁺ ADNP ⁺ EIF ⁺ DE ⁺ DH ⁺ QV ⁺ RVQF ⁺ GL ⁺ IDGEEIAE....SKKDE....AAQVDS ⁺ .VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ EN ⁺ AK ⁺ RYL ⁺ ADHP ⁺ QI ⁺ FD ⁺ ED ⁺ DK ⁺ RV ⁺ VKF ⁺ GL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ ADNP ⁺ EIF ⁺ DD ⁺ ID ⁺ HK ⁺ V ⁺ RVQY ⁺ GL ⁺ IEEDNTEEKQSSKEK.....ETD ⁺ EK ⁺ .ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ LGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ GL ⁺ DNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGREN ⁺ AK ⁺ NYL ⁺ ADHED ⁺ VED ⁺ EV ⁺ RL ⁺ KV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEK ⁺ TIAY ⁺ IA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VAM ⁺ IRAGNAGEAPALAPAAPEAA...EA.....	363
DKKL ⁺ GGQREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ AD ⁺ EIT ⁺ KAT ⁺ QNSM ⁺ TEGMI....SGSEDD ⁺ E....GEE ⁺	343
DKKL ⁺ GGQREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEI....MPLPDEP.....LEE ⁺ ME.....	347
DKKL ⁺ GGQREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEI....MPLPDEP.....LEE ⁺ ME.....	347
DTKL ⁺ GGQGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGQGK ⁺ NN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IRNTL ⁺ ASPN ⁺ NS....VLKATASDSN...DES ⁺ DVEEFSEEL.....	372
GAKIGQGK ⁺ DN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMHI....TEG.....T...QDET ⁺ DGERPEE.....	348
GAKIGQGK ⁺ DN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMHI....TEG.....T...QDET ⁺ DGERPEE.....	348
GAKIGQGK ⁺ DN ⁺ RV ⁺ VL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMHI....TEG.....T...QDET ⁺ DGERPEE.....	348
GERIGQGRD ⁺ NC ⁺ REFL ⁺ REN ⁺ AE ⁺ LARE ⁺ IE ⁺ EN ⁺ KV ⁺ REHL ⁺ GV ⁺ TPMG....AVTL.AEEVE....ED.....	352
GDKIGQGK ⁺ ANA ⁺ ISW ⁺ LKEN ⁺ PEIAA ⁺ AK ⁺ EIKK ⁺ VRELLLNQDS....KPDFVVD.....GAD ⁺ AETNEDF.....	352
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GDKIGQGK ⁺ ANA ⁺ CKYL ⁺ KEN ⁺ PEIAKT ⁺ LD ⁺ KKL ⁺ REMLLNPNEM....QLIAETSSAA...DDVE ⁺ F ⁺ GAVPEEF.....	354
GSKIGQGK ⁺ ANA ⁺ AKYL ⁺ LEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ IRAKLL ⁺ VT ⁺ SAN....TKATPVAEDL...ADAD ⁺ I.....	347
GNKIGQGK ⁺ NN ⁺ VIRY ⁺ LEEN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQLLT ⁺ KASD....QTAA.HDETE...EEP ⁺ DLLES.....	349
GNKIGQGK ⁺ NN ⁺ VIRY ⁺ FEEN ⁺ NC ⁺ QIAE ⁺ IE ⁺ ERN ⁺ IREQLLT ⁺ TG ⁺ TN....GAVQ.I.EDE...EEP ⁺ DLLES.....	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388
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consensus

 non conserved
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 ≥ 50% conserved