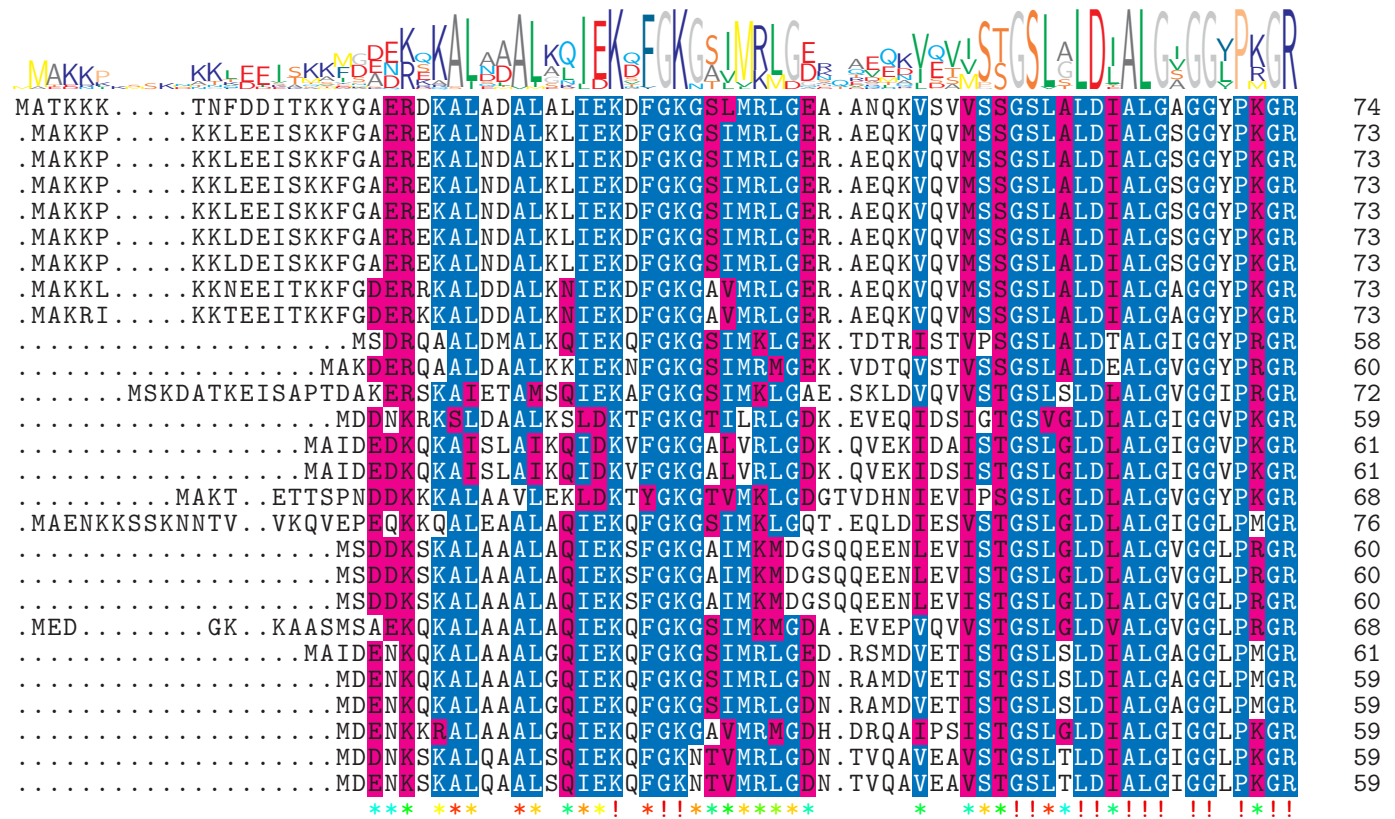


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consensus

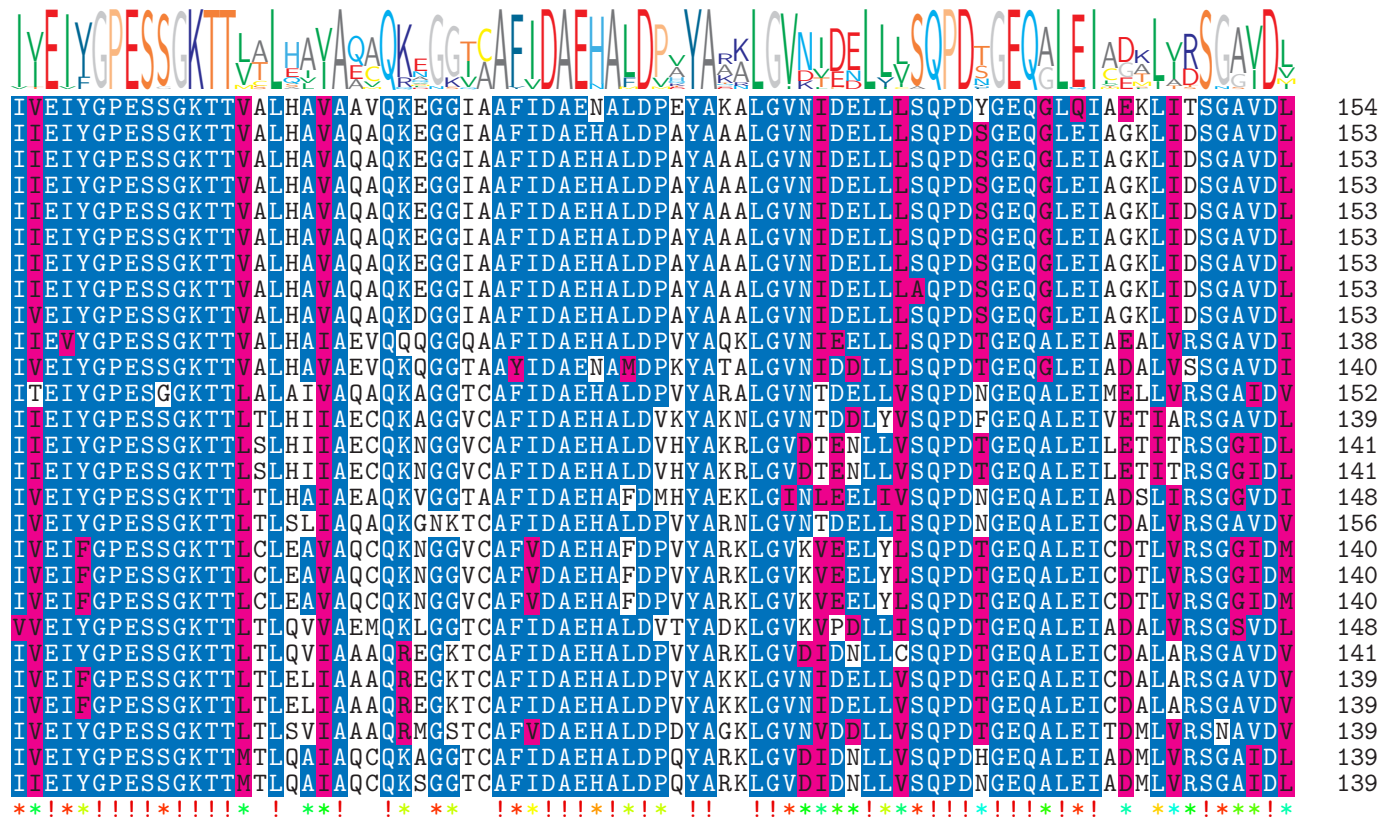
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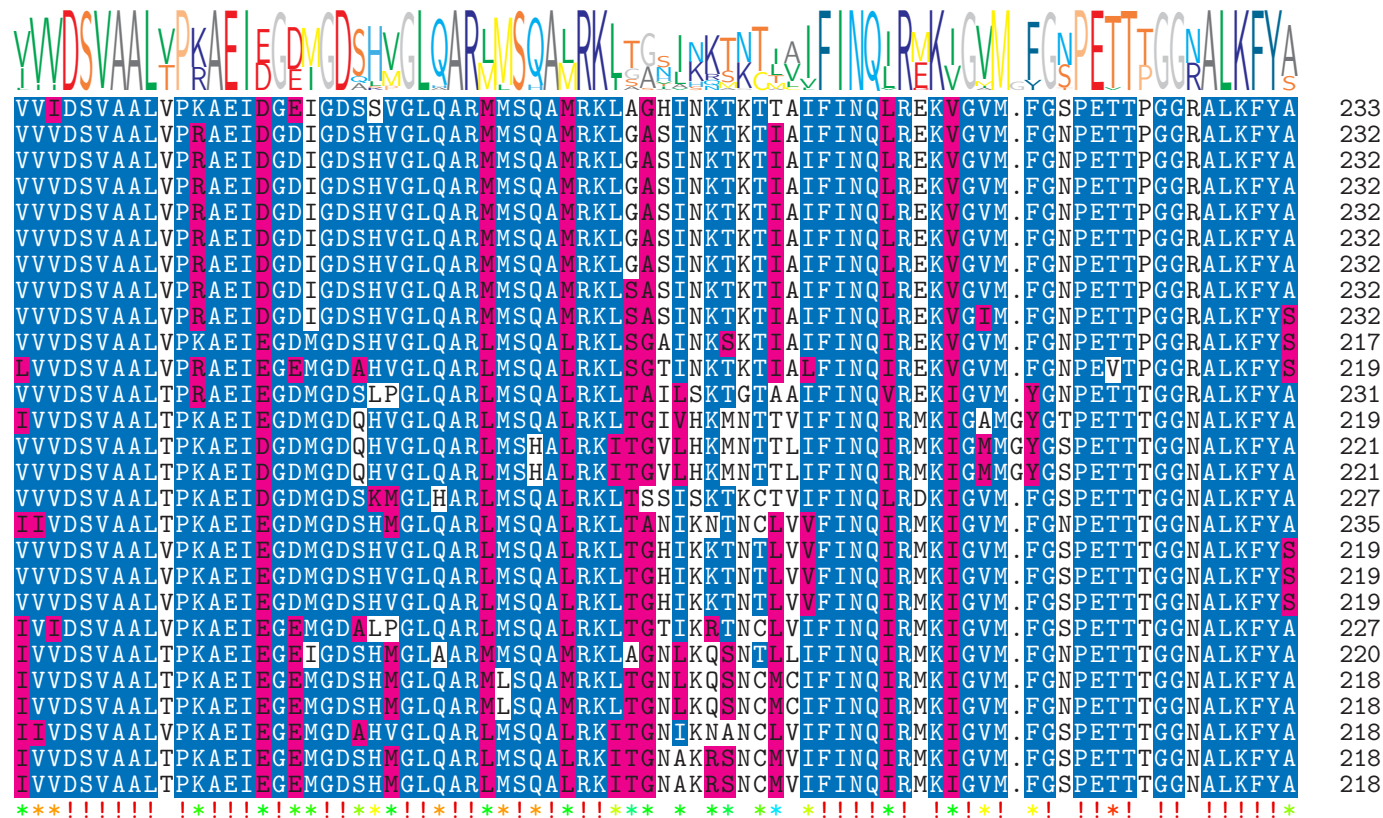
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consensus

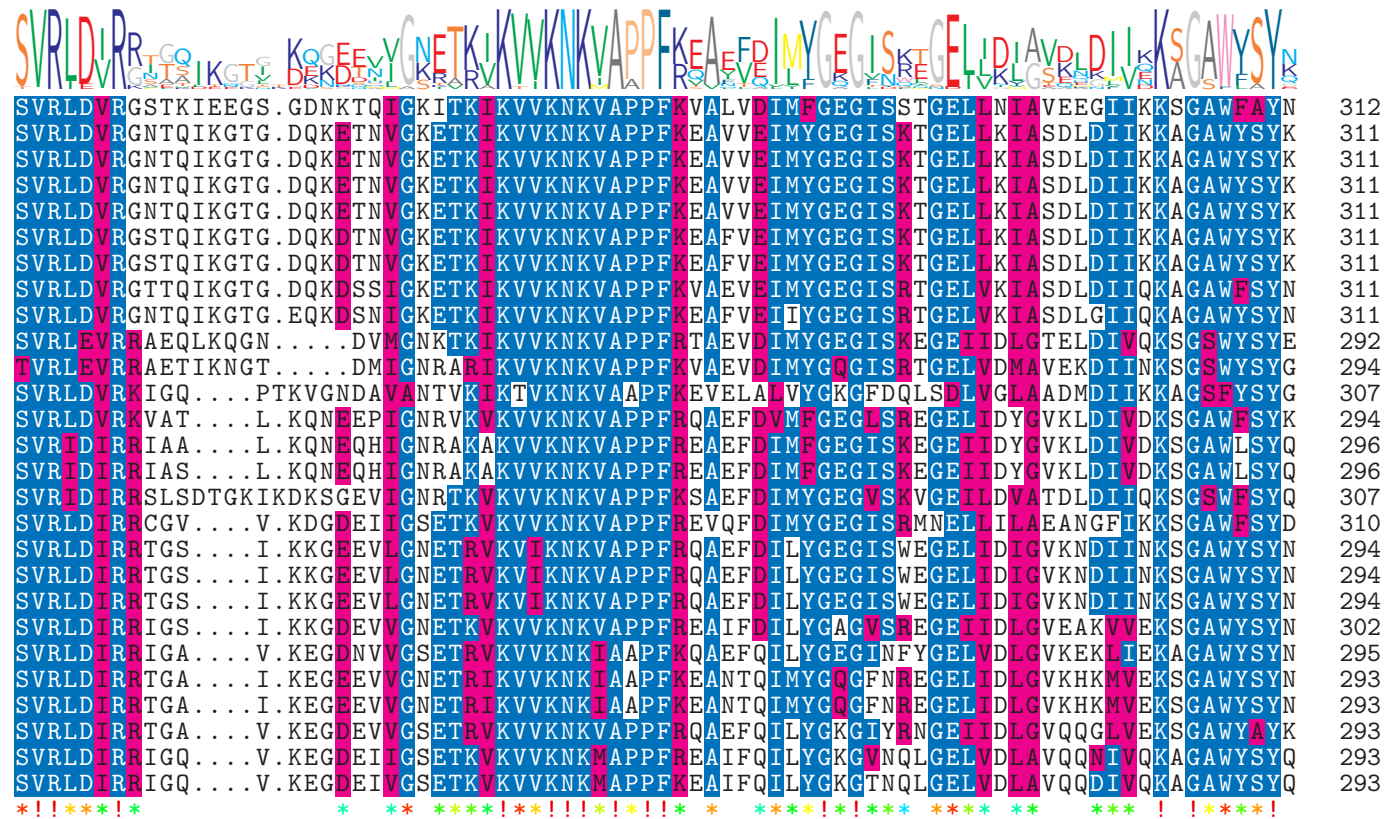
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NTDB id 1022 ACIAD RS06390 WP 0004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ DHK ⁺ V ⁺ RAAH ⁺ CI ⁺ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AEHP ⁺ EI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ ADNP ⁺ EI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ VQF ⁺ CL ⁺ IDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ ADNP ⁺ EI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ VQF ⁺ CL ⁺ IDGEEAAS....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS ⁺ EN ⁺ AK ⁺ RYL ⁺ ADHP ⁺ QI ⁺ FD ⁺ EID ⁺ DK ⁺ VR ⁺ VKF ⁺ CL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGGGS ⁺ EN ⁺ AK ⁺ FL ⁺ ADNP ⁺ EI ⁺ FD ⁺ DD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ CL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ LGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CL ⁺ DNNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGGGR ⁺ EN ⁺ AK ⁺ NYL ⁺ ADHED ⁺ VE ⁺ DV ⁺ RLK ⁺ V ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKE ⁺ KTI ⁺ AYI ⁺ AE ⁺ RP ⁺ EME ⁺ QE ⁺ IRDR ⁺ VMA ⁺ IRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKL ⁺ LGQGR ⁺ EN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PEI ⁺ AD ⁺ EIT ⁺ KAT ⁺ QNSM ⁺ CI ⁺ EGM....ISGSEDD ⁺ EG....EE.....	343
DKKL ⁺ LGQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ESIG ⁺ SNEE....IMPLPDEPL....EE..ME.....	347
DKKL ⁺ LGQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ESIG ⁺ SNEE....IMPLPDEPL....EE..ME.....	347
DTKL ⁺ LGQGR ⁺ D ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGGQK ⁺ NN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IRNT ⁺ LASNPN....SVLKATASDSN...DESDVEEFSEEL.....	372
GAKIGGQK ⁺ D ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMH....ITEG.....T...QDET ⁺ DGERPEE.....	348
GAKIGGQK ⁺ D ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMH....ITEG.....T...QDET ⁺ DGERPEE.....	348
GAKIGGQK ⁺ D ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NGVEMH....ITEG.....T...QDET ⁺ DGERPEE.....	348
GERIGGQ ⁺ RD ⁺ NC ⁺ REFL ⁺ REN ⁺ AE ⁺ LARE ⁺ EI ⁺ EN ⁺ KV ⁺ REHL ⁺ GV ⁺ TPM....GAVTLAE.EVE...ED.....	352
GEKIGGQK ⁺ AN ⁺ ATT ⁺ WL ⁺ KEN ⁺ PEI ⁺ ATA ⁺ KIE ⁺ KRV ⁺ RELLSNQN....ATPDFAVD....DSEGVAETNEDF.....	353
GDKIGGQK ⁺ AN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF.....	354
GDKIGGQK ⁺ AN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF.....	354
GSKIGGQK ⁺ AN ⁺ AAK ⁺ YLE ⁺ EN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ IRAK ⁺ LLV ⁺ TSA....NTKATPVAEDL...ADADI.....	347
GNKIGGQK ⁺ NN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ ISTE ⁺ EIE ⁺ AVI ⁺ REQLLTKAS....DQTAA.HDETE...EEPDLLES.....	349
GNKIGGQK ⁺ NN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ IAE ⁺ IE ⁺ ERN ⁺ IREQLLTGT....NGAVQ.I.EDE...EEPDLLES.....	349

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved