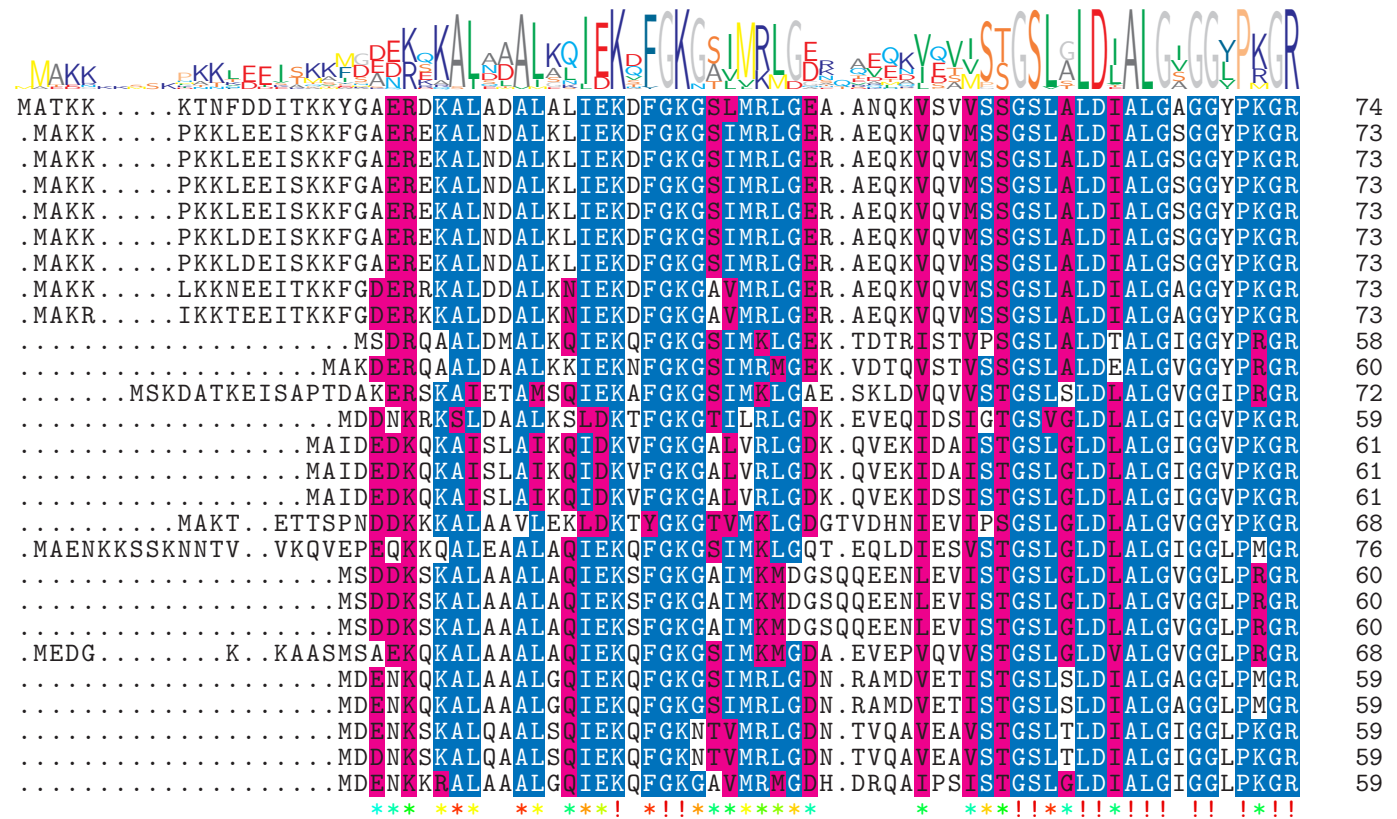


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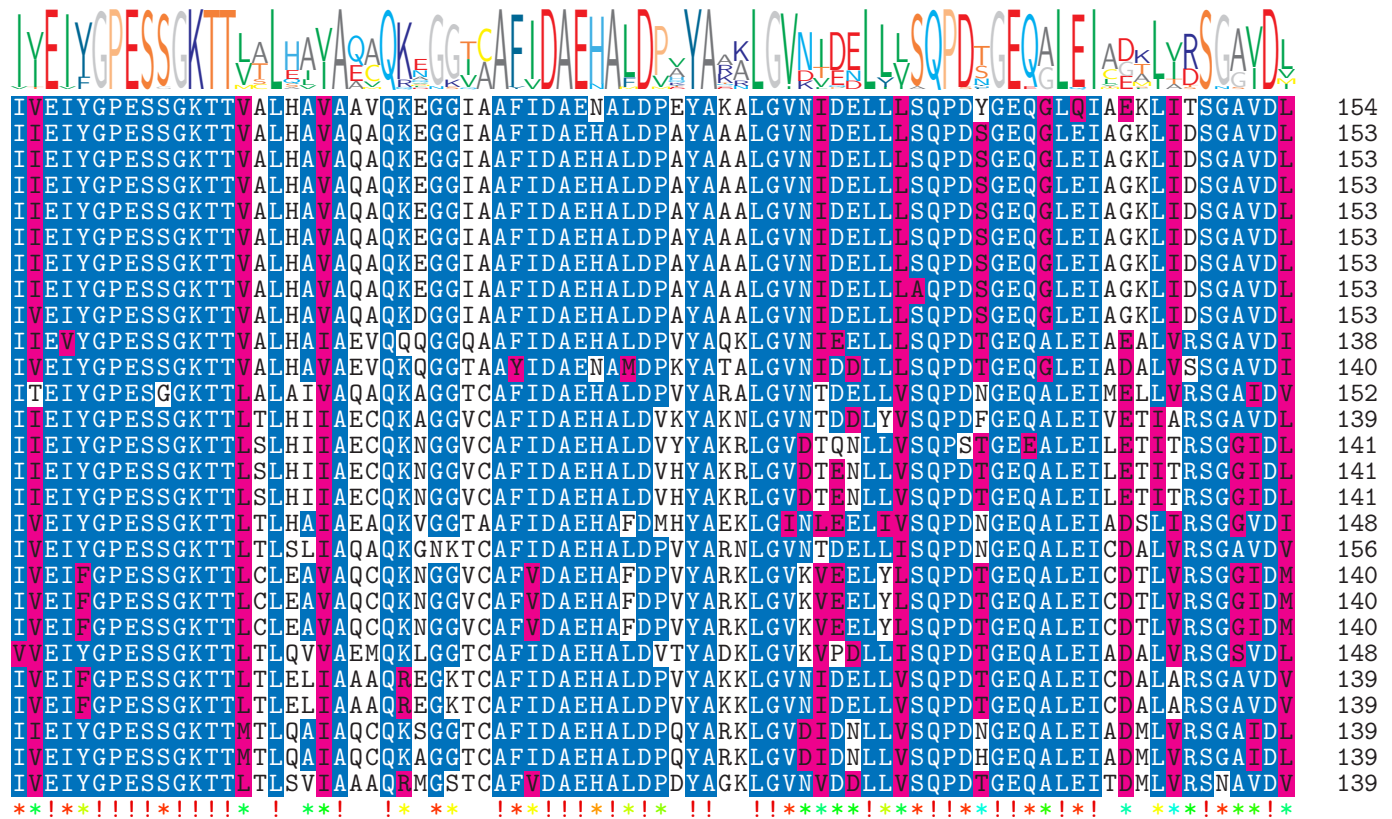
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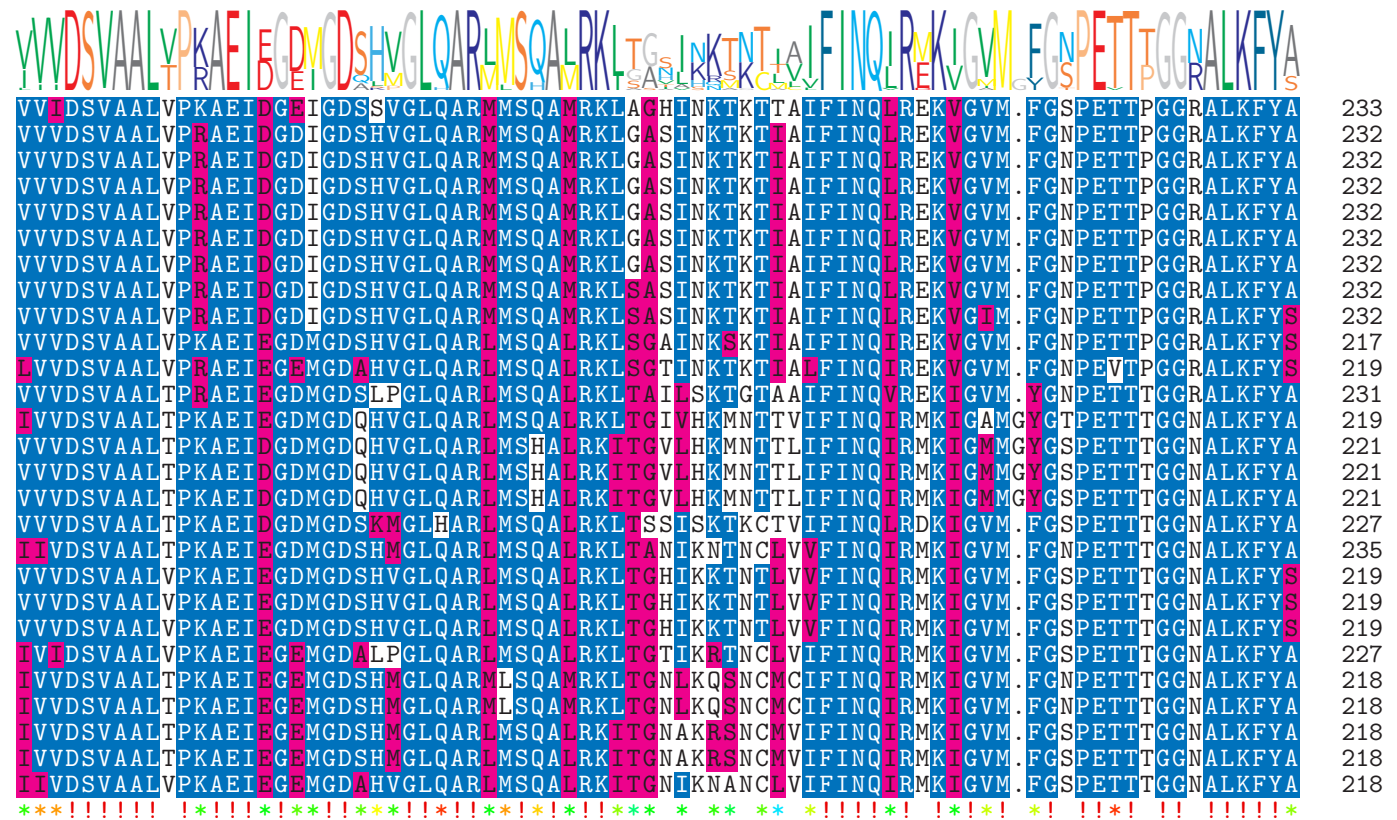
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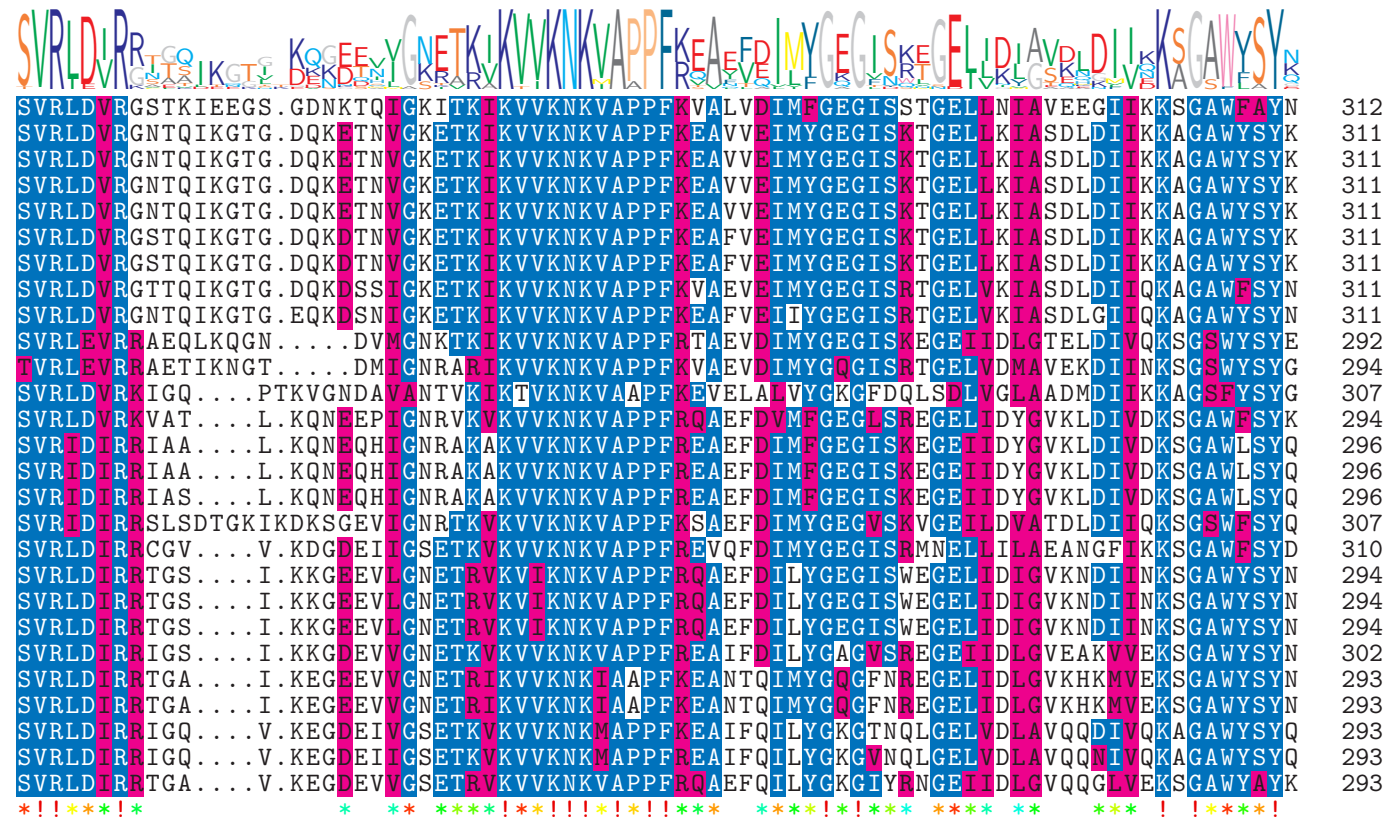
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
DEKIGGGA ⁺ EA ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FE ⁺ DE ⁺ DK ⁺ VR ⁺ AA ⁺ HC ⁺ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SK ⁺ FC ⁺ LIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SK ⁺ FC ⁺ LIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ VR ⁺ SK ⁺ FC ⁺ LIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ DE ⁺ DH ⁺ QV ⁺ RV ⁺ QF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGQGS ⁺ EN ⁺ AK ⁺ RYL ⁺ AD ⁺ HP ⁺ QL ⁺ FE ⁺ DE ⁺ DR ⁺ KV ⁺ VK ⁺ FC ⁺ LEESEEEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ IDH ⁺ KV ⁺ RV ⁺ QY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LI ⁺ QE ⁺ QI ⁺ RE ⁺ HY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ EN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DEV ⁺ RL ⁺ KV ⁺ RA ⁺ AY ⁺ CHSDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGK ⁺ EK ⁺ TI ⁺ AY ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IR ⁺ DR ⁺ MA ⁺ AT ⁺ RAG ⁺ NAGE ⁺ AP ⁺ AL ⁺ AP ⁺ AA ⁺ PE ⁺ AA ⁺ EA.....	363
DKKL ⁺ GGGREN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IT ⁺ QNSM ⁺ CTEGMIS....GSEDD..EGEE.....	343
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ ITL ⁺ KI ⁺ KES ⁺ IGS ⁺ NEEIM....PLPDE..PLEEME.....	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ ITL ⁺ KI ⁺ KES ⁺ IGS ⁺ NEEIM....PLPDE..PLEEME.....	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ ITL ⁺ KI ⁺ KES ⁺ IGS ⁺ NEEIM....PLPDE..PLEEME.....	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LA ⁺ EE ⁺ LE ⁺ AK ⁺ IRE ⁺ KLQAK.....	343
GTKIGGK ⁺ NN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QI ⁺ RN ⁺ TL ⁺ AS ⁺ NP ⁺ NS ⁺ SV....LKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGGK ⁺ KD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RA ⁺ LN ⁺ GV ⁺ EM ⁺ HIT....EGTQDETD.....GERPEE.....	348
GAKIGGK ⁺ KD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RA ⁺ LN ⁺ GV ⁺ EM ⁺ HIT....EGTQDETD.....GERPEE.....	348
GAKIGGK ⁺ KD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RA ⁺ LN ⁺ GV ⁺ EM ⁺ HIT....EGTQDETD.....GERPEE.....	348
GERIGGGRD ⁺ NC ⁺ REF ⁺ LR ⁺ EN ⁺ AE ⁺ L ⁺ ARE ⁺ IE ⁺ KN ⁺ VR ⁺ EH ⁺ LCV ⁺ TPMGA....V.TLAEVEEED.....	352
GDKIGGK ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LR ⁺ EM ⁺ LL ⁺ NP ⁺ EN ⁺ MQ....LIAETSSAADDVE..FGAVPEEF.....	354
GDKIGGK ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LR ⁺ EM ⁺ LL ⁺ NP ⁺ EN ⁺ MQ....LIAETSSAADDVE..FGAVPEEF.....	354
GNKIGGK ⁺ KNN ⁺ VIR ⁺ YFE ⁺ ENN ⁺ QIA ⁺ EE ⁺ IE ⁺ RN ⁺ IRE ⁺ QL ⁺ LT ⁺ TGT ⁺ NG....AVQ.I.EDEEEEPD....LLES.....	349
GNKIGGK ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IRE ⁺ QL ⁺ LT ⁺ TAS ⁺ DQ....TAA.HDETEEEPD....LLES.....	349
GSKIGGK ⁺ KANA ⁺ KYLE ⁺ EN ⁺ PE ⁺ IG ⁺ EE ⁺ EQ ⁺ IR ⁺ AK ⁺ LL ⁺ VS ⁺ TANT....KATPVAEDLADAD....I.....	347

logo

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consensus			

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