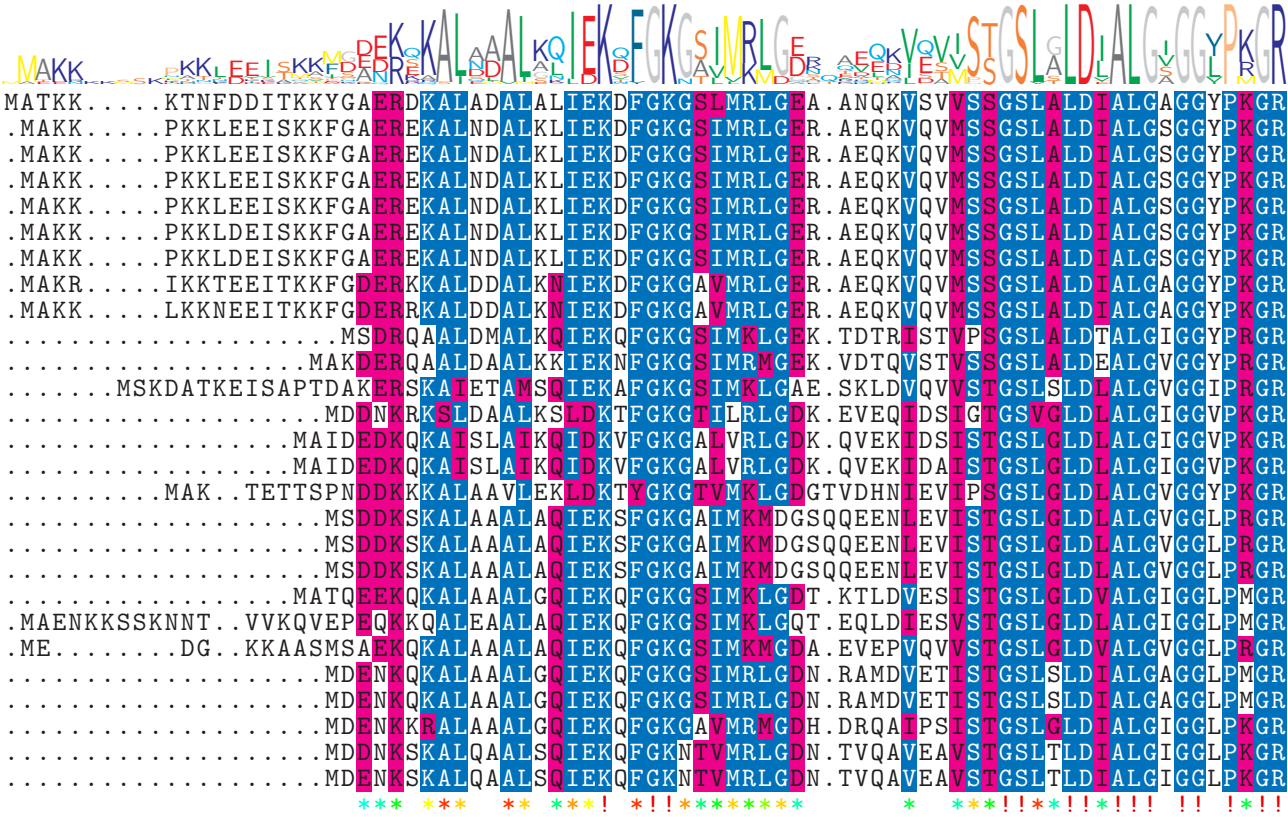


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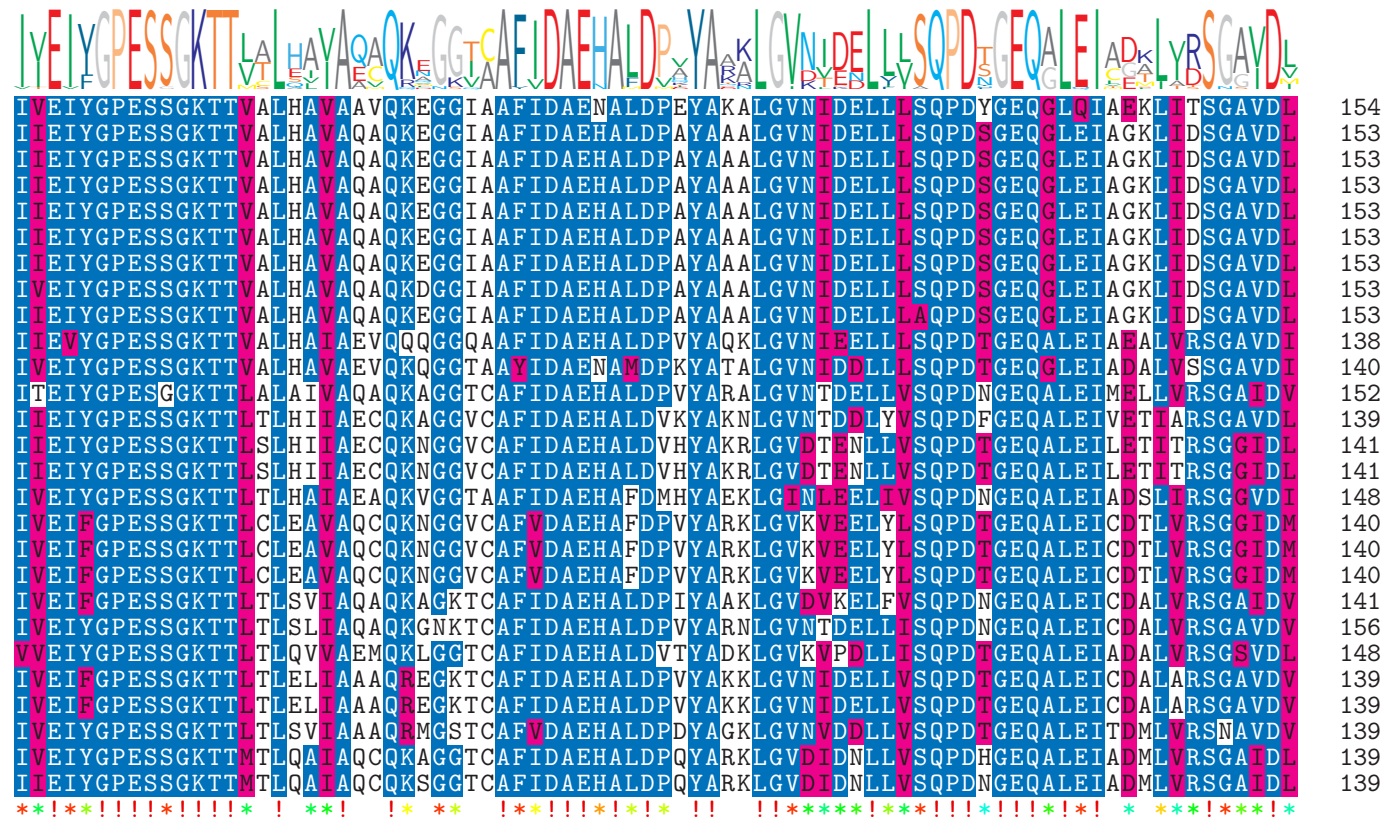


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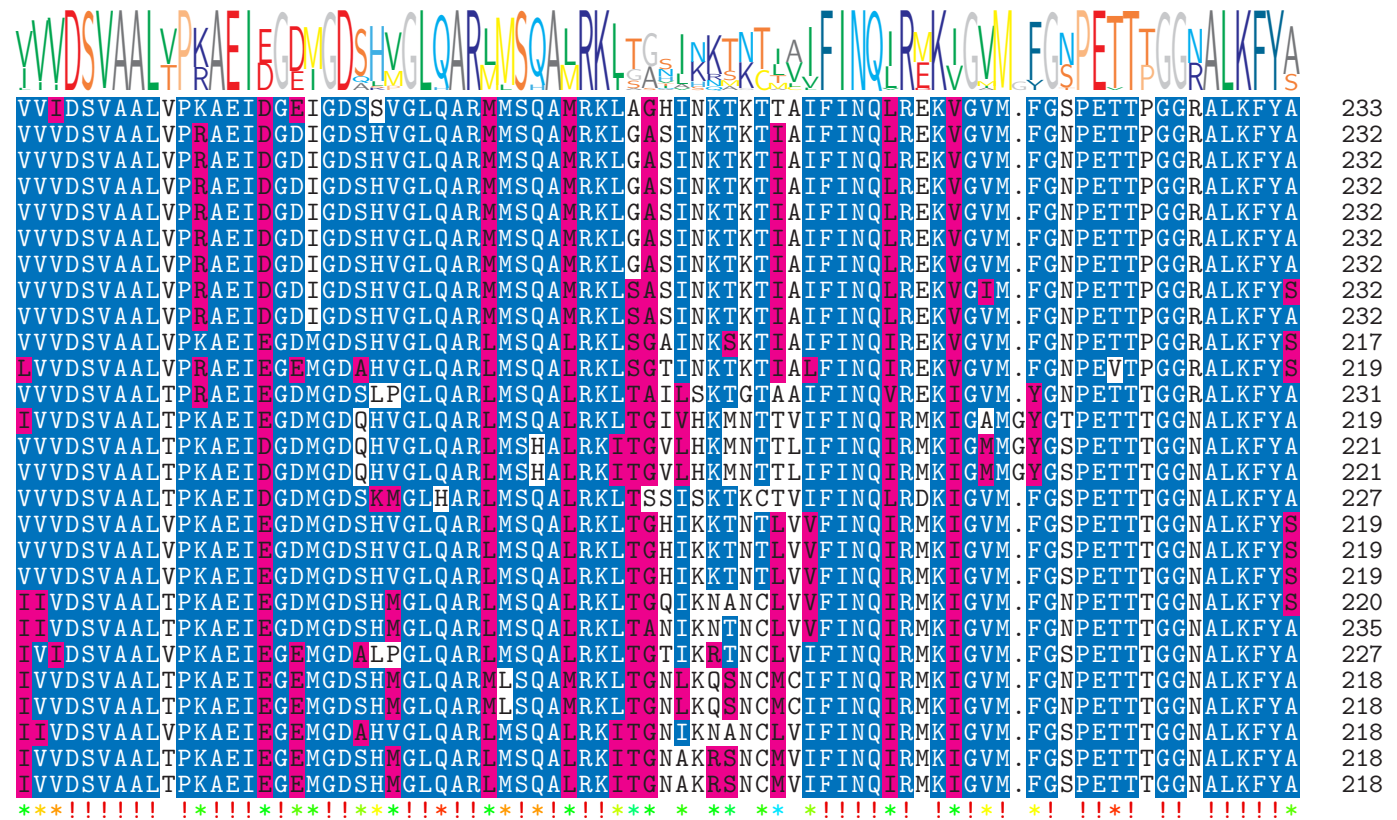
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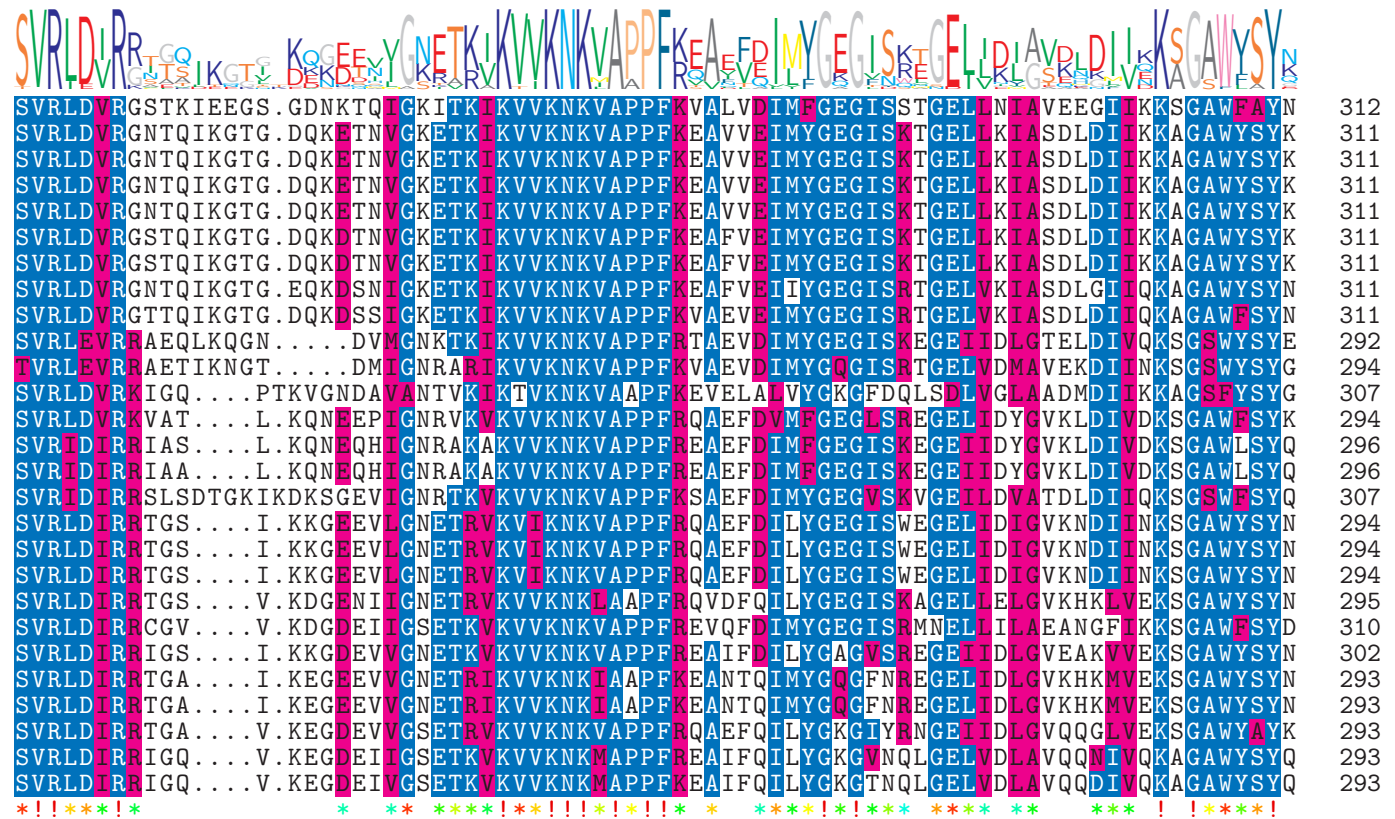
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DH ⁺ QV ⁺ RVQF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPEI ⁺ VFAEI ⁺ DH ⁺ QV ⁺ RVQF ⁺ CLIDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPEI ⁺ FDDI ⁺ DHKV ⁺ RVQY ⁺ CLIEDNTTEEKQ.SSKEK.....ETDEK..ADKNLVLEDDTIEL	381
GEKIGQGS ⁺ ENAK ⁺ KRYLAD ⁺ HQP ⁺ LFDEI ⁺ DRKV ⁺ RVKF ⁺ CLLEESEEEESAM.AVASE.....E.....TDDLALDLNIGIEI	376
EERL ⁺ GGGREN ⁺ AKQFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQA.EETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VEDEV ⁺ RLKV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPT.TEDE.QI.NILPDDST....EE.....	355
DERIGQG ⁺ KEKTI ⁺ AYIA ⁺ ERPE ⁺ MEQE ⁺ IRDRV ⁺ MAATRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEI ⁺ DEIT ⁺ TKAT ⁺ IQNSM ⁺ CI ⁺ EGMISGS..EDDEGE..E.....	343
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADEI ⁺ TLK ⁺ IKES ⁺ IGS ⁺ NEEIMPL..PDEPLE..EME.....	347
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADEI ⁺ TLK ⁺ IKES ⁺ IGS ⁺ NEEIMPL..PDEPLE..EME.....	347
DTKL ⁺ GGGRD ⁺ TVKEL ⁺ IKDN ⁺ PELA ⁺ ELE ⁺ EAKI ⁺ REKLQAK.....	343
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GEKIGQGG ⁺ KANS ⁺ MKWL ⁺ NEN ⁺ IEKS ⁺ DELE ⁺ ARL ⁺ RAEL ⁺ VANPEQALM..ADIEQSENNTESSEDFE.....EEL.....	354
GTKIGQGG ⁺ KNNAV ⁺ KWLKEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQE ⁺ IRNTL ⁺ ASN ⁺ PSVLK..ATASDSND ⁺ ESDVE.EFSE.....EEL.....	372
GERIGQGRD ⁺ NCRE ⁺ FLREN ⁺ AE ⁺ LARE ⁺ IKN ⁺ KV ⁺ REHL ⁺ GV ⁺ TPMGAV...TLAEEVEED.....	352
GDKIGQGG ⁺ KANACK ⁺ YLKEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DKKL ⁺ REMLLN ⁺ PENMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GDKIGQGG ⁺ KANACK ⁺ YLKEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DKKL ⁺ REMLLN ⁺ PENMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GSKIGQGG ⁺ KANA ⁺ AKY ⁺ LEEN ⁺ PEI ⁺ GQE ⁺ IEQQ ⁺ IRAKLL ⁺ TSANTKA..TPVAEDLADADI.....	347
GNKIGQGG ⁺ KNNVIR ⁺ YLEEN ⁺ PEI ⁺ QISTE ⁺ IE ⁺ BAVIRE ⁺ QLLT ⁺ TKASDQTA..A.HDETEEE ⁺ PDLL..ES.....	349
GNKIGQGG ⁺ KNNVIR ⁺ YLEEN ⁺ PEI ⁺ QISTE ⁺ IE ⁺ BAVIRE ⁺ QLLT ⁺ GTGNAGV..Q.I.EDEEE ⁺ PDLL..LE.....S.....	349

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved