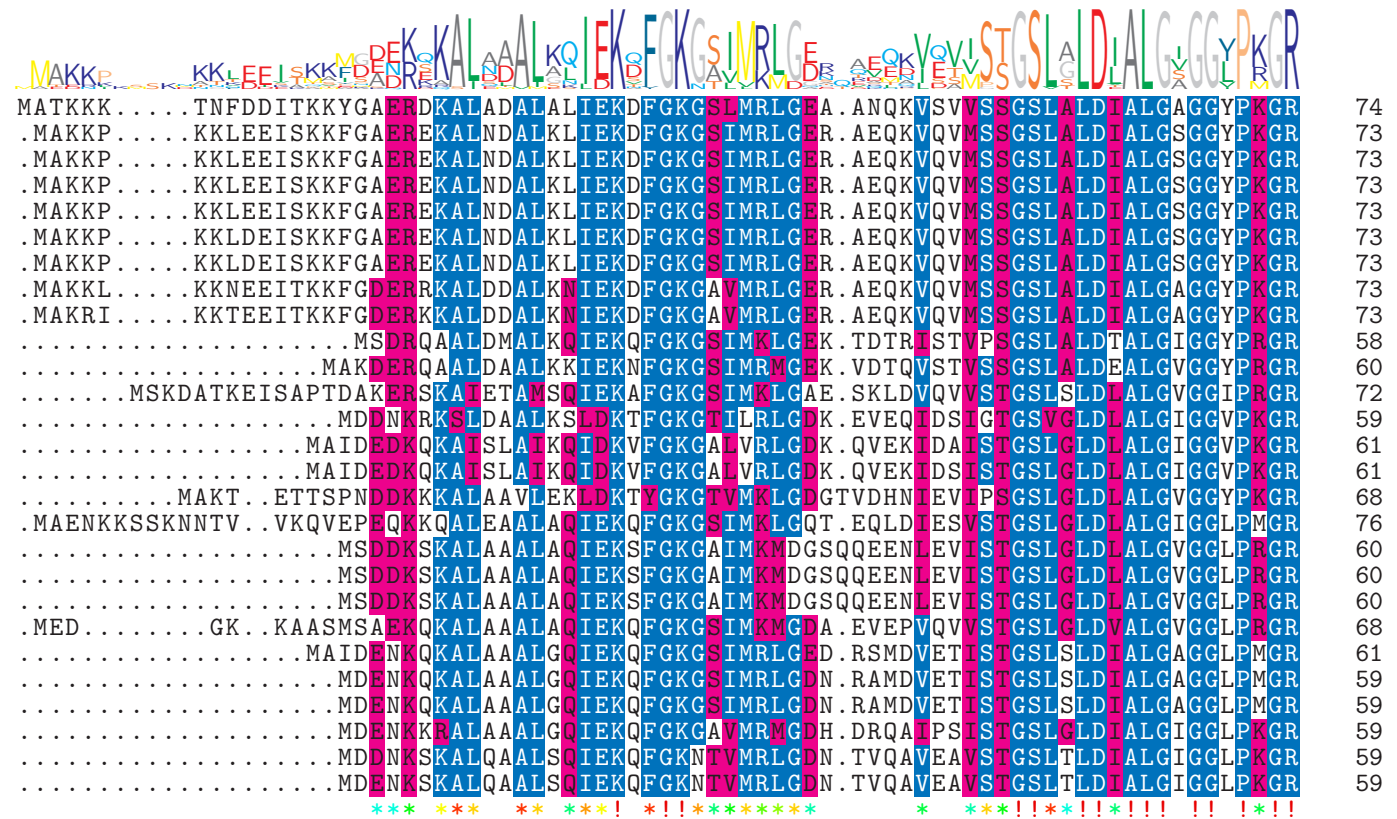


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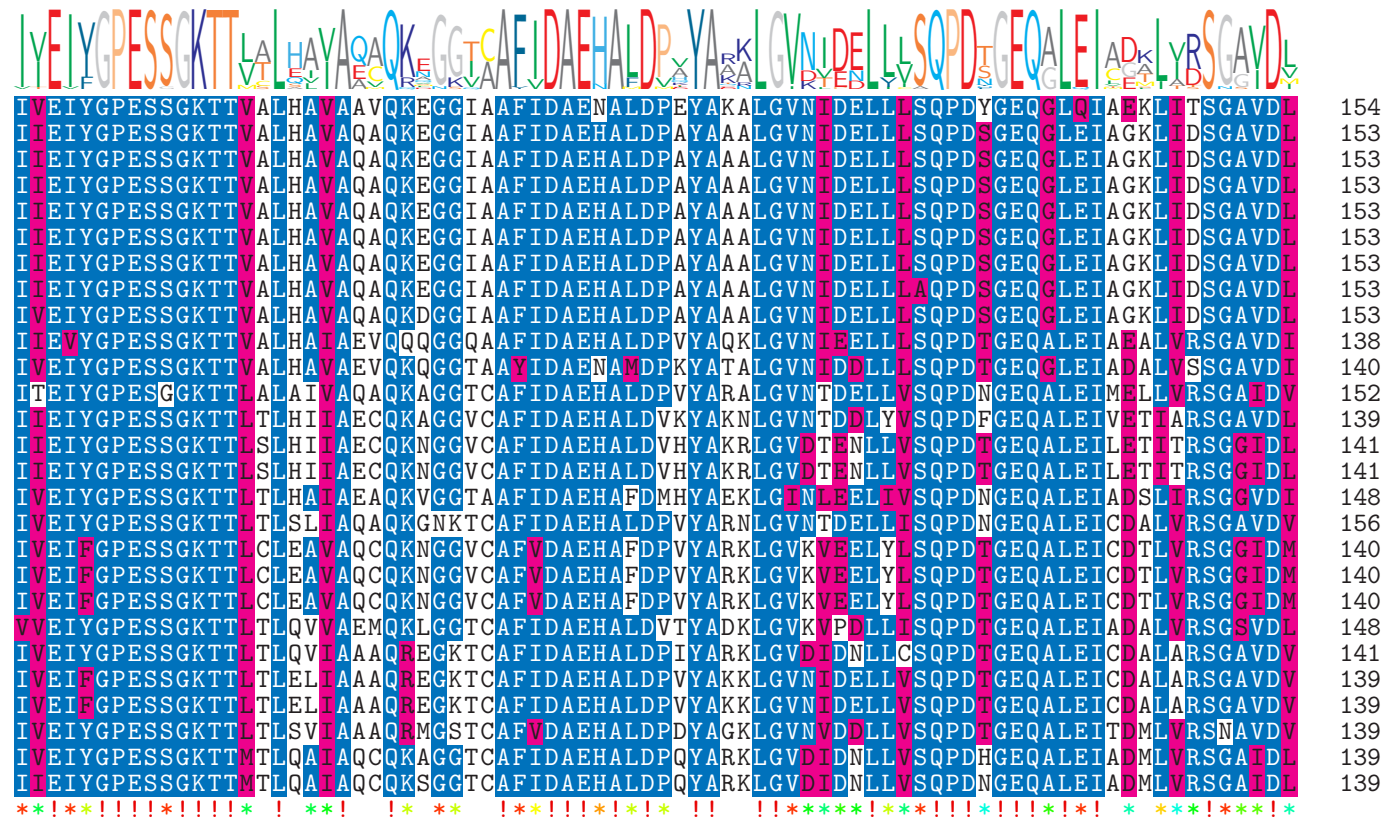
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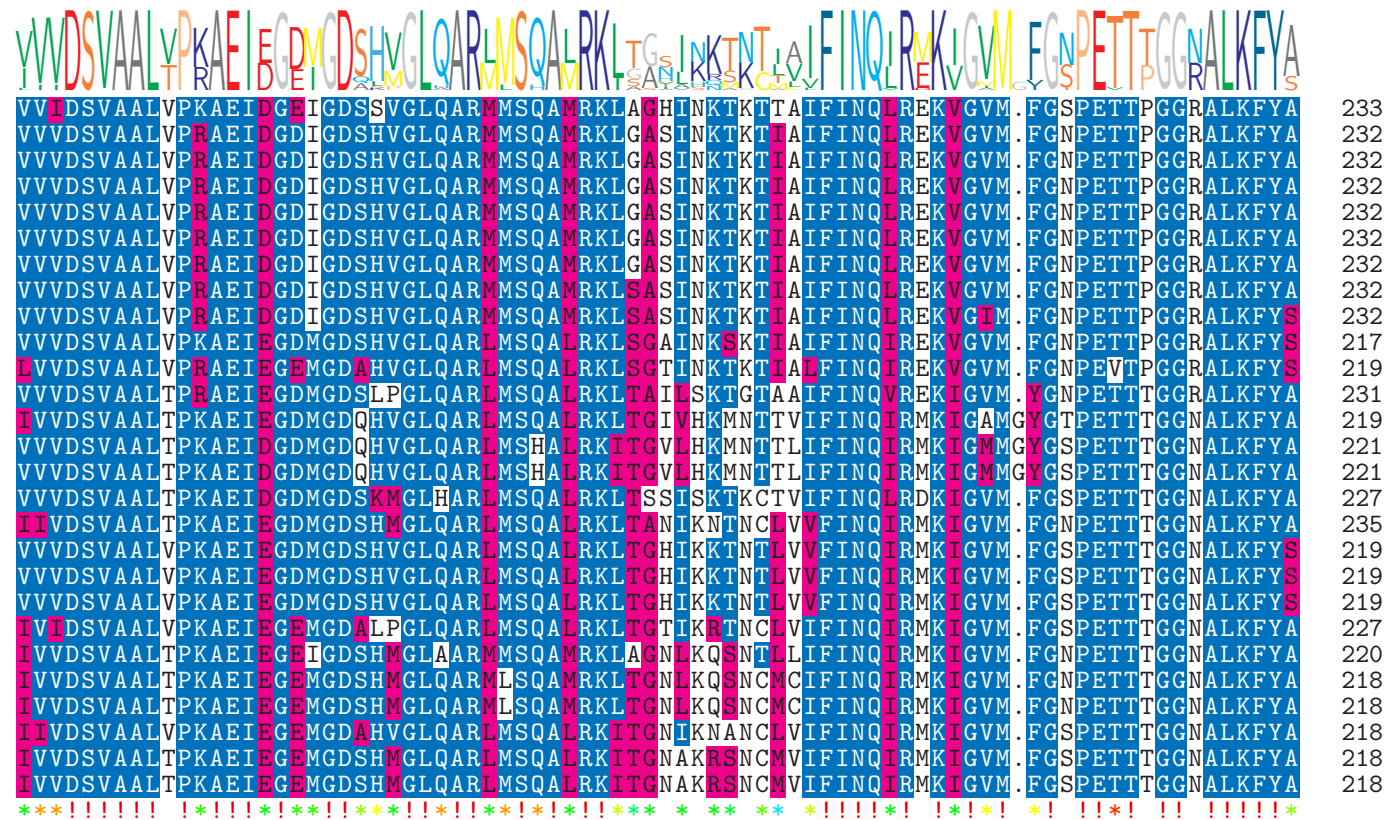
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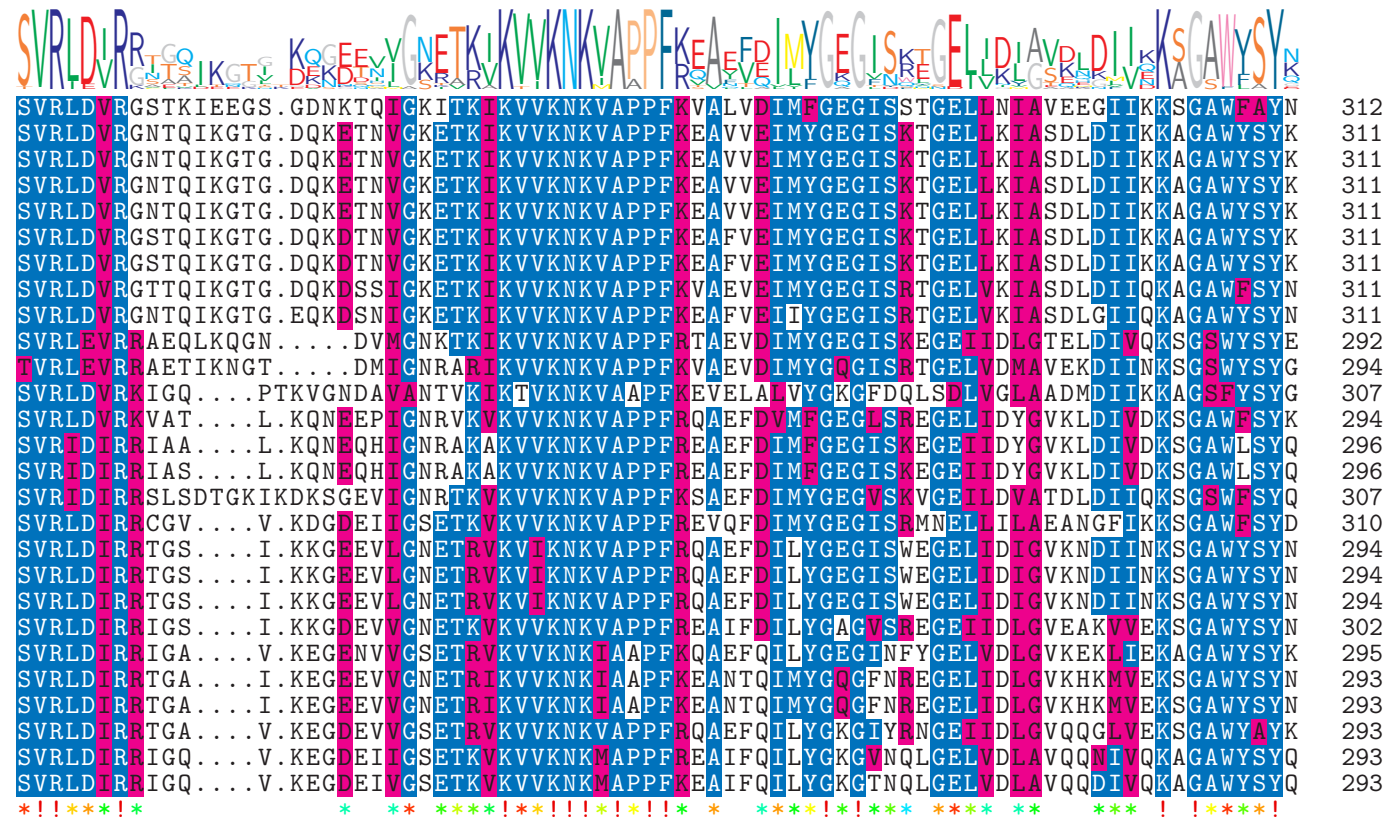
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ QV ⁺ RSK ⁺ FLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ QV ⁺ RSK ⁺ FLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ QV ⁺ RSK ⁺ FLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEE ⁺ AA ⁺ .VNEEVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ DE ⁺ DH ⁺ QV ⁺ RV ⁺ QF ⁺ FLIDGEEIAES ⁺KKDE ⁺AAQV ⁺ DS ⁺ .VNEEVTLDLGDELEIE ⁺	381
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GEKIGGGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ IDH ⁺ KV ⁺ RV ⁺ QY ⁺ GLIEEDNTEEKQSSKEK ⁺ETD ⁺ E ⁺ K ⁺ .ADKNLVLELDDTIELE ⁺	382
EE ⁺ RL ⁺ LGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL ⁺ .EFE ⁺ .E ⁺	348
SERIGGGR ⁺ EN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ VRAAY ⁺ GISDVPEEDLPTTEDE ⁺ .QI ⁺ .NILPDDST ⁺EE ⁺	355
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DKKL ⁺ GGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEIA ⁺ DEIT ⁺ KAT ⁺ QNSM ⁺ TEGM ⁺ISGSEDD ⁺ EG ⁺EE ⁺	343
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADEIT ⁺ TLK ⁺ IKES ⁺ GSNEE ⁺IMPLPDEPL ⁺EEME ⁺	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADEIT ⁺ TLK ⁺ IKES ⁺ GSNEE ⁺IMPLPDEPL ⁺EEME ⁺	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK ⁺	343
GTKIGQGK ⁺ NNAV ⁺ KWL ⁺ KEN ⁺ PEIA ⁺ ADKLE ⁺ QEI ⁺ RNTL ⁺ ASNP ⁺ N....SVLKATASDSN ⁺ ...DES ⁺ DVEEFSEEL ⁺	372
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMH ⁺ITEG ⁺T ⁺ ...QDET ⁺ DGERPEE ⁺	348
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMH ⁺ITEG ⁺T ⁺ ...QDET ⁺ DGERPEE ⁺	348
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMH ⁺ITEG ⁺T ⁺ ...QDET ⁺ DGERPEE ⁺	348
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GNKIGQGK ⁺ NNVIR ⁺ YLEEN ⁺ PEI ⁺ QISTE ⁺ IE ⁺ AVI ⁺ REQLLT ⁺ TKAS ⁺DQTAA ⁺ .HDETE ⁺ ...EED ⁺ LLLES ⁺	349
GNKIGGQK ⁺ NNVIR ⁺ YLEEN ⁺ PEI ⁺ QIAE ⁺ IE ⁺ ERN ⁺ IREQLLTGT ⁺NGAVQ ⁺ .I ⁺ .EDE ⁺ ...EED ⁺ LLLES ⁺	349

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved