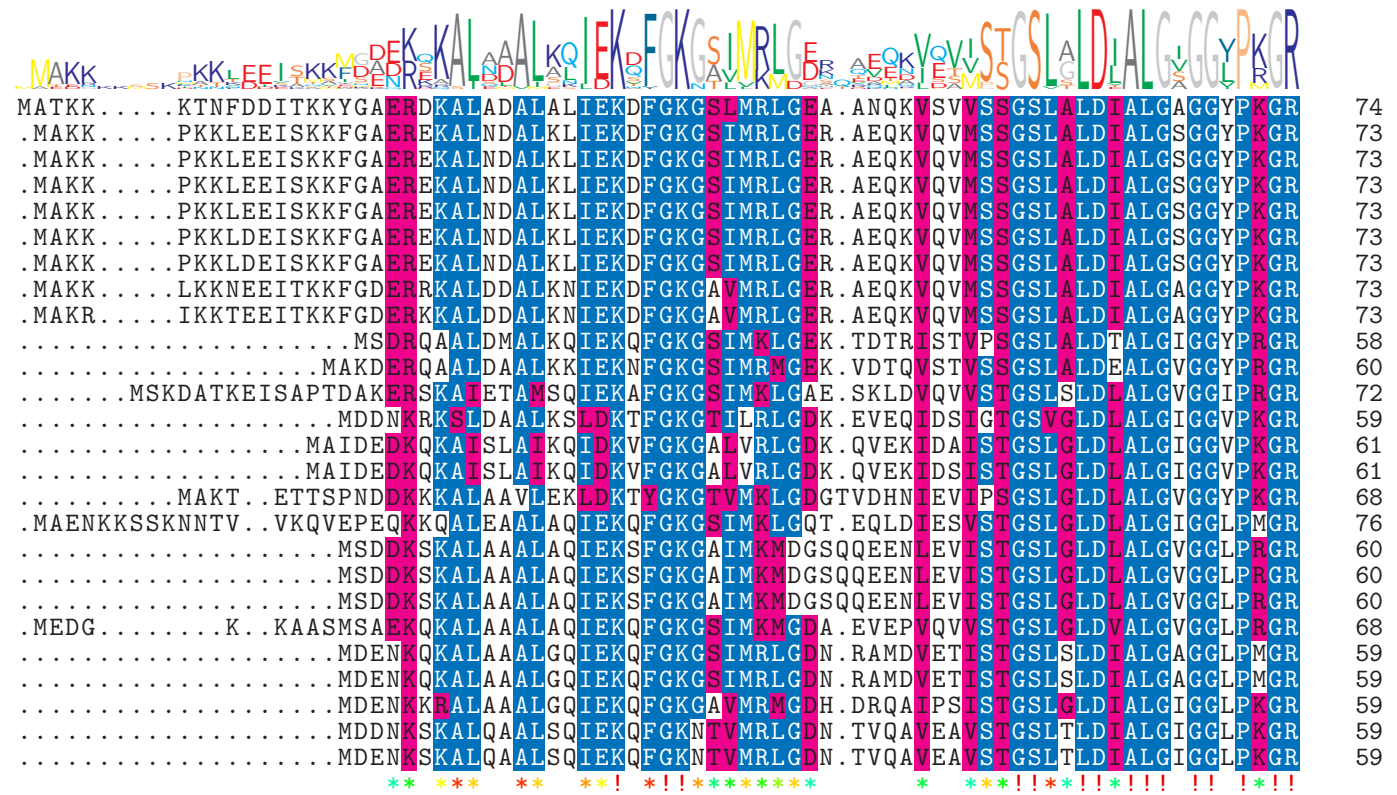


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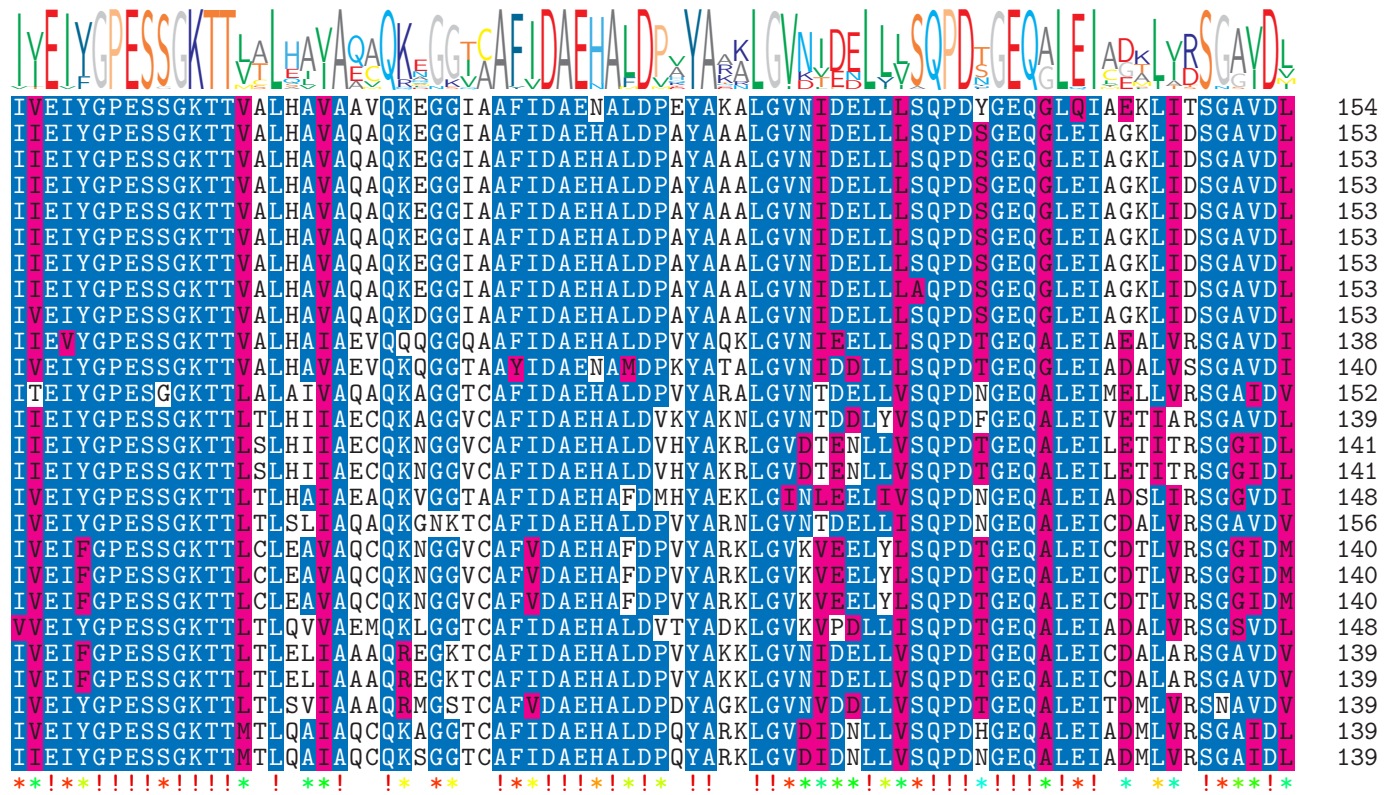
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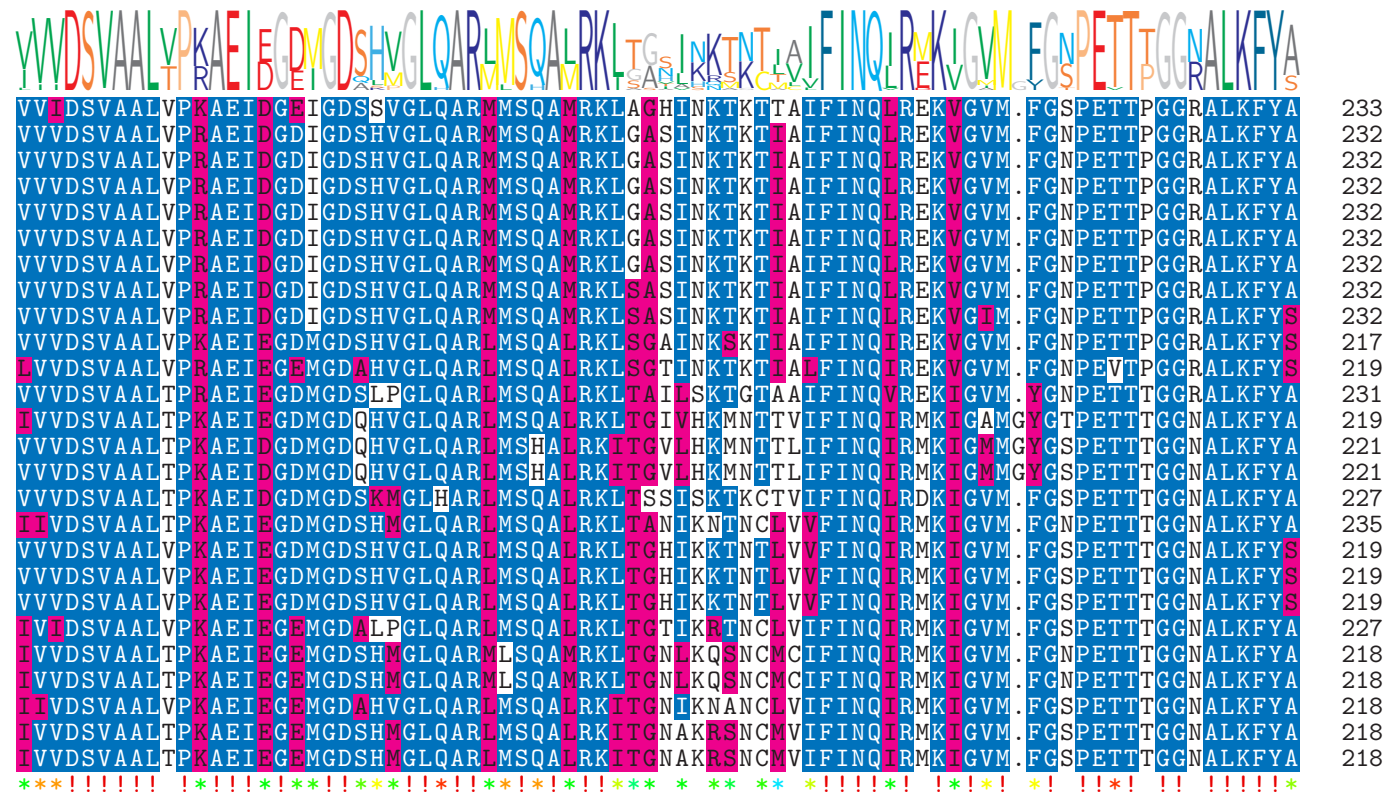
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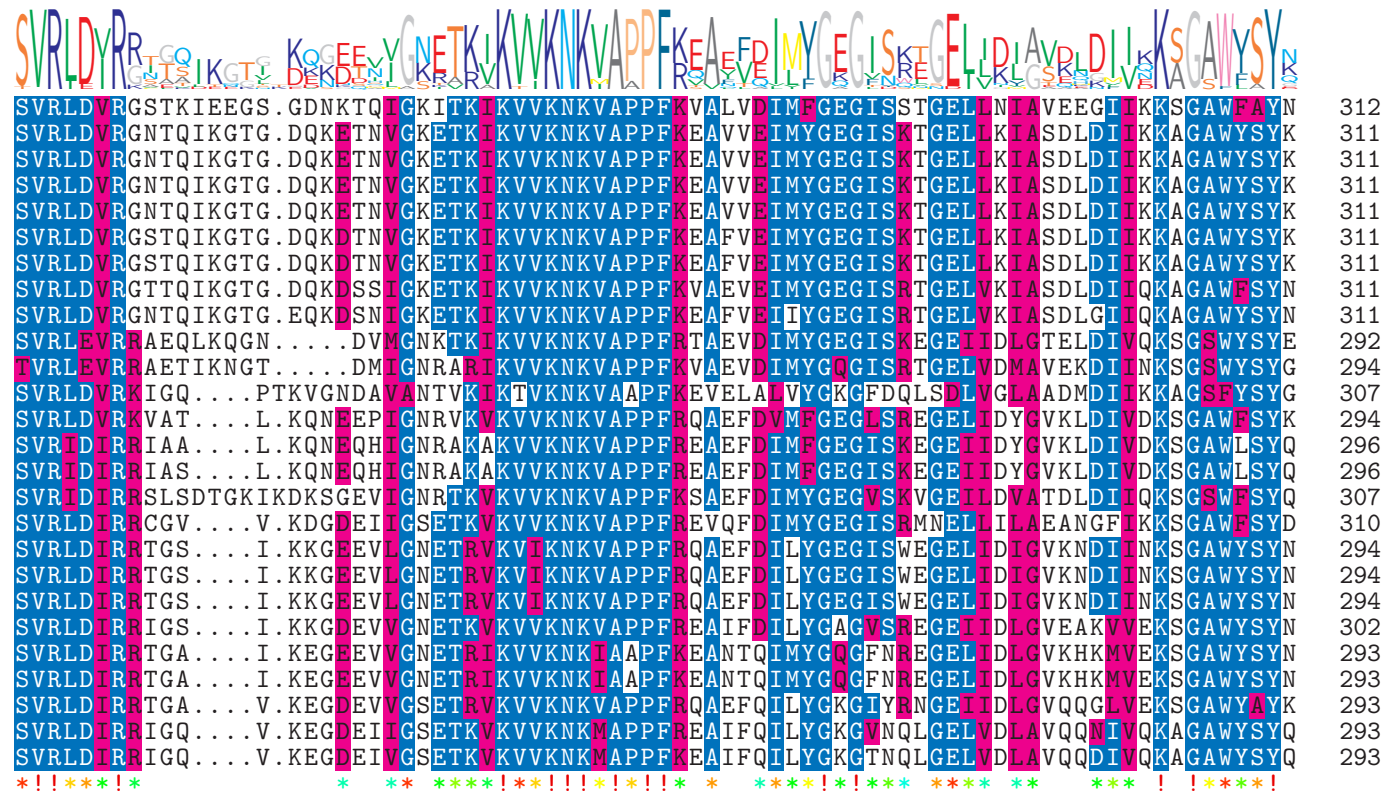
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ ID ⁺ QK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ ID ⁺ QK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DE ⁺ ID ⁺ QK ⁺ VR ⁺ SKF ⁺ GLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ VF ⁺ AE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQF ⁺ GLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ FDE ⁺ ID ⁺ RV ⁺ VR ⁺ VKF ⁺ GLIDEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQY ⁺ CLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EER ⁺ LGGGREN ⁺ AK ⁺ FLKEN ⁺ KD ⁺ IMLM ⁺ IQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SER ⁺ IGGGREN ⁺ AK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DEV ⁺ LR ⁺ KV ⁺ RAAY ⁺ GISDVPEEDLPTTEDE.QI.NILP ⁺ DST.....EE.....	355
DER ⁺ IGGQKEKT ⁺ IAY ⁺ I ⁺ AE ⁺ RP ⁺ EME ⁺ Q ⁺ EIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE...A.....	363
DKKLGGGREN ⁺ SKA ⁺ FLKEN ⁺ PEI ⁺ ADE ⁺ IT ⁺ KAI ⁺ QNSM ⁺ GTIEGMI....SGSEDDE..GE..E.....	343
DKKLGGGREN ⁺ AK ⁺ ALLKED ⁺ KALADE ⁺ IT ⁺ LK ⁺ IKES ⁺ IGSNEEI....MPLPDEP..LE..EME.....	347
DKKLGGGREN ⁺ AK ⁺ ALLKED ⁺ KALADE ⁺ IT ⁺ LK ⁺ IKES ⁺ IGSNEEI....MPLPDEP..LE..EME.....	347
DTKLGGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IKD ⁺ NPE ⁺ LAEE ⁺ LEAK ⁺ IREKLQAK.....	343
GTKIGGGKNN ⁺ AVK ⁺ WLKEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IRNTLASNPNS....VLKATASDSND..ESDVVEEFSEEEEL.....	372
GAKIGGGKDN ⁺ VR ⁺ VWLKEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GAKIGGGKDN ⁺ VR ⁺ VWLKEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GAKIGGGKDN ⁺ VR ⁺ VWLKEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGT.....Q..DET ⁺ DGERPEE.....	348
GER ⁺ IGQGRDNC ⁺ REFL ⁺ RNAEL ⁺ LARE ⁺ EN ⁺ KVR ⁺ EHLC ⁺ VTPMG....AV.TLAEVEVE..D.....	352
GDKIGGGKAN ⁺ ACKYLKEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGGGKAN ⁺ ACKYLKEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGGGKAN ⁺ AAKYLEEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ RAKL ⁺ YTSAN....TKATPVAEDLA..DADI.....	347
GNKIGGGKNN ⁺ VIRYLEEN ⁺ PEI ⁺ ISTE ⁺ IEA ⁺ VIRE ⁺ QLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGGGKNN ⁺ VIRYFEEN ⁺ PEI ⁺ AE ⁺ IE ⁺ ERN ⁺ IRE ⁺ QLLTTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

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NTDB id 408 SMU RS09530 WP 002262392.1	D..	383
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved