

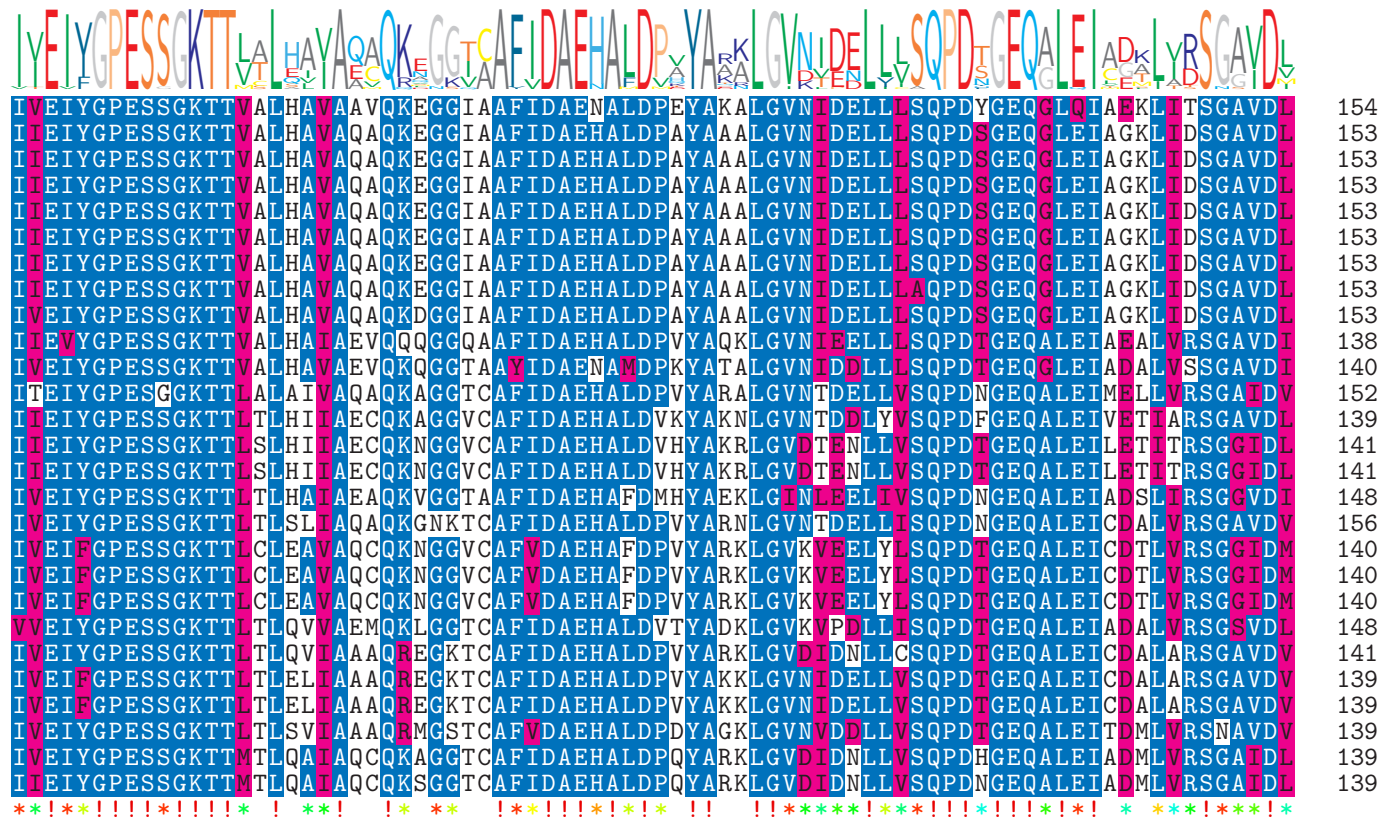
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consensus	***	***	*	***!	***!	*****	*	***!!*!!*!!*!!*!!*!!	*	***!!*!!*!!*!!*!!	!!	!!	!!	!!	!!	!!		

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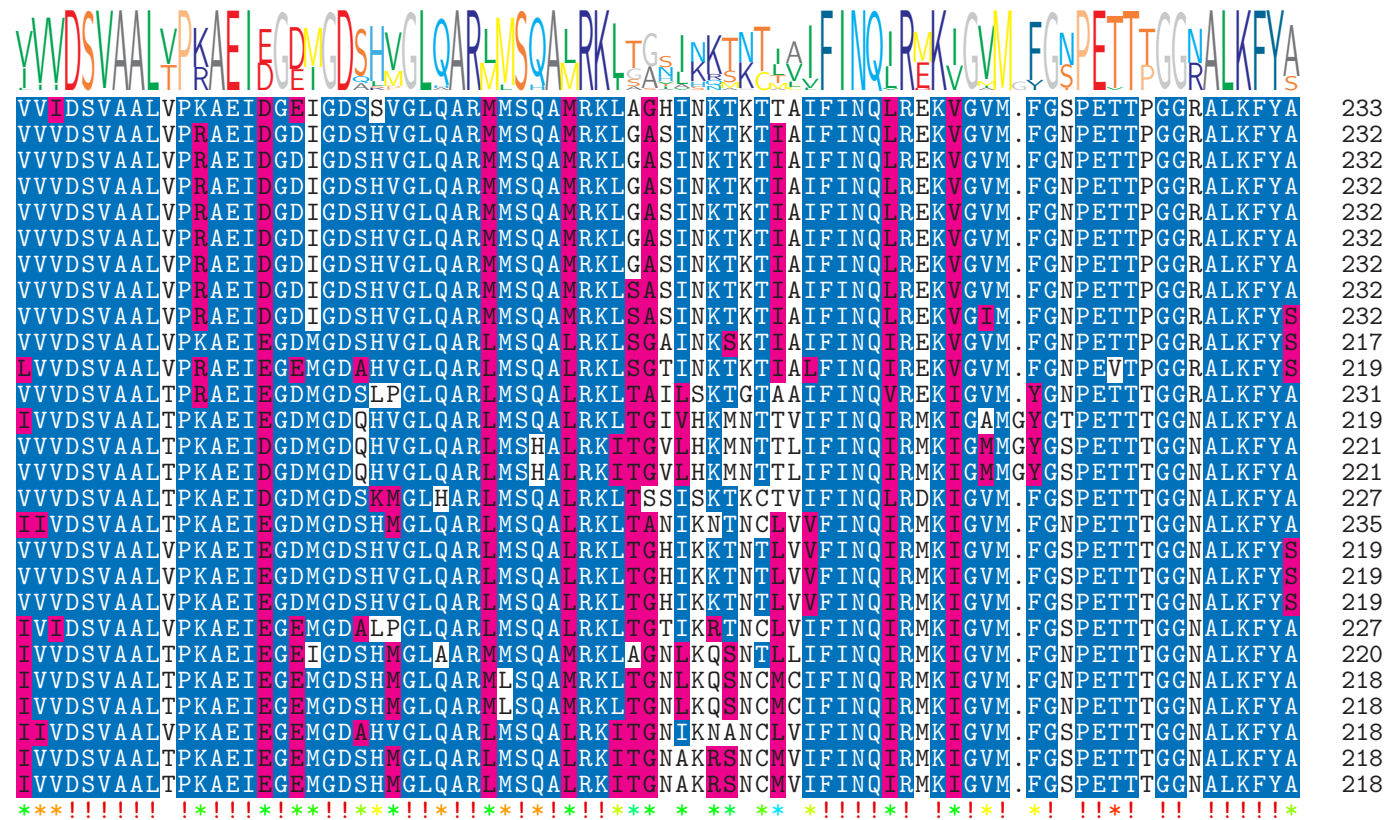
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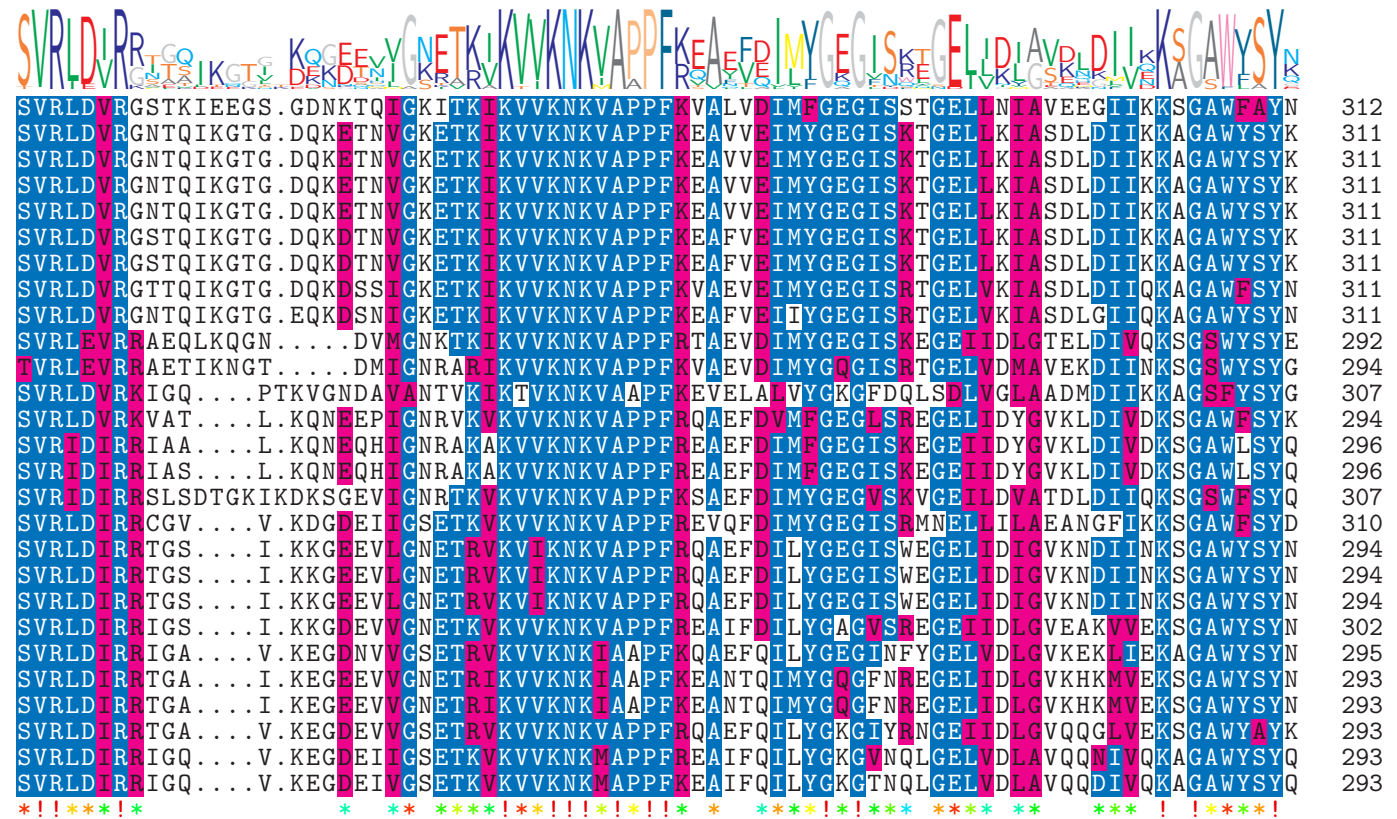
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDH ⁺ QV ⁺ RVQF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGGGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ IFDE ⁺ IDR ⁺ KV ⁺ VKF ⁺ CLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGGGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IFDD ⁺ IDHK ⁺ V ⁺ RVQY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGGGS ⁺ REN ⁺ AK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ V ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQ ⁺ KEK ⁺ TIAY ⁺ IA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VMA ⁺ IRAGNAGEAPALAPAPAAPEAA...EA.....	363
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DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALAD ⁺ EITL ⁺ KIK ⁺ ESIG ⁺ SNEE....IMPLPDEPL....EE..ME	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGGQ ⁺ KNN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEIAD ⁺ KL ⁺ EQE ⁺ IRNTL ⁺ ASNPN....SVLKATASDSN...DESDVEEFSEEL.....	372
GAKIGGQ ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMH....ITEG.....T...QDET ⁺ DGERPEE	348
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GERIGGQ ⁺ RD ⁺ NCRE ⁺ FLREN ⁺ AE ⁺ LARE ⁺ IE ⁺ ENK ⁺ VREHL ⁺ GVTPM....GAVTLAE.EVE...ED	352
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GNKIGGQ ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PEI ⁺ QIAE ⁺ IE ⁺ ERN ⁺ IRE ⁺ QLLTGT....NGAVQ.I.EDE...EEPDLLES	349

logo

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consensus

 non conserved
 similar
 ≥ 50% conserved