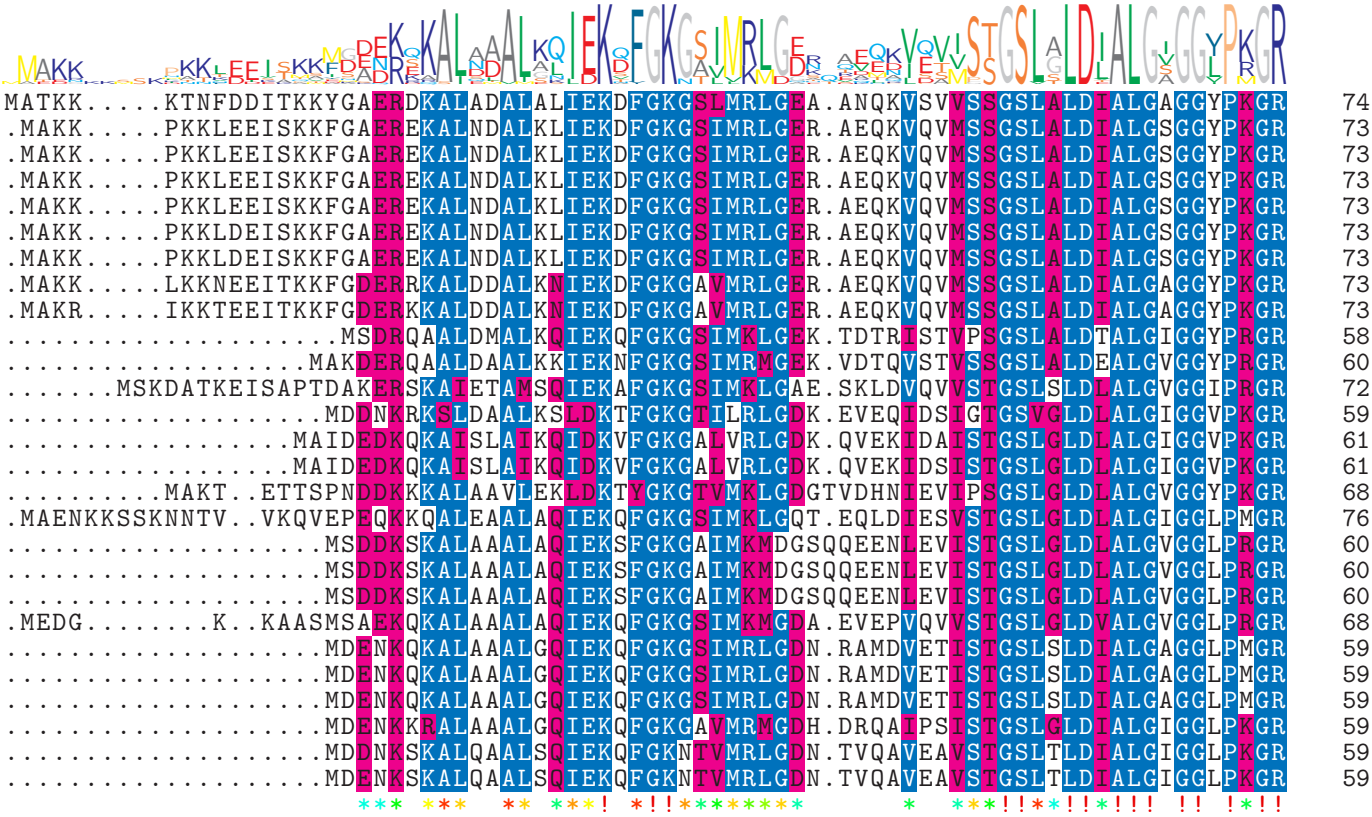


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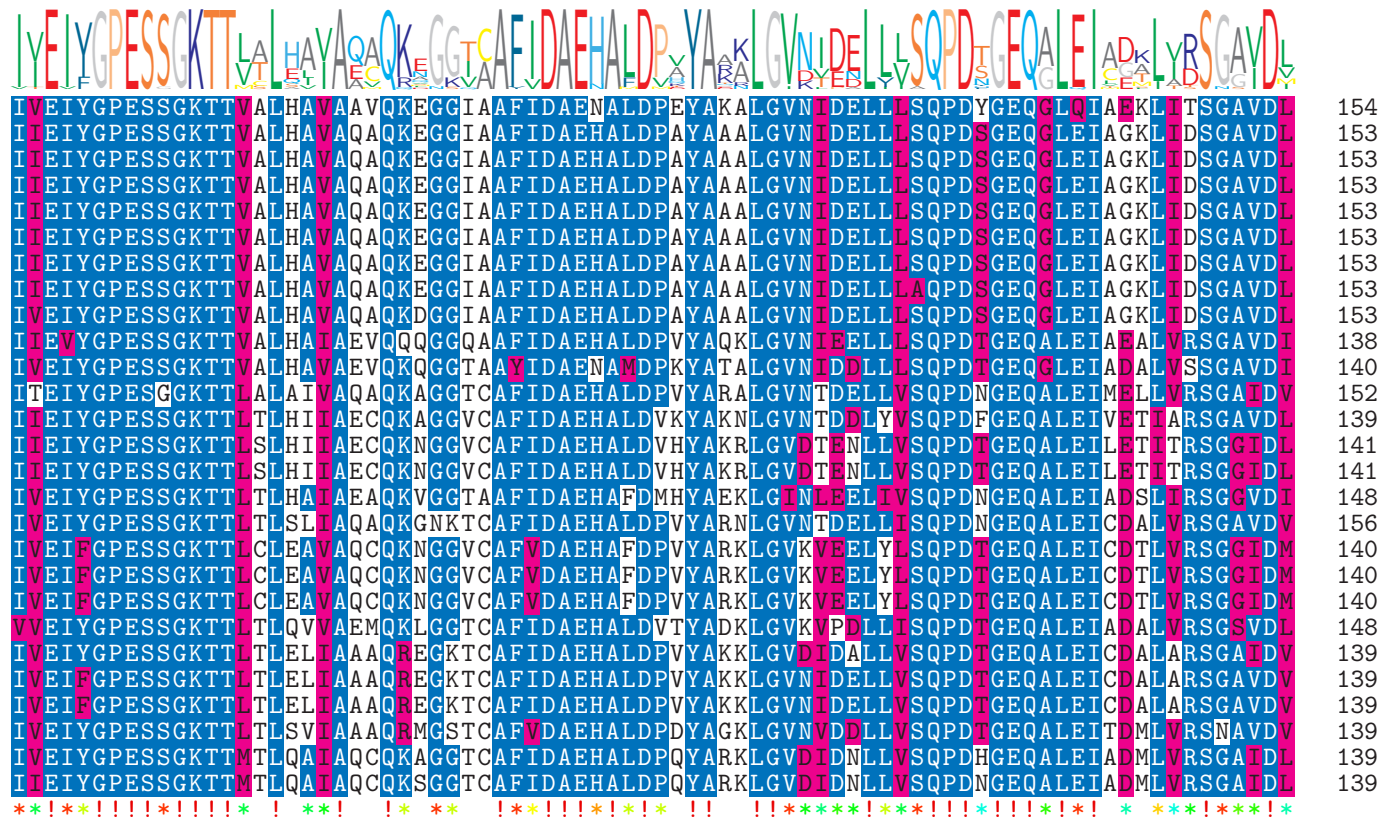
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consensus

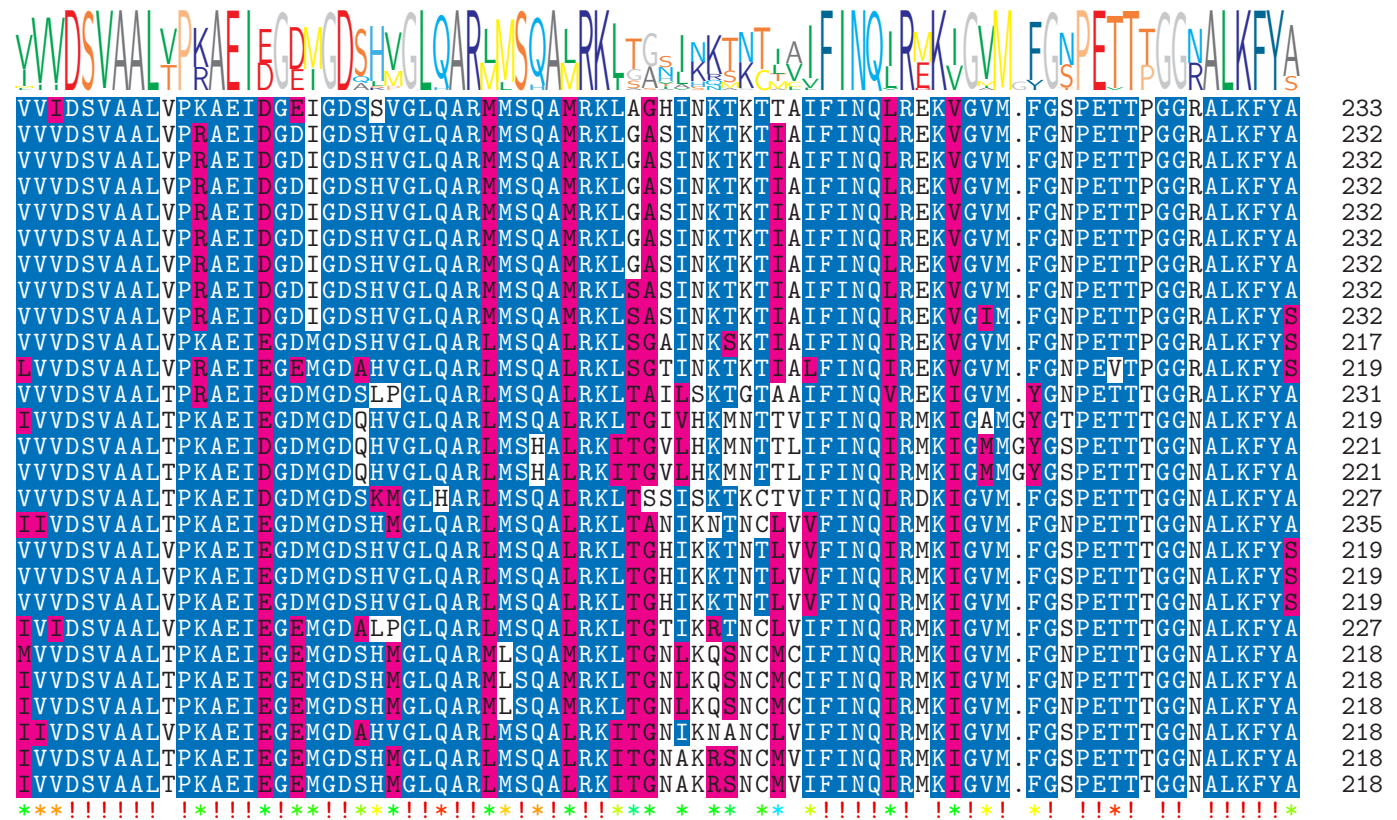
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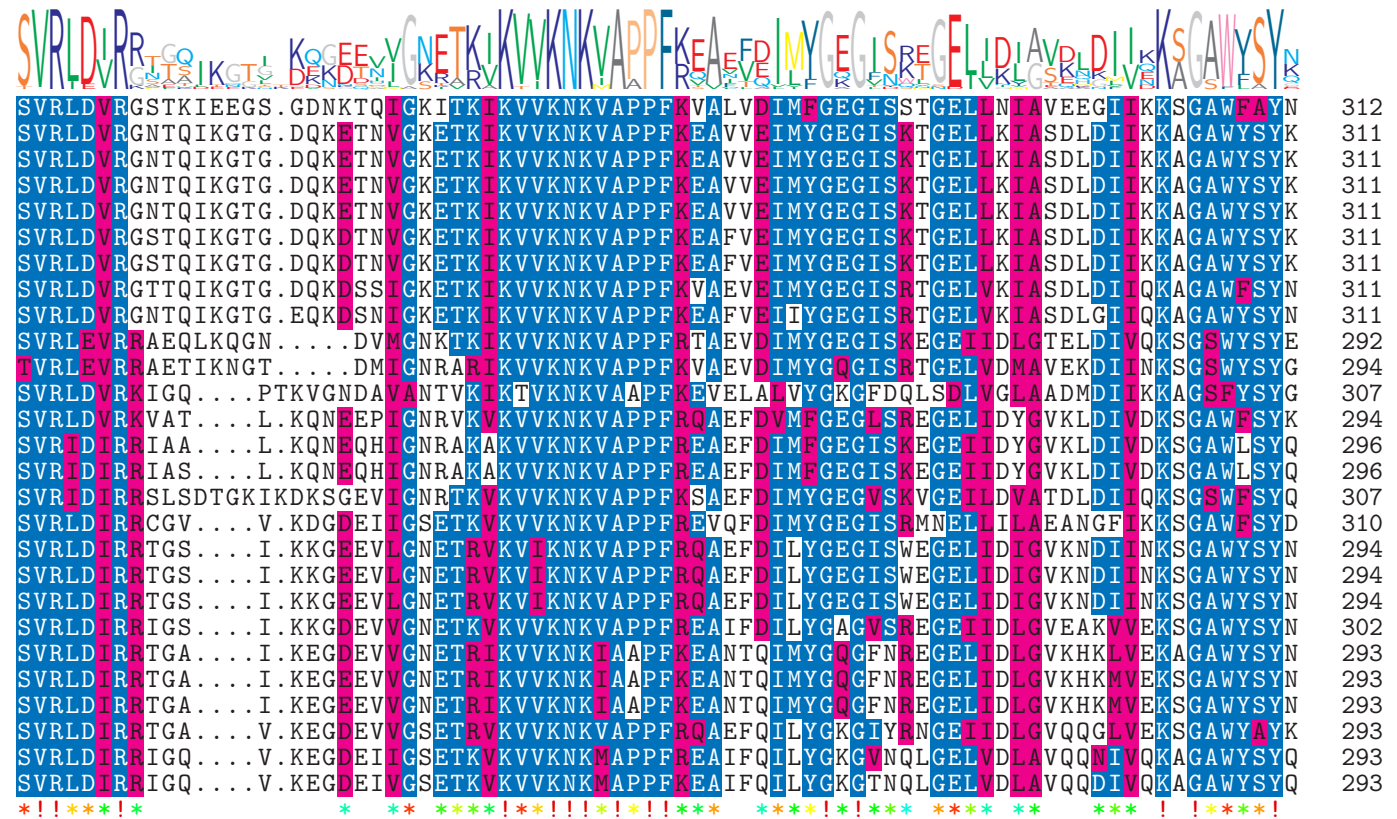
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consensus

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Sequence	Score
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DEKIGQGS EN AKKYLA ADNP EIFD ED DHQRVVFQ CL IDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS EN AKKYLA ADNP EVFA ED DHQRVVFQ CL IDGEEAAS....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS EN AKRYLADHP QL FD ED DRKRVVKF CL LEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGQGS EN AKKFLADNP EIFD DD ED DHKRVVQY CL IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE RL LGQGR EN AKQFLKEN KD IMLMIQEQIREHY CL DNNGVVQQQA ET QEEL.EFE.E.....	348
SERIGQGR EN AKNYLADHED VE EVRLKVR AA Y CT SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAYIA ERP EME QET IRDRVAA SN IRAGNAGEAPALAPAAPEAAEA.....	363
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DKKLGGGREN AK ALLKEDKALADEITLKIKESIGSNEEIM....PLPD.....EPLLEE..ME.....	347
DKKLGGGREN AK ALLKEDKALADEITLKIKESIGSNEEIM....PLPD.....EPLLEE..ME.....	347
DTKLGGGRD TV KELIKDN PE LAE ELE AKIREKLQAK.....	343
GAKIGQGGK NN AVKWLKEN PE IA DK LEQ IR N TL ASNPNSV....LKATASDSNDES D VEE..FSEEEEL.....	372
GDKIGQGGK DN RVVWLKEN PE IS DE IDA KTR ALN GV EMHIT....E.....GTQDET D GE..RPEE.....	348
GAKIGQGGK DN RVVWLKEN PE IS DE IDA KTR ALN GV EMHIT....E.....GTQDET D GE..RPEE.....	348
GAKIGQGGK DN RVVWLKEN PE IS DE IDA KTR ALN GV EMHIT....E.....GTQDET D GE..RPEE.....	348
GERIGGGRD NC REFLRENA EL ARE EN KVREHL GV TPMGA....VTL.AEEVEED.....	352
GDKIGQGGK ANA CNYLREH PE IA KT ID TKL REMLLS PA QPE....APAAGEKPEQE EE F.....	347
GDKIGQGGK ANA CKYLKEN PE IA KT LD KKL REMLLN PN EMQ....LIAETSSAADD V EFGA..VPEEF.....	354
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GSKIGQGGK ANA AKYLEEN PE IGQ EIE QQIRAK LL YTSANT....KATPVAEDLADADI.....	347
GNKIGQGGK NN VIRYLEEN PQ ISTE IE IAVIREQLLT KA SDQ....TAA.HDETEEE P DL...LES.....	349
GNKIGQGGK NN VIRYLEEN PQ IAE IE IRNIREQLLT GT NG....AVQ.I.EDEEE P DL...LLES.....	349

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349

consensus

 non conserved
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 ≥ 50% conserved