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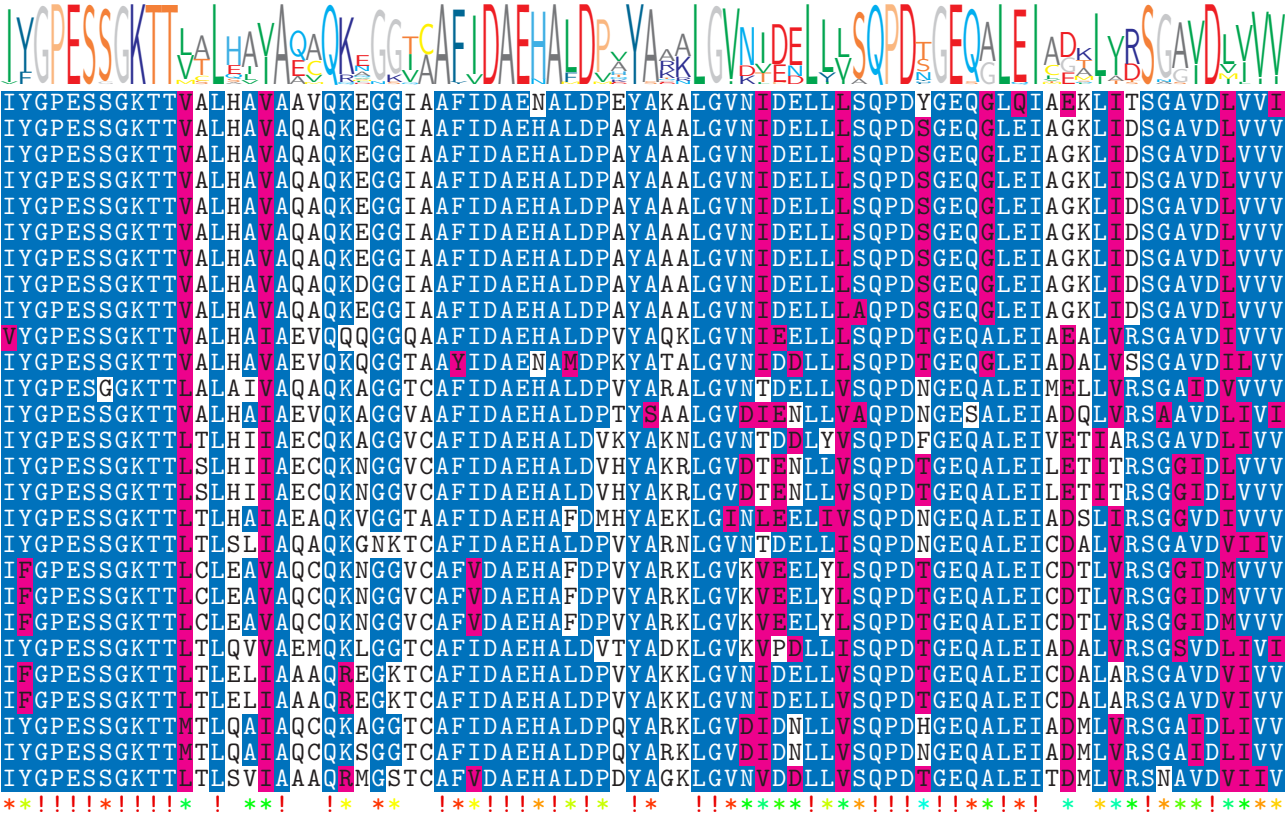
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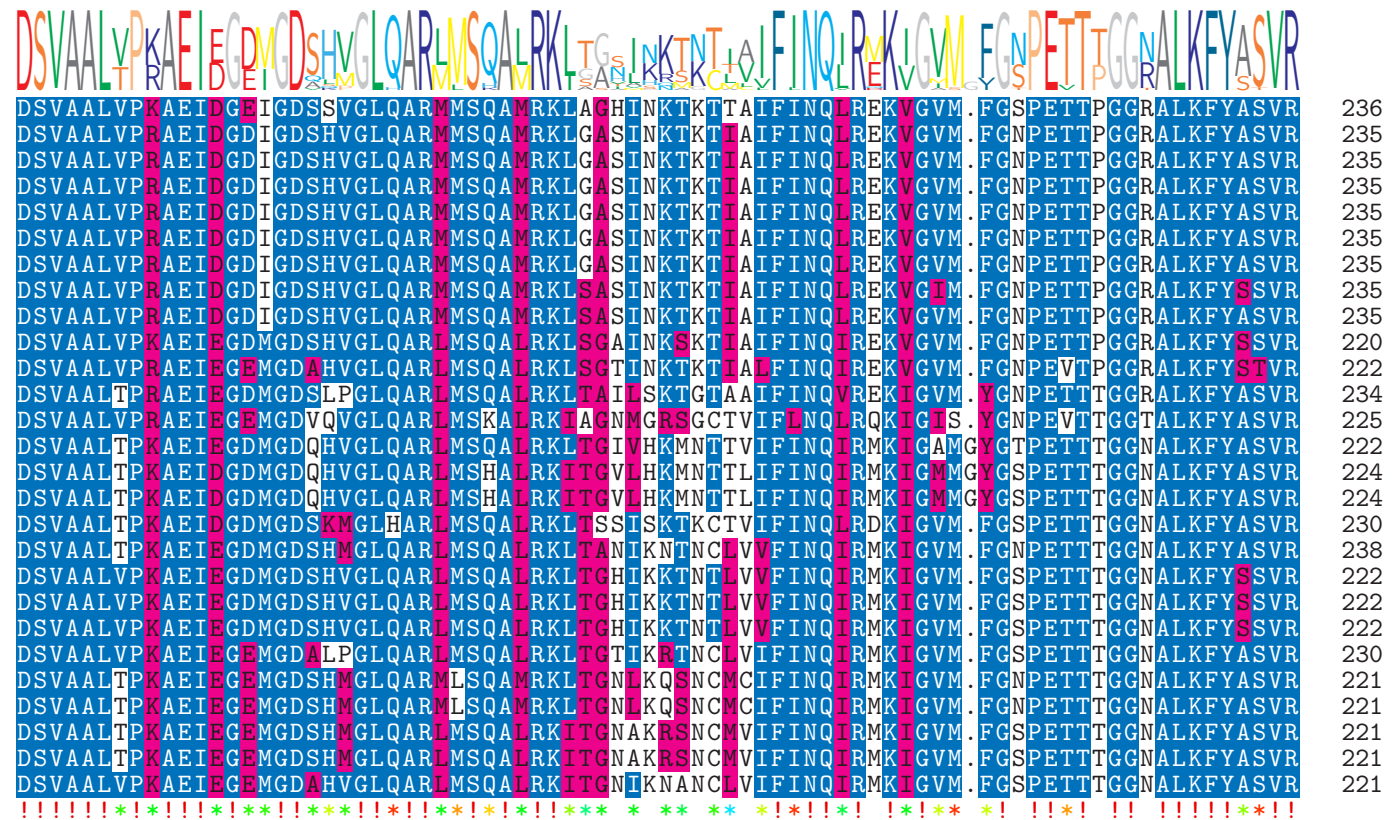


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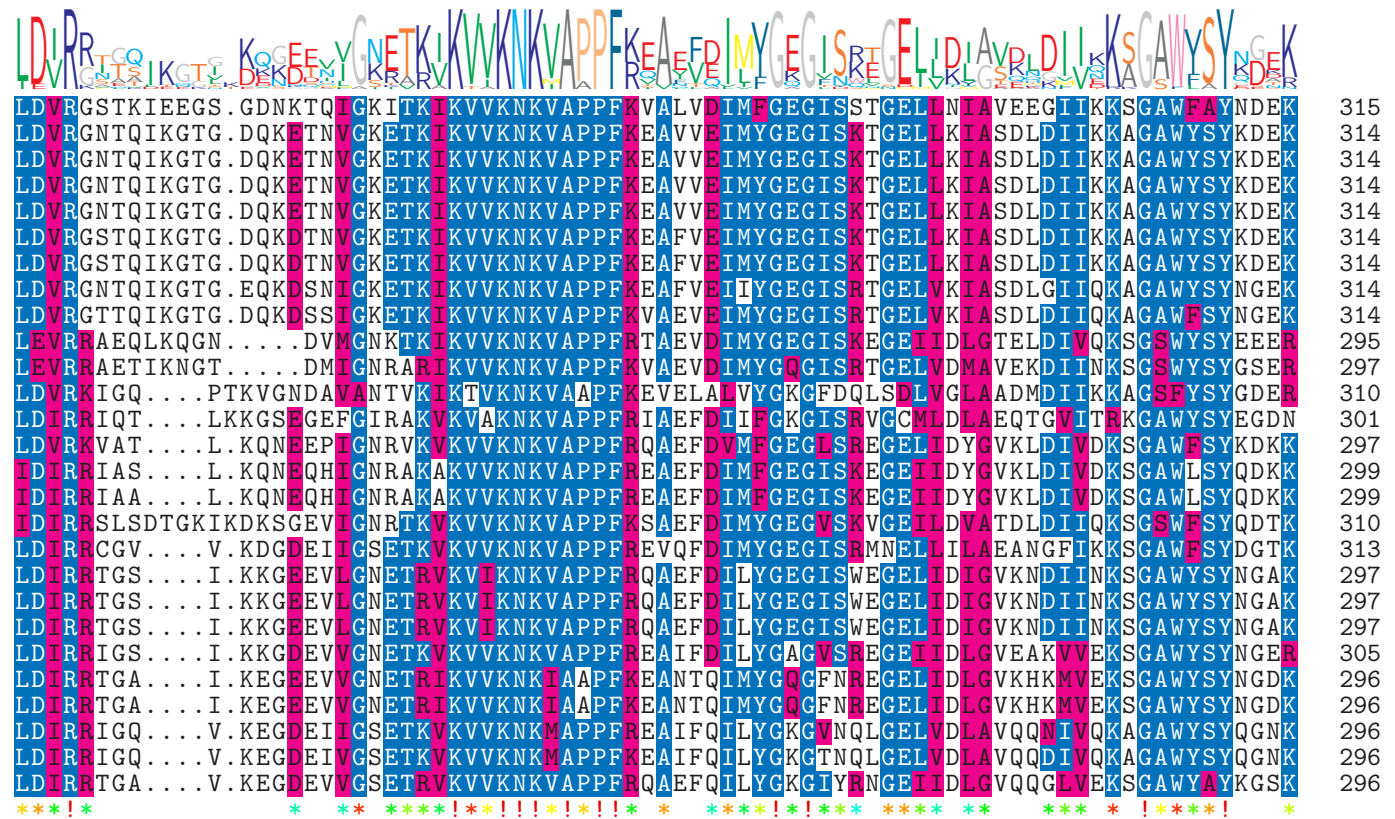
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Sequence	Score
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IGGGS EN AKKYLA EH PEIF DE IDKQVRSKFG L IDGEEVSEQDTENKK. DEPKKEEA..VNEEVPLDLGDELEIEIE	387
IGGGS EN AKKYLA EH PEIF DE IDKQVRSKFG L IDGEEVSEQDTENKK. DEPKKEEA..VNEEVPLDLGDELEIEIE	387
IGGGS EN AKKYLA EH PEIF DE IDKQVRSKFG L IDGEEVSEQDTENKK. DEPKKEEA..VNEEVPLDLGDELEIEIE	387
IGGGS EN AKKYLA DN PEVFAEID H QVVRVQFGL L IDGEEAAE....SKK. DEVAQVDS..VNEEVTLDLGDELEIEIE	383
IGGGS EN AKKYLA DN PEIF DE IDHQRVVRVQFGL L IDGEEIAE....SKK. DEAAQVDS..VNEEVTLDLGDELEIEIE	383
IGGGS EN AKKFLA DN PEIF DD IDHKVRVQYGL L IEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED.	383
IGGGS EN AKRYLA DHP QLF DE IDRKVRVKFGL L EESEEEESAMAVASE.....E.....TDDLALDLDNNGIEIED.	378
LGQGR EN AKQFL KEN KD IM LMIQEQIREHYGL DN NGVVQQQAEETQE. EL .EFE.E.....	348
IGQGR EN AKNYLA DH EDVE DE VLRLKVR AA YGL IS DVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
IGCGK E KTIAYIA ER PEMEQEI IR DRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
IAQGR DN AVKYLE EN PDVA AI VTQKVRENLD M SSMGFGDEHH..TTEE.....	348
LGQGR EN SKAFL KEN PEIA DE ITKAIQNSMG L EGMISGSEDD...EGE.....	343
LGQGR EN AKALL KED KALADEITLKIKESIGSNEEIMPLPDE...PLEEME.....	347
LGQGR EN AKALL KED KALADEITLKIKESIGSNEEIMPLPDE...PLEEME.....	347
LGQGR DN TVKELIK DN PELA EE LAKIREKLQAK.....	343
IGGKK NN AVKWL KEN PEIA DK LEQEI RN TLASNPNSVLKATA..SDSN ES DVEE.....FSEEEL.....	372
IGGKK DN VVRVWL KEN PEIS DE IDAKIRALNGVEMHITEGTQD..ETDGER.....PEE.....	348
IGGKK DN VVRVWL KEN PEIS DE IDAKIRALNGVEMHITEGTQD..ETDGER.....PEE.....	348
IGGKK DN VVRVWL KEN PEIS DE IDAKIRALNGVEMHITEGTQD..ETDGER.....PEE.....	348
IGGGR DN CRFL RE LAELAREIENKVREHLGVTPMGAVTLA..EEVEED.....	352
IGGKKANACKY L KENPEIAKTLDKKLREMLLNPNMQLIAET..SSAADVEFGA.....VPEEF.....	354
IGGKKANACKY L KENPEIAKTLDKKLREMLLNPNMQLIAET..SSAADVEFGA.....VPEEF.....	354
IGGKK NN VIRYLE EN PQISTEIEAVIREQLLTKASDQTAA.H.DETE EP DLL.....ES.....	349
IGGKK NN VIRYFE EN NQIA E EIERNIREQLLTGTNGAVQ.I..EDE EP DLL.....LES.....	349
IGGKKANA AKY LE EN PEIGQEIEQQIRAKLLVTSANTKATPV..AEDLADADI.....	347

logo

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consensus

 non conserved
 similar
 ≥ 50% conserved