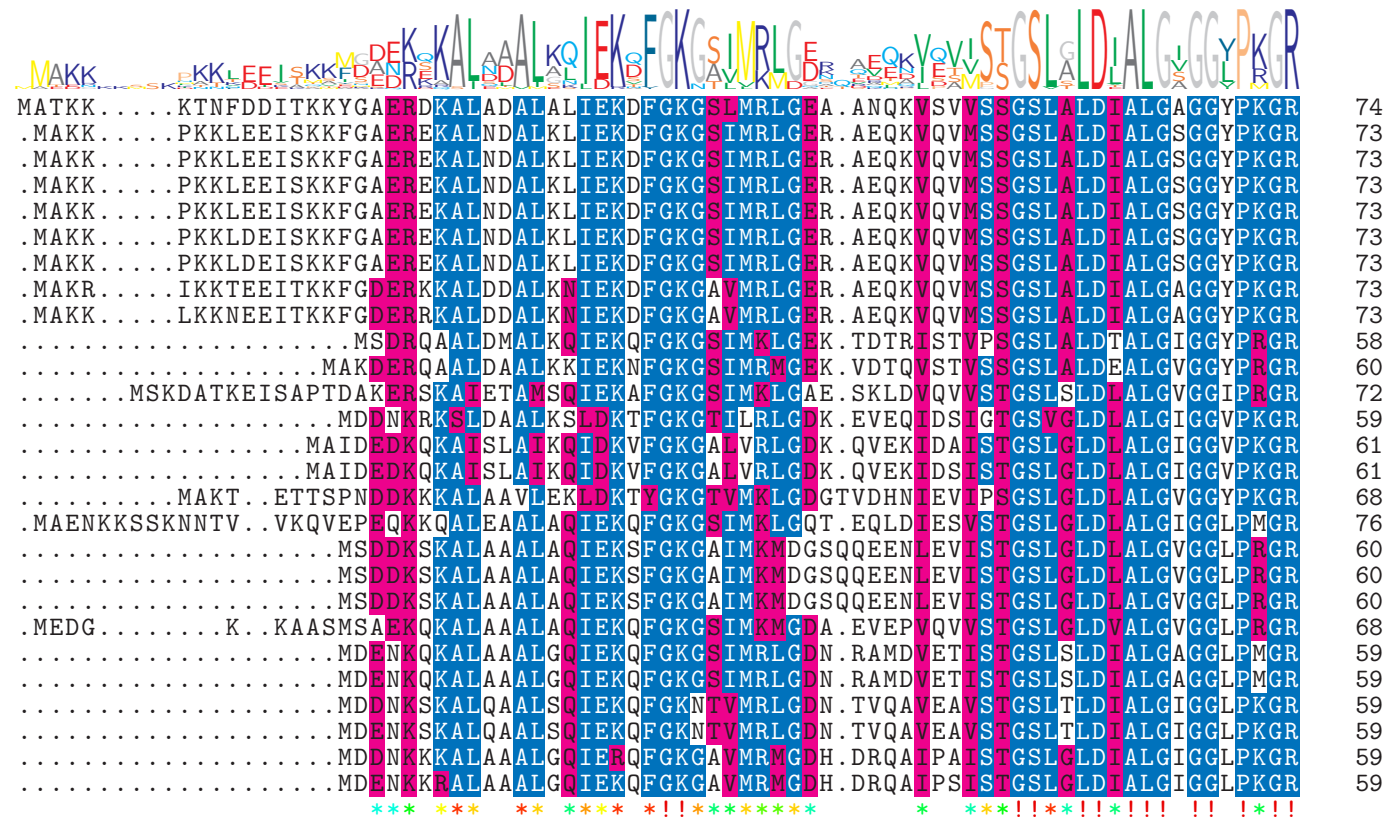


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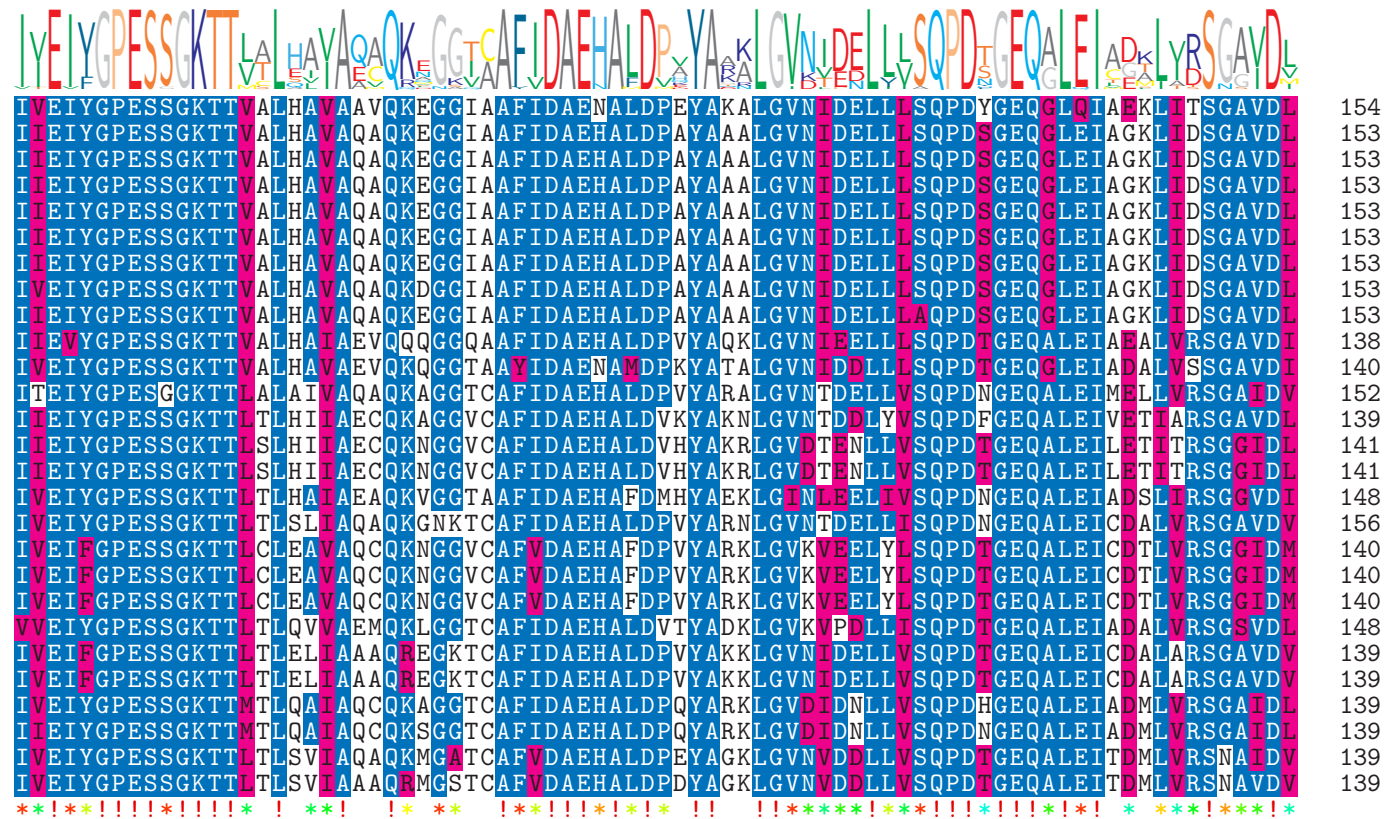
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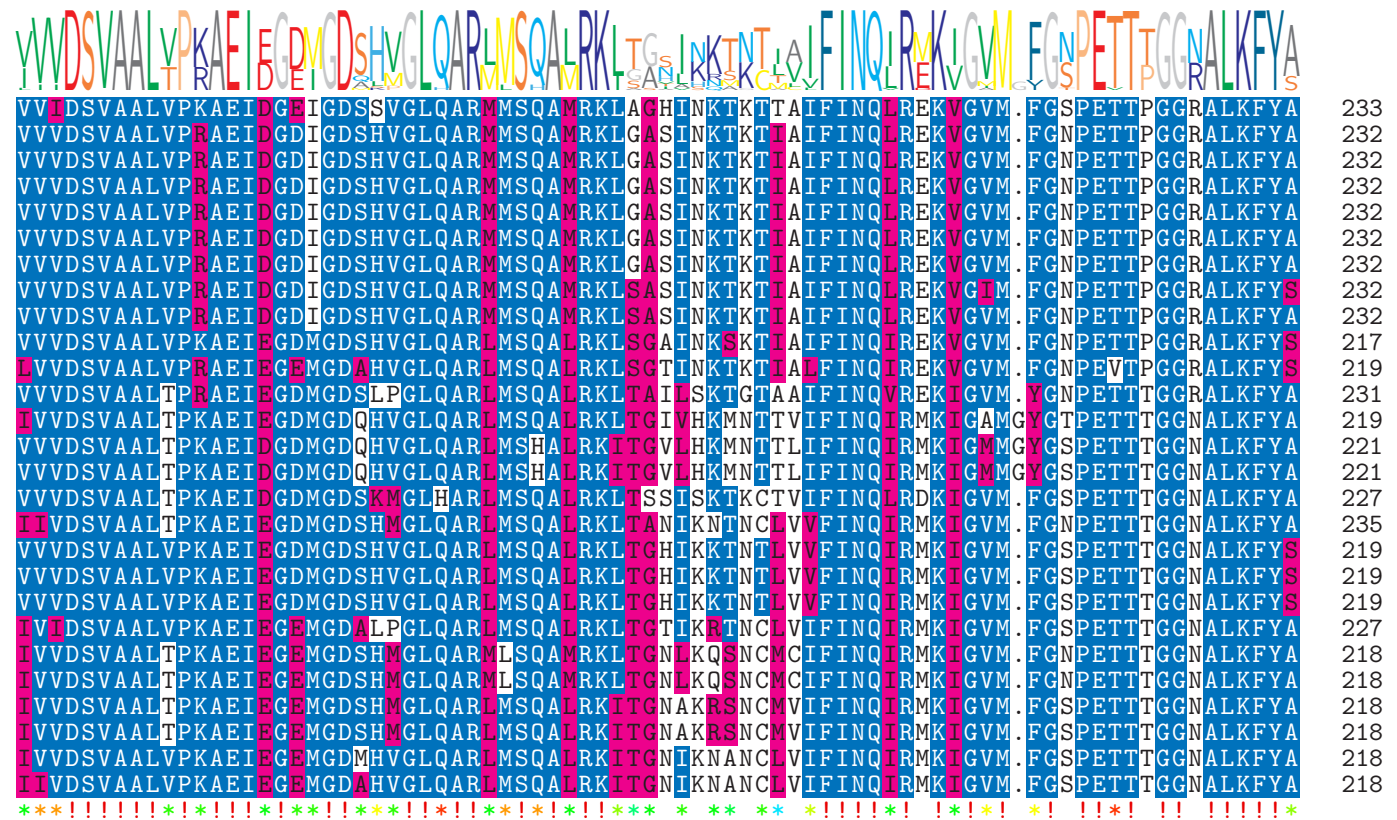
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consensus

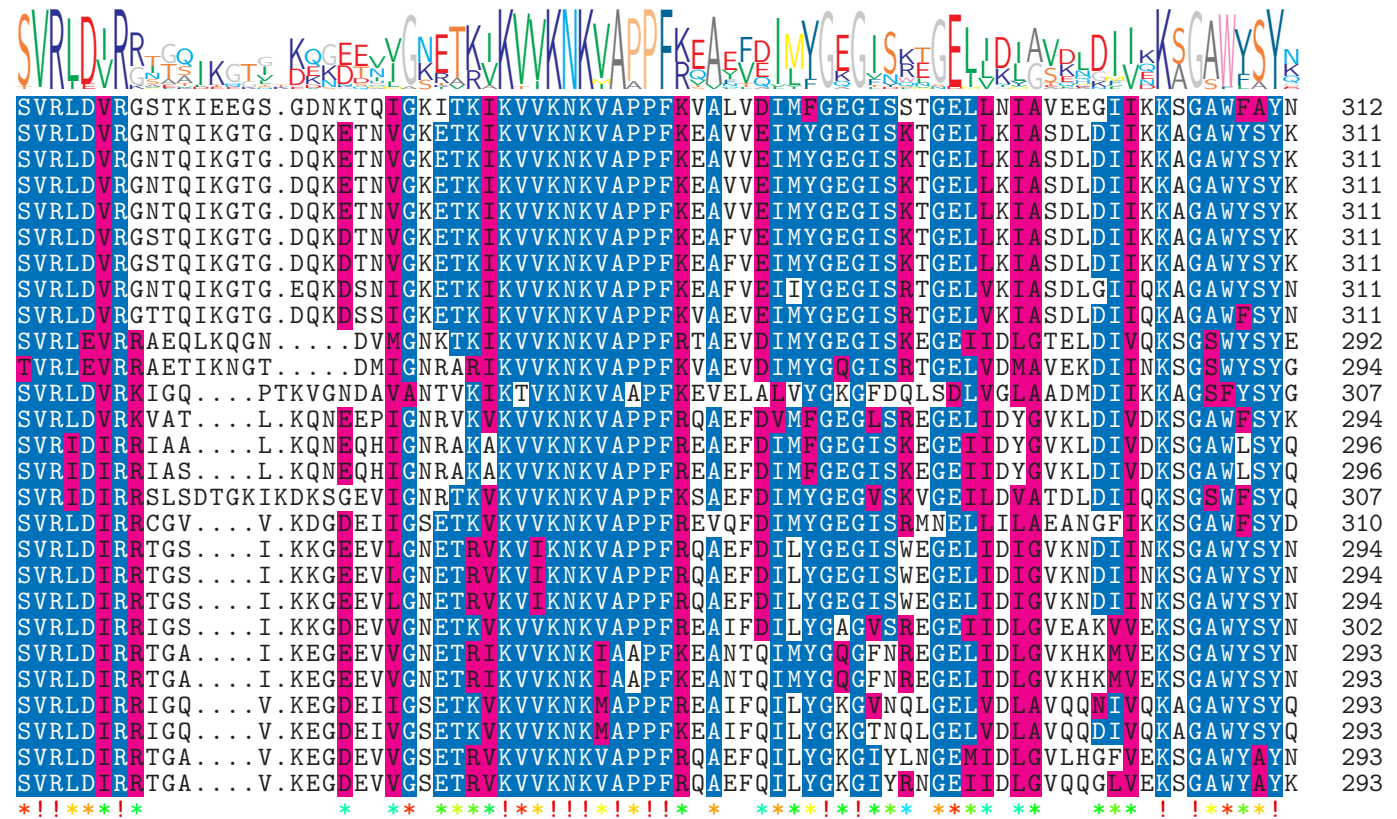
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consensus

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
DEKIGQGA ⁺ AKAKNYL ⁺ LKEHQ ⁺ DV ⁺ FDEID ⁺ HKV ⁺ RAAH ⁺ GL ⁺ LDSEVAETEEETTAS ⁺ KT ⁺ KAKAKKEEKAVET ⁺ E ⁺ EIELELED.....	387
DEKIGQGS ⁺ ENAKKYL ⁺ LAHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKD ⁺ E....PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAKKYL ⁺ LAHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKD ⁺ E....PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAKKYL ⁺ LAHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKD ⁺ E....PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAKKYL ⁺ ADNPEVFA ⁺ EID ⁺ HQV ⁺ RVQF ⁺ GL ⁺ IDGEEAAE...SKKD ⁺ E....VAQVDS...VNEEVTLDLGDELEIE	381
DEKIGQGS ⁺ ENAKKYL ⁺ ADNPEIF ⁺ DEID ⁺ HQV ⁺ RVQF ⁺ GL ⁺ IDGEEAAE...SKKD ⁺ E....AAQVDS...VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ ENAKKFL ⁺ ADNPEIF ⁺ DD ⁺ IDHKV ⁺ RVQF ⁺ GL ⁺ IEEDNTEEEKSSKEK.....ETDEK...ADKNLVLELDDDTIELE	382
GEKIGQGS ⁺ ENAKRYL ⁺ ADHPQLF ⁺ DEID ⁺ RKV ⁺ RVKF ⁺ GL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EE ⁺ RLGQGR ⁺ ENAKQFL ⁺ KENKDIMLMIQE ⁺ QIREHY ⁺ GLD ⁺ NNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAKNYL ⁺ ADHEDVE ⁺ DEV ⁺ RLKV ⁺ RAAY ⁺ GIS ⁺ SDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQG ⁺ KEKTIAY ⁺ IAERP ⁺ MEQE ⁺ IRDRV ⁺ MAAIRAGNAGEAPALAPAPAAP ⁺ E.....A.AEA.....	363
DKKLGGGREN ⁺ AKFL ⁺ KENPEIAD ⁺ EITKA ⁺ IQNSM ⁺ GIEGMISGSEDD...EGE...E.....	343
DKKLGGGREN ⁺ AKALLKEDKALADEITL ⁺ KIKESIG ⁺ SNEEIMPLPDE...PLE...EME.....	347
DKKLGGGREN ⁺ AKALLKEDKALADEITL ⁺ KIKESIG ⁺ SNEEIMPLPDE...PLE...EME.....	347
DTKLGGGRD ⁺ TVKEL ⁺ IKDNPEL ⁺ AEELEAK ⁺ IREKLQAK.....	343
GTKIGQGK ⁺ NNAVK ⁺ VLKENPEIAD ⁺ KLQE ⁺ IRNTL ⁺ ASNPNVLKATASDSNDES.....DVEEF.SEEEL.....	372
GAKIGGQK ⁺ DNVRVWLKENPEIS ⁺ DEIDAK ⁺ IRALNG ⁺ VMHITEGTQDET ⁺ D..GE.....RPEE.....	348
GAKIGGQK ⁺ DNVRVWLKENPEIS ⁺ DEIDAK ⁺ IRALNG ⁺ VMHITEGTQDET ⁺ D..GE.....RPEE.....	348
GAKIGGQK ⁺ DNVRVWLKENPEIS ⁺ DEIDAK ⁺ IRALNG ⁺ VMHITEGTQDET ⁺ D..GE.....RPEE.....	348
GERIGQGRD ⁺ NCREFLRENAELAR ⁺ EIENK ⁺ VREHL ⁺ GVTPMGA.VTLAEV...EE...D.....	352
GDKIGQGK ⁺ ANACKYLKENPEIAKT ⁺ LDKKL ⁺ REMLLNPNMQLIAETSSA..AD....DVEFG.AVPEEF.....	354
GDKIGQGK ⁺ ANACKYLKENPEIAKT ⁺ LDKKL ⁺ REMLLNPNMQLIAETSSA..AD....DVEFG.AVPEEF.....	354
GNKIGQGK ⁺ NNVIRYLEENPQIST ⁺ EIEAV ⁺ IREQLLT ⁺ TKASDQTAAHDET.....EE..EPDLL.ES.....	349
GNKIGQGK ⁺ NNVIRYFEENNQIA ⁺ EIEIERN ⁺ IREQLLT ⁺ TGTNGAVQI..ED.....EE..EPDLL.LES.....	349
GSKIGQGGK ⁺ ANS ⁺ AKFL ⁺ ADNPDI ⁺ AATLEK ⁺ QIRDKLL ⁺ TPAPDVKAAANREP..VD.....EMEEA..DTDI.....	352
GSKIGQGGK ⁺ ANAKYLENPEI ⁺ IGQ ⁺ EIEQQ ⁺ IRAKLL ⁺ VTSANTKATPVAED..LA.....D.....ADI.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347

consensus

 non conserved
 similar
 ≥ 50% conserved