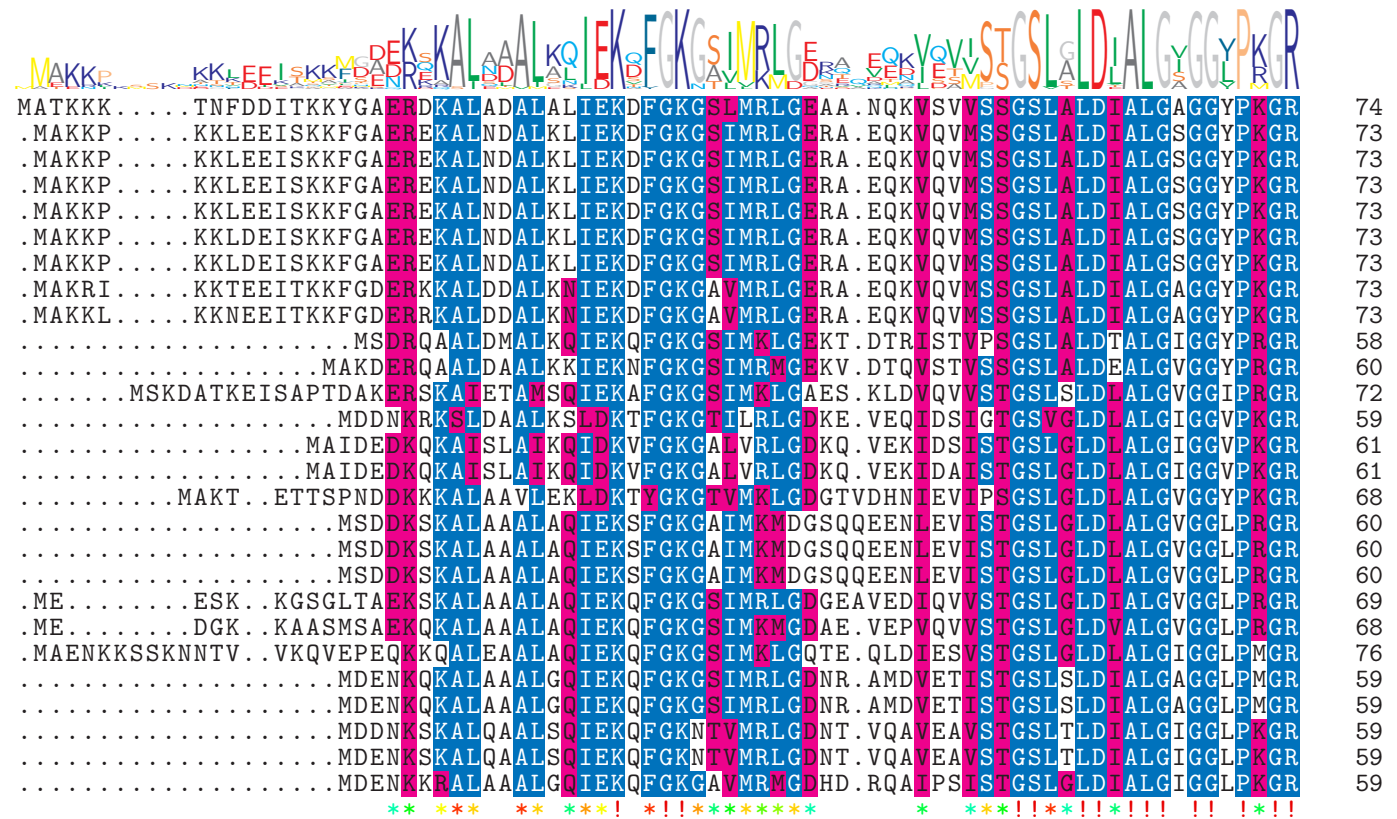


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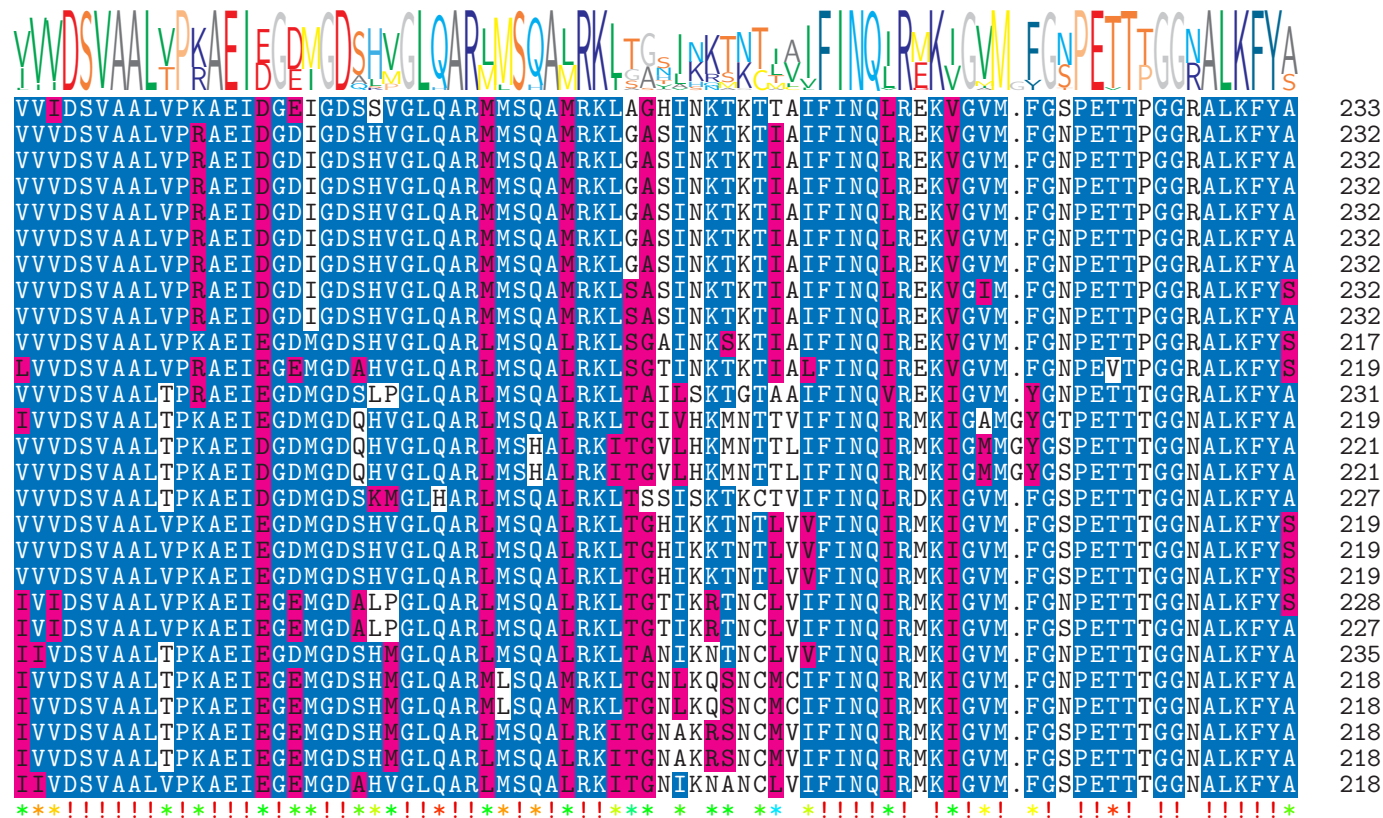
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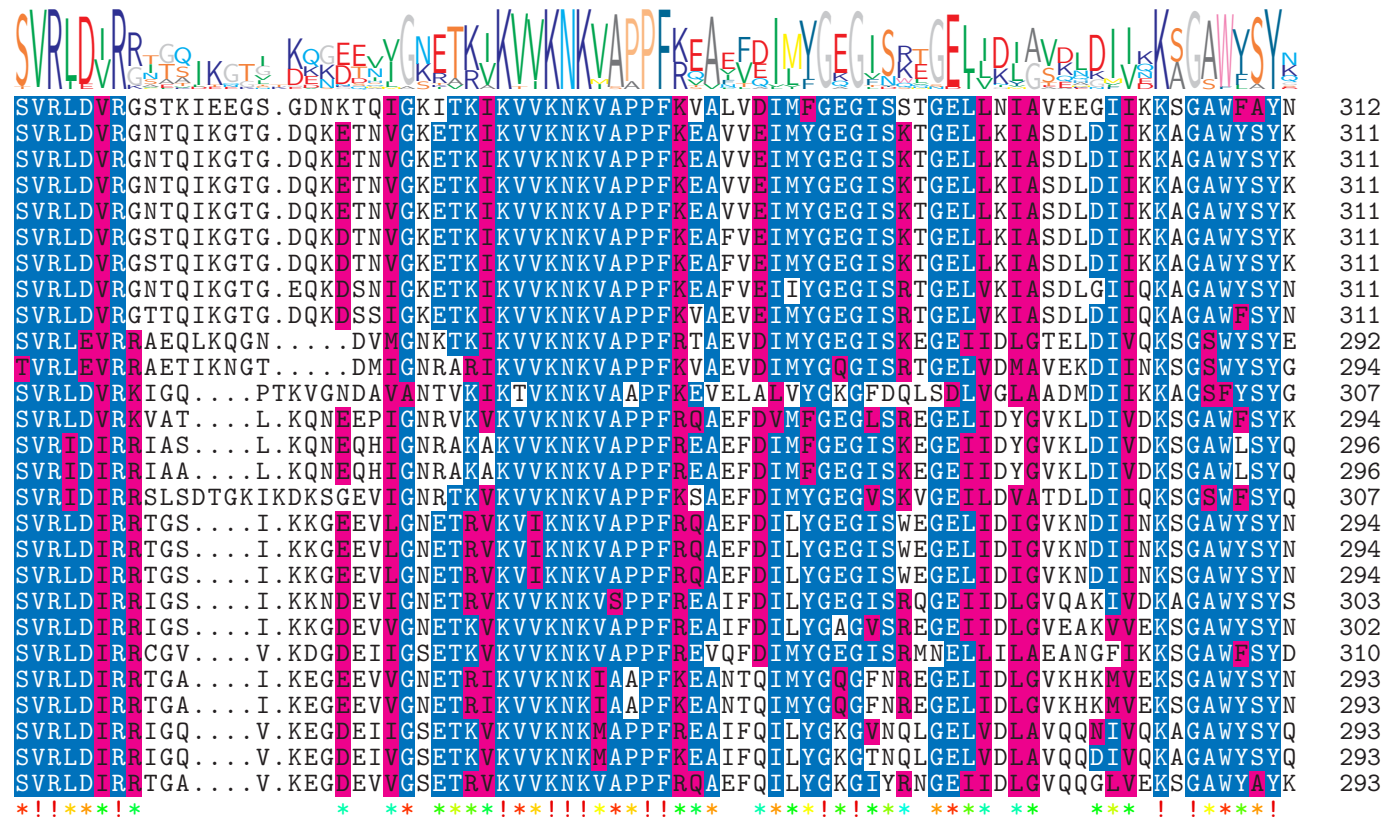
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ ID ⁺ KQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ ID ⁺ KQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ ID ⁺ KQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ ID ⁺ KQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE ⁺PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ IFDE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ VFAE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CLIDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IFDD ⁺ ID ⁺ HK ⁺ VR ⁺ VQY ⁺ CLIEDNTTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIEIE	382
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EERL ⁺ CGGREN ⁺ AKQFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DEV ⁺ RLK ⁺ VRAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPD ⁺ DST.....EE.....	355
DERIGQG ⁺ KEKTIAY ⁺ IA ⁺ ERP ⁺ MEQE ⁺ IRDR ⁺ MAA ⁺ IRAGNAGEAPALAPAPA ⁺ PEAA ⁺ ..EA.....	363
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	343
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	343
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	343
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	343
DTKL ⁺ GGGRD ⁺ TVKEL ⁺ IKDN ⁺ PELA ⁺ EEL ⁺ EAK ⁺ IREKLQAK.....	343
GAKIGQGG ⁺ KDNVR ⁺ VWLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	348
GAKIGQGG ⁺ KDNVR ⁺ VWLKEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHIT.....EGTQDE ⁺ TD..GER.....PEE.....	348
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GEKIGQGG ⁺ KDNARE ⁺ FLREN ⁺ PEIARE ⁺ IE ⁺ NR ⁺ IRESLCVAAMPQ....GAGSEAEIM..DEE.....E.....	356
GERIGQGRD ⁺ NCRE ⁺ FLREN ⁺ AEARE ⁺ IE ⁺ NK ⁺ VREHL ⁺ CVTPMGA....VT..LAEV..EED.....	352
GT ⁺ KIGQGG ⁺ KNNAV ⁺ KWLKEN ⁺ PEIAD ⁺ KLE ⁺ QEIR ⁺ N ⁺ TAL ⁺ SNPNSV.....LKATAS ⁺ SN..DES ⁺ DVEEFSEEL.....	372
GDKIGQGG ⁺ KANACK ⁺ YLKEN ⁺ PEIAKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PENMQ....LIAETSSAA..D ⁺ VEFGAVPEEF.....	354
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GNKIGQGG ⁺ KNNVIR ⁺ YLEEN ⁺ PQISTE ⁺ IE ⁺ AVIREQLLT ⁺ TKASDQ....TAA.HDETE..EEP ⁺ DLL..ES.....	349
GS ⁺ KIGQGG ⁺ KANAKY ⁺ LEEN ⁺ PEIGQE ⁺ IE ⁺ QQ ⁺ IRAK ⁺ LVTSANT.....KATPVAE ⁺ DL..ADADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved