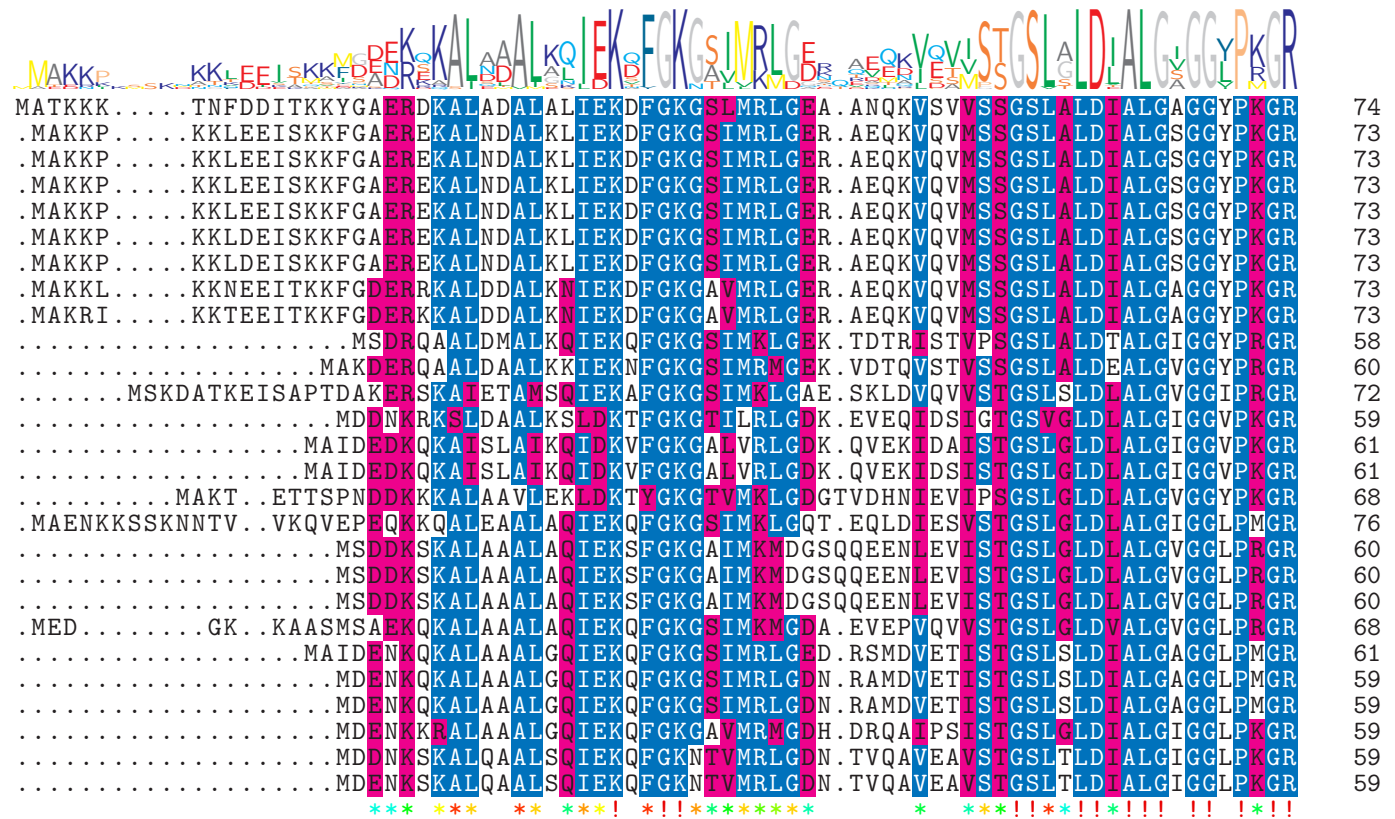


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGQGA ⁺ EA ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ DHK ⁺ V ⁺ RAAH ⁺ CI ⁺ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ VFAE ⁺ IDHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEAAE....SKKDE....VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ IFDE ⁺ IDHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAE....SKKDE....AAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QIFDE ⁺ IDRK ⁺ VR ⁺ VKF ⁺ CLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IFDD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ LGQGR ⁺ ENAK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQE ⁺ QIREHY ⁺ CLDNNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DVRL ⁺ KV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQG ⁺ KEK ⁺ TIAY ⁺ IA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VMAA ⁺ IRAGNAGEAPALAPAAPEAAEA.....	363
DKKL ⁺ GGQGR ⁺ ENSKA ⁺ FL ⁺ KEN ⁺ PEIA ⁺ DEIT ⁺ KA ⁺ TQNSM ⁺ TEGMI....SGSEDDGEE.....	343
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEI....MPLPDEPLEEME.....	347
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEI....MPLPDEPLEEME.....	347
DTKL ⁺ GGQGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELEAK ⁺ IREKLQAK.....	343
GAKIGQG ⁺ KNN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEIAD ⁺ KL ⁺ EQE ⁺ IRNTL ⁺ ASPN ⁺ NS....VLKATASDSNDES ⁺ DVEE...FSEEL.....	372
GDKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEM ⁺ HI....TEGTQDET....DGERPEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEM ⁺ HI....TEGTQDET....DGERPEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEM ⁺ HI....TEGTQDET....DGERPEE.....	348
GERIGQGRD ⁺ NCRE ⁺ FLREN ⁺ AEL ⁺ ARE ⁺ EIEN ⁺ KV ⁺ REHL ⁺ GVTPM ⁺ G....AVTLA.EEEVED.....	352
GDKIGQG ⁺ KANA ⁺ ISWL ⁺ KEN ⁺ PEAA ⁺ AE ⁺ EKKV ⁺ RELLSN ⁺ QDA....TPDFAVDGNSEAE ⁺ TEQD...F.....	352
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KEN ⁺ PEIA ⁺ KTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIA...ETSSAADDVE...FGAVPEEF.....	354
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KEN ⁺ PEIA ⁺ KTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIA...ETSSAADDVE...FGAVPEEF.....	354
GSKIGQG ⁺ KANAACK ⁺ YLEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ RAKL ⁺ LVTSAN....TKATPVAEDLADADI.....	347
GNKIGQG ⁺ KNN ⁺ VIR ⁺ YLEEN ⁺ PEI ⁺ STE ⁺ EIE ⁺ AVI ⁺ REQLLT ⁺ KASD....QTAA.HDETEEEPD ⁺ LLE...S.....	349
GNKIGQG ⁺ KNN ⁺ VIR ⁺ YLEEN ⁺ PEI ⁺ STE ⁺ EIE ⁺ ERN ⁺ IREQLLT ⁺ TG ⁺ TN....GAVQ.I.EDEEEPD ⁺ LLL...ES.....	349

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved