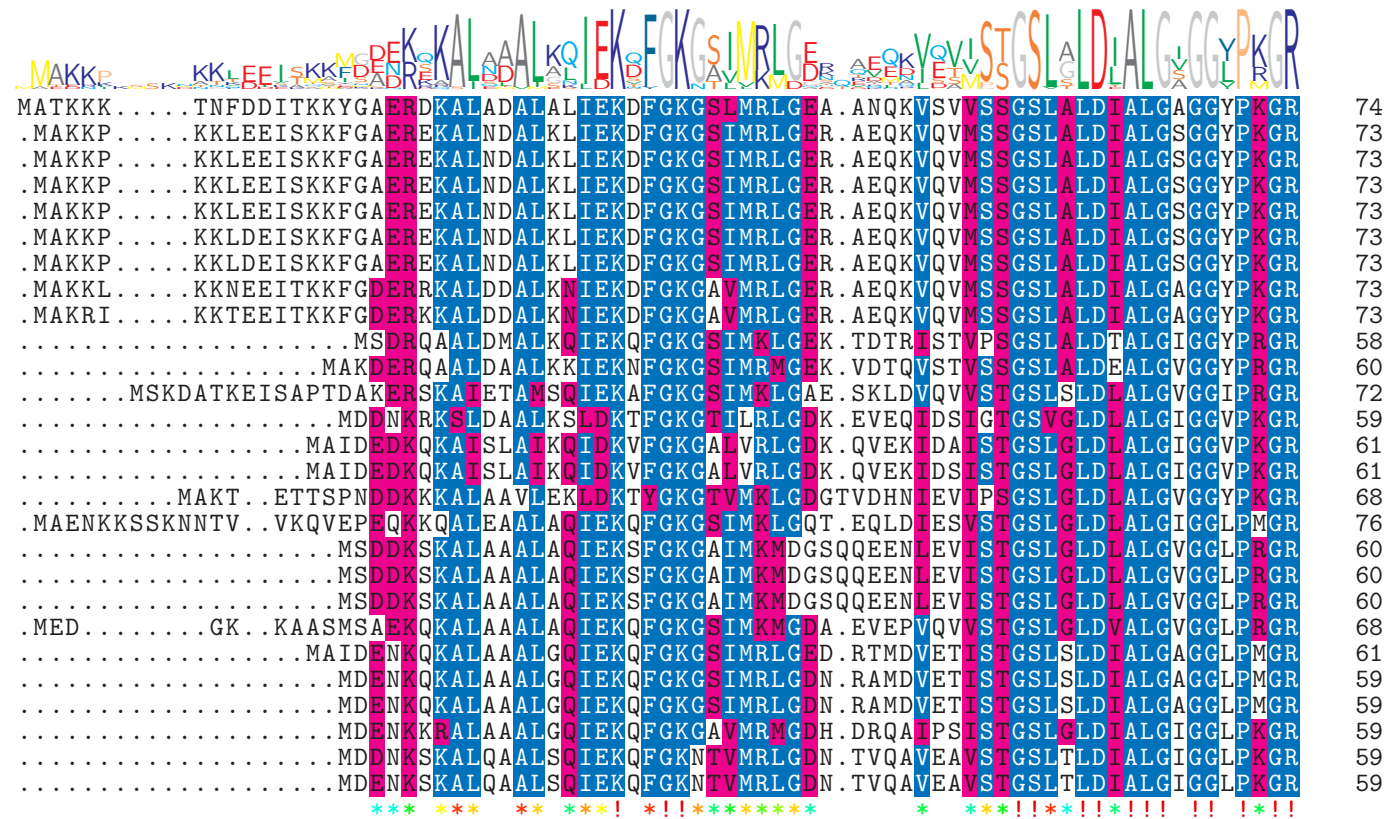


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NTDB id 1205 PSJM300 05545 AFN77183.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGA ⁺ EA ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ DHK ⁺ V ⁺ RAAH ⁺ CI ⁺ LDDSEVAETEET ⁺ TASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFDE ⁺ IDK ⁺ QV ⁺ RSKF ⁺ CLIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ ADNP ⁺ EVFA ⁺ EID ⁺ HQ ⁺ V ⁺ RVQF ⁺ CLIDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ ADNP ⁺ EVFA ⁺ EID ⁺ HQ ⁺ V ⁺ RVQF ⁺ CLIDGEEAAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS ⁺ ENAK ⁺ RYLA ⁺ DHP ⁺ QLFDE ⁺ IDR ⁺ KV ⁺ VKF ⁺ CLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGGGS ⁺ ENAK ⁺ KFLAD ⁺ NPE ⁺ IFDD ⁺ IDHK ⁺ V ⁺ RVQY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERL ⁺ GGGREN ⁺ AKQFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGGGREN ⁺ AKNYL ⁺ ADHED ⁺ VEDEV ⁺ RLK ⁺ V ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEK ⁺ TIAY ⁺ IA ⁺ ERP ⁺ MEQE ⁺ IRDR ⁺ V ⁺ MAA ⁺ IRAGNAGEAPALAPAPAA.PEAAEA.....	363
DKKL ⁺ GGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIA ⁺ DEIT ⁺ KAT ⁺ IQNSM ⁺ CI ⁺ EGMISGSEDDE..GE.E.....	343
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KI ⁺ KESIG ⁺ SNEEIMPLPDEP..LE.EME.....	347
DKKL ⁺ GGGREN ⁺ AKALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KI ⁺ KESIG ⁺ SNEEIMPLPDEP..LE.EME.....	347
DTKL ⁺ GGGRD ⁺ TVK ⁺ ELI ⁺ KDN ⁺ PELA ⁺ EEL ⁺ EAK ⁺ IREKLQAK.....	343
GAKIGGQKN ⁺ NAV ⁺ KLKEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQE ⁺ IRNT ⁺ LASN ⁺ PN ⁺ SVLKATAS..D...SNDES ⁺ DVEEFSEEE..L.....	372
GAKIGGQKDN ⁺ RV ⁺ VWLKEN ⁺ PEIS ⁺ DE ⁺ IDAK ⁺ IRAL ⁺ NCV ⁺ EMHITEGTQDE..TD.....GERPEE.....	348
GAKIGGQKDN ⁺ RV ⁺ VWLKEN ⁺ PEIS ⁺ DE ⁺ IDAK ⁺ IRAL ⁺ NCV ⁺ EMHITEGTQDE..TD.....GERPEE.....	348
GAKIGGQKDN ⁺ RV ⁺ VWLKEN ⁺ PEIS ⁺ DE ⁺ IDAK ⁺ IRAL ⁺ NCV ⁺ EMHITEGTQDE..TD.....GERPEE.....	348
GERIGGGRD ⁺ NC ⁺ REFL ⁺ REN ⁺ AEL ⁺ ARE ⁺ IE ⁺ ENK ⁺ V ⁺ REHL ⁺ CVTPMGAVTLAAE..VE.ED.....	352
GD ⁺ KIGGQKAN ⁺ AIT ⁺ WLKEN ⁺ PEIA ⁺ AAAK ⁺ EIE ⁺ BKV ⁺ RELLLNQDAKPD..FV..VD.GNDAEETE ⁺ EQDF.....	352
GDKIGGQKAN ⁺ ACKY ⁺ LKEN ⁺ PEIA ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLNPN ⁺ MQLI..AE.....TSSAADDVEFGAVPEEF.....	354
GDKIGGQKAN ⁺ ACKY ⁺ LKEN ⁺ PEIA ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLNPN ⁺ MQLI..AE.....TSSAADDVEFGAVPEEF.....	354
GSKIGGQKAN ⁺ AAKY ⁺ LEEN ⁺ PEIG ⁺ QEI ⁺ EQQ ⁺ IRAKLL ⁺ TSANTKA..TP..VA.EDLADADI.....	347
GNKIGGQKNN ⁺ VIRY ⁺ LEEN ⁺ PQISTE ⁺ IE ⁺ BAV ⁺ IREQLLTGASDQTA..A...HD.ETEEEPD ⁺ LLES.....	349
GNKIGGQKNN ⁺ VIRY ⁺ FEEN ⁺ NQIA ⁺ EIE ⁺ ERN ⁺ IREQLLTGTGNGAV..Q...I..EDEEEPD ⁺ LLES.....	349

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
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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