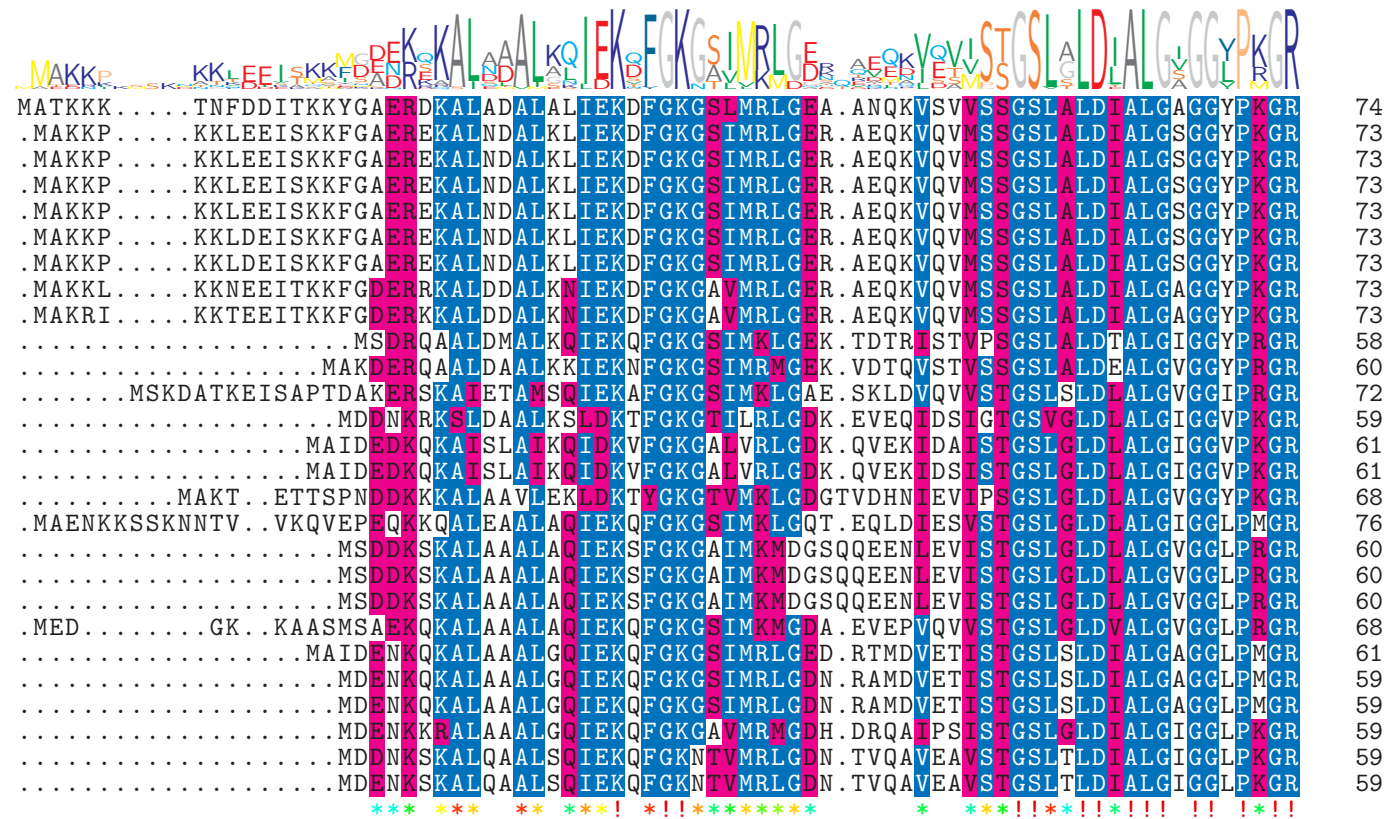


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ HK ⁺ V ⁺ RAAH ⁺ CL ⁺ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGSENAKKYLA ⁺ EHPE ⁺ IFDE ⁺ IDKQ ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLA ⁺ EHPE ⁺ IFDE ⁺ IDKQ ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLA ⁺ EHPE ⁺ IFDE ⁺ IDKQ ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLA ⁺ ADNP ⁺ EVFA ⁺ EID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CL ⁺ IDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLA ⁺ ADNP ⁺ EVFA ⁺ EID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CL ⁺ IDGEEAAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSSENAKRYLAD ⁺ HP ⁺ Q ⁺ IFDE ⁺ IDR ⁺ KV ⁺ VK ⁺ F ⁺ CL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGQGSSENAKKFLAD ⁺ NPE ⁺ IFDD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ CL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ LGQGR ⁺ ENAK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQE ⁺ QIREHY ⁺ CL ⁺ DMNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGQGRENAKNYLAD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ VRAAY ⁺ CT ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAYIA ⁺ ERP ⁺ EME ⁺ QE ⁺ IRDR ⁺ VMAAIRAGNAGEAPALAPAPAA.PEAAEA.....	363
DKKL ⁺ GGQGR ⁺ ENSKA ⁺ FL ⁺ KEN ⁺ PEIA ⁺ DEIT ⁺ KAT ⁺ IQNSM ⁺ CT ⁺ EGMISGSEDDE..GE.E.....	343
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEIMPLPDEP..LE.EME.....	347
DKKL ⁺ GGQGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEIMPLPDEP..LE.EME.....	347
DTKL ⁺ GGQGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGQGKNNAV ⁺ KWL ⁺ KEN ⁺ PEIA ⁺ ADK ⁺ LQE ⁺ IRNTL ⁺ ASNPNSVLKATAS..D...SNDES ⁺ DVEEFSEEE..L.....	372
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHITEGTQDE..TD.....GERPEE.....	348
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHITEGTQDE..TD.....GERPEE.....	348
GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRALN ⁺ GVEMHITEGTQDE..TD.....GERPEE.....	348
GERIGQGRD ⁺ NCRE ⁺ FLREN ⁺ AEL ⁺ ARE ⁺ EIEN ⁺ KV ⁺ REHL ⁺ GVTPMGAVTLAAE..VE.ED.....	352
GDKIGQGGKANAT ⁺ WL ⁺ KEN ⁺ PEIAA ⁺ AE ⁺ EKKV ⁺ RELLLNQDAKPD..FV..VD.GNDAEETE ⁺ QDF.....	352
GDKIGQGGKANACKYL ⁺ KEN ⁺ PEIAKT ⁺ LD ⁺ KKL ⁺ REMLLNPNEMQLI..AE.....TSSAADDVEFGAVPEEF.....	354
GDKIGQGGKANACKYL ⁺ KEN ⁺ PEIAKT ⁺ LD ⁺ KKL ⁺ REMLLNPNEMQLI..AE.....TSSAADDVEFGAVPEEF.....	354
GSKIGQGGKANAAKY ⁺ LEEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ IRAKLL ⁺ VT ⁺ SANTKA..TP..VA.EDLADADI.....	347
GNKIGQGGKNNVIR ⁺ YLEEN ⁺ PEI ⁺ QISTE ⁺ EIE ⁺ AVIRE ⁺ QLLTKASDQTA..A...HD.ETEEEPD ⁺ LLES.....	349
GNKIGQGGKNNVIR ⁺ YLEEN ⁺ PEI ⁺ QIAE ⁺ EIRN ⁺ IRE ⁺ QLLTTGTNGAV..Q...I..EDEEEPD ⁺ LLES.....	349

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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