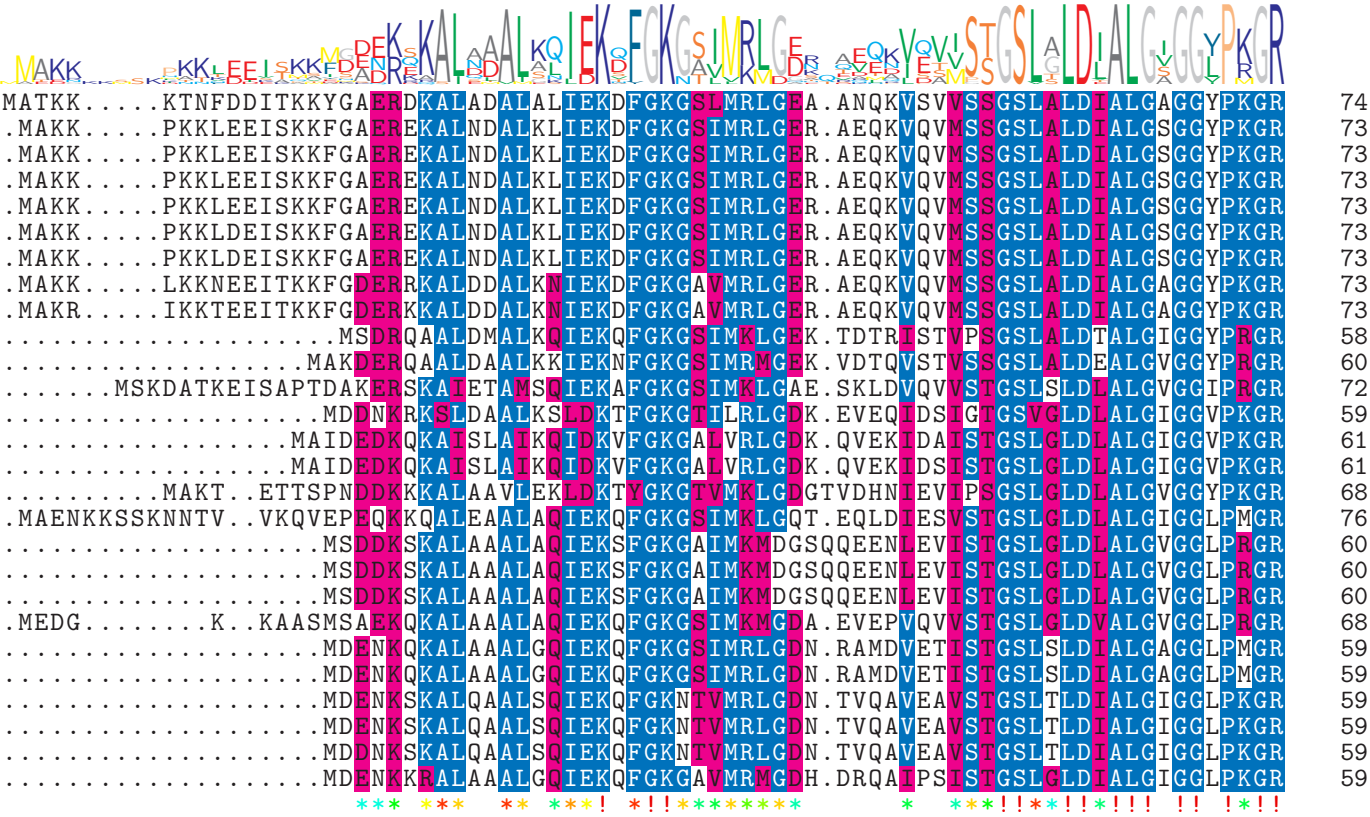


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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus



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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 Q5545 AEN77183.1

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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KNYLKEHQ ⁺ DV ⁺ FEID ⁺ HKVRAAHG ⁺ LDDSEVAETEEEE.TTAS ⁺ KTK..AKAKKEEKAVETEEIELELED..	387
DEKIGQGSEN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGD ⁺ EL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGD ⁺ EL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGD ⁺ EL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ DNPEVFA ⁺ EID ⁺ HQVRVQFGLIDGEEAAE.....SKKD ⁺ E.....VAQVDS..VNEEVTLDLGD ⁺ EL	378
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ DNPEIF ⁺ DEID ⁺ HQVRVQFGLIDGEEIAE.....SKKD ⁺ E.....AAQVDS..VNEEVTLDLGD ⁺ EL	378
GEKIGQGS ⁺ EN ⁺ AKRYLADHPQLF ⁺ DEID ⁺ RKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGS ⁺ EN ⁺ AKKFLADNPEIF ⁺ DDID ⁺ HKVRVQYGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGREN ⁺ AKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAAEE.TQEEL.E..FE.E.....	348
SERIGGGREN ⁺ AKNYLADHEDVEDEVRLK ⁺ VRAAYG ⁺ ISDVPEEDLPTTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGGQKE ⁺ KTIAYIA ⁺ ERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGGREN ⁺ SKAFLKENPEIA ⁺ DEITKAIQNSMGIEGMISGS..EDDEGE..E.....	343
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD ⁺ TVKELIKDNPELAE ⁺ ELEAKIREKLQAK.....	343
GTKIGQGKNN ⁺ AVKWLKENPEIADKLEQEI ⁺ RNTLASNPNSVLK..ATASDSND ⁺ ESDVEEFSE.....EEL.....	372
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGGQKDN ⁺ VRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGGGRDN ⁺ CREFLRENAELAREIENK ⁺ VREHLGVTPMGAV..TLAEEVEED.....	352
GDKIGGQKAN ⁺ ACKYLKENPEIAK ⁺ LDKKLREMLLNPNMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GDKIGGQKAN ⁺ ACKYLKENPEIAK ⁺ LDKKLREMLLNPNMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GNKIGGQKNN ⁺ VIRYFEENTQIAE ⁺ EIERNIREQLLTGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQKNN ⁺ VIRYFEENNQIAE ⁺ EIERNIREQLLTGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQKNN ⁺ VIRYLEENPQISTEIE ⁺ EAVIREQLLTKASDQTA..A.HDETEE ⁺ EPD..LLES.....	349
GSKIGGQKANA ⁺ KYLEENPEIG ⁺ EIEEQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

	E	I	E	E	E	
NTDB id 600 KW2 RS01765 WP 011675413.1						387
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE					388
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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved