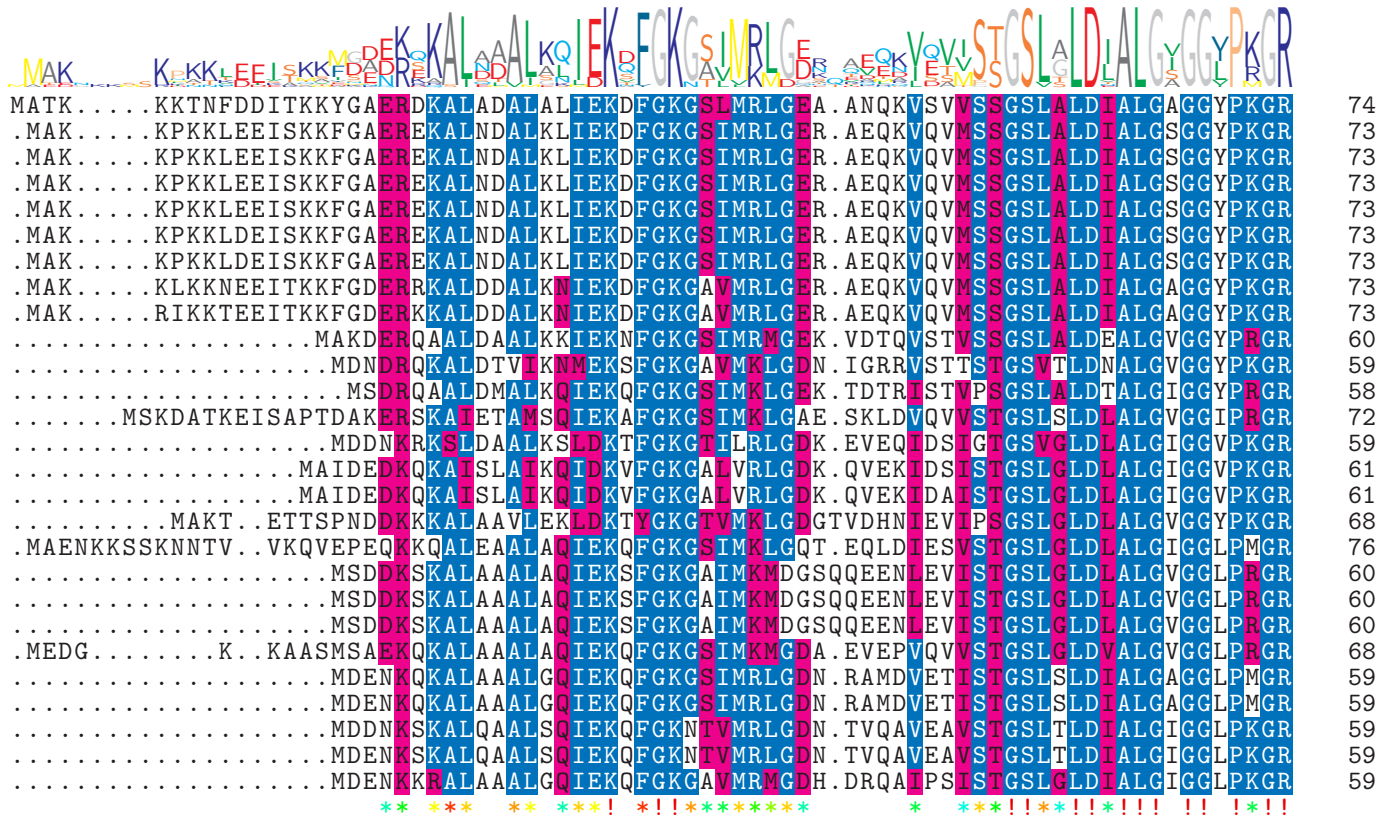


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consensus



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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
SERIGQGR ENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTTEDEQINILPDDSTEE	355
GERMGQGG KENVKMYLKENPQIKEEIDRKLRKLGISDGDVEETEDA . . PKSLFDEE	347
EERLGGGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQQAETQEELEFEE	348
DERIGQGEKKTIAIYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAEA	363
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DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDE . PLEEME	347
DTKLGGGRD TVKELIKDNPELAEELEAKIREKLQAK	343
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GERIGQGRDNCREFLRN AELAREIENKVRHGLVTPMG AVTLA . EEEVE	352
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GNKIGQGKNN VIRYLEENPQISTEIEAVIREQLLTKASD QTAA . HDETEEEPD . LL . ES	349
GNKIGQGKNN VIRYFEENNQIAEIEIERNIREQLLTTGTN GAVQ . I . EDEEEPD . LL . LES	349
GSKIGQGGKANAACKYLENPEI GQIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved