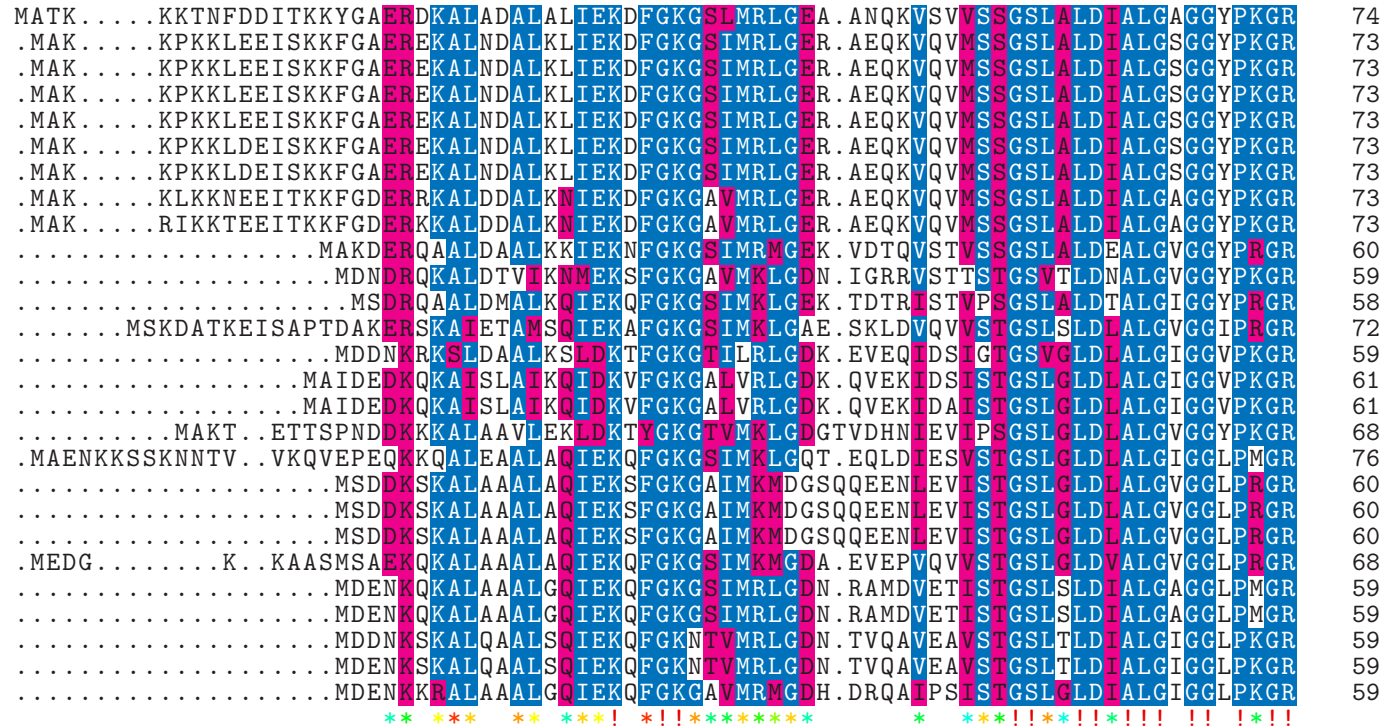


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consensus

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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 ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
SERIGQGR ENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTTEDEQINILPDDSTEE	355
GERMGQGG KENVKMYLKENPQIKEEIDRKLRKLGISDGDVEETEDA . . PKSLFDEE	347
EERLGGGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQAAETQEELEFEE	348
DERIGQGEKKTIAIYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA	363
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DKKLGQGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDE . PLEEME	347
DKKLGQGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDE . PLEEME	347
DTKLGQGRD TVKELIKDNPELAEELEAKIREKLQAK	343
GKIGQGKNN AVKWLKENPEIADKLEQEI RNTLASNPNS VLKATASDSNDESD . VEEFSEEEL	372
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMG AVTLA . EEEVE	352
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD QTAA . HDETEEEPD . LL . ES	349
GNKIGQGKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN GAVQ . I . EDEEEPD . LL . LES	349
GSKIGQGKANAAKYYLENPEI GQIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved