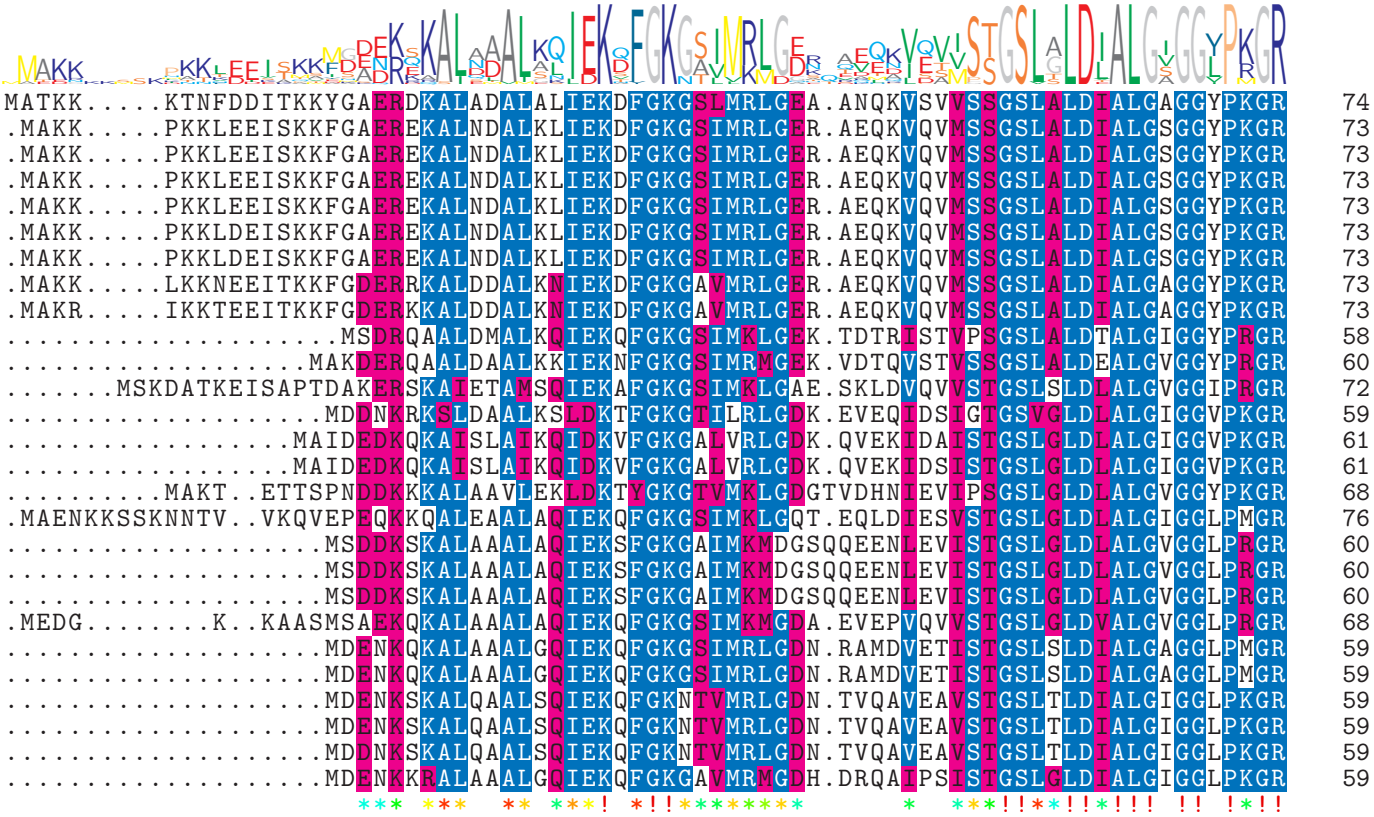


logo

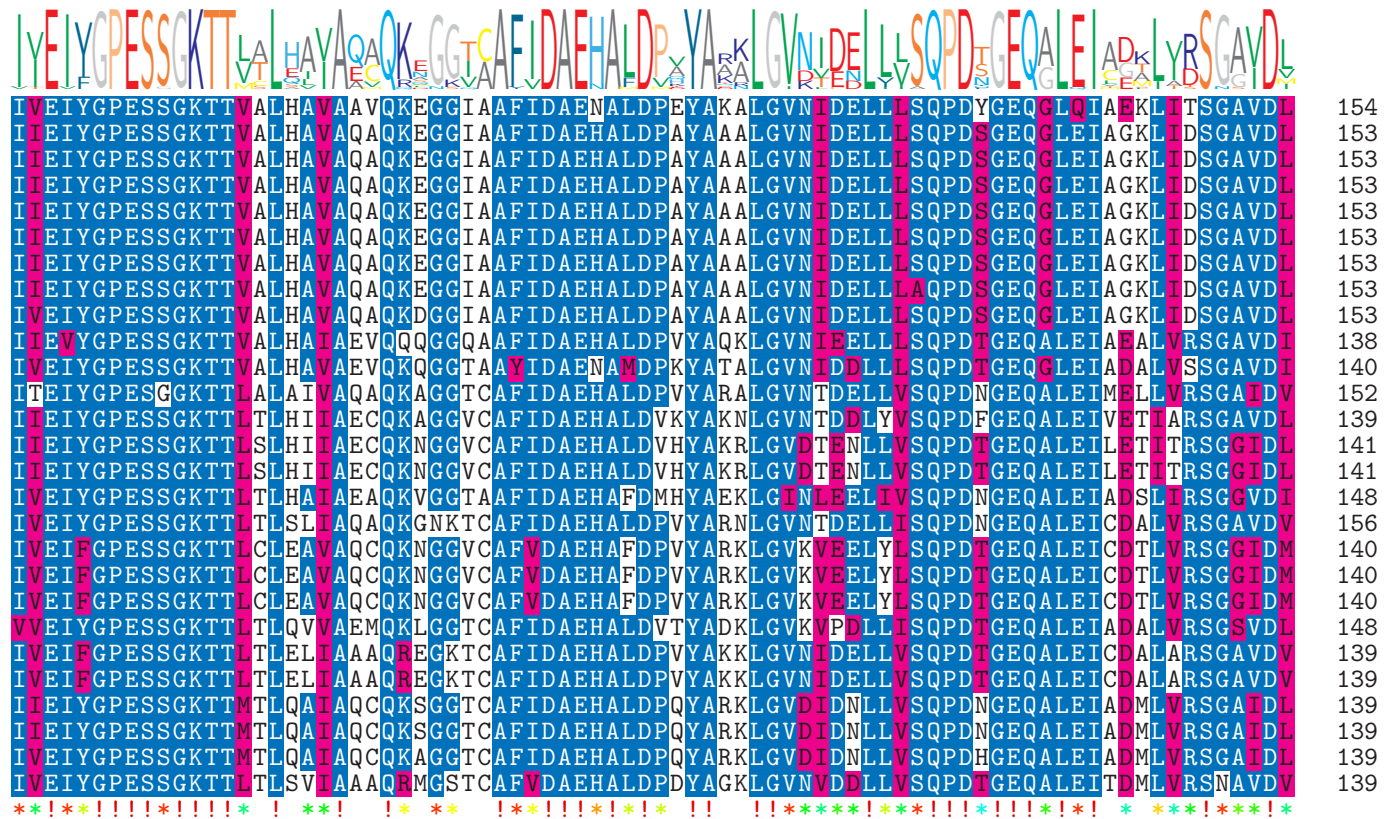
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 207735 BS065 RS07975 WP 000344169.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus



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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGD	382
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGD	382
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGD	382
DEKIGQGS ENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE.....SKKDE.....VAQVDS..VNEEVPLDLGD	378
DEKIGQGS ENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE.....SKKDE.....AAQVDS..VNEEVPLDLGD	378
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGG RENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGGG RENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGQG KEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA..	363
DKKLGGG RENSKAFLKENPEIADEITKAIQNSMGI EGMISGS..EDDEGE..E.....	343
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGG RDTVKELIKDNPELAEELEAKIREKLQAK..	343
GTKIGQG KNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK..ATASDSND ESDVEEFSE.....EEL.....	372
GAKIGQG KDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGQG KDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGQG KDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGQG RDNCREFLRENAELAREIENKVRHGLVTPMGAV..TLAEEVEED.....	352
GDKIGQG KANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAAD VFEFGAVPE.....EF.....	354
GDKIGQG KANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAAD VFEFGAVPE.....EF.....	354
GNKIGQG KNNVIRYFEENTQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
GNKIGQG KNNVIRYFEENNQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
GNKIGQG KNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..A.HDETEEPPD..LLES.....	349
GSKIGQG KANAACKYLENPEIQEIEQQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

	E	I	E	L	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