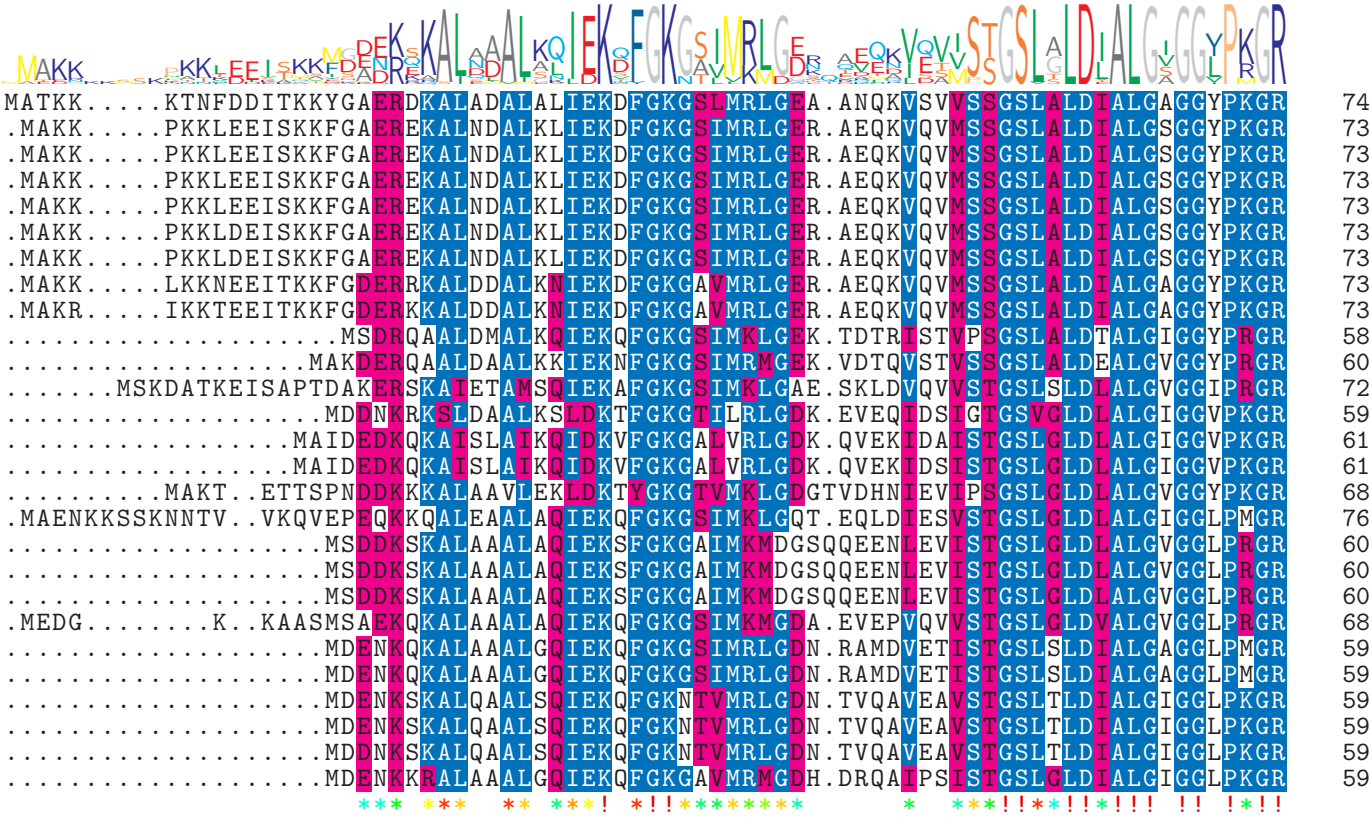


logo

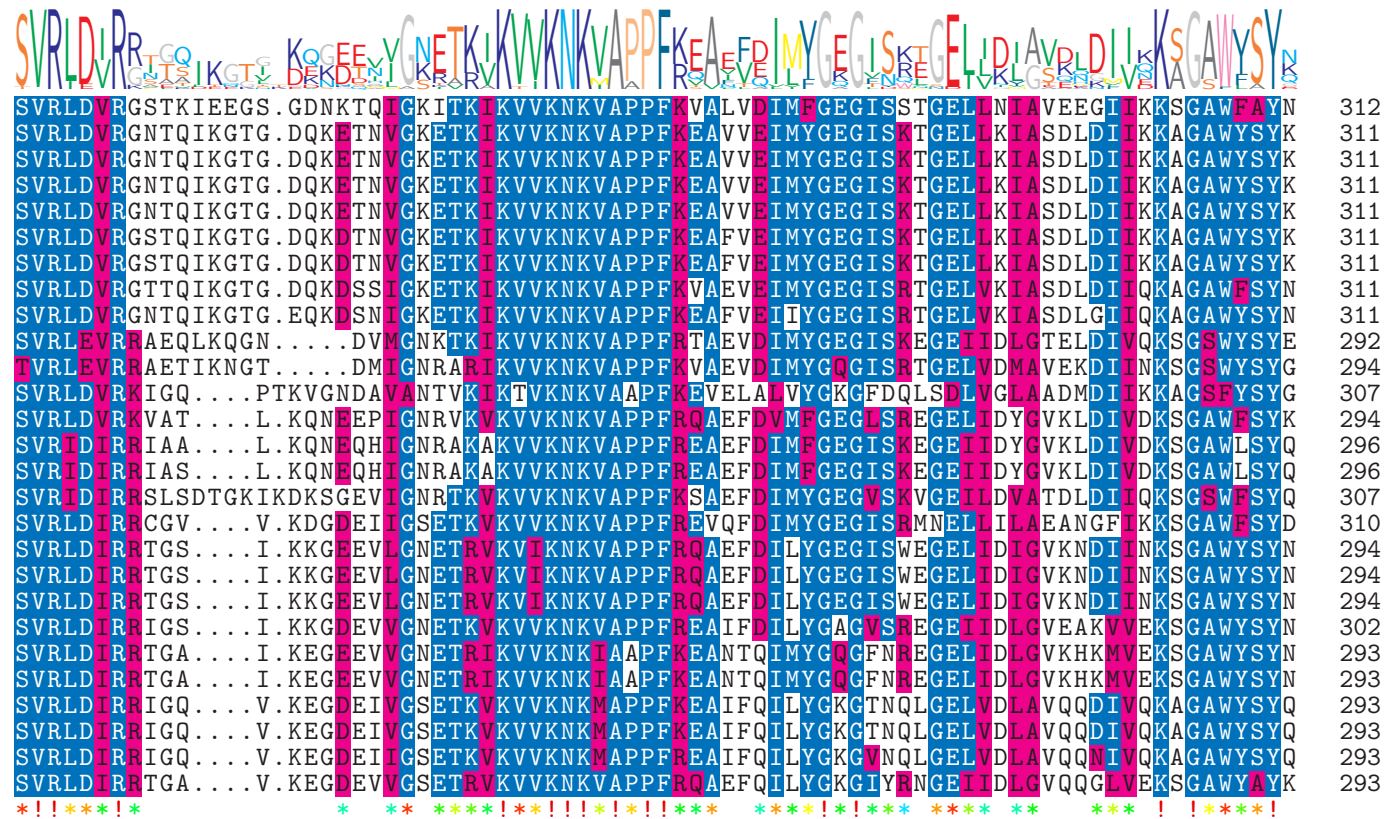
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
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NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
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NTDB id 1245 Cj1673c YP 002345041.1
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NTDB id 1334 RAOC RS04870 WP 004918236.1
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NTDB id 1124 NGFG RS03960 WP 003688695.1
NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
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NTDB id 272165 C5B74 RS07955 WP 000344169.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus




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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
DEKIGQGA EKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEE.TTASKTK..AKAKKEEKAVETEEIELELED..	387
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..ADKNLVLEDDTI	379
EERLGGG RENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGGG RENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGQG EKTITAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA..	363
DKKLGGG RENSKAFLKENPEIADEITKAIQNSMGI EGMISGS..EDDEGE..E.....	343
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGG RDTVKELIKDNPELAELEAKIREKLQAK..	343
GTKIGQG KNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK..ATASDSND ESDVEEFSE.....EEL.....	372
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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 KANAAYLEENPEIQEIEQQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

			E	I	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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NTDB id 1205 PSJM300 05545 AFN77183.1		347					
consensus							

-  non conserved
-  similar
-  ≥ 50% conserved