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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
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NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
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NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
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NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus



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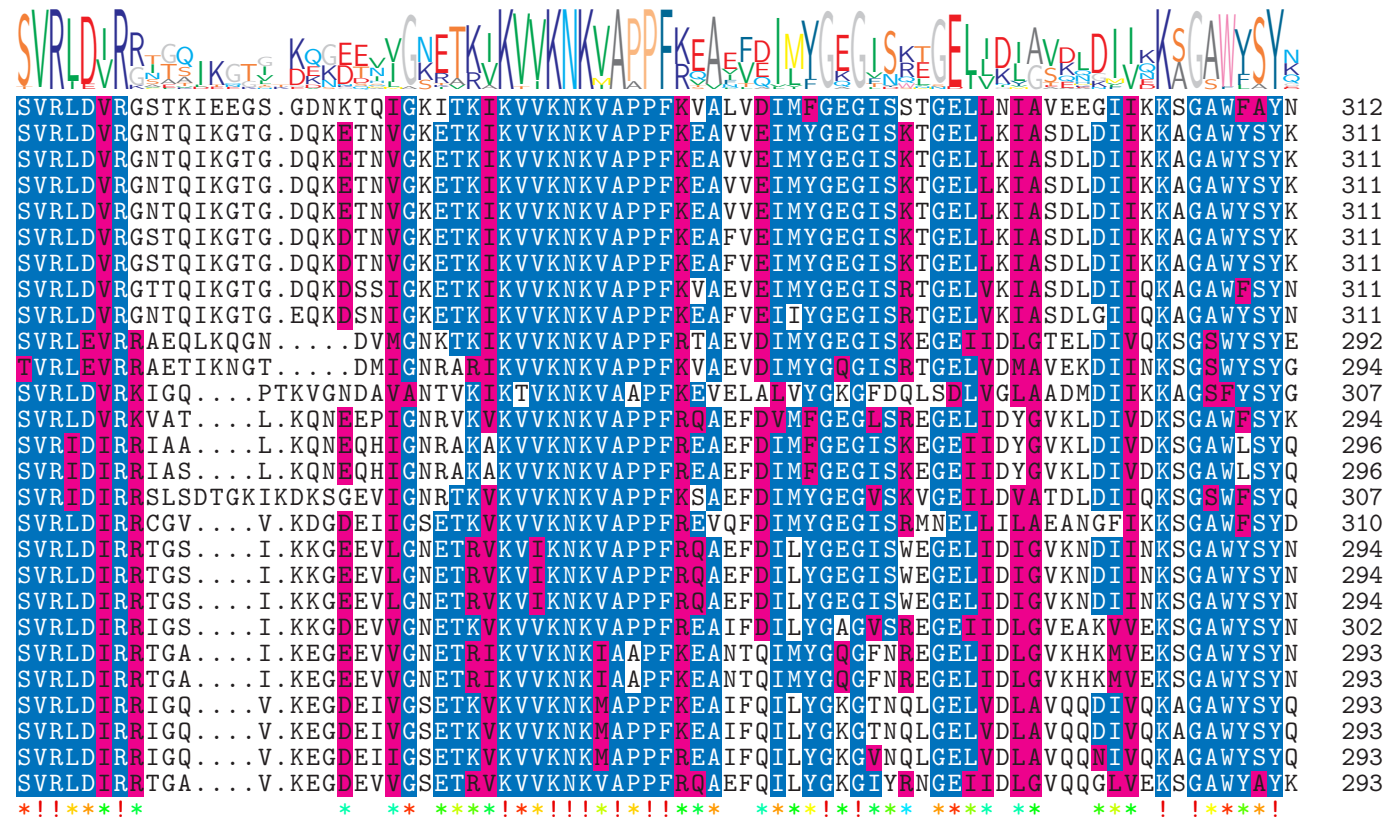
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NTDB id 1205 PSJM300 Q5545 AEN77183.1

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consensus

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
EERLGQGR ENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGQGR ENAKNYLADHEDVEDEVRLKVRVQYGLSDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGQG EKIITAIARPEMEQETIDRVMAAIRAGNAGEAPALAPAPAPEAAEA	363
DKKLGGGR ENSKAFLKENPEIADEITKAIQNSMGTIEGMISGS..EDDEGE..E.....	343
DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD TVKELIKDNPELAEELEAKIREKLQAK	343
GTKIGQG KNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK..ATASDSND ESDVEEFSE.....EEL.....	372
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGQGRD NCREFLRENAELAREIENKVRHGLVTPMGAV..TLAEEVEED.....	352
GDKIGQG KANACKYLKENPEIAKTLKKLREMLLNPNMQLI..AETSSAAD VFEFGAVPE.....EF.....	354
GDKIGQG KANACKYLKENPEIAKTLKKLREMLLNPNMQLI..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

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			E	I	E	L	E	E	
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NTDB id 194 SPR RS08825 WP 001085462.1	EIEIEE	388							
NTDB id 159 SP RS09750 WP 001085462.1	EIEIEE	388							
NTDB id 527 SMSK321 RS11065 WP 001085454.1	EIEIEE	384							
NTDB id 499 SM12261 RS08315 WP 078228268.1	EIEIEE	384							
NTDB id 453 Spy49 1753c ACI62003.1	EIED..	378							
NTDB id 408 SMU RS09530 WP 002262392.1	ELED..	383							
NTDB id 115 BSU 16940 NP 389576.2		348							
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NTDB id 1313 DR RS12030 WP 010888966.1		363							
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NTDB id 1022 ACIAD RS06390 WP 004925639.1		349							
NTDB id 1205 PSJM300 05545 AFN77183.1		347							
consensus									

-  non conserved
-  similar
-  ≥ 50% conserved