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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
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
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
NTDB id 1130 NGFG RS03960 WP 003688695.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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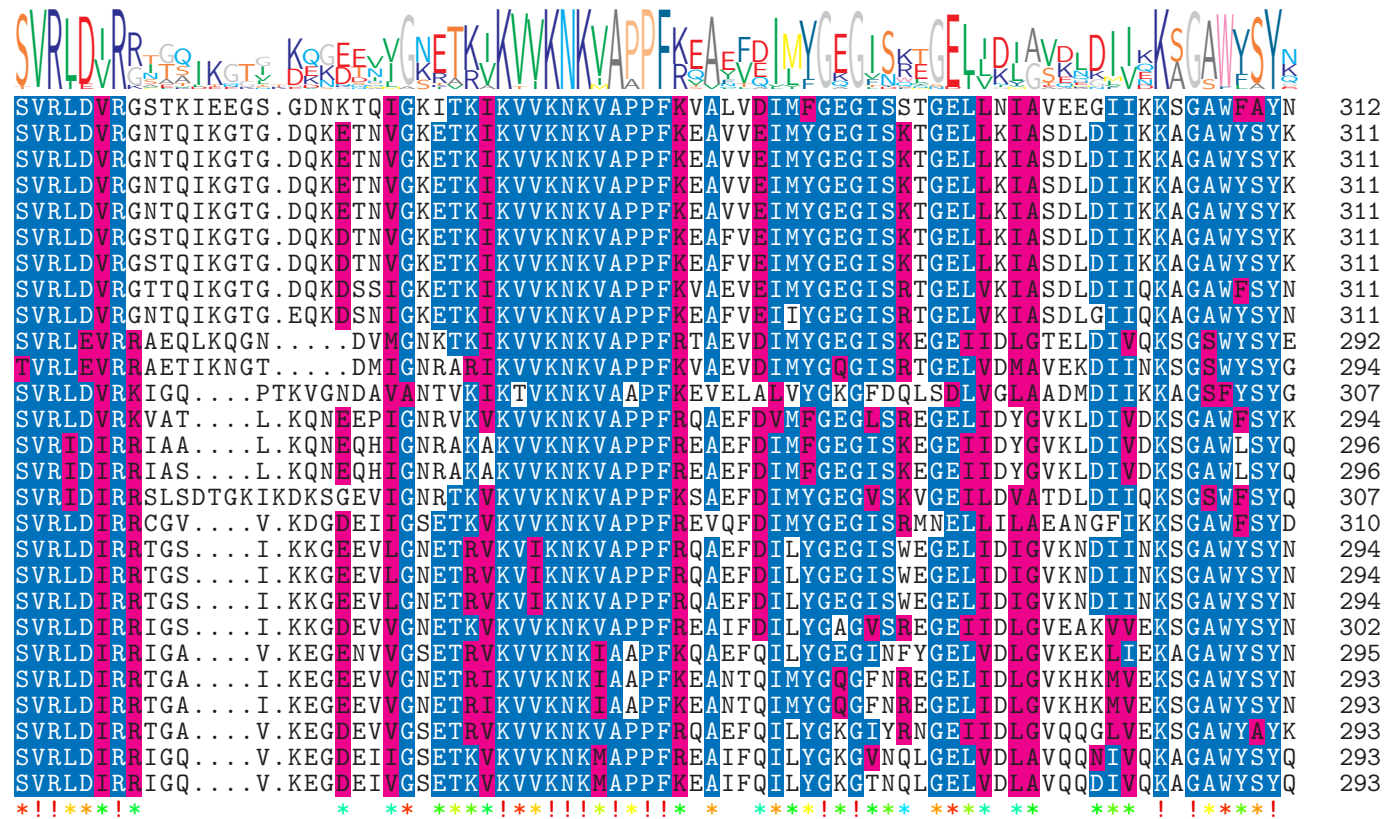
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Sequence	Score
DEKIGQGAETAKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKKEKAVETEEIEIELEDED.....	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAHNPEIFDEIDHQVRVQFGLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPFIIDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGQKEKTIATYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAA...EA.....	363
DKKLGQGRNSKAFLLKENPEIADIEITKATQNSMGIEGMI.....SGSEDD.....EGEE.....	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE.....PLEEME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE.....PLEEME.....	347
DTKLGQGRDITVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGKNNNAVKWLKENPEIADKLEQIRNTLASNPNS.....VLKATASDSN.....DESQVEEFSEEL.....	372
GAKIGQKQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TE.....GT...QDETGDGERPEE.....	348
GAKIGQKQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TE.....GT...QDETGDGERPEE.....	348
GAKIGQKQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TE.....GT...QDETGDGERPEE.....	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMG.....AVTLA.EEVE...ED.....	352
GEKIGQKQKANATAWLKENPATAKIEKKVRELLSNQDS.....TPDFSVDNN.....GEGVKETNEDF.....	354
GDKIGQKQKANACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAA...DDVEFGAVPEEF.....	354
GDKIGQKQKANACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAA...DDVEFGAVPEEF.....	354
GSKIGQKQKANAAKYLEENPEIGQIEEQQIRAKLLVTSAN.....TKATPVAEDL...ADADI.....	347
GNIKIGQKQKNNVIRYLEENPQISTEIEAVIREQLLTKASD.....QTAA.HDETE...EEPDLLES.....	349
GNKIGQKQKNNVIRIFYENNQIAEIERNIREQLLTGTN.....GAVQ.I.EDE...EEPDLLES.....	349

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		IEE	
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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved