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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
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
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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 1142 GTF74 RS11550 WP 000344154.1
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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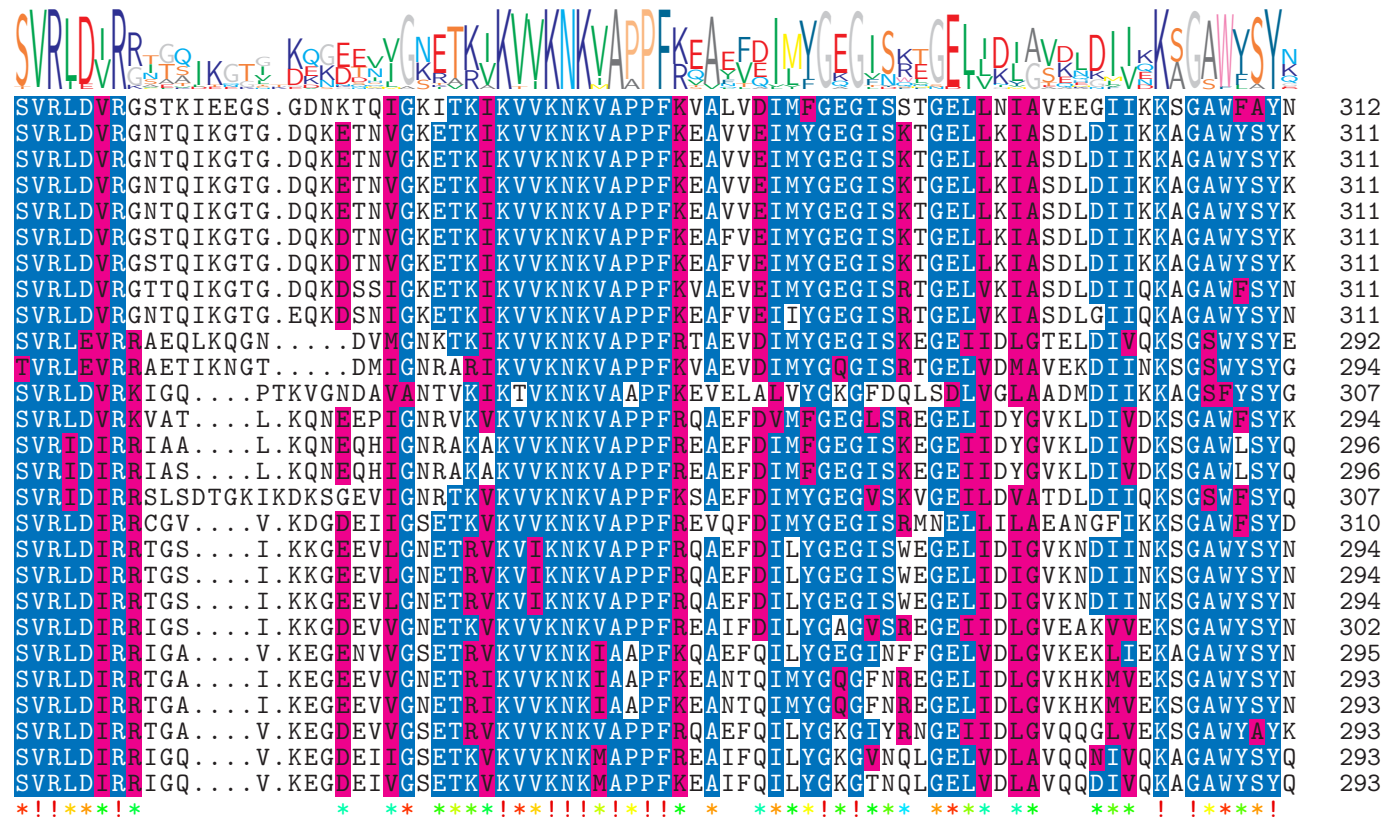
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Sequence	Score
DEKIGQGA EKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKEEKAVETEEIEIELEDED....	387
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST.....EE	355
DERIGGQKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAAA	363
DKKLGQGRNSKAFLEKNPEIADEITKAIQNSMGI EGM.....ISGSEDDEG..EE	343
DKKLGQGRNNAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL..EEM.....E	347
DKKLGQGRNNAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL..EEM.....E	347
DTKLGQGRDVTVKELIKDNPELAEELEAKIREKLQAK.....	343
GTKIGQGKNNAVKWLKENPEIADKLEQIRNTLASNP.....SVLKATASDSNDES DV.....EEFSFEEL.....	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEG.....TQDETD...GERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEG.....TQDETD...GERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEG.....TQDETD...GERPEE	348
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPM.....GAVT L.AEEVEED.....	352
GEKIGQKANAIAWLKENPAAAEIEKKVRELLNNQD.....PTPAF.....TVDDNDV...AETS EDF	352
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPN.....MQLIAETSSAADDVEF...GAVP EEF	354
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPN.....MQLIAETSSAADDVEF...GAVP EEF	354
GSKIGGQKANAAKYLEENPEIGQEIEQQIRAKLLVTSA.....NTKATPVAEDLADADI	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS.....DQTAA.HDETEEEPDL...LES	349
GNKIGGQKNNVIRIFYENNQIAEIEIRNIREQLLTGT.....NGAVQ.I.EDEEPPDL...LLES	349

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		IEE	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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