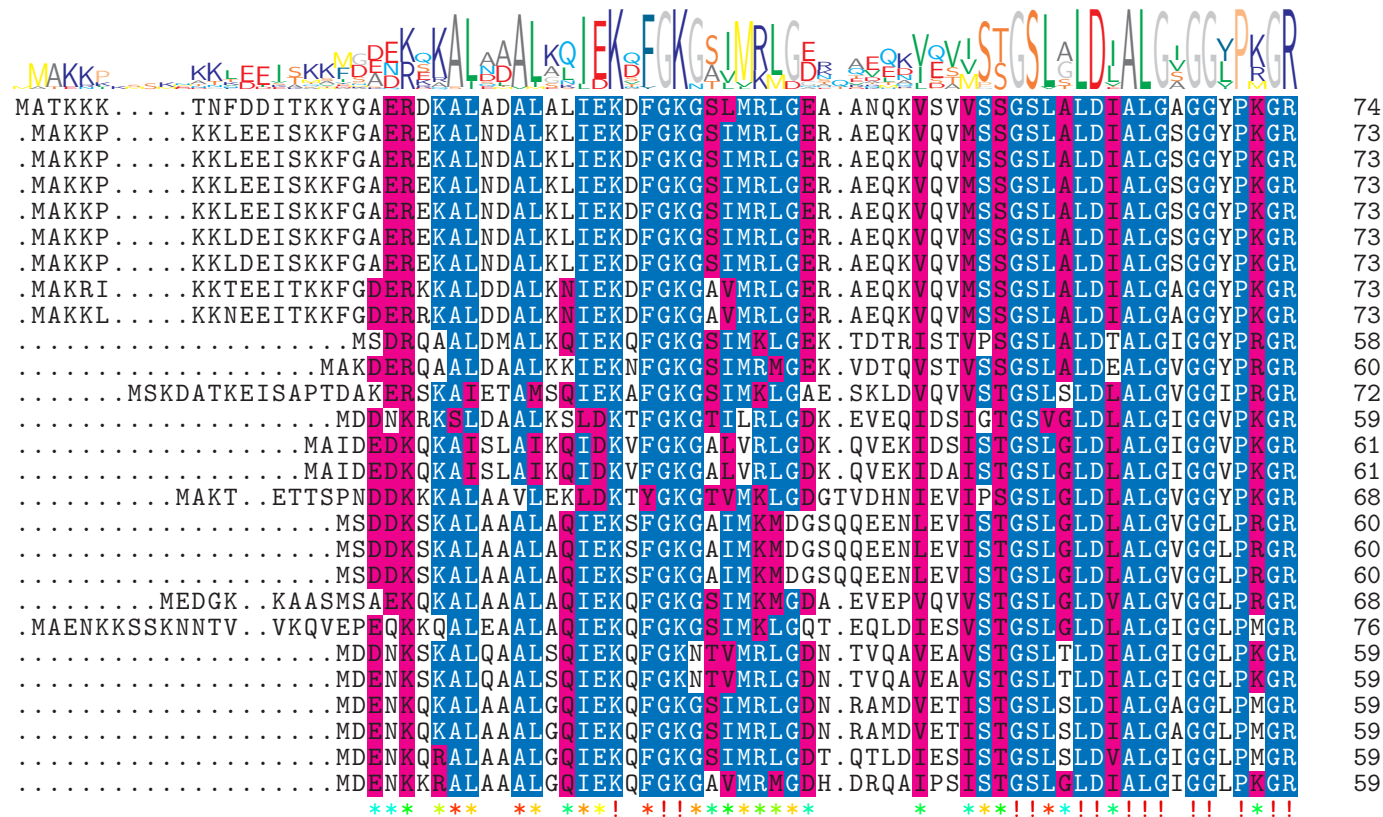


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NTDB id 453 Spy49 1753c ACI62003.1
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NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1211 C694 RS00795 WP 000963128.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 249449 CPU03 RS11025 WP 005281921.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

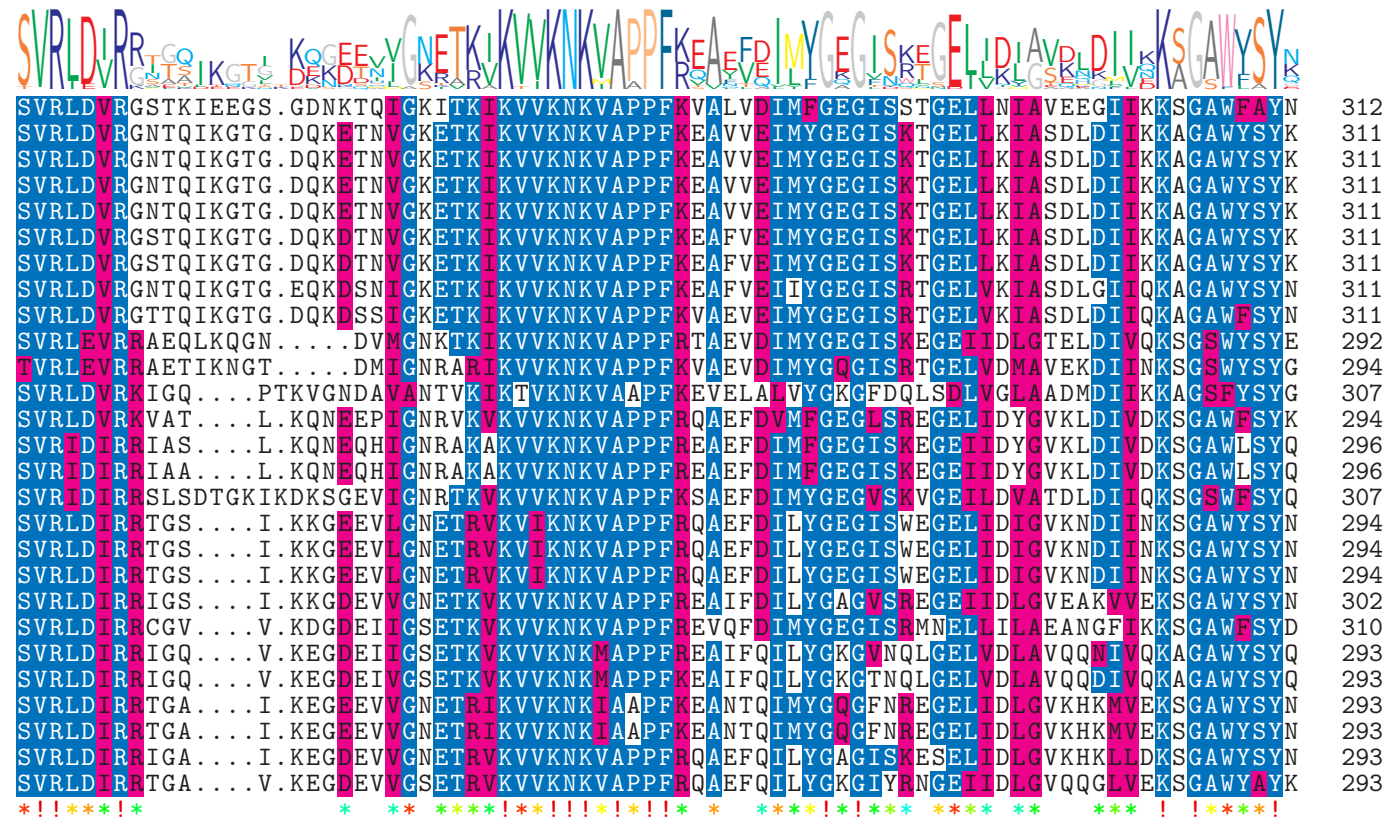
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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQSSKEK....ETDEK..ADKNLVLELDDTTIELE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE	355
DERIGGQKEKTIATYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEA..AEA	363
DKKLGGGRENAAKFLKENPEIADEITKAIQNSMGTIEGMIS.....GSEDDEGE..E.....	343
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIM....PLPDEPLE..E..ME	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIM....PLPDEPLE..E..ME	347
DTKLGGGRDVTVKELIKDNPELAELEAKIREKLQAK.....	343
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT....EGT.....QDETGDGER.PEE	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT....EGT.....QDETGDGER.PEE	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT....EGT.....QDETGDGER.PEE	348
GERIGGGRDNCREFLRNAAELAREIENKVRHGLVTPMGA....VTLA.EEV..EED	352
GTKIGGQKNNAVKWLKENPEIADKLEQEIRNTLASNPNSV....LKATASDS..NDESVDVEEF.SEEEL	372
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTASDQ....TAAHDETE....EEPDL.LES	349
GNKIGGQKNNVIRIFYEENQIAEIEIERNIREQLLTTGTNG....AVQI.EDE....EEPDL.LLES	349
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNENMQ....LIAETSSA..ADDVEFGAV.PEEF	354
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNENMQ....LIAETSSA..ADDVEFGAV.PEEF	354
GDKIGGQKANSMKFLQENPAISAELEGKIRELLSHAAAT....DAD...RA..KGEVDDDDAM.PDDENF	353
GSKIGGQKANAAYLEENPEIQEIEQQIRAKLLVTSANT....KAT...PV..AEDLADADI	347

logo

		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	IEE		388
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NTDB id 249449 CPU03 RS11025 WP 005281921.1	...		353
NTDB id 1205 PSJM300 05545 AFN77183.1	...		347
consensus			

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