

Figure S1 (Traag et al.)

A. 100% conservation

SsgA_Sgold	1	-----MSFLVS-----EELSFR	PVELRYETC-DPYAVRLTFHLP---GDAPVTW
SsgA_Sscab	1	-----MSFLVS-----EELSFR	PVELRYETC-DPYAVRLTFHLP---GDAPVTW
SsgA_Saver	1	-----MSFLVS-----EELSFR	PVELRYETC-DPFAVQLTFHLP---GDAPVTW
SsgA_Scoel	1	-----MSFLVS-----EELSFR	PVELRYETR-DPYAVRLTFHLP---GDAPVTW
SsgA_Snetr	1	-----MRESVQAEVLSFLVS-----EELSFK	PVELRYETR-DPYAVRMTFHLPL---GDAPVTW
SsgA_Sgris	1	-----MSFLVS-----EELSFR	PVELRYEVEG-DPYAVRMTFHLPL---GDAPVTW
SsgA_Salbu	1	-----MSFLVS-----EELAFR	PVELRYETV-DPYAVRLTFHLP---GDAPVTW
SsgB_Scoel	1	-----MNTTVSCELHLRLVVS-----SESSLP	PAGLRYDTA-DPYAVHATFHTG---AEETVEW
SsgB_Sscab	1	-----MNTTVSCELHLRLVVS-----SESSLP	PAGLRYDTA-DPYAVHATFHTG---AEETVEW
SsgB_Saver	1	-----MNTTVSCELHLRLVVS-----SESSLP	PAGLRYDTA-DPYAVHATFHTG---AEETVEW
SsgG_Scoel	1	----MHTNPTGPTVVERELELRLVLS-----PESGIP	PARLGYHTD-DPYAVHITFHID---SGHPVHW
SsgG_Sscab	1	----MRHTVVERELELGLVLS-----PEHTLP	PAKLGERSD-DPYAVHITFHIN---SDRPVHW
SsgY_Saver	1	-----MQLVVP-----HEISAP	SMRLRYEPS-DPYVVRAAFTAVD---SDETVEW
SsgZ_Saver	1	-----MESLKTVMQEVAVQLVVS-----RTYSL	CMSLRYEPT-DPYVVRATFFTH---TDEPTEW
SsgD_Scoel	1	-----MSTVIEQVPEARLVAA-----APRMPS	PATLHYDRA-DPFAVRMTFPAPATLEGVEVCW
SsgD_Saver	1	-----MSTVIEQVPEARLVAA-----APRMPS	PATLHYDRS-DPFAVRMTFPAPATLEGVEVCW
SsgD_Sscab	1	-----LSTVIEQVPEARLVAA-----APRMPS	PATLHYDRS-DPFAVRMTFPAPATLEGVEVCW
SsgE_Saver	1	-----MSVVEQYARAHVVSD-----APEAQDT	PVVLRYDPEVDPDRSVRIGLPG-----PHEW
SsgE_Sscab	1	-----MSVVEQYARAHVVSD-----TPDDRDT	PVVLRYDPDNDASAVRVLPG-----PDEW
SsgE_Scoel	1	-----MSVVEQYARAHLLTDGDLDPQDDGGA	PVVLRYDQLDPSKVCVALPGRGGRASGSEW
SsgV_Sscab	1	-----MTVTLEQPARALLVTA-----EDREVP	PASLRYRSD-DPLAVHLDFFADISLNGTMVTV
SsgW_Sscab	1	-----MHPAQPTMPTPPALEQARARCLITP-----AYEEVP	RTTLRYTDP-DPLAVHLDFFAGVSAGDSVTV
SsgF_Scoel	1	MSGDHHGVQAQHSAAQALLPLSLCLSQMTG-ALEWED	PAEFRYDPD-HPLLVTIRFAPEG---APPVTW
SsgC_Scoel	1	-----MNTVVHKTLVVQLQAG-----GTADRFP	LAHLAYDAA-DPFAVTVVFSHDG---RVLARW
consensus	1		i y v w

SsgA_Sgold	42	AFGRELLIDCGPRPCGD	CDVHIA	PADPETFGEVL	IRLQV----	GSDQAM	FRVGTAP	VAFT	DRD	DKIV
SsgA_Sscab	42	AFGRELLIDCGVGRPCGD	CDVHIA	PADPETFGEVL	IRLQV----	GTDQAM	FRVGTAP	VAFT	DRD	DKIV
SsgA_Saver	42	TFGRELLIDCGVGRPCGD	CDVHIA	PADREAFGEVL	IRLQV----	GGDHAI	FRSGAVP	VTF	DRD	DKIV
SsgA_Scoel	42	AFGRELLVDCVGRPCGD	CDVRI	APVEPEPLAEVL	IRLQV----	GSDQAM	FRSSAAP	VAFT	DRD	DKIV
SsgA_Snetr	52	AFGRELLLDGINRPSGD	CDVHIA	APTDEGLSDVS	IRLQV----	GADRAI	FRAGAPP	VAFT	DRD	DKSV
SsgA_Sgris	42	AFGRELLLDGLNSPSGD	CDVHIA	GTEPEGLGDVH	IRLQV----	GADRAI	FRAGTAP	VAFT	DRD	DKIV
SsgA_Salbu	42	VFGRELLVECVLDAAGD	CDVRI	CPVQGTATREVH	ITLQV----	GSEQAM	FRVGKAP	LAFT	DRD	DQGL
SsgB_Scoel	52	VFARDLLAECGLHRPTGT	CDVRI	WPSRSHGQGVV	CHALSS----	PEGEAL	LEAPARA	ESFT	KRT	DAAV
SsgB_Sscab	52	VFARDLLAECGLHRPTGT	CDVRI	WPSRSHGQGVV	CHALSS----	PEGEAL	LEAPARA	ESFT	KRT	DAAV
SsgB_Saver	52	VFARDLLAECGLHRPTGT	CDVRI	WPSRSHGQGVV	CHALSS----	PEGEAL	LEAPARA	ESFT	KRT	DAAV
SsgG_Scoel	58	TFARDLLVECVFRPSGH	CDVRI	WPSKTEGRSVV	VALSS----	PDGDAL	LEAPTPO	SAWL	ERT	LRAV
SsgG_Sscab	53	TFARELLVECVFRPCGQ	CDVRI	WPTKVSGRGVV	VALSS----	PDGDAL	LEAPAAA	SAWL	ERT	LRVV
SsgY_Saver	43	IIGRDLLIDCLEGSPVGE	CDIS	WPADGPRSDSY	ILLNP----	PAGTAL	LKARTHE	KTFT	QGT	EDLV
SsgZ_Saver	54	VLGRDLLADCLRGSAGC	CDIR	WPAVGRGDKAMY	IVLGA----	PAGTAL	LEVVPQD	KTFT	ESAE	EALV
SsgD_Scoel	55	TFSRELLIACMQEPNGH	CDVRI	RP---YAYDRTV	EFHA----	PEGTAV	IHVRSGE	RRFL	QAAG	EELV
SsgD_Saver	55	TFARELLASGMEEPVGH	CDVRI	RP---YGYDRTV	EFHA----	PEGTAV	VHVRSGE	RRFL	ERT	TEL
SsgD_Sscab	55	TFARELLVTGMEESVGH	CDVRI	RP---YGYERLV	EFHA----	PEGTAV	VHVHAGE	RRFL	EGT	IDLV
SsgE_Saver	49	AFSRDLLERCLRTPTGT	CEVRI	WP---CGRVQAV	MEFHS----	AQGVAV	VEFEAKT	FRFL	DRTY	LAT
SsgE_Sscab	50	TFPRELLERCLRTPTTS	CEVSI	WP---CGRVQAV	MEFHS----	AQGVAV	MQFDTKA	IRFL	DRTY	YAT
SsgE_Scoel	60	TFSRELLLEQLRAPAGS	CEVRI	WP---CGRVQAV	MEFHS----	PQGCSV	VQFENKA	IRFL	DRTY	YAT
SsgV_Sscab	55	TFSRELLLEKCVGAPSGN	CDVRI	WP---CGRLRTV	VELHS----	PYGTAL	LRFEKAA	QRFL	DRSY	GVV
SsgW_Sscab	64	AFARALLAECILTASAGI	CDVRI	WP---CGPAHTV	VELRS----	PHGMAM	IRFDTP	RRFL	DRRS	YAVV
SsgF_Scoel	66	HVGRDLLHECLRTTSGL	CDVRI	WADTPTDRETAV	IQVNA----	HGDIAT	FSLPVP	EEW	DRTY	LHV
SsgC_Scoel	53	TLDREMVAECLTRPVGV	CDVRI	RPESRGMWDEL	RHELLGDGRADGERHRA	VVFVWAAV	WEAFT	DR	RETHAV	
consensus	71	R 11 G	G v i	i	m	l	f l			

SsgA_Sgold	106	PLGQERSLADFDALLDEALDR	ILAEEQNASG
SsgA_Sscab	106	PLGQERSLADFDLLDEALDR	ILAEEQNASG
SsgA_Saver	106	PLGQECSLADFD AHLDEALDR	ILAEEQNASG
SsgA_Scoel	106	PLGQEGALADFD SHLDEALDR	ILAEEQNASG
SsgA_Snetr	116	PLGQEQLTGDGFEDSLEAALGK	ILAEEQNASG
SsgA_Sgris	106	PLGQEHTLGDGFDGNLEDALGR	ILAEEQNASG
SsgA_Salbu	106	SLGSERAHADFD SHLDDALNRS	LAEEQNASG
SsgB_Scoel	116	PPGTEHRHFDDLDQELSHILAES	-----
SsgB_Sscab	116	PPGTEHRHFDDLDQELSHILAES	-----
SsgB_Saver	116	PPGTEHRHFDDLDTELSHILAES	-----
SsgG_Scoel	122	PPGTEGAQLGIDDGLAELLAR	-----
SsgG_Sscab	117	PPGSEFDMLGFDDGLAELLAR	-----
SsgY_Saver	107	PRGAEPGHIDLDTSLAHFLAEG	-----
SsgZ_Saver	118	PRGTESGHIDWDREVANLFAKG	-----
SsgD_Scoel	116	PVGLEHLQLDLDHDLAELMRGSC	-----
SsgD_Saver	116	PVGLEHLQIDLDHDLAELMRDAC	-----
SsgD_Sscab	116	PLGLEHHVLDLDHDLAQLMRDAC	-----
SsgE_Saver	110	PVPH-----	-----
SsgE_Sscab	111	PVAH-----	-----
SsgE_Scoel	121	AQPVAH-----	-----
SsgV_Sscab	116	PAGREELGPALDRGLTSLLRGV	-----
SsgW_Sscab	125	PLGGEGLGPAFDDGLASLLDGV	-----
SsgF_Scoel	130	PAGTESRRLGTD AFLSKLFDEPEASSR	---
SsgC_Scoel	123	RPGREE--VRVDDFLAELTAEG	-----
consensus	141		

**Figure S1 (contd.)**  
**B. 50% conservation**

```

SsgA_Sgold 1 -----MSFLVS-----EELSFRLPVELRYETC-DPYAVRLTFHLP---GDAPVTW
SsgA_Sscab 1 -----MSFLVS-----EELSFRLPVELRYETC-DPYAVRLTFHLP---GDAPVTW
SsgA_Saver 1 -----MSFLVS-----EELSFRLPVELRYETC-DPYAVRLTFHLP---GDAPVTW
SsgA_Scoel 1 -----MSFLVS-----EELSFRLPVELRYETR-DPYAVRLTFHLP---GDAPVTW
SsgA_Snetr 1 -----MRESVQAEVLSFLVS-----EELSFRLPVELRYETR-DPYAVRLTFHLP---GDAPVTW
SsgA_Sgris 1 -----MSFLVS-----EELSFRLPVELRYEYVG-DPYAVRLTFHLP---GDAPVTW
SsgA_Salbu 1 -----MSFLVS-----EELAFRLPVELRYETV-DPYAVRLTFHLP---GDAPVTW
SsgB_Scoel 1 -----MNTIVSCEHLRLVVS-----SESSLPVPAGLRYDTA-DPYAVHATFFHTG---AETVVEW
SsgB_Sscab 1 -----MNTIVSCEHLRLVVS-----SESSLPVPAGLRYDTA-DPYAVHATFFHTG---AETVVEW
SsgB_Saver 1 -----MNTIVSCEHLRLVVS-----SESSLPVPAGLRYDTA-DPYAVHATFFHTG---AETVVEW
SsgG_Scoel 1 ----MHTNPTGPTVVEREELRLVLS-----PEGIPVPEARLGYHID-DPYAVHATFFHID---SGHPVHW
SsgG_Sscab 1 ----MRHIVVEREELRLVLS-----PEHLPVPAKLGFRSD-DPYAVHATFFHIN---SDRPVHW
SsgY_Saver 1 -----YQLVVP-----HEISAPVSMRLRYEFS-DPYVVRAAFVAVD---SDETVEW
SsgZ_Saver 1 ----MESLKTVMQEVAVQLVVS-----RTYSLVCMSLRYEPT-DPYVVRATFFTH---TDETEW
SsgD_Scoel 1 ----MSIVLEQVPEARLVAA-----APRMPSPATLHYDRA-DPYAVRMTFPAPATLEGVEVWCW
SsgD_Saver 1 ----MSIVLEQVPEARLVAA-----APRMPSPATLHYDRS-DPYAVRMTFPAPATLEGVEVWCW
SsgD_Sscab 1 ----LSIVLEQVPEARLVAA-----APRMPSPATLHYDRS-DPYAVRMTFPAPATLEGVEVWCW
SsgE_Saver 1 ----MSVVEQYARAHVSD-----APEAQDTVPVVLRYDPEVDPRSVRGLPG-----EHEW
SsgE_Sscab 1 ----MSVVEQYARAHVSD-----TPDDRDTVPVVLRYDPEVDPRSVRGLPG-----EDEW
SsgE_Scoel 1 ----MSVVEQYARAHVSD-----TPDDRDTVPVVLRYDPEVDPRSVRGLPG-----EDEW
SsgV_Sscab 1 ----MTVILEQPARALLVTA-----EDREVPVHSLRYRSD-DPYAVHATFFPADISLNGTMTW
SsgW_Sscab 1 ----MHPAQPTMPTPALRQARACLITP-----AYEEVVRTTLRYTPD-DPYAVHATFFPAGVSAQVSVTW
SsgF_Scoel 1 MSGDHHGVQAQHSAAQALPLSLCLQSMGTG-ALEWEDVFAEFRYDPD-HPLLVTRFAPEG---APPVTW
SsgC_Scoel 1 ----MNTIVVHKTIVVQLQAG-----GTADRFPVLAHLAYDAA-DPYAVRLTFVSHDG---RVLARW
consensus 1 t v v m lvvs e s vpv lryet dpyavrltfh gd pv W

```

```

SsgA_Sgold 42 AFGRELLIDGGRPCGGDGDVHILAPADPETFGEVLIIRLQV-----GSDQAMFRVGTAPLVAFLDRTDKIV
SsgA_Sscab 42 AFGRELLIDGGRPCGGDGDVHILAPADPETFGEVLIIRLQV-----GTDQAMFRVGTAPLVAFLDRTDKIV
SsgA_Saver 42 TFGRELLIDGGRPCGGDGDVHILAPADREAFGEVLIIRLQV-----GGDHALFRSGAVPLVTFDRTDKIV
SsgA_Scoel 42 AFGRELLVDGGRPCGGDGDVHILAPVEPEPLAEVLIIRLQV-----GSDQALFRSSAAPLVAFLDRTDKIV
SsgA_Snetr 52 AFGRELLLDGINRPSGDDGDVHILAPTDPEGLSDVSIIRLQV-----GADRALFRAGAPLVAFLDRTDKIV
SsgA_Sgris 42 AFGRELLLDGLNSPSGDDGDVHILGTEPEGLGDVHILRQV-----GADRALFRAGTAPLVAFLDRTDKIV
SsgA_Salbu 42 VFGRELLVGVLDAAAGDGDVVRVCPVQGTATREVVHITLQV-----GSEQALFRVGKAPLVAFLDRTDQGL
SsgB_Scoel 52 VFARDLLAELHRRPTGTIGDVRVWPSRSHGQGVVCHALSS-----PEGEALLEAPARAESEFLKRTDAAV
SsgB_Sscab 52 VFARDLLAELHRRPTGTIGDVRVWPSRSHGQGVVCHALSS-----PEGEALLEAPARAESEFLKRTDAAV
SsgB_Saver 52 VFARDLLAELHRRPTGTIGDVRVWPSRSHGQGVVCHALSS-----PEGEALLEAPARAESEFLKRTDAAV
SsgG_Scoel 58 TFARDLLVEGFRPSCGHGDVRVWPSKTEGRSVVLMALSS-----PDGDALLEAPTQVSAWLERLTLRAV
SsgG_Sscab 53 TFARELLVEGFRPCGGDGDVRVWPTKVSGRGVLMALSS-----PDGDALLEAPAAAWSAWLERLTLRVV
SsgY_Saver 43 IIGRDLLIDGLEGVGEGDISLWADGPDPRSDSYILLNP-----PAGTALLKARTHEKTFIQGTEDLV
SsgZ_Saver 54 VLERDILLADGLRGSAGCGDIRVWPVAVGRGDKAVYIVLGA-----PAGTALLEVPVQDKTFLESAAHALV
SsgD_Scoel 55 TFSRELLIAGMQEENGHGDVVRVPE---YAYDRTVLEFHA-----PEGTAVVHVRSGEIRRFQAAAGELV
SsgD_Saver 55 TFARELLASGMEEPVGHGDVVRVPE---YGYDRTVLEFHA-----PEGTAVVHVRSGEIRRFLERTTELV
SsgE_Sscab 55 TFARELLVTGMEESVGHGDVVRVPE---YGYERLVLEFHA-----PEGTAVVHVRSGEIRRFLEGTIDLV
SsgE_Saver 49 AFSRDLLERGLRPTGTGCEVRVWPE---CGRVQAVMEFHS-----AQQVAVVEFEAKTFRFRRTTYLAT
SsgE_Sscab 50 TPRELLERGLRPTTSCPVSTWPE---CGRVQAVMEFHS-----AQQVAVMQFDTKALIRFRRTTYTAV
SsgE_Scoel 60 TFSRELLEQLRABAGSGEVRVWPE---CGRVQAVMEFHS-----PQGCVVQFENKALIRFRRTTYAAT
SsgV_Sscab 55 TFSRELLEKGVGAPSGNGDVHILWPE---CGRVQAVMEFHS-----PYGTALLRFEKAALQRFLLRSYGVV
SsgW_Sscab 64 AFARDLLAELGLTASAGIGDVHILWPE---CGPAHTVVELRS-----PHGMAMIRFDTPTRFRFRRSYAVV
SsgF_Scoel 66 HVGRDLLHEGLRSTTSGLDVQVWADTPTDRETAWLQVNA-----HGDIAIFSLPVPPEEHWDRTYLHV
SsgC_Scoel 53 TLDREMVVAGLTRVGVGDVVRVPEESRGMWDEIRTEELGSDGRADGERHRAVVFVWAAAVAEAFRETHAVV
consensus 71 fgRelidGl p g Gdvrvwp g vli l p g allr l fldrtd iv

```

```

SsgA_Sgold 106 PLGQERSLADFDALLDEALDRILAEEQNAG
SsgA_Sscab 106 PLGQERSLADFDTLDEALDRILAEEQSAG
SsgA_Saver 106 PLGQECSLADFDALHDEALDRILAEEQSAG
SsgA_Scoel 106 PLGQEGALADFDSHLDEALDRILAEEQSAG
SsgA_Snetr 116 PLGQEQLGDFEDSLEAALGKILAEEQNAG
SsgA_Sgris 106 PLGQEHTLGDFDGNLEDALGRILAEEQNAG
SsgA_Salbu 106 SLGSERAHADFDSHLDDALNRSLAEEQSAG
SsgB_Scoel 116 PPGTEHRRHFDLDQELSHLLAES-----
SsgB_Sscab 116 PPGTEHRRHFDLDQELSHLLAES-----
SsgB_Saver 116 PPGTEHRRHFDLDTELSHLLAES-----
SsgG_Scoel 122 PPGTEGAQLGIDDCGLAELLAR-----
SsgG_Sscab 117 PPGSEFDMLGFDDGLAELLAR-----
SsgY_Saver 107 PRGAEFGHIDLDTSLAHFLAEG-----
SsgZ_Saver 118 PRGTESGHIDWDREMANLFAKG-----
SsgD_Scoel 116 PVGLEHLQLDLDHDLAELMRGSC-----
SsgD_Saver 116 PVGLEHLQLDLDHDLAELMRDAC-----
SsgD_Sscab 116 PVGLEHHHVLDLDHDLAELMRDAC-----
SsgE_Saver 110 PVPH-----
SsgE_Sscab 111 PVAH-----
SsgE_Scoel 121 AQPVAH-----
SsgV_Sscab 116 PAGREELGPALDRGLTSLLRGV-----
SsgW_Sscab 125 PLGGEGLGPAFDGCLASLDGV-----
SsgF_Scoel 130 PAGTESSRLGTDALSKLFDEPEASSR---
SsgC_Scoel 123 RFGREE--VRVDDFLAELTAEG-----
consensus 141 plg e d d l il

```

**Figure S1. Alignment of SsgA-like proteins (SALPs).** Conserved residues are highlighted by black shading (complete conservation) or grey shading (includes so-called conserved changes, such as Arg or Lys). Figures represent 100% conservation (A) or 50% conservation among all SALPs analysed (B). Nomenclature is based on highest sequence homology to the *S. coelicolor* SALP homologues. Contigs refer to short sequence files extracted from the *S. scabies* database ([www.sanger.ac.uk/Projects/S\\_scabies](http://www.sanger.ac.uk/Projects/S_scabies)). The complete genome sequences of *S. avermitilis* (Ikeda *et al.*, 2003) and *S. coelicolor* (Bentley *et al.*, 2002) have been published. Proteins, abbreviations and accession numbers are presented in the Table below. Alignment was produced using the ClustalW algorithm and presentation produced using the BoxShade webserver (see Materials and Methods section).

Short name	SALP	Organism of origin	Database or contig number
SsgA_Scoel	SsgA	<i>S. coelicolor</i>	SCO3926
SsgB_Scoel	SsgB	<i>S. coelicolor</i>	SCO1541
SsgC_Scoel	SsgC	<i>S. coelicolor</i>	SCO7289
SsgD_Scoel	SsgD	<i>S. coelicolor</i>	SCO6722
SsgE_Scoel	SsgE	<i>S. coelicolor</i>	SCO3158
SsgF_Scoel	SsgF	<i>S. coelicolor</i>	SCO7175
SsgG_Scoel	SsgG	<i>S. coelicolor</i>	SCO2924
SsgA_Saver	SsgA	<i>S. avermitilis</i>	SAV4267
SsgB_Saver	SsgB	<i>S. avermitilis</i>	SAV6810
SsgD_Saver	SsgD	<i>S. avermitilis</i>	SAV1687
SsgE_Saver	SsgE	<i>S. avermitilis</i>	SAV3605
SsgY_Saver	SsgY	<i>S. avermitilis</i>	SAV570
SsgZ_Saver	SsgZ	<i>S. avermitilis</i>	SAV580
SsgA_Sscab	SsgA	<i>S. scabies</i>	contig: scab0274d04.q1k
SsgB_Sscab	SsgB	<i>S. scabies</i>	contig: scab0975f02.p1k
SsgD_Sscab	SsgD	<i>S. scabies</i>	contig: scab0372d01.q1k
SsgE_Sscab	SsgE	<i>S. scabies</i>	contig: scab0136f09.q1k
SsgG_Sscab	SsgG	<i>S. scabies</i>	contig: sab0313c04.q1k
SsgV_Sscab	SsgV	<i>S. scabies</i>	contig: scab0162c08.q1k
SsgW_Sscab	SsgW	<i>S. scabies</i>	contig: scab0039b09.q1k
SsgA_Salbu	SsgA	<i>S. albus</i>	AF195771
SsgA_Sgold	SsgA	<i>S. goldeniensis</i>	AF195773
SsgA_Sgris	SsgA	<i>S. griseus</i>	BAA21558
SsgA_Snetr	SsgA	<i>S. netropsis</i>	AF195772