SUPPLEMENTARY MATERIAL

belonging to the manuscript

A novel taxonomic marker that discriminates between morphologically complex actinomycetes

by

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Table S1. Number of SALPs and developmental characteristics of completely sequenced actinomycetes. For a list of all protein sequences and their accession numbers see Supplemental Data file 5.

Species	NCBI reference sequence	genome size (Mbp)	Nr of SALPs	cell morphology, development
Streptomyces avermitilis	NC_003155	9	6	aerial mycelium, long spore chains
Streptomyces coelicolor	NC_003888	8.7	7	
Streptomyces griseus	NC_010572	8.5	5	
Streptomyces scabiei	NC_013929	10.1	7	
Streptomyces clavuligerus	NZ_CM001015	9.1	6	
Kitasatospora setae	NC_016109	8.8	12	
Amycolatopsis mediterranei U32	NC_014318	10.2	5	short spore chains
Frankia alni	NC_008278	7.5	5	multisporous sporangium
Frankia sp. CcI3	NC_007777	5.4	3	
Frankia sp. EAN1pec	NC_009921	9	3	
Frankia sp. QA3	NZ_CM001489	7.6	4	
Frankia symbiont of Datisca glomerata	NC_015656	5.3	2	sporangium
Actinosynnema mirum	NC_013093	8.3	2	dome like structures with Synnemata
Pseudonocardia dioxanivorans	NC_015312	7.4	2	budding and fragmenting aerial mycelium
Saccharomonospora viridis	NC_013159	4.3	2	single spores in aerial mycelium
Saccharothrix espanaensis	NC_019673	9.4	2	nocardioform mycelia and rod-shaped spores
Saccharopolyspora erythraea	NC_009142	8.2	3	spore chains with spiny spores
Saccharopolyspora spinosa NRRL 18395	NZ_AEYC00000000	8.5	8	
Streptosporangium roseum	NC_013595	10.4	2	sporangia on aerial hyphae
Acidothermus cellulolyticus	NC_008578	2.4	1	long slender filaments, no spores
Actinoplanes missouriensis	NC_017093	8.8	1	sporangium in mycelium
Blastococcus saxobsidens DD2	NC_016943	4.9	1	aggregated cocci or rods forming multiseptate filaments
Catenulispora acidiphila	NC_013131	10.5	1	chains of cylindrical arthrospores
Cellulomonas fimi	NC_015514	4.3	1	irregular rod shape, no spores
Geodermatophilus obscurus	NC_013757	5.3	1	aggregated cocci or rods forming multiseptate filaments
Kineococcus radiotolerans	NC_009664	5.0	1	multicellular structures
Micromonospora	NC_014391	7.0	1	single spores from vegetative

aurantiaca				mycelium
Modestobacter marinus	NC_017955	5.6	1	aggregated cocci or rods forming multiseptate filaments
Nakamurella multipartita	NC_013235	6.1	1	cocci in small irregular clusters; no spores
Nocardioides sp. JS614	NC_08699	5.3	1	rods or cocci, no spores
Nocardiopsis alba	NC_018524	5.9	1	hyphae that fragment into smooth rod-shaped spores
Salinispora arenicola	NC_009953	5.8	1	single spores from vegetative mycelium
Salinispora tropica	NC_009380	5.2	1	
Stackebrandtia nassauensis	NC_013947	6.8	1	fragmenting aerial hyphae
Thermobifida fusca	NC_007333	3.6	1	single spores borne on branched sporophores
Thermobispora bispora	NC_014165	4.2	1	aerial mycelia branch monopodally and bear longitudinal pairs of spores
Thermomonospora curvata	NC_013510	5.7	1	single, warty spores on sporophores (on vegetative and aerial hyphae)
Verrucosispora maris	NC_015434	6.7	1	single spores from mycelium

Figure S1. Maximum-likelihood tree based on the alignment of SALPs proteins from a range of morphologically complex actinomycetes. For input sequences and their accession numbers see Supplemental Data file 5.

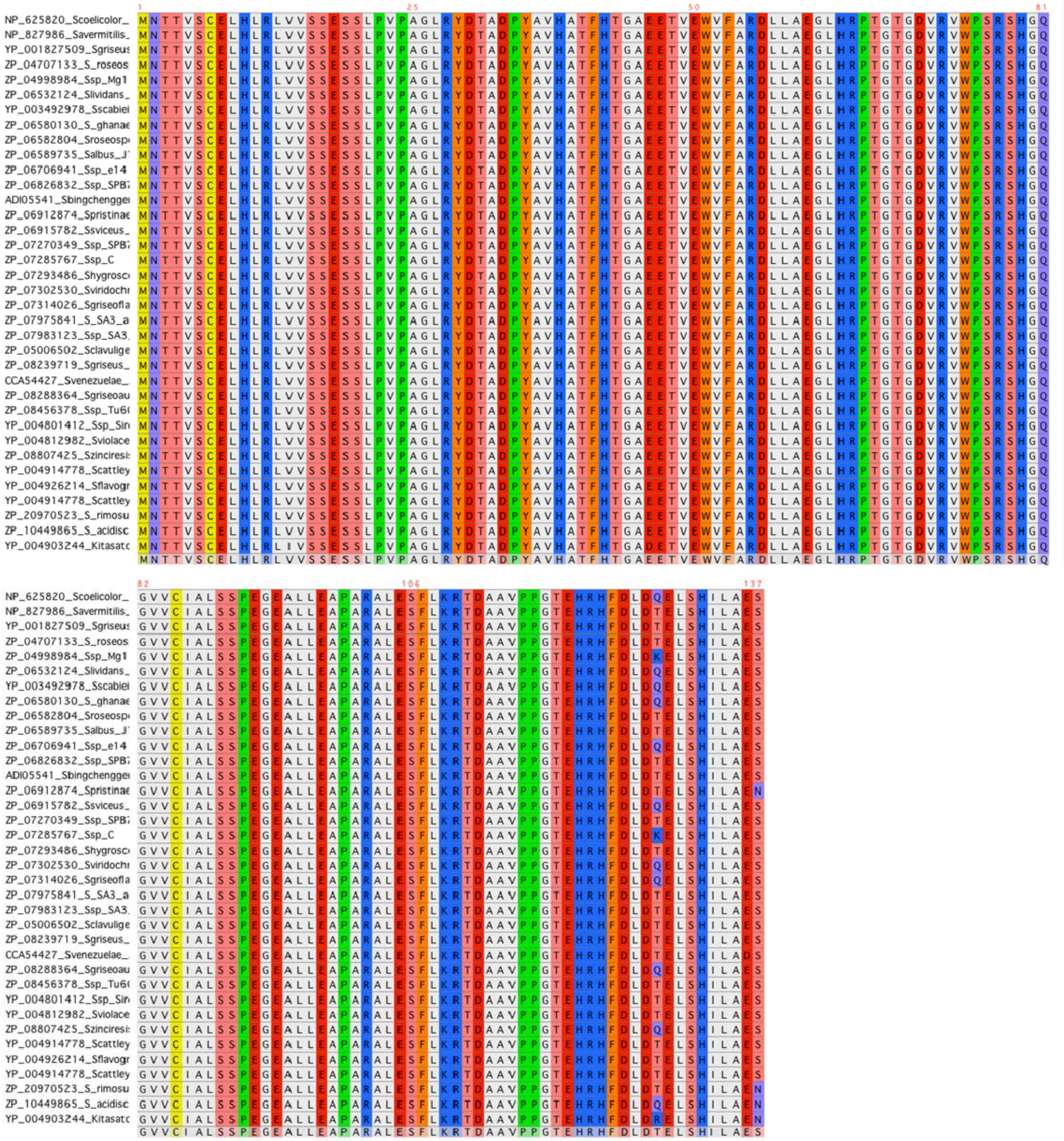

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Figure S2. Alignment of SsgB orthologues. All species are *Streptomyces* sp., except *Kitasatospora setae* at the bottom. For input sequences and their accession numbers see Supplemental Data file 5.

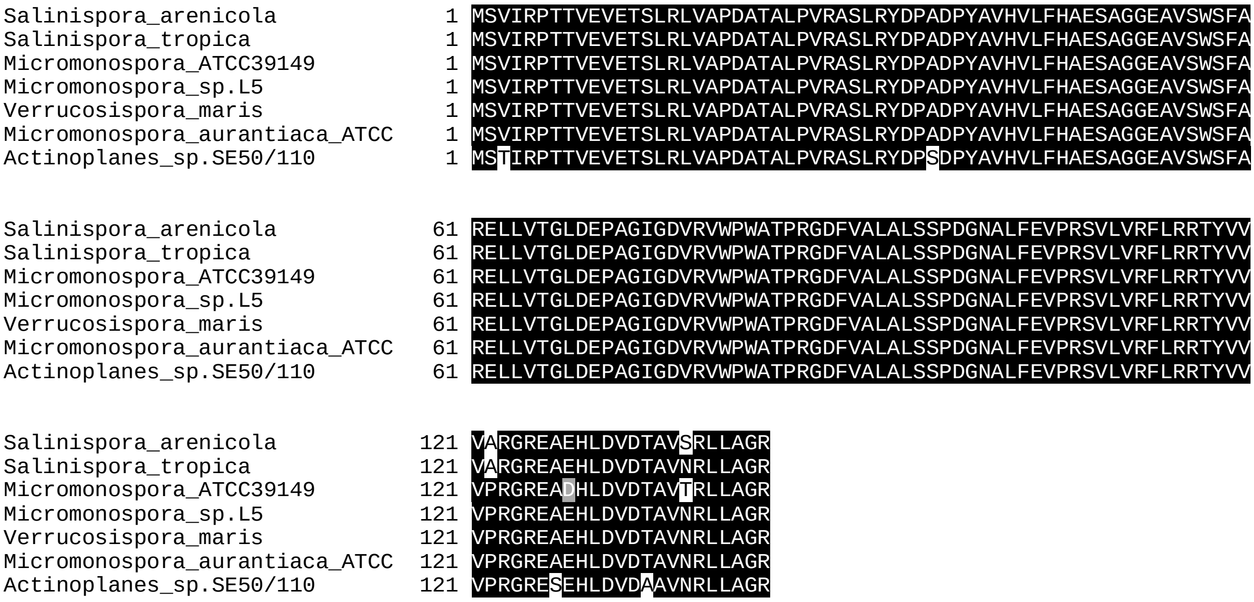

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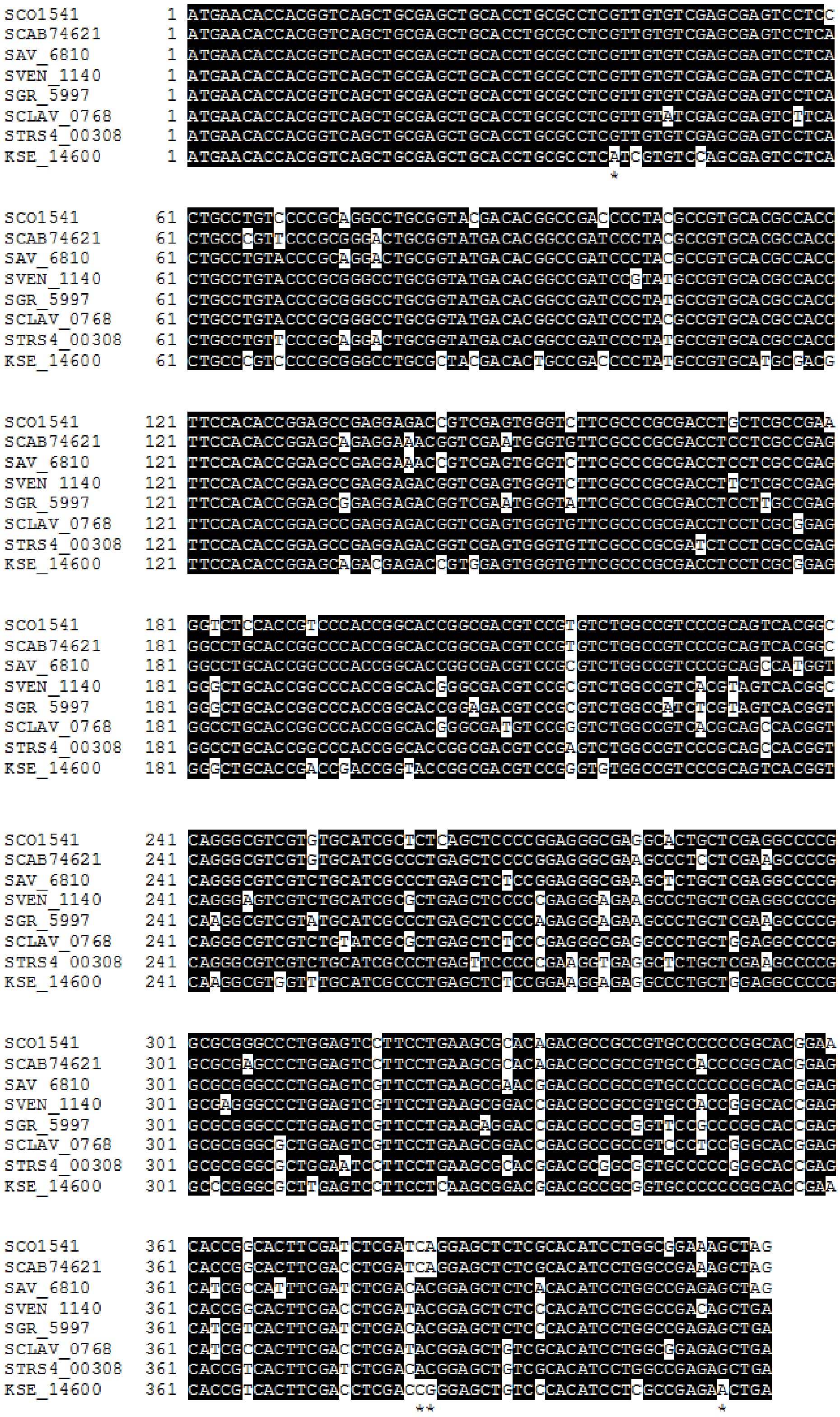
Figure S3. Alignment of SsgB proteins from *Micromonospora*, *Salinispora* and *Verrucosispora*. Species from which SsgB orthologues originate are indicated on the left. For shading, at least 50% of the aligned proteins should share the same or similar aa residues. Identical residues shaded black, similar residues shaded grey. For input sequences and their accession numbers see Supplemental Data file 1.



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SGR_5997     301 GCGCGGGCCCTGGAGTCGTTCCTGAAGAGGACCGACGCCGCGGTTCCGCCCGGCACCGAG
SCLAV_0768   301 GCGCGGGCGCTGGAGTCGTTCCTGAAGCGGACCGACGCCGCCGTCCCTCCGGGCACGGAG
STRS4_00308  301 GCGCGGGCGCTGGAATCCTTCCTGAAGCGCACGGACGCGGCGGTGCCCCCGGGCACCGAG
KSE_14600    301 GCCCGGGCGCTTGAGTCCTTCCTCAAGCGGACGGACGCCGCGGTGCCCCCCGGCACCGAA

SCO1541      361 CACCGGCACTTCGATCTCGATCAGGAGCTCTCGCACATCCTGGCGGAAAGCTAG
SCAB74621    361 CACCGGCACTTCGACCTCGATCAGGAGCTCTCGCACATCCTGGCCGAAAGCTAG
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STRS4_00308  361 CACCGTCACTTCGATCTCGACACGGAGCTGTCGCACATCCTGGCCGAGAGCTGA
KSE_14600    361 CACCGTCACTTCGACCTCGACCGGGAGCTGTCCCACATCCTCGCCGAGAACTGA
                                      **                           *
```

Figure S4. Alignment of *ssgB* genes from *Streptomyces* and *Kitasatospora*. The locus of each gene within corresponding genomes is indicated. The *ssgB* genes are from the genome sequences of *Streptomyces coelicolor* (SCO1541), *S. scabies* (Scab74621), *S. avermitilis* (SAV_6810), *S. venezuelae* (SVEN1140), *S. griseus* (SGR_5997) *S. clavuligerus*

(SCLAV_0768), *S. sp. S4* (STRS4_00308) and *Kitasatospora setae* (KSE_14600).

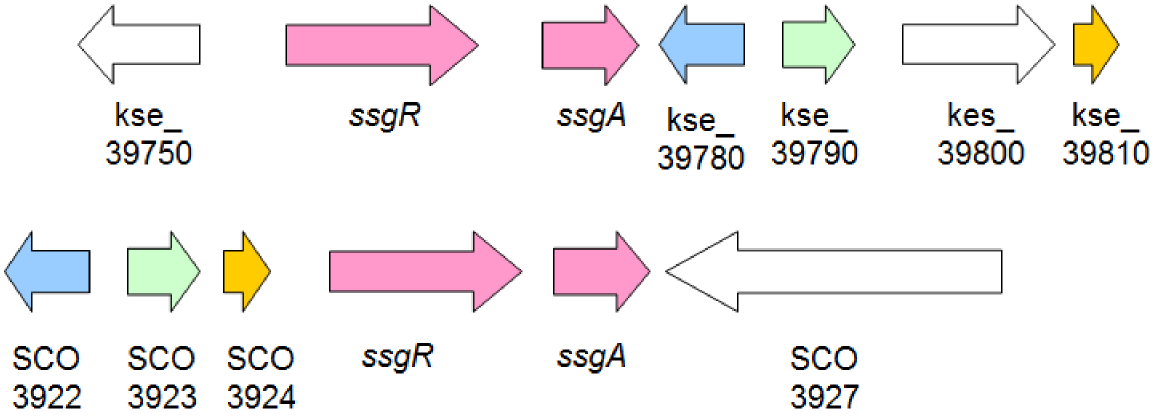
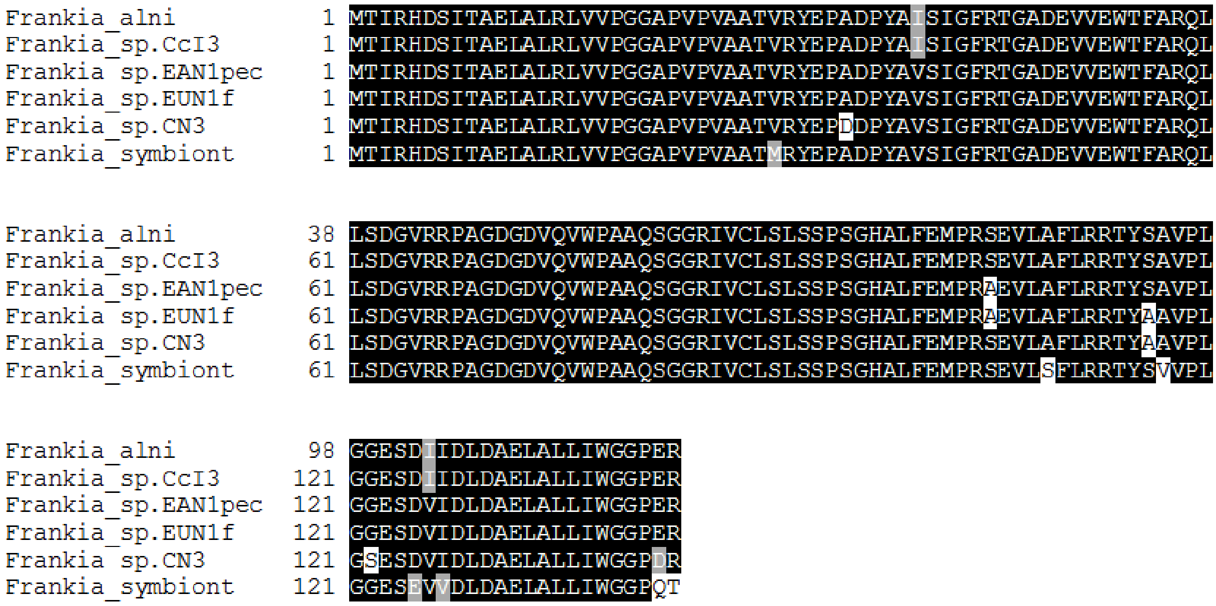


Figure S5. Gene synteny around *ssgA* from *Streptomyces coelicolor* and *Kitasatospora setae*. Direct orthologues are presented in the same colours (white genes are not related).



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Frankia_sp.EAN1pec      1 MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAVSIGFRTGADEVVEWTFARQL
Frankia_sp.EUN1f        1 MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAVSIGFRTGADEVVEWTFARQL
Frankia_sp.CN3          1 MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPDDPYAVSIGFRTGADEVVEWTFARQL
Frankia_symbiont        1 MTIRHDSITAELALRLVVPGGAPVPVAATMRYEPADPYAVSIGFRTGADEVVEWTFARQL

Frankia_alni           38 LSDGVRRPAGDGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYSAVPL
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Frankia_sp.EAN1pec     61 LSDGVRRPAGDGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRAEVLAFLRRTYSAVPL
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Frankia_sp.CN3         61 LSDGVRRPAGDGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYAAVPL
Frankia_symbiont       61 LSDGVRRPAGDGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLSFLRRTYSVVPL

Frankia_alni           98 GGESDIIDLDAELALLIWGGPER
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Frankia_symbiont      121 GGESEVVDLDAELALLIWGGPQT
```

Figure S6. Alignment of SsgB orthologues from different *Frankia* species. Species from which SsgB orthologues originate are indicated on the left. For shading, at least 50% of the aligned proteins should share the same or similar aa residues. Identical residues shaded black, similar residues shaded grey. For input sequences and their accession numbers see Supplemental Data file 1.

Supplemental Data file 1. 16S rRNA sequences from actinomycetes used as input for Figure 1.

```
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complete genome
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Supplemental Data file 2. RpoB protein sequences from actinomycetes used as input for Figure 2.

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JS614]
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PLMTPKGTFIINGTERVVVSQLVRSPGVYFDRSLDKASDKDIYGCRIIPSRGAWLEFEIDKRDNVGVRID
RKRKQPVTVLLKALGWTEARIREHFGAYESMNITLEKDHTSGQDDALLDIYRKLRPGEPPTKESAQALLE
NLYFNPKRYDLAKVGRYKVNKKLGLRLDMNQGTLTEDDIVATIEYLVRLHAGEEEAVLTAAGPEGVSVPI
```

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EIDDIDHFGNRRLRTVGELIQNQVRLGLARMERVVRERMTTQDVEAITPQTLINIRPVVASIKEFFGTSQ
LSQFMDQTNPLAGLTHKRRLSALGPGGLSRERAGFEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSAYGR
VNPFGFIETPYRKVVDGRVTDEIHYLTADEEDRYIKAQANSPLNPDGTFAEEKVLVRTKGGEIEYLPPEE
VHYMDVSPRQMTSVATAMIPFLEHDDANRALMGSNMQRQAVPLLRSEAPLVGTGMEYRAATDAGDVILAE
KPGVVEEVSADYITVLNDDGTRTTYRVAKFKRSNQGTCFNQKPIVDEGQRVEAGQVIADGPCTDQGEMAL
GKNLLVAFMPWEGHNYEDAIILSQRLVQDDVLSSIHIEEHEVDARDTKLGPEEITRDIPNVSEEVLADLD
ERGIIRIGADVVPGDILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGEQGKVIGVRVFSR
EEGDELPPGVNELVRVYVAQKRKITDGDKLAGRHGNKGVIAKILPVEDMPFLEDGTPVDIILNPLGVPGR
MNVGQVLETHLGWVASQGWKIEGDDADWKRSLQAIGATEAGPWTKTATPVFDGAREEEITGLLSCTLPNR
DGMRLIGPNGKAKLYDGRTGEPFKDPIAVGYIYILKLLHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQ
RFGEMEVWALEAYGAAYALQELLTIKSDDVLGRVKVYEAIVKGENIPEPGIPESFKVLIKEMQSLCLNVE
VLSSDGMSIEMRDSDEDVFRAAEELGIDLSRREPSSVEEV
>gi|330470182|ref|YP_004407925.1| rpoB gene product [Verrucosispora
maris AB-18-032]
MAASRPAKTSRTSSAFAPRRVSFGRITEHLEVPNLLAIQNESFDWLVGNEAWQGRSADDPHARSGLAEIL
DEISPIEDFSGTMSLSFSAPRFDEVKASIEECKEKDLTYCAPLFVTAEFTNNTTGEIKSQTVFMGDFPMM
TPKGTFIINGTERVVVSQLVRSPGVYFDKQPDKTSDRDLSSVKVIPSRGAWLEFDIDKRDTVGVRIDRKR
RQAVTVLLKAIGWSAERIREKFGWSELMMTTLEKDHIAGQDEALLDIYRKLRPGEPPTRENAQTLLDNLF
FNPKRYDVAKVGRYKFNKKLELDVPITTGTLTEDDIVATVEYLCRLHAGEEGYEADDIDHFGNRRLRTVG
ELIQNQVRVGLSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIREFFGTSQLSQFMDQTNPLAGLTHR
RRLSALGPGGLSRERAGFEVRDVHPSHYGRMCPIETPEGPNIGLIGALSTFARVNPFGFIETPYRKVVDG
RVTDQIDYLTADEEDRFVKAQANAPLRADGTFAEDRVLVRRKGGETEDVPPAAVDYMDVSPRQMTSVATA
MIPFLEHDDANRALMGANMQRQAVPLVKAESPLVGTGMEYRAAVDAGDVVVAEVGGVVEDLCADYITVHQ
DDGHRRTYLLHKFRRSNAGSCVNQKPVVFEGDRVEAGQVIADGPCTDEGEMALGRNLLVAFMCWEGHNYE
DAIILSQRLVQQDVLTSIHIEEHEVDARDTKLGPEEITRDIPNVSEEMLADLDERGIIRIGAEVVPGDIL
VGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGETGTVIGVRTFSREDGDELPPGVNELVRVY
VAQKRKIQDGDKLAGRHGNKGVISKILPVEDMPFLEDGTPVDIVLNPLGVPSRMNIGQVLETHLGWVAKT
GWKVEGDDAEWKRQLQSIGADSSEPDTNVATPVFDGAREEEISGLLASTLPNRDGKQLIGATGKAQLFDG
RSGEPLPDPIAVGYIYILKLNHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAY
ALQELLTIKSDDVLGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGVALEMRETDDE
VFRAAEELGIDLSRREPSSVEEV
```

Supplemental Data file 3. SsgB protein sequences from actinomycetes used as input for Figure 3.

```
>gi|117928576|ref|YP_873127.1| sporulation and cell division protein
SsgA [Acidothermus cellulolyticus 11B] (Acel_1369)
MNASVHIIEVTEFHLLLDGDSRVITARLHYDPADPYVITVHFDTGVTWVLGRDLLADGLH
MEIGDGDVHLRPEGDQLFLTLRSPSGEALLAASRSAIAGFMADTERVVPRGTEHLRVDLD
KELARLLP
>gi|383781699|ref|YP_005466266.1| unnamed protein product [Actinoplanes
missouriensis 431] SsgB 40% AMIS_65300
MSTIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGRESDHLDVDAAVNRLL
AGR
>gi|359839220|gb|AEV87661.1| sporulation and cell division protein SsgA
[Actinoplanes sp. SE50/110] ACPL_6779 SCO1541 50%
MSTIRPTTVEVETSLRLVAPDATALPVRASLRYDPSDPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGRESEHLDVDAAVNRLL
AGR
>gi|256376149|ref|YP_003099809.1| sporulation and cell division protein
SsgA [Actinosynnema mirum DSM 43827] (Amir_2015)
mrndhvtlrstavfdllaprtpavpvqvelrydtkdpyaviaafrtgragwvewvfardl
ladgliadagdgdvrirpaaddpevvvielsspsghamfeasaqeladfldrtydvvvpg
nehlwvdvdealthlisndls
>gi|399539086|ref|YP_006551748.1| sporulation and cell division protein
SsgA [Amycolatopsis mediterranei S699]
MRNDHVTLRSTAVFDLLAPRTPAVPVKVELRYDTRDPYAVVAAFRTGRAGWVEWVYARDLLADGLLADAG
DGDVRIRPSVEDPEAVLIELNSPSGHAMFEASAQELADFLDRTYDVVLPGNEHLWVDVDDALTHLIPHDL
A
>gi|300787203|ref|YP_003767494.1| sporulation and cell division protein
SsgA [Amycolatopsis mediterranei U32] (Amed_5330)
mrndhvtlrstavfdllaprtpavpvkvelrydtrdpyavvaafrtgragwvewvyardl
ladglladagdgdvrirpsvedpeavlielnspsghamfeasaqeladfldrtydvvlpg
nehlwvdvddalthliphdla
>gi|379735734|ref|YP_005329240.1| unnamed protein product [Blastococcus
saxobsidens DD2] BLASA_2304 SsgB 40%
MPGHISPITLQLIGPQSWTEVPALLCYDPADPFAVRIAFGDPGEQDPADGDEGIAWLVSRELLQAGLEHP
AGDGDVRVWPAHATADVLFLHLRAPSGEALFELSRGTVAAFLRHTEALVPTGSETGLLHLDQELDALLSN
GGPDAPGR
>gi|256391413|ref|YP_003112977.1| sporulation and cell division protein
SsgA [Catenulispora acidiphila DSM 44928] (Caci_2217)
msssvtcelqlrlvisgdsslpvpaglrydtadpyavhatfhtggqdtvdwvfarellae
glrrptgtgdvrvwpsrsrgqaivclalsspegealleaparalesflkrtntavppgle
hrfydldaelvhlfadn
>gi|332670552|ref|YP_004453560.1| sporulation and cell division protein
SsgA [Cellulomonas fimi ATCC 484] Celf_2043
MTQSSYDVVEVVAMQLIGSDASVIPVSAELSFRTSDPYTVRAVFTGPHTMSTWLLGRELLSLGMLASADA
PAGTGDVQVWRDEDPDYTLVSLNGVEGSALLAAPTEPITRFLASTEALVPLGAESARMESEITALIAALL
TA
>gi|296129627|ref|YP_003636877.1| unnamed protein product [Cellulomonas
flavigena DSM 20109] (Cfla_1781)
madtsydvievvamqligsdatvipvsaemcfrtsdpytvravftgahtmstwllgrell
aqgvhavadapagtgdvqvwrdddpdytlvslsgvegsallaaptepllrflaateslvp
igaesdkmegeitaliaallta
>gi|336320679|ref|YP_004600647.1| sporulation and cell division protein
SsgA [Cellulomonas gilvus ATCC 13127] Celgi_1568
MTHSSYDVVEVVAMQLIGSDASVIPVSAELSFRTTDPYTVRAVFTGPHTMSTWLIGRELLSMGMHAAADA
PAGSGDVQVWRDEDPDYALVSLSGVEGSALLAAPSEPILRFLATTESLVPLGSESDRMESEISAFIAALL
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TA
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ACN14a] (FRAAL2127)
MPVAATVRYEPADPYAISIGFRTGADEVVEWTFARQLLSDGVRRPAGDGDVQVWPAAQSG
GRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYSAVPLGGESDIIDLDAELALLIWGGPER
>gi|158316914|ref|YP_001509422.1| sporulation and cell division protein
SsgA [Frankia sp. EAN1pec] Franean1_5158
MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAVSIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRAEVLAFLRRTYSAVPLGGESDVIDLDAELALLIWGG
PER
>gi|86740065|ref|YP_480465.1| sporulation and cell division protein
SsgA [Frankia sp. CcI3] Francci3_1359
MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAISIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYSAVPLGGESDIIDLDAELALLIWGG
PER
>gi|358463323|ref|ZP_09173392.1| sporulation and cell division protein
SsgA [Frankia sp. CN3] FrCN3DRAFT_8065
MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPDDPYAVSIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYAAVPLGSESDVIDLDAELALLIWGG
PDR
>gi|288922741|ref|ZP_06416912.1| sporulation and cell division protein
SsgA [Frankia sp. EUN1f] FrEUN1fDRAFT_6610
MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAVSIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRAEVLAFLRRTYAAVPLGGESDVIDLDAELALLIWGG
PER
>gi|392943918|ref|ZP_10309560.1| sporulation and cell division protein,
SsgA [Frankia sp. QA3]
MTIRHDSITAELALRLVVPGGAPVPVAATVRYEPADPYAISIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLAFLRRTYSAVPLGGESDIIDLDAELALLIWGG
PER
>gi|336178472|ref|YP_004583847.1| sporulation and cell division protein
SsgA [Frankia symbiont of Datisca glomerata] FsymDg_2563
MTIRHDSITAELALRLVVPGGAPVPVAATMRYEPADPYAVSIGFRTGADEVVEWTFARQLLSDGVRRPAG
DGDVQVWPAAQSGGRIVCLSLSSPSGHALFEMPRSEVLSFLRRTYSVVPLGGESEVVDLDAELALLIWGG
PQT
>gi|284991618|ref|YP_003410172.1| sporulation and cell division protein
SsgA [Geodermatophilus obscurus DSM 43160] (Gobs_3195)
minratpgytcpttlhlvgpqswtevpallsyeirdpfavritfgdhaeedgiswlvgrd
llhagldqpagegdvrlwpsrtsgdvlflhlrapsgealfevsrgtvagflqltasvvpf
geessvlqvdgelaallsnggadptgr
>gi|152967013|ref|YP_001362797.1| sporulation and cell division protein
SsgA [Kineococcus radiotolerans SRS30216]
mpalphrktevdvdvslrlrttsgpglpvpaslhygaddpyaihavfrggdtdvewvfar
dllreglsapagagdvqvqpcsdspdgrprvllrlsspdgnaeleadesdvrrflrrada
lvppgretrhldldeliarlvs
>gi|357388405|ref|YP_004903244.1| ssgB gene product [Kitasatospora
setae KM-6054]
mnttvscelhlrlivssesslpvpaglrydtadpyavh
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aparalesflkrtdaavppgtehrhfdldrelshilaen
>SsgB_Kutzneria_sp744_KUTG_02305 not on GenBank
MRNDHVTLRSTAVFDLLAPRTPAVPVQVELRYDTRDPYAVVAAFRTGRAGWVEWVYARDL
LADGLIAEAGDGDVRIKPATDDPEVVVIELNSPSGHATFEAASEELADFLDRTYDVVVPG
NEHLWVNVDQALTHLISNDMS
>gi|302866229|ref|YP_003834866.1| sporulation and cell division protein
SsgA [Micromonospora aurantiaca ATCC 27029]
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGREAEHLDVDTAVNRLL
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AGR
>gi|443289776|ref|ZP_21028870.1| Sporulation and cell division protein
SsgA [Micromonospora lupini str. Lupac 08]
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGREAEHLDVDTAVNRLL
AGR
>gi|238063620|ref|ZP_04608329.1| sporulation and cell division protein
ssgA [Micromonospora sp. ATCC 39149] (Mcag_04586)
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGREADHLDVDTAVTRLL
AGR
>gi|315502787|ref|YP_004081674.1| sporulation and cell division protein
ssga [Micromonospora sp. L5]
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGREAEHLDVDTAVNRLL
AGR
>gi|389865025|ref|YP_006367266.1| sporulation and cell division
protein, SsgA [Modestobacter marinus]
MARSSRSGCTARTTFHLVGPQSWTAVPAALVYDSSDPFAVRVRFGDGATDDVEPALYDDPDDDGGVEWLL
SRDLLRAGLTGPVGEGDVRLWPARGGLDVLFLQLRAPSGEAMFELSGAVVGDFLRETELLVPAGGESDLL
RVDEELSALLRGGTDNPTGR
>gi|258653633|ref|YP_003202789.1| sporulation and cell division protein
SsgA [Nakamurella multipartita DSM 44233] (Namu_3475)
mydfntveyrmtatvtemvlisdptmppvhaelryrsddpfavqlllsidqspaitwvfg
rdllvegvqapagigdvqvfpvldgtvielrsgeqvasllahtqdlaafldhsieivpsg
sesayfeieadlrdlpihdafea
>gi|326331443|ref|ZP_08197733.1| sporulation and cell division protein
SsgA [Nocardioidaceae bacterium Broad-1]
MSDIKHPAVQQDIKISCLDPWGRTVEVPTTLGYRENDPYAVSLTFHSGAGDVEWVVSRTLMLQGLSAPAG
EGDVKIYPSIDEDAKAVAVFDFSSPDGRLIATADSGEVQTFLGKSFSAVPVGSESQHMDLDALIADLLSS
SFDAE
>gi|119716595|ref|YP_923560.1| unnamed protein product [Nocardioides
sp. JS614] (Noca_2368)
mdlpatfgydpadpwavwitfrgprdevrwavgrdlllqgltdpagegdiqlwpsidehg
raavvmelcspdgrlvtqlhthelyrfltrtlaivpvgseaidlddlvaeltgisrae
>gi|403507738|ref|YP_006639376.1| putative regulator [Nocardiopsis alba
ATCC BAA-2165]
MNSSDITATAELGLRLVVPERTAVPLVARLDYSADDPYAIRVAFHTGEDSPVEWIFARELLTVGIVRPVG
EGDVRVWPSKSEGGERSVSISLSSPFGQAEFDTQVSPLAEFLHRTYEIVPAGQEGSFVDLDEEIQQHLHS
>gi|297562209|ref|YP_003681183.1| sporulation and cell division protein
SsgA [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111]
(Ndas_3271)
mnssdttataelglrlvvpertavplvarldysaddpyairvafhtgednpvewifarel
ltvgivrpvgegdvrvwpskddngdrsvsialsspfgqaefdtqvsplaeflhrtyeivp
agqegqfvnldeeiqqhlhs
>gi|331695878|ref|YP_004332117.1| sporulation and cell division protein
SsgA [Pseudonocardia dioxanivorans CB1190]
MRDVTNIICKQTVFELIAPDSTVTVNVELTYSFRDPFAVEASFRTGNSQPVVWVFARDLLADGLTEATGD
GDVTVAPIGHGQVELVLTSPSGHARFHADAAELSSFLEHTYAAVPEGAEYSWLDFDAALTELLDEKARD
>gi|418459703|ref|ZP_13030816.1| sporulation and cell division protein,
SsgA [Saccharomonospora azurea SZMC 14600]
MRNEHVTLRSTAVFDLLAPRTPPVPVKVELRYDTRDPYAVVAAFRTGRAGWVEWVFARDLLADGLLGEAG
DGDVRLKPSIEDPDSVFVELNSPSGHAMFEASAQELADFLDQTYDVVLPGNEHLWVDVDDALTRLIPHDL
G
>gi|257055521|ref|YP_003133353.1| sporulation and cell division
protein, SsgA [Saccharomonospora viridis DSM 43017] (Svir_14890)
MRNDHVTLRSTAVFDLLAPRTPPVPVKVELRYDTRDPYAVVAAFRTGRAGWVEWVFARDL
LSDGLLGEAGDGDVRIRPSMEDPDSVFVELNSPSGHAMFEASAQELADFLDQTYDVVLPG
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NEHLWVDVDDALTRLIPHDLG
>gi|134098535|ref|YP_001104196.1| regulator [Saccharopolyspora
erythraea NRRL 2338] (SACE_1961)
MRNDHVTLRSTAVFDLLAPQTPAVPVQVELRYDTRDPYAVVAAFRTGRAGWVEWVFARDL
LADGLIAHAGVGDVTIRPAVDDPEVVVIELSSPSGHAVFEASAQELADFLDRTYDVVVPG
NENLWVNVDDALTRLLPHDLS
>gi|348170571|ref|ZP_08877465.1| regulator [Saccharopolyspora spinosa
NRRL 18395]
MTLRSTAVFDLLAPQTPAVPVQVELRYDTRDPYAVVAAFRTGRAGWVEWVFARDLLADGLIAHAGEGDVT
IRPAVDAPEVVAIELSSPSGHAVFEASAQELADFLDRTYDVVVPGNENLWVDVDEALTRLLPHDLG
>gi|433604679|ref|YP_007037048.1| Sporulation and cell division protein
[Saccharothrix espanaensis DSM 44229]
MRNDHVTLRSTAVFDLLAPRTPAVPVQVELRYDTKDPYAVVAAFRTGRAGWVEWVYARDLLADGLIADAG
DGDVRIRPAADDPEVVVIELSSPSGHAMFEASAQELADFLDRTYDVVVPGNEHLWVDVDEALTHLISNDL
T
>gi|159037194|ref|YP_001536447.1| sporulation and cell division protein
SsgA [Salinispora arenicola CNS-205] Sare_1560
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVARGREAEHLDVDTAVSRLL
AGR
>gi|145594147|ref|YP_001158444.1| unnamed protein product [Salinispora
tropica CNB-440] (Strop1600)
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFA
RELLVTGLDEPAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVV
VARGREAEHLDVDTAVNRLLAGR
>gi|291300584|ref|YP_003511862.1| sporulation and cell division protein
SsgA [Stackebrandtia nassauensis DSM 44728] (Snas_3098)
mattrpatvevdttmrfvatdfttvnvrasmrydaddpyaihvmfhpgnpdaeqvswsfa
rellaaglveptgmgdvrvwpwstprgdaialalsspdgnalfevsrslvsrflrrsyal
vpkgkegdsldmdatvaklladr
>gi|21220041|ref|NP_625820.1| regulator [Streptomyces coelicolor A3(2)]
(SCO1541)
MNTTVSCELHLRLVVSSESSLPVPAGLRYDTADPYAVH
ATFHTGAEETVEWVFARDLLAEGLHRPTGTGDVRVWPSRSHGQGVVCIALSSPEGEALLE
APARALESFLKRTDAAVPPGTEHRHFDLDQELSHILAES
>gi|345854610|ref|ZP_08807425.1| regulator [Streptomyces zinciresistens
K42]
MNTTVSCELHLRLVVSSESSLPVPAGLRYDTADPYAVHATFHTGAEETVEWVFARDLLAEGLHRPTGTGD
VRVWPSRSHGQGVVCIALSSPEGEALLEAPARALESFLKRTDAAVPPGTEHRHFDLDQELSHILAES
>gi|302527908|ref|ZP_07280250.1| regulator [Streptomyces sp. AA4]
MRNDHVTLRSTAVFDLLAPRTPAVPVKVELRYDTRDPYAVVAAFRTGRAGWVEWVYARDLLADGLLADAG
DGDVRIRPSVEDPESVLIELNSPSGHAMFEASAQELADFLDRTYDVVLPGNEHLWVDVDDALTHLIPNDL
A
>gi|271967422|ref|YP_003341618.1| unnamed protein product
[Streptosporangium roseum DSM 43021] (Sros_6145)
mnsatvsaelglrlvvpdrttvpllaglsytaddpyairmafhvgndepvewifarellt
vgivrrvgdgdvqvwparadgertlhisltspfgqalfevplaplteflhrtyelvpagr
etdfmdldaelsnmlwss
>gi|72162510|ref|YP_290167.1| unnamed protein product [Thermobifida
fusca YX] (Tfus_2111)
MSSSGTSITCEVGLQLIVPDRAPVPLVARLDYSVDDPYAIRAAFHVGDDEPV
EWIFARELLTVGIIRETGEGDVRIWPSQDGKERMVNIALSSPFGQARFHAQV
APLSEFLHRTYELVPAGQESDYIDIDAEIAEHLS
>gi|296270068|ref|YP_003652700.1| sporulation and cell division protein
SsgA [Thermobispora bispora DSM 43833] (Tbis_2095)
mnsitvsaelglrlvvpdrttipltasltytatdpyairmafhvgndepvewifarellt
igmvrrvgegdvqvwartegeqslnisltspfgqalfevplapltaflnrtyelvpagr
esdfmdldqelsnmlwss
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>gi|269126283|ref|YP_003299653.1| sporulation and cell division protein
SsgA [Thermomonospora curvata DSM 43183] (Tcur_2048)
mdssrtisaelglrlvvpdrttvpllaeveyatddpyairmsfyvgndepvewifarell
tvgivrrvgdgdvqvwpaepggdrivhialsspfgdalfevplpplaeflhrtyravpag
reaefidmeaelenllwps
>gi|330466623|ref|YP_004404366.1| sporulation and cell division protein
ssga [Verrucosispora maris AB-18-032] VAB18032_13260
MSVIRPTTVEVETSLRLVAPDATALPVRASLRYDPADPYAVHVLFHAESAGGEAVSWSFARELLVTGLDE
PAGIGDVRVWPWATPRGDFVALALSSPDGNALFEVPRSVLVRFLRRTYVVVPRGREAEHLDVDTAVNRLL
AGR
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Supplemental Data file 4. SsgA protein sequences.

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>gi|395772008|ref|ZP_10452523.1| regulator [Streptomyces acidiscabies
84-104]
MNFLVSEELSFRIPVGLEYEPDDPYAVRLTFHLPGDAPVTWTFGRELLIDGVGRPCGEGDVRVAPTDPES
LGEVLIRLQVGADQAVFRSSAAPLIAFLDRTDRVVPLGQEGSFADFDAHLDEALGRILAEEQSAG
>gi|11066161|gb|AAG28482.1|AF195771_1 SsgA [Streptomyces albus]
MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTA
TREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG
>gi|291452710|ref|ZP_06592100.1| SsgA [Streptomyces albus J1074]
MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTA
TREVHITLQVGSEQALFRVGKAPLLAFLDRTDRLVPLGSERAHADFDSHLDDALNRILAEEQSAG
>gi|398784277|ref|ZP_10547541.1| SsgA protein [Streptomyces auratus
AGR0001]
MSFVVSDELAFRIPVELDFASADPFAVRLTFDLPGDAPVTWAFGRELLLDGLSRPSGEGDVRIEPASP
EHLSDVFISLQVGSERALFRVSAAPLVAFLDRTDRLVPLGKEEVCDTLEAVLDRILTEAPAG
>gi|29830810|ref|NP_825444.1| cell division protein, regulatory protein
[Streptomyces avermitilis MA-4680]
MSFLVSEELSFRIPVELRYETCDPFAVQLTFHLPGDAPVTWTFGRELLIDGVGRPCGDGDVHIAPADREA
FGEVLIRLQVGGDHALFRSGAVPLVTFLDRTDKLVPLGQECSLADFDAHLDEALDRILAEEQSAG
>gi|374988085|ref|YP_004963580.1| SsgA protein [Streptomyces
bingchenggensis BCW-1]
MTFLVSQDLSFRIPVELSYDSSDPYAVEITFHLPGDAPVSWAFARELLLDGLSKPSGEGDVRIAPASPEG
LSDVFIRLQVGAERALFRAGAAPLVAFLDRTDRVVPFGQEQAACDPVGDLDAELDRILAEDRYAG
>gi|418467927|ref|ZP_13038780.1| regulator [Streptomyces coelicoflavus
ZG0656]
MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD
VRIAPVDPEPLAEVLIRLQVGSDQALFRSSAAPLVAFLDRTDKLVPLGQEGALADFDSHLDEALDRILAE
EQSAG
>gi|21222332|ref|NP_628111.1| regulator [Streptomyces coelicolor A3(2)]
MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGDVRIAPVEPE
PLAEVLIRLQVGSDQALFRSSAAPLVAFLDRTDKLVPLGQEGALADFDSHLDEALDRILAEEQSAG
>gi|185534933|gb|ACC77835.1| SsgA [Streptomyces clavuligerus]
MNFLVSEELSFRIPVELRYETDDPYAVRMTFHLPGDAPVTWAFSRDLLVGGVTGPTGDG
DVHIAPTGPGRRADLGIRLQVGQERAYFVVGAPPVVAFLDRTDRLVPLGQERAYGNCAGDLDSALCGILA
EEQNAG
>gi|185534923|gb|ACC77830.1| SsgA [Streptomyces collinus]
MSFLVSEELSFRIPVELRYESSDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCGEGD
VRVTPVEPDALGEVLIRLQVGSDQALFRSSTAPLVAFLDRTDKLVPLGQEGSLADFDAHLDEALDRILAE
QGAG
>gi|408530778|emb|CCK28952.1| hypothetical protein BN159_4573
[Streptomyces davawensis JCM 4913]
MSFLVSEELSFRIPVELRYATSDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRACGEGD
VRVSPADPETLGDVLIRLQVGGDHALFRSSSAPLIAFLDRTDKLVPLGQEGALSDFDASLDEALDRILAE
EQSAG
>gi|185534927|gb|ACC77832.1| SsgA [Streptomyces diastatochromogenes]
MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCGEGD
VHIAPVDAEVLGEVLIRLQVGCDHALFRSSTPPLVAFLDRTDKLVPLGQEGALADFDAHLDEALDRILAE
EQNAG
>gi|185534919|gb|ACC77828.1| SsgA [Streptomyces filamentosus]
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EQNAG
>gi|185534929|gb|ACC77833.1| SsgA [Streptomyces filipinensis]
MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCGEGD
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EQSAG
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LSDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEEALGRILAKEQNAG
>gi|185534925|gb|ACC77831.1| SsgA [Streptomyces fradiae]
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VRIAPVDPEPLAEVLIRLQVGTDQALFRSSAAPLVAFLDRTDKLVPLGQEGALADFDAHLDEALDRILAE
EQNAG
>gi|291438568|ref|ZP_06577958.1| regulatory protein [Streptomyces
ghanaensis ATCC 14672]
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>gi|411003756|ref|ZP_11380085.1| SsgA protein [Streptomyces globisporus
C-1027]
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>gi|11066159|gb|AAG28481.1|AF195770_1 SsgA [Streptomyces goldeniensis]
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>gi|185534935|gb|ACC77836.1| SsgA [Streptomyces granaticolor]
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>gi|302559712|ref|ZP_07312054.1| conserved hypothetical protein
[Streptomyces griseoflavus Tu4000]
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VRVSPLDPEALGEVLIRLQVGGDQALFRSSTAPLVAFLDRTDKLVPLGQEGALADFDAHLDDALDRILAE
QSAG
>gi|182437448|ref|YP_001825167.1| SsgA protein [Streptomyces griseus
subsp. griseus NBRC 13350]
MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE
GLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG
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SsgA [Streptomyces griseus XylebKG-1]
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LGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG
>gi|329938685|ref|ZP_08288081.1| SsgA-like sporulation/cell division
regulator [Streptomyces griseoaurantiacus M045]
MSFLVSEELSFRIPVELRYETCDPFAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGDVHIA
PADPHAIGEVLIRLQVGADRAVFKSGAAPLVAFLDRTDKLVPLGQERSLADFDTLLDEALDRILAEEQSA
G
>gi|386841227|ref|YP_006246285.1| regulator [Streptomyces hygroscopicus
subsp. jinggangensis 5008]
MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCGEGD
VHIAPADSEVLGEVLIRLQVGGDQALFRSSAPPLVAFLDRTDKLVPLGQEGALADFDAHLDEALDRILAE
EQSAG
>gi|429201636|ref|ZP_19193088.1| hypothetical protein STRIP9103_04759
[Streptomyces ipomoeae 91-03]
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EQSAG
>gi|11066163|gb|AAG28483.1|AF195772_1 SsgA [Streptomyces netropsis]
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>gi|297193350|ref|ZP_06910748.1| SsgA protein [Streptomyces
pristinaespiralis ATCC 25486]
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EENAG
>gi|185534931|gb|ACC77834.1| SsgA [Streptomyces ramocissimus]
MSFLVSKELSFRIPVELSYEAADPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCG
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LAEEQSAG
>gi|441142623|ref|ZP_20962491.1| SsgA protein [Streptomyces rimosus
subsp. rimosus ATCC 10970]
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LSDVFIGLQVGDERALFRAGAPPLVAFLDRTDRLVPIGEEEVCDTLDSTLDRILSEAQKAG
>gi|239989179|ref|ZP_04709843.1| SsgA protein [Streptomyces roseosporus
NRRL 11379]
MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE
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>gi|291446185|ref|ZP_06585575.1| ssgA [Streptomyces roseosporus NRRL
15998]
MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE
GLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG
>gi|290959050|ref|YP_003490232.1| unnamed protein product [Streptomyces
scabiei 87.22]
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VHIAPADPETFGEVLIRLQVGTDQAMFRVGTAPLVAFLDRTDKLVPLGQERSLADFDTLLDEALDRILAE
EQSAG
>gi|408825596|ref|ZP_11210486.1| sporulation and cell division protein
SsgA [Streptomyces somaliensis DSM 40738]
MSFIVSEELSFRIPVELGYETRDPFAVRMTFHLPGDAPVTWTFGRELLVDGINDATGDGDVRIEPSETEE
LSDVHIRLRVGADQALFRASAPPLVAFLDRTDKLVPLGQECSLGDFDEGLDEVLGRILADENAG
>gi|302535619|ref|ZP_07287961.1| SsgA protein [Streptomyces sp. C]
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VHIAPTDPDELSDVHIRLQVGGDRALFRAGAGPLVAFLDRTDRLVPLGQERNLGDFEESLDQALGRILSE
SQHDERKAG
>gi|185534943|gb|ACC77840.1| SsgA [Streptomyces sp. Che26]
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EQNAG
>gi|294630283|ref|ZP_06708843.1| regulatory protein [Streptomyces sp.
e14]
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VRISPADSDSLSEVLIRLQVGPDRALFRSSTAPLVAFLDRTDKLVPLGQEGALADFDAHLDEALDRILAE
EQSAG
>gi|185534941|gb|ACC77839.1| SsgA [Streptomyces sp. Gre54]
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EQNAG
>gi|254384822|ref|ZP_05000159.1| SsgA [Streptomyces sp. Mg1]
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LSDVHIRLQVGCDRALFRASAAPLVAFLDRTDRLVPLGQERNLGDFEESLDEALCKILAQSRQNEQNAG
>gi|302520469|ref|ZP_07272811.1| regulator [Streptomyces sp. SPB78]
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HRILAEEPSAG
>gi|359150781|ref|ZP_09183584.1| regulator [Streptomyces sp. S4]
MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQT
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>gi|318075542|ref|ZP_07982874.1| SsgA-like sporulation/cell division
regulator [Streptomyces sp. SA3_actF]
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VRVSPVEPEPLLDGEGPGELHIRLQVGTDQALFRVGMAPIVAFLDRTDRLVPLGEERACADFESHLDDAL
HRILAEEPSAG
>gi|318059016|ref|ZP_07977739.1| SsgA-like sporulation/cell division
regulator [Streptomyces sp. SA3_actG]
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VRVSPVEPEPLLDGEGPGELHIRLQVGTDQALFRVGMAPIVAFLDRTDRLVPLGEERACADFESHLDDAL
HRILAEEPSAG
>gi|345000910|ref|YP_004803764.1| sporulation and cell division protein
SsgA [Streptomyces sp. SirexAA-E]
MSFLVSEELSFRIPVELRYEVSDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIAPTEPEG
LSDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGSLEEALGRILAKEQNAG
>gi|421740505|ref|ZP_16178755.1| sporulation and cell division protein,
SsgA [Streptomyces sp. SM8]
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VRVCPVGQTATREVHITLQVGSEQALFRAGKAPLLAFLDRTDRLVPLGSERAHADFDSHLDDALNRILAE
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>gi|295837801|ref|ZP_06824734.1| regulator [Streptomyces sp. SPB74]
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Tu6071]
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HRILAEEPSAG
>gi|365864743|ref|ZP_09404422.1| SsgA protein [Streptomyces sp. W007]
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EQNAG
>gi|297200889|ref|ZP_06918286.1| regulator [Streptomyces sviceus ATCC
29083]
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VRVSPAGSDLLGDVLIRLQVGGDQALFRSSTAPIIAFLDRTDKLVPLGQEAALADFDTHLDEALDRILAE
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[Streptomyces turgidiscabies Car8]
MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGVGRPCGDGD
VRIAPADTDVLGEVLIRLQVGGDQALFRSGAAPLVAFLDRTDKLVPLGQERSLADFDAHLDEALDRILAE
EQSAG
>gi|185534937|gb|ACC77837.1| SsgA [Streptomyces venezuelae]
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EEQSAG
>gi|328883752|emb|CCA56991.1| putative regulator [Streptomyces
venezuelae ATCC 10712]
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LSDVSIRLQVGGDRALFRASAPPLVAFLDRTDKLVPLGQERTLGDFEDNLEAALGRILAEESAGPTA
>gi|345016399|ref|YP_004818753.1| sporulation and cell division protein
SsgA [Streptomyces violaceusniger Tu 4113]
MTFLVSQDLSFRIPVELSYDSSDPYAVEITFHLPGDAPVSWAFARELLLDGLSRPTGEGDVRIAPASPEG
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QGAG
>gi|443626097|ref|ZP_21110527.1| putative SsgA-like sporulation/cell
division regulator [Streptomyces viridochromogenes Tue57]
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EQSAG
>gi|345849305|ref|ZP_08802318.1| SsgA-like sporulation/cell division
regulator [Streptomyces zinciresistens K42]
MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGGPCGEGD
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Supplemental Data file 5. SALP protein sequences from actinomycetes.

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>Streptomyces_coelicolor_SsgB (SCO1541)
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>Streptomyces_coelicolor_SsgE (SCO3158)
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WIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR*
>Streptomyces_coelicolor_SsgG (SCO2924)
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ELLTDGLHTSVGIGDVIIWPGPQRPGDTQRIFIRLRPPGSTALLSLDHDDALEFLETTQPLPQNPSATAR
TAVLATWEQELRDLICPSPGE
>Streptomyces_griseus_subsp_griseus_NBRC_13350_SsgD
MSSVIEQSVQARMVASAPRMETLPATLQYDRQYPFAVRMAFPAPATLEGTEVSWEFSRELLTTGVDSPAG
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>Streptomyces_griseus_subsp_griseus_NBRC_13350_SsgA
MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE
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>Streptomyces_griseus_subsp_griseus_NBRC_13350_SsgE
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WPCGRTQLIVELHSTDGVEVFQFEIRTLIRFLARTRAQTPATAPDTGREAPPRPPSRTTRPERGTPERGA
RTEQRDARAGRGAQTARG
>Streptomyces_griseus_subsp_griseus_NBRC_13350_SsgG
MMSIVERELELKLVLSPERSIPVPARLTYRTDDPYAVHIAFHIGSESPVHWTFARELLVEGVFRPCGHGD
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DLWLSDPWQSDDAPSQDGEA
>Streptomyces_griseus_subsp_griseus_NBRC_13350_SsgB
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TEHRHFDLDTELSHILAES
>Streptomyces_bottropensis_ATCC_25435_SBD_2172
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DDEADSRPAAPTDAEEAAQEVQLLRCGILIGATSTGKSAVLAALLAYRHLSLGSRRQLLAPRFWMDPSAA
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QAMQLLAPDIQMHASPTLHTLGWAWAGRKQQRLQNLRHMIEPWAHPAQPLFSATPTGLLVHPAPAARLHI
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HIEERESLALTSSLHTRLTYRVSDPYAVEARFRADDQGETVWIFARDLLRDGLERRNGLGDVSVWPDVGK
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