Signalling pathways that control development and antibiotic production in streptomyces

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APPENDICES

SUPPLEMENTARY INFORMATION BELONGING TO CHAPTER III

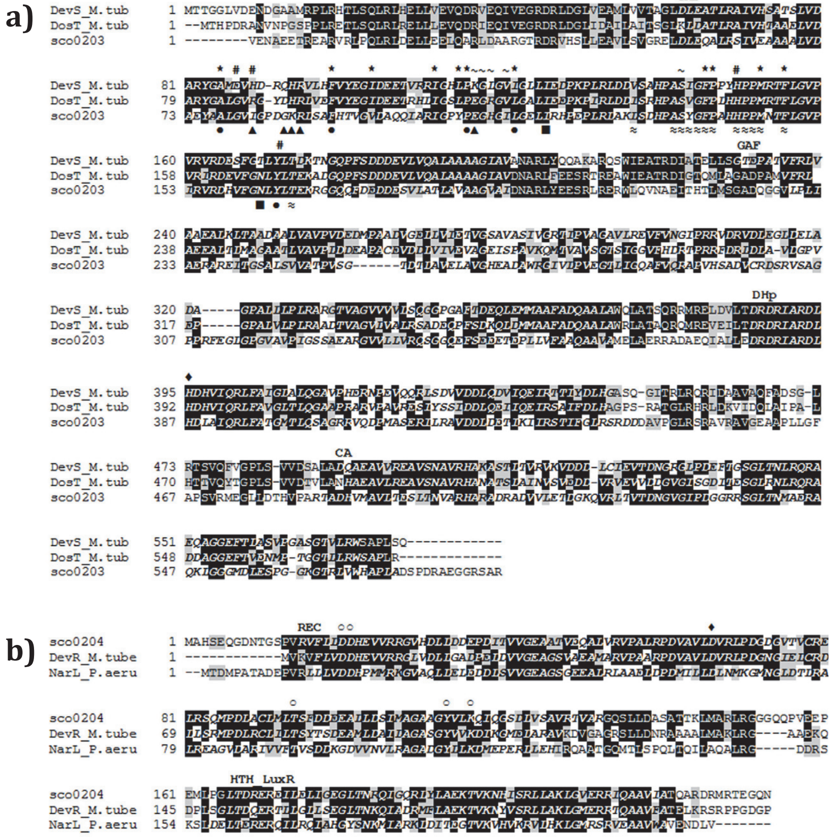


FIGURE S1: Alignment of SCO0203 (OsdK) and SCO0204 (OsdR).
Multiple alignments of OsdK with DevS and DosT of *M. tuberculosis* (A) and OsdR with DevR of *M. tuberculosis* and NarL of *P. aerigunosa* (B) are created with ClustalW (digits indicate the amino acid number). The different protein domains are indicated in italic. Amino acids conserved in at least 80% of the sequences are shaded: identical amino acids in black and amino acids with similar properties in grey. Important amino acids of DosT and DevS are indicated beneath and above the alignment, respectively. GAF, GAF domain; DHp, dimerization and histidine phosphotransfer domain; CA, C-terminal catalytic and ATP binding domain; REC, receiver domain; HTH_LuxR, helix-turn-helix-LuxR domain; ⧫, phosphorylation site; ○, RR activation; #, H-bond network from iron to surface; * hydrophobic space surrounding heme; ~, contact with propionate groups heme; ●, ligand binding; ▲, surface crevice; □≈, heme binding; ■, cavity next to ligand binding pocket.

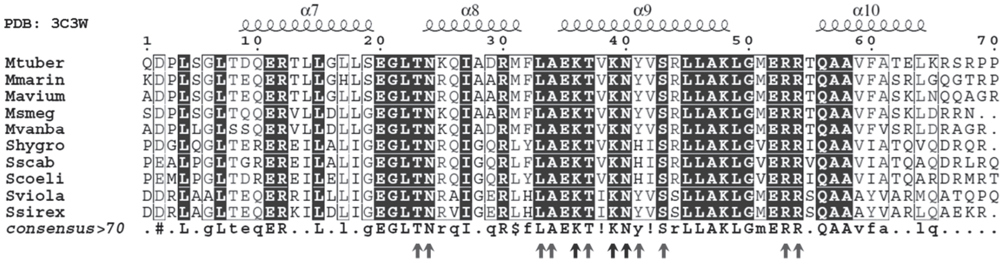


FIGURE S2. Sequence alignment of the DNA-binding domain of DevR with *Streptomyces* and *Mycobacterium* orthologues.
The secondary structure prediction was based on the crystal structure of DevR (PDB ID: 3C3W; Wisedchaisri et al., 2005), and is shown on top. Conserved residues are shown in grey, and boxes denote conservative substitutions. A symbol shows residues involved in interactions with DNA, where lighter gray arrows represent residues contacting nucleotide bases and dark gray arrows indicate residues making DNA phosphate oxygen contacts. Abbreviations (M., *Mycobacterium*; S., *Streptomyces*): Mtuber, *M. tuberculosis*; Mmarin, *M. marinum*; Mavium, *M. avium*; Msmeg, *M. smegmatis*; Mvanba, *M. vanbaalenii;* Shygro, *S. hygroscopicus*; Sscab, *S. scabies*; Scoeli, *S. coelicolor*; Sviola, *S. violaceoruber;* Ssirex, *S. sp. sirex*. For accession numbers see Methods.

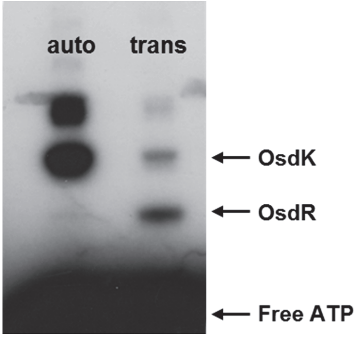
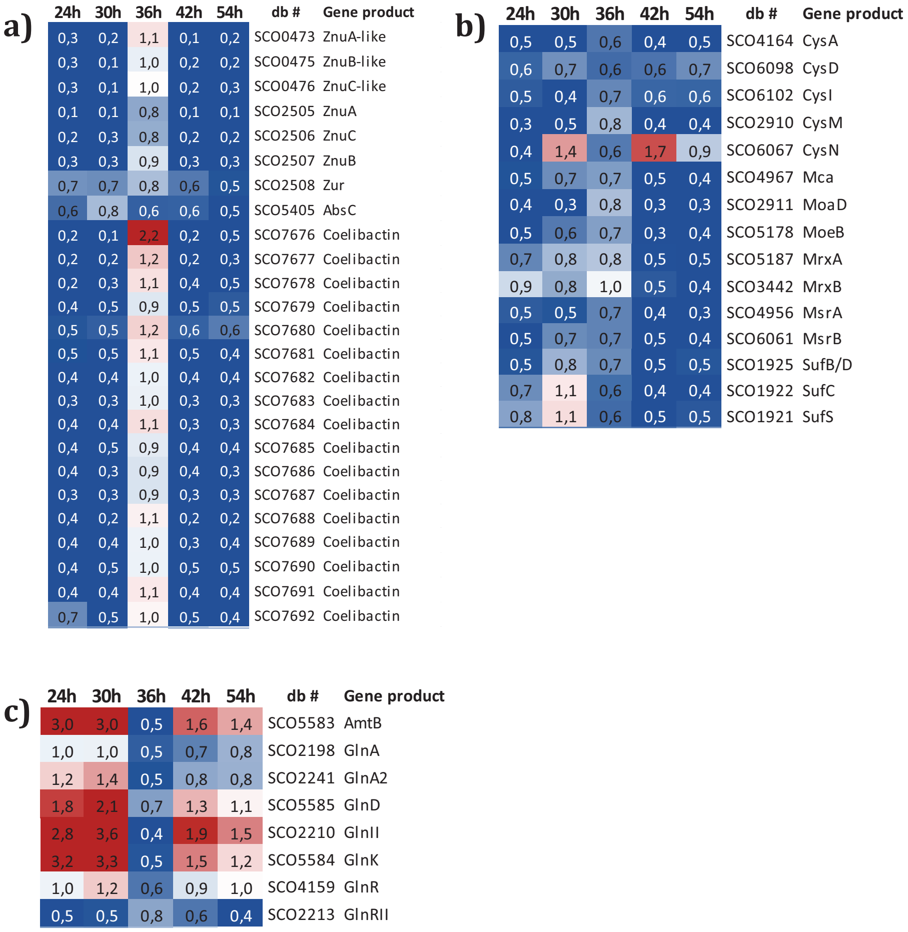


FIGURE S3. In vitro auto-phosphorylation and trans-phosphorylation of OsdRK.
OsdK was first auto-phosphorylated in the presence of unlabelled and [32P]-radiolabelled ATP, as described previously Wang *et al.* (2009). OsdK was readily phosphorylated as shown by the large band in the lane 'auto'. Using auto-phosphorylated OsdK, OsdR was trans-phosphorylated as shown by the presence of a band of phosphorylated OsdR and OsdK in lane 'trans'. However, there was significant phosphosignal loss observed (decrease in band intensity in time). The reactions were run on 3.5% acrylamide gels in 0.5x Tris-Borate-EDTA (TBE) buffer. Gels were dried and then submitted to autoradiography for analysis.



a)

24h	30h	36h	42h	54h	db #	Gene product
0,3	0,2	1,1	0,1	0,2	SCO0473	ZnuA-like
0,3	0,1	1,0	0,2	0,2	SCO0475	ZnuB-like
0,3	0,1	1,0	0,2	0,3	SCO0476	ZnuC-like
0,1	0,1	0,8	0,1	0,1	SCO2505	ZnuA
0,2	0,3	0,8	0,2	0,2	SCO2506	ZnuC
0,3	0,3	0,9	0,3	0,3	SCO2507	ZnuB
0,7	0,7	0,8	0,6	0,5	SCO2508	Zur
0,6	0,8	0,6	0,6	0,5	SCO5405	AbsC
0,2	0,1	2,2	0,2	0,5	SCO7676	Coelibactin
0,2	0,2	1,2	0,2	0,3	SCO7677	Coelibactin
0,2	0,3	1,1	0,4	0,5	SCO7678	Coelibactin
0,4	0,5	0,9	0,5	0,5	SCO7679	Coelibactin
0,5	0,5	1,2	0,6	0,6	SCO7680	Coelibactin
0,5	0,5	1,1	0,5	0,4	SCO7681	Coelibactin
0,4	0,4	1,0	0,4	0,4	SCO7682	Coelibactin
0,3	0,3	1,0	0,3	0,3	SCO7683	Coelibactin
0,4	0,4	1,1	0,3	0,3	SCO7684	Coelibactin
0,4	0,5	0,9	0,4	0,4	SCO7685	Coelibactin
0,4	0,3	0,9	0,4	0,3	SCO7686	Coelibactin
0,3	0,3	0,9	0,3	0,3	SCO7687	Coelibactin
0,4	0,2	1,1	0,2	0,2	SCO7688	Coelibactin
0,4	0,4	1,0	0,3	0,4	SCO7689	Coelibactin
0,4	0,5	1,0	0,5	0,5	SCO7690	Coelibactin
0,4	0,4	1,1	0,4	0,4	SCO7691	Coelibactin
0,7	0,5	1,0	0,5	0,4	SCO7692	Coelibactin

b)

24h	30h	36h	42h	54h	db #	Gene product
0,5	0,5	0,6	0,4	0,5	SCO4164	CysA
0,6	0,7	0,6	0,6	0,7	SCO6098	CysD
0,5	0,4	0,7	0,6	0,6	SCO6102	CysI
0,3	0,5	0,8	0,4	0,4	SCO2910	CysM
0,4	1,4	0,6	1,7	0,9	SCO6067	CysN
0,5	0,7	0,7	0,5	0,4	SCO4967	Mca
0,4	0,3	0,8	0,3	0,3	SCO2911	MoaD
0,5	0,6	0,7	0,3	0,4	SCO5178	MoeB
0,7	0,8	0,8	0,5	0,5	SCO5187	MrxA
0,9	0,8	1,0	0,5	0,4	SCO3442	MrxB
0,5	0,5	0,7	0,4	0,3	SCO4956	MsrA
0,5	0,7	0,7	0,5	0,4	SCO6061	MsrB
0,5	0,8	0,7	0,5	0,5	SCO1925	SufB/D
0,7	1,1	0,6	0,4	0,4	SCO1922	SufC
0,8	1,1	0,6	0,5	0,5	SCO1921	SufS

c)

24h	30h	36h	42h	54h	db #	Gene product
3,0	3,0	0,5	1,6	1,4	SCO5583	AmtB
1,0	1,0	0,5	0,7	0,8	SCO2198	GlnA
1,2	1,4	0,5	0,8	0,8	SCO2241	GlnA2
1,8	2,1	0,7	1,3	1,1	SCO5585	GlnD
2,8	3,6	0,4	1,9	1,5	SCO2210	GlnII
3,2	3,3	0,5	1,5	1,2	SCO5584	GlnK
1,0	1,2	0,6	0,9	1,0	SCO4159	GlnR
0,5	0,5	0,8	0,6	0,4	SCO2213	GlnRII

FIGURE S4. Heat maps of genes related to zinc import (A), sulphur metabolism and thiol homeostasis (B) and nitrogen metabolism (C) that are significantly differentially expressed between the *osdR* mutant and its parent *S. coelicolor* M145.
RNA was isolated from mycelium grown on MM with 1% mannitol during vegetative growth (24 h), vegetative/aerial growth (30 h), aerial growth/early sporulation (42 h) and sporulation (54 h). Only genes with a pfp value less than 0.010 and a fold change (Δ*osdR* expression/M145 expression) of more than 2.0 are presented. The levels of the fold changes are indicated with colours as represented by the scale bar.

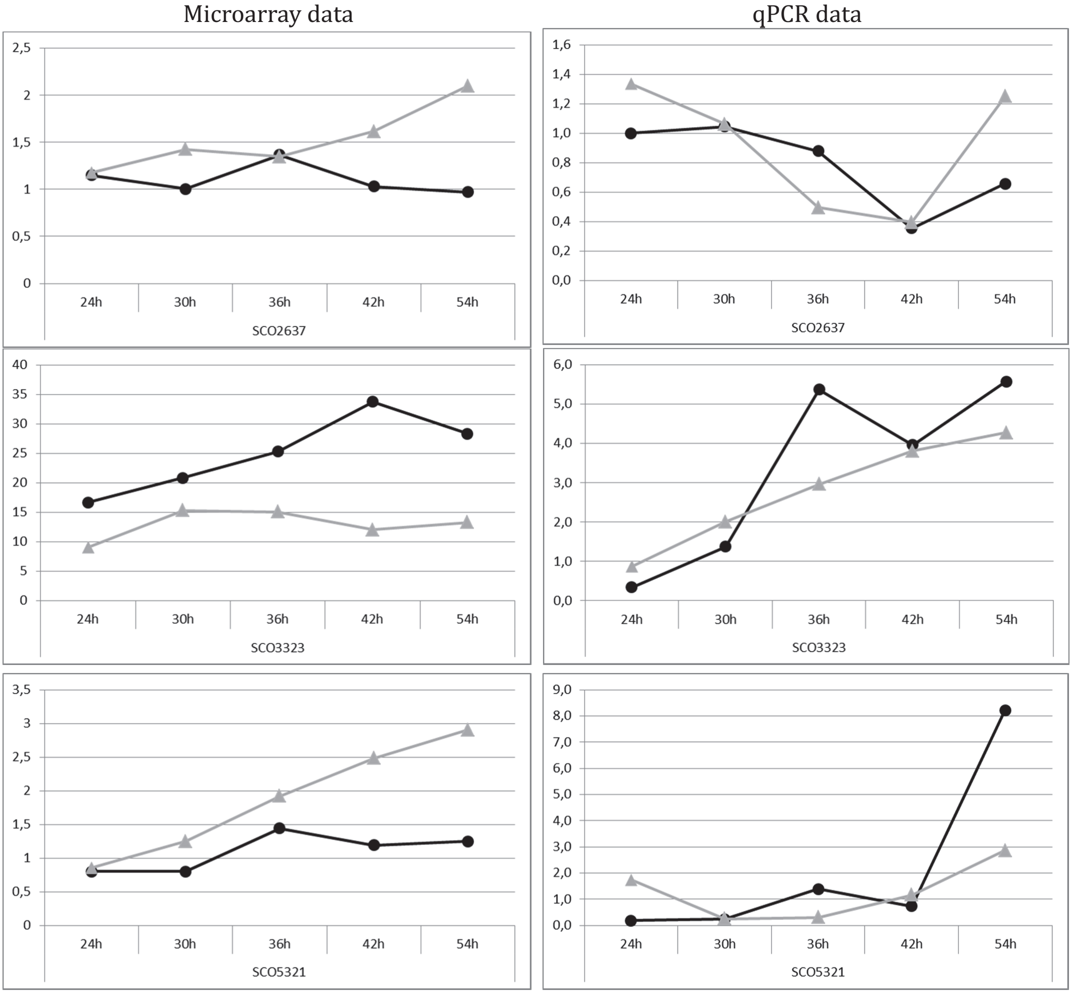


FIGURE S5. Microarray and RT-qPCR expression profiles of genes deregulated in the *osdR* mutant.
RNA was isolated, for microarray analysis (left) and RT-qPCR (right) profiling, from independent cultures grown on MM with 1% mannitol during vegetative growth (24 h), vegetative/aerial growth (30 h), aerial growth (36 h), aerial growth/early sporulation (42 h) and sporulation (54 h). The expression profiles in wild type (black, ●) and the osdR mutant (grey, ▲) over time were compared between the microarray data (left) and RT-qPCR (right). Genes of interest tested: SCO2637, SCO3323 (*bldN*) SCO5321 (*whiE*).

TABLE S1. Bacterial strains, plasmids and constructs.
[a] IFD, in-frame deletion.

Strains/plasmids	Genotype/description	Reference
Bacterial strain		
S. coelicolor A3(2) M145	SCP1$^-$ SCP2$^-$	(Kieser et al., 2000)
M512	M145 Δ*actII-ORF4* Δ*redD*	(Floriano & Bibb, 1996)
GSTC1	M145 ΔSCO0203 (::*aacC4*)	this work
GSTC2	M145 ΔSCO0204 (::*aacC4*)	this work
GSTC3	M145 ΔSCO0204 (IFD[a])	this work
GSTC4	M145 ΔSCO0203/SCO0204 (IFD[a])	this work
GSTC6	M512 ΔSCO0204 (::*aacC4*)	this work
E. coli JM109	*See reference*	(Sambrook et al., 1989)
E. coli ET12567	*See reference*	(MacNeil et al., 1992)
Plasmid		
pWHM3	*E. coli - Streptomyces* shuttle vector (multi-copy in both hosts)	(Vara et al., 1989)
pHJL401	*E. coli-Streptomyces* shuttle vector with multiple copies in *E. coli* and 1-5 copies per chromosome in *Streptomyces*	(Larson & Hershberger, 1986)
pIJ2587	pHJL401 derivative with promoterless reporter gene *redD*	(van Wezel et al., 2000)
pGWS345	pIJ2587 harbouring the -395/+122 region relative to the start of whiG	this work
pGWS1059	pIJ2587 harbouring the -250/+38 region relative to the start of SCO0204	this work
pGWS1058	pIJ2587 harbouring the -211/+74region relative to the start of SCO0200	this work
pGWS1060	pIJ2587 harbouring the -341/+60 region relative to the start of SCO0207	this work
pGWS376	pWHM3 with 4 kb fragment for SCO0204 replacement by *aacC4*	this work
pGWS377	pWHM3 with 3 kb fragment for SCO0204 in-frame deletion	this work
pGWS378	pWHM3 with 3.4 kb fragment for SCO0203 replacement by *aacC4*	this work
pGWS380	pWHM3 with 2.7 kb fragment for SCO0203-0204 in-frame deletion	this work
pET0203	pET28b (Novagen) protein expression vector for SCO0203	(Wang et al., 2009)
pET0204	pET28b (Novagen) protein expression vector for SCO0204	(Wang et al., 2009)

TABLE S2. Oligonucleotides

Primers for cloning and RT-qPCR reactions

	Target *	**Specification ^**	**Sequence(5'-> 3') #**
Construction of mutants	SCO0203L	F-1162	GTACGAATTCTGGATCAGGTACGTCCTGGTGC
		R+16	CGATTGGCTGAGCTCATGAAGTTCTAGACACCCTGGCCTCGCGGGTCTC
	SCO0203R	F+1720	CTGCATAACCCTGCTTCGGGGTCTAGATCCCCCGACAGGGCGGAAGGC
		R+2931	GTACAAGCTTACCCGACGCCGAAAGTCCGCACC
	SCO0204L	F-1439	GTACGAATTCGCGGTATCACCTTGGTGCACGTC
		R+16	CGATTGGCTGAGCTCATGAAGTTCTAGAGCTTCCCGTGTTGTCGCCCTG
	SCO0204R	F+670	CTGCATAACCCTGCTTCGGGGTCTAGACGGGACCGGATGCGCACCGAA
		R+2120	GTACAAGCTTAGCGGAGGCCGAAGATCGTCGAC
Verification of mutants	SCO0203	F-1253	CGACGTCCCCATGTACCGGAAGC
		R+3037	CCGAACCACGATGCGTGGACTGG
	SCO0204	F-1529	TGGAGTACGACATCGCGGTGG
		R+2241	ACGTGCGTGTCGAGCAGGCCCTC
	aacC4	F+783	TGCACGACATTGCACTCCAC
		R+219	TCTCGAGAATGACCACTGCTG
Promoter probing	pSCO0200	F-250	GTCAGAATTCTGATCGCGCTGGCCGCTGTCT
		R+38	GTCAGGATCCGGCGAGCCGTCGAGTCCTACGGT
	pSCO0204	F-211	GTCAGAATTCCCGCCAAGTACGACGCCCTG
		R+74	GTCAGGATCCACCACTTCGTGGTCGTCCAGGAG
	pSCO0207	F-341	GTCAGAATTCCGTGCACCAAGGTGATACCGCTC
		R+60	GTCAGGATCCACCGAGAAGTCCGGCCATGTC
RT-qPCR primers	SCO0200	F+387	CACCGAGACGCCGGTGATCCT
		R+461	ATGCCGGTGGGGTCCTTGAG
	SCO0204	F+331	GCCGGCTACGTCCTGAAGCA
		R+481	TGGCGTCCAGCAGCGACTGG
	SCO2637	F+1015	CAGGTCGGGTACTTCGGCAC
		R+1121	TTGGCACCGGCGGAGTTGTA
	SCO5320	F+359	AACCGCTGGCGACCTGCGTC
		R+489	GGTGAGGGCGTGCCGTACGA
	SCO5321	F+1017	CCACAACCTCGCCTGGAAGC
		R+1090	TGTCGTACGTGTCCAGCAGG
	SCO1541	F+205	GAGACCGTCGAGTGGGTCTT
		R+337	GGGAGCTGAGAGCGATGCAC
	SCO3323	F+313	CTCTACGACCAGTACAGCGA
		R+407	AGAAAGGTCTCGCTGGTGAG
	SCO4735	F+227	ACTACTTCCCGAACAAGGTGC
		R+306	GACGTCGTAGCGGTTGTCCAG

Oligonucleotides and primers for EMSA experiments

	Target *	**Location ^**	**Sequence(5'-> 3') #**
50mers	pSCO0200 wt	50F	CCCATCACCCTGCGGGCAGGGACGGTCGGCCCCGTCCCGGGACCACAGGC
		50R	GCCTGTGGTCCCGGGACGGGGCCGACCGTCCCTGCCCGCAGGGTGATGGG
	pSCO0200 50a	50aF	CCCATCACCCTGCGGGCAGGGACGGTCGGCACCGTCCCGGGACCACAGGC
		50aR	GCCTGTGGTCCCGGGACGGTGCCGACCGTCCCTGCCCGCAGGGTGATGGG
	pSCO0200 50b	50bF	CCCATCACCCTGCGGGCAGGGAAGGTCGGCCCCGTCCCGGGACCACAGGC
		50bR	GCCTGTGGTCCCGGGACGGGGCCGACCTTCCCTGCCCGCAGGGTGATGGG
	pSCO0200 50ab	50abF	CCCATCACCCTGCGGGCAGGGAAGGTCGGCACCGTCCCGGGACCACAGGC
		50abR	GCCTGTGGTCCCGGGACGGTGCCGACCTTCCCTGCCCGCAGGGTGATGGG
	pSCO0200 50x	50xF	CCCATCACCCTGCGGGCAGTGAATGTAGGCACCGTCCCGGGACCACAGGC
		50xR	GCCTGTGGTCCCGGGACGGTGCCTACATTCACTGCCCGCAGGGTGATGGG
S. coelicolor targets	pSCO0200	F-250	GTCAGAATTCTGATCGCGCTGGCCGCTGTCT
		R+38	GTCAGGATCCGGCGAGCCGTCGAGTCCTACGGT
	pSCO0204	F-211	GTCAGAATTCCCGCCAAGTACGACGCCCTG
		R+74	GTCAGGATCCACCACTTCGTGGTCGTCCAGGAG
	pSCO0207	F-341	GTCAGAATTCCGTGCACCAAGGTGATACCGCTC
		R+60	GTCAGGATCCACCGAGAAGTCCGGCCATGTC
	pSCO1541	F-355	GCCGACGACGAAAACGCCGACC
		R+98	TCGGCCGTGTCGTACCGCAG
	pSCO2637	F-182	GTCAGAATTCTGTGTCCCCGATGGCGCATGG
		R+36	GTCAGGATCCGCCCGGTATCGGTTCGCGCT
	pSCO2967	F-218	GTCAGAATTCACGAAGCTGCCGCTCATCCTGG
		R+11	GTCAGGATCCCTCGCGAACACCAAGGTCAG
	pSCO5314	F-109	GCAGATGGCGCTGATCCGGGACC
		R+82	CGCTGTCGGACTCCGCGAACACC
	pSCO5316	F-139	GCGCGGCCTCATGGGGTCGAACT
		R+68	GCGGTGCGCTTCATCAGCGCCGA
	pSCO5319	F-190	TCCGTATGACGCCCCTGACCGA
		R+50	TTCGGGGCGATGTCGCCGAG
	pSCO5321	F-374	CATCCGTCGCTACGACGGGAGAG
		R+106	AGGTCGACAGGCCCACCAGGGAC
	pSCO5979	F-293	GTCAGAATTCCGTGTGCTCCAGCTCGGCCA
		R+50	GTCAGGATCCAGGTGCCGCCACTCGGGGGT
	pSCO6041	F-300	GTCAGAATTCTGCCGTCGTGCCTGCATCATGG
		R+56	GTCACTGCAGTGTCCGGGTTCCTGTTCCGGTGG
	pdasR	F+479	GCGCGAAGCGCTTCCCCGCCCTG
		R+675	GTCCTGGGAGTGCCGGGAGAGCATCAGCATG
M. tuberculosis targets	Rv3134c	R8	CCACCCGTGCGATAGGTGAGATTC
		R9c	CTCATCGACCGCCCACAACG
	devR	53R1	GTCAGCGCGGTTGTCGCGGAG
		R3	GACCTTTACCACCAGGGCACC
	hspX	hspXF2	TCTGAACGGCGGTTGGCAGACA
		hspXR	CGGGAAGGGTGGTGGCCATTTG

* target gene given as gene or SCO database number; nucleotide position is given relative to first nucleotide of the relevant gene.
p refers to promoter; 50mers denoted with '50'; primers for *M. tuberculosis* genes were described previously (Chauhan et al)

^ Forward (F) or reverse (R) primer; nucleotide position relative to first nucleotide of target gene.
\# Restriction sites underlined: GGATCC, BamHI; GAATTC, EcoRI; AAGCTT, HindIII; CTGCAG, PstI; GAGCTC, SacI; TCTAGA, XbaI.

TABLE S3. Position weight matrix for the OsdR binding site.

OsdR Position weight matrix

(Minimum score : -39.68; Maximum score : 16.45)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
A	0.91	-2.48	-2.48	-2.48	0.25	-2.48	-2.48	1.12	-0.38	-2.48	-2.48	-2.48	-2.48	-2.48	-2.48	-2.48
C	-1.16	-2.48	-2.48	-1.16	0.77	0.97	-1.16	-2.48	-0.61	0.97	-2.48	-2.48	0.97	0.97	0.97	-1.16
G	0.39	0.97	0.97	0.77	-2.48	-2.48	0.87	-0.61	-2.48	-2.48	0.97	0.87	-2.48	-2.48	-2.48	-2.48
T	-2.48	-2.48	-2.48	-0.38	-2.48	-2.48	-2.48	0.91	1.58	-2.48	-2.48	-0.38	-2.48	-2.48	-2.48	1.80

SUPPLEMENTARY INFORMATION BELONGING TO CHAPTER IV

TABLE S1. Bacterial strains and plasmids.

Bacterial strain		
Strains and genotype		**Reference**
E. coli JM109	See reference	Sambrook et al., 1989
E. coli ET12567	See reference	MacNeil et al., 1992
E. coli Rosetta(DE3)pLysS	See reference	Novagen
M145	*S. coelicolor* A3(2) M145 SCP1- SCP2- prototroph	Kieser et al., 2000
Δ*nagB*	M145 Δ*nagB* ^{d}	Swiatek et al., 2012a
SMA11	M145 Δ*nagB* ^{SMA11} suppressor	Swiatek, 2012
ΔSCO4393	M145 ΔSCO4393^{d}	This work
ΔSCO4393Δ*nagB*	M145 ΔSCO4393^{d}ΔnagB^{d}	This work
Δ*nagA* ΔSCO4393	M145 Δ*nagA* ^{a} ΔSCO4393^{d}	This work
ΔSCO4393Δ*nagA*	M145 ΔSCO4393^{a}Δ*nagA* ^{d}	This work
Plasmids		
Plasmid	**Description**	**Reference**
pHJL401	*E. coli - Streptomyces* shuttle vector, 1-5 copies per chromosome in *Streptomyces*	Larson & Hershberger, 1986
pWHM3	*E. coli - Streptomyces* shuttle vector (multi-copy in both hosts)	Vara et al., 1989
pET15b	See reference	Novagen
pUWLcre	pUWL*ori* T derivative with *cre(a)* gene under *ermE** promoter	Fedoryshyn et al, 2008
pGWS1051	pHJL401 harbouring SCO4393 gene under control of its own promoter	This work
pGWS1052	pWHM3 harbouring the SCO4393 flanking regions with *loxP-aac(3)IV-loxP*	This work
pGAM1	pWHM3 harbouring the *nagA* flanking regions with *loxP-aac(3)IV-loxP*	Swiatek et al., 2012a
pET4393	pET15b harbouring the SCO4393 gene	This work

^{a}, Aprr, apramycin resistant. ^{D} deletion

TABLE S2. Oligonucleotides.

Gene*	Name^	Sequence#
SCO4393	compF-217	GTACgaattcCCCCTCGATGAGATTGCCGGAGG
	compR+762	GTCAaagcttGTGCGTTCAGCGGCGGTAGAAGA
SCO4393	pETF-1	GTACgaattcatATGAGCGACCACAAGCCGGCC
	pETR-756	GTACggatccCCGGGGCACCGGGTGCGTTCA
SCO4393	LF-1438	gtcagaattcacgtcgatgcgccgcgccatagg
	LR+15	gaagttatccatcacctctagaCTTGTGGTCGCTCATGCG
	RF+768	gaagttatcgcgcatctctagaCGCCGCTGAACGCACCCGGTG
	RR+2157	gtcaaagcttgcgacgctccattcgagcagagg

* SCO database number; nucleotide position is given relative to first nucleotide of therelevant gene

^ Forward (F) or reverse (R) primer, (L and R indicate left or right flank, where applicable); nucleotide position relative to first nucleotide of target gene

Restriction sites underlined: GAATTC, EcoRI; AAGCTT, HindIII; CATATG, NedI; CTGCAG, PstI; TCTAGA, XbaI

SUPPLEMENTARY INFORMATION BELONGING TO CHAPTER V

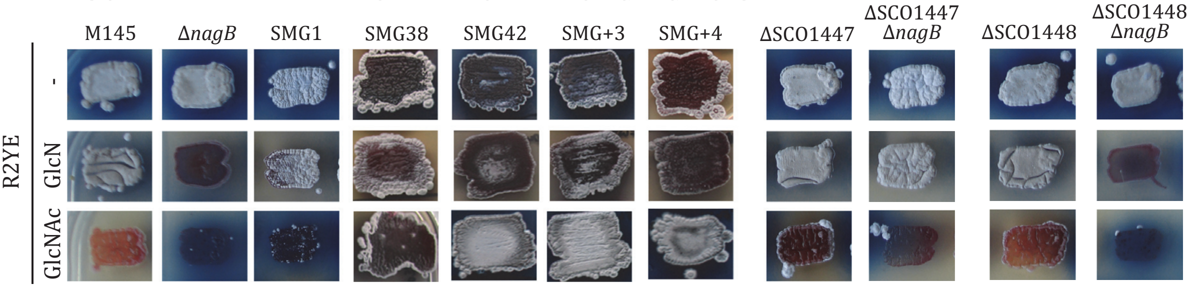


FIGURE S1. Phenotypic analysis of *S. coelicolor* mutants on R2YE
Spores of *S. coelicolor* wildtype (M145), suppressor mutants and deletion mutants were plated onto rich glucose-containing media (R2YE) and supplemented with glucosamine (GlcN) or N-acetylglucosamine (GlcNAc) as indicated.

TABLE S1. Bacterial strains and plasmids.

Strains/plasmids	Genotype/description	Reference
Bacterial strain		
E. coli JM109	See reference	Sambrook et al., 1989
E. coli ET12567	See reference	MacNeil et al., 1992
M145	*S. coelicolor* A3(2) M145 SCP1- SCP2-	Kieser et al., 2000
GAM4	M145 *nagA*	Swiatek et al., 2012a
GAM5	M145 *nagB*	Swiatek et al., 2012a
GAM6	M145 *nagK*	Swiatek et al., 2012a
GAM8	M145 *nagKA*	Swiatek et al., 2012a
	M145 *nagBA*	this work
	M145 *nagKAB*	this work
	M145 SCO1447	this work
	M145 SCO1447*nagB*	this work
	M145 SCO1448	this work
	M145 SCO1448*nagB*	this work
Plasmids		
pWHM3	E. coli - Streptomyces shuttle vector (multi-copy in both hosts)	Vara et al., 1989
pHJL401	E. coli-Streptomyces shuttle vector with multiple copies in E. coli and 1-5 copies per chromosome in Streptomyces	Larson & Hershberger, 1986
pUWLcre	pUWL*ori* T derivative with *cre(a)* gene under *ermE* * promoter	Fedoryshyn et al, 2008
pGWS961	pHJL401 harbouring SCO4284 gene (+1/+1146) with promoter sequence (-136/-3) of the SCO4284-SCO4285 operon	this work
pGAM1	pWHM3 harbouring flanking regions of *S. coelicolor* SCO4284 with *apra-loxP* inserted between the flanks	Swiatek et al., 2012a
pGAM2	pWHM3 harbouring flanking regions of *S. coelicolor* SCO5236 with *apra-loxP* inserted between the flanks	Swiatek et al., 2012a
pGWS948	pWHM3 harbouring flanking regions of *S. coelicolor* SCO1447 with *apra-loxP* inserted between the flanks	this work
pGWS955	pWHM3 harbouring flanking regions of S. coelicolor SCO1448 with *apra-loxP* inserted between the flanks	this work

TABLE S2. Oligonucleotides

Gene*	Name^	Sequence#
SCO4285	F-136	gtcagaattcACCCTGACTGCTCGTTCGCGCGT
	R-1	gtcacatatgGGTGCCGCCCACATCGAG
SCO4284	F+1	gtcacatATGGCCCCAAGCAAGGTTCTCGCC
	R+1146	gtcaaagcttTCAGCCCAGGTGGGGATCGAC
SCO1447	LF-1251	gtcagaattcACCCTCGCGAACACCACCAGGCA
	LR+3	gaagttatccatcacctctagaCATGCCGGGATCCTTCCAGAT
	RF+1200	gaagttatcgcgcatctctagaTTCGCACCGCCGGAGCGGTAG
	RR+2565	gtcaaagcttGCATGCGCAGGCCGTCAAGC
SCO1448	LF-1422	gtcagaattcTGCTGCCGACGGTACTCGGGTGG
	LR+9	gaagttatccatcacctctagaTGTGTTCATGGTCCACCCCTC
	RF+1221	gaagttatcgcgcatctctagaCCGGCAGTCCTGAACGCCTCGC
	RR+2603	gtcaaagcttTCTCCGCGATCAGGGCGATGACG

* SCO database number; nucleotide position is given relative to first nucleotide of therelevant gene

^ Forward (F) or reverse (R) primer, (L and R indicate left or right flank, where applicable); nucleotide position relative to first nucleotide of target gene

Restriction sites underlined: GAATTC, EcoRI; AAGCTT, HindIII; CATATG, NedI; TCTAGA, XbaI

TABLE S3. Mutations identified in GlcN-derived *S. coelicolor nagB* suppressor mutants.

Position[d]	nt[f]	GSM38			GSM42*			GSM+3			GSM+4			SCO #[e]	Annotation
		Type[a]	nt[b]	aa[c]	Type[a]	nt[b]	aa[c]	Type[a]	nt[b]	aa[c]	Type[a]	nt[b]	aa[c]		
521609i	C	-	-	-	Ins	A	-	-	-	-	-	-	-	SCO0492	peptide synthetase
1020977	G	-	-	-	-	-	-	SNP	T	-	-	-	-	SCO0968	hypothetical protein
1544534	G	Del	GAP	fs	-	-	-	-	-	-	-	-	-	SCO1447	transcriptional regulator
1749870	G	-	-	-	-	-	-	-	-	-	SNP	C	P71R	SCO1635	hypothetical protein
1760847	C	-	-	-	-	-	-	SNP	A	A315S	-	-	-	SCO1647	Pup deamidase/depupylase
3435930	G	-	-	-	-	-	-	SNP	A	-	-	-	-	SCO3134	two-component system response regulator
3849222i	C	-	-	-	Ins	C	fs	Ins	C	fs	-	-	-	SCO3485	LacI family transcriptional regulator
3850016	G	Del	GAP	fs	-	-	-	-	-	-	-	-	-		
3850017	C	Del	GAP	fs	-	-	-	-	-	-	-	-	-		
4692947 - 4699275		-	-	-	Unc	U	-	-	-	-	Unc	U	-	SCO4277- SCO4283	
4699483	G	-	-	-	Unc	U	-	-	-	-	SNP	C	A354G	SCO4284	N-acetylglucosamine-6-phosphate deacetylase
4699603	T	-	-	-	Unc	U	-	SNP	C	K314R	SNP	C	K314R		
4700074	C	-	-	-	Unc	U	-	SNP	T	G157E	SNP	T	G157E		
4700217	G	-	-	-	Unc	U	-	SNP	A	-	SNP	A	-		
4700568	G	-	-	-	Unc	U	-	-	-	-	SNP	A	A319V	SCO4285	sugar kinase
4700569	C	-	-	-	Unc	U	-	-	-	-	SNP	T	A319T		
4700571	G	-	-	-	Unc	U	-	-	-	-	SNP	T	A318D		
4700573i	C	-	-	-	-	-	-	-	-	-	Ins	T	fs		
4700574	G	-	-	-	Unc	U	-	-	-	-	SNP	A	T317M		
4700575	T	-	-	-	Unc	U	-	-	-	-	SNP	C	T317A		
4700745	C	-	-	-	Unc	U	-	-	-	-	Unc	U	-		
4781962	C	SNP	T	-	SNP	T	-	SNP	T	-	SNP	T	-	SCO4367	oxidoreductase
5586261i1	C	-	-	-	Ins	C	fs	-	-	-	Ins	C	fs	SCO5138	hypothetical protein
5586264i4	C	-	-	-	Ins	G	fs	-	-	-	Ins	G	fs		
5586264i1	C	-	-	-	Ins	G	fs	-	-	-	Ins	G	fs		
5586264i3	C	-	-	-	Ins	A	fs	-	-	-	Ins	A	fs		
5586264i2	C	-	-	-	Ins	G	fs	-	-	-	Ins	G	fs		
5586265i1	G	-	-	-	Ins	G	fs	-	-	-	Ins	G	fs		
7050737	C	-	-	-	SNP	T	A139T	-	-	-	SNP	T	A139T	SCO6384	integral membrane lysyl-tRNA synthetase
7190566	A	-	-	-	-	-	-	-	-	-	SNP	C	K498Q	SCO6496	dehydrogenase
7265819	C	SNP	G	H424Q	-	-	-	-	-	-	-	-	-	SCO6563	integral membrane transporter
7778607	T	-	-	-	-	-	-	-	-	-	SNP	G	V388G	SCO7004	carbohydrate kinase
7778749	C	-	-	-	-	-	-	-	-	-	SNP	G	-	SCO7004	carbohydrate kinase

SUPPLEMENTARY INFORMATION BELONGING TO CHAPTER VI

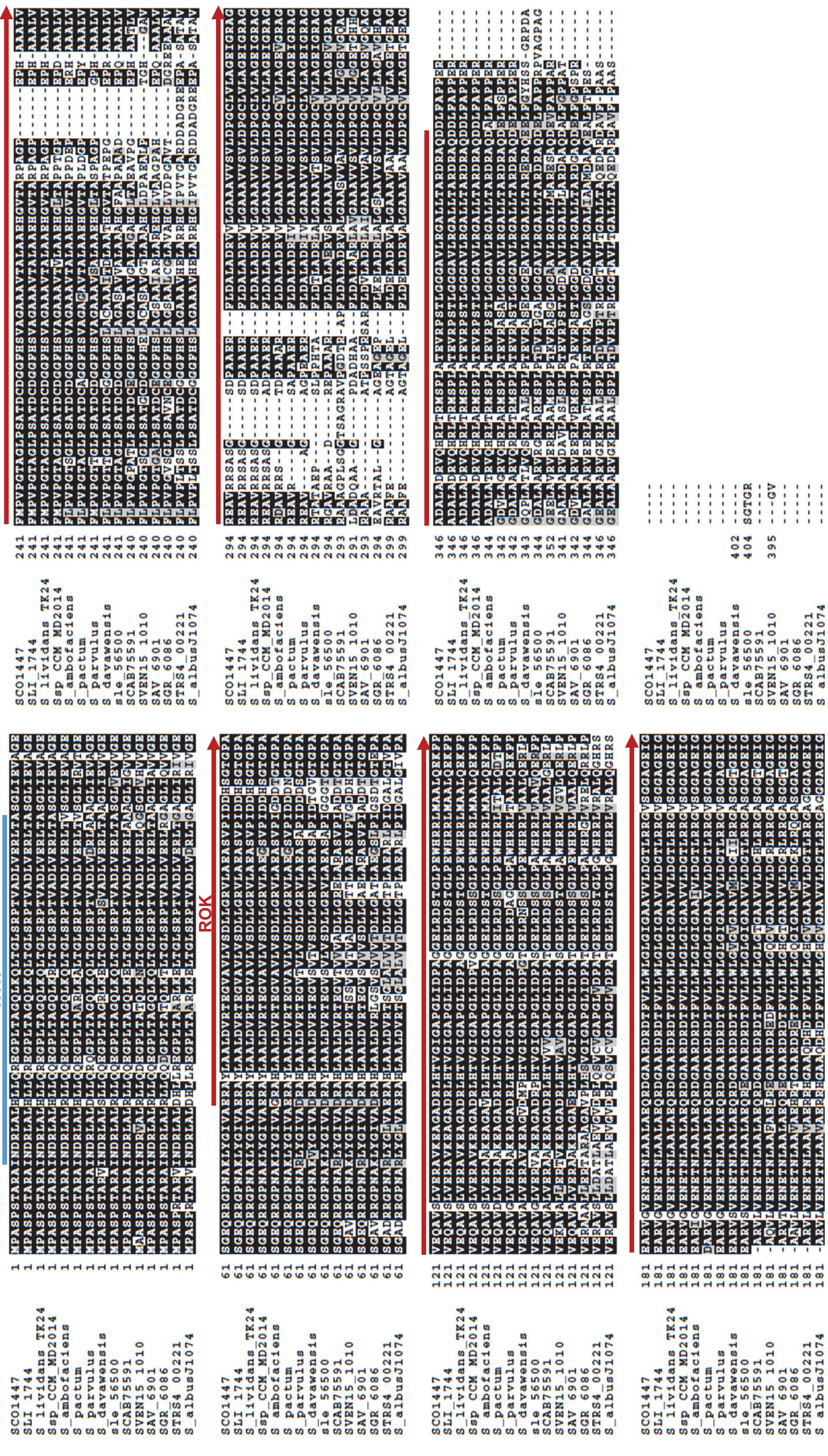


FIGURE S1. Sequence alignment of RokL6.
Alignment of the RokL6 (SCO1447) protein sequence with homologs from other *Streptomyces* species. Identical amino acids are shaded black and amino acids with similar properties are in grey. The HTH-domain of RokL6 is indicated as is the ROK-family domain, which begins at position 78 of RokL6. The image was generated using Boxshade.

TABLE S1. Bacterial strains and plasmids.

Bacterial strain		
Strains and genotype		**Reference**
E. coli JM109	See reference	Sambrook et al., 1989
E. coli ET12567	See reference	MacNeil et al., 1992
E. coli Rosetta(DE3)pLysS	See reference	Novagen
M145	*S. coelicolor* A3(2) M145 SCP1- SCP2- prototroph	Kieser et al., 2000
M512	M145 ΔredD ΔactII-ORF4	van Wezel et al., 2000
ΔnagB	M145 Δ*nagB*[d]	Swiatek et al., 2012a
GAM4	M145 *nagA*	Swiatek et al., 2012a
GAM5	M145 *nagB*	Swiatek et al., 2012a
	M145 *nagBA*	This work
	M145 SCO1447	This work
	M145 SCO1447*nagB*	This work
	M145 SCO1448	This work
	M145 SCO1448*nagB*	This work
ΔSCO6110	M145 ΔSCO6110	This work
ΔSCO6110Δ*nagB*	M145 ΔSCO6110[a]Δ*nagB*[d]	This work
ΔSCO6110Δ*rokL6*	M145 ΔSCO6110[a]Δ*rokL6*[d]	This work
Δ6110-14	M145 ΔSCO6110-14	This work
ΔS6110-14Δ*nagB*	M145 ΔSCO6110-14[a]Δ*nagB*[d]	This work
Plasmids		
Plasmid	**Description**	**Reference**
pHJL401	*E. coli - Streptomyces* shuttle vector, 1-5 copies per chromosome in *Streptomyces*	Larson & Hershberger, 1986
pWHM3	*E. coli - Streptomyces* shuttle vector (multi-copy in both hosts)	Vara et al., 1989
pUWLcre	pUWL*ori* T derivative with *cre(a)* gene under *ermE** promoter	Fedoryshyn et al, 2008
pGWS948	pWHM3 harbouring flanking regions of *S. coelicolor* SCO1447 with *apra-loxP* inserted between the flanks	this work
pGWS953	pWHM3 harbouring flanking regions of *S. coelicolor* SCO6110 with *apra-loxP* inserted between the flanks	this work
pGWS954	pWHM3 harbouring flanking regions of *S. coelicolor* SCO6110-14 with *apra-loxP* inserted between the flanks	this work

[a], Aprr, apramycin resistant. [D] deletion

TABLE S2. Oligonucleotides.

Gene*	Name^	Sequence#
SCO6110	6110LF-1198	gtcagaattctgctgatcgccgacgagcccac
	6110LR+6	gaagttatccatcacctctagaGCTCACCCCTGCTCCTCCGTC
	6110RF+927	gaagttatcgcgcatctctagaCACGAGCTGACCGCCCGCTGA
	6110RR+2197	gtcaaagcttgccaacggctatgtgcgcgaggt
SCO6110-14	6114LF-1306	gtcagaattcAGGACGGCTCGTTCGATGGCGAG
	6114LR+9	gaagttatccatcacctctagaAGTGGACATGTATCTCCTCCA
	6110RF+927	as above
	6110RR+2197	as above

* SCO database number; nucleotide position is given relative to first nucleotide of the relevant gene

^ Forward (F) or reverse (R) primer, L and R indicate left or right flank; nucleotide position relative to first nucleotide of target gene

Restriction sites underlined: GAATTC, EcoRI; AAGCTT, HindIII; TCTAGA, XbaI

TABLE S3. Proteomic comparison of *S. coelicolor* M145 and its *rokL6* mutant.

	GlcN-Mann		1447-wt			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO6010	1.379	1.288	1.580	1.475	SCO6010	Probable ABC-transport system ATP binding protein
SCO5869	1.389		1.796	1.273	SCO5869	Uncharacterized protein
SCO3967	1.851		10.400	6.011	SCO3967	Conserved hypothetical membrane protein
SCO5895			0.278	0.378	SCO5895	Putative methyltransferase
SCO2661	1.304	1.892	1.393	2.022	SCO2661	Putative sugar hydrolase
SCO5880			0.368	0.192	SCO5880	RedY protein
SCO5293	1.196		1.667	1.397	SCO5293	Putative oxygenase subunit
SCO5554	1.785			0.571	SCO5554	3-isopropylmalate dehydratase small subunit
SCO5113	1.305	1.071	1.419	1.165	SCO5113	BldKB_ putative ABC transport system lipoprotein
SCO1245			2.186	1.968	SCO1245	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
SCO7417	1.307	0.904	2.241	1.551	SCO7417	Putative cytochrome P450-family protein
SCO3349	1.216		1.804	1.668	SCO3349	Uncharacterized protein SCO3349
SCO2280			0.445	0.601	SCO2280	Putative TetR-family transcriptional regulator
SCO2256			0.224	0.242	SCO2256	3-methyl-2-oxobutanoate hydroxymethyltransferase
SCO5259			1.827	1.509	SCO5259	Permease
SCO5512			0.489	0.300	SCO5512	Acetolactate synthase
SCO4979			2.293	1.884	SCO4979	Phosphoenolpyruvate carboxykinase [GTP]
SCO3089				0.307	SCO3089	Putative ABC transporter ATP-binding protein
SCO2620	1.406		1.754		SCO2620	Trigger factor
SCO3963			0.508	0.463	SCO3963	Uncharacterized protein
SCO6375			2.595	2.286	SCO6375	Putative secreted protein
SCO4055			2.862	3.066	SCO4055	Putative alcohol dehydrogenase
SCO1901	0.829	0.650	1.462	1.146	SCO1901	Putative zinc-binding dehydrogenase
SCO3097		1.668		0.408	SCO3097	Putative secreted protein
SCO1923			1.892	1.609	SCO1923	Putative dioxygenase ferredoxin subunit
SCO2182			0.823	0.850	SCO2182	Putative gntR-family transcriptional regulator
SCO5024			2.597	1.852	SCO5024	Putative oxidoreductase
SCO2117		0.782	1.822	1.730	SCO2117	Putative anthranilate synthase
SCO2630	1.467		0.627	0.417	SCO2630	Putative biotin synthase
SCO2225	1.717	1.559			SCO2225	Putative isomerase
SCO6540	1.471	1.191	1.242		SCO6540	Putative pterin-4-alpha-carbinolamine dehydratase
SCO3202	1.741			0.672	SCO3202	RNA polymerase principal sigma factor HrdD
SCO2780			0.726	0.667	SCO2780	Putative secreted protein
SCO1476	1.625		1.727		SCO1476	S-adenosylmethionine synthase
SCO3618			1.981	1.794	SCO3618	Recombination protein RecR
SCO0247			1.652	1.375	SCO0247	Uncharacterized protein
SCO0477	1.424	1.499		1.172	SCO0477	Uncharacterized protein
SCO1760			1.524	1.156	SCO1760	Cytidylate kinase
SCO2616		0.887	1.397	1.183	SCO2616	Putative membrane protein
SCO3731	1.443		1.448	1.219	SCO3731	Cold-shock protein
SCO1169				0.441	SCO1169	Xylose isomerase
SCO6659	1.486	1.371		0.867	SCO6659	Glucose-6-phosphate isomerase 1
SCO2164			0.759	0.590	SCO2164	Putative integral membrane efflux protein
SCO3182	1.205		1.436		SCO3182	UTP--glucose-1-phosphate uridylyltransferase
SCO1872			2.136	1.541	SCO1872	Putative IclR-family transcriptional regulator
SCO7477		0.257		5.862	SCO7477	Putative membrane protein
SCO1486	1.653		1.885		SCO1486	Dihydroorotase
SCO1406	0.857		2.354		SCO1406	Uncharacterized protein
SCO5745			1.851	1.407	SCO5745	Ribonuclease J
SCO3956			0.619	0.697	SCO3956	Putative ABC transporter ATP-binding protein
SCO3928			1.718	1.217	SCO3928	Phosphomethylpyrimidine synthase
SCO4653	1.662		1.860		SCO4653	50S ribosomal protein L7/L12
SCO5553	1.337			0.767	SCO5553	3-isopropylmalate dehydratase large subunit
SCO4472				0.442	SCO4472	Putative secreted protein
SCO2548	1.794	1.289	1.479		SCO2548	Putative Hit-family protein
SCO1666			1.610	1.252	SCO1666	Putative phosphatase
SCO6057	1.200		1.295	1.121	SCO6057	Putative ATP/GTP-binding integral membrane protein
SCO1045				1935	SCO1045	Putative metal associated protein
SCO1773			1.501		SCO1773	Alanine dehydrogenase
SCO5472				0.434	SCO5472	Aminomethyltransferase
SCO2093	1.197	1.067	1.280	1.140	SCO2093	Carbonic anhydrase
SCO3615	1.265			0.864	SCO3615	Aspartokinase
SCO5047	0.728		0.664	0.873	SCO5047	Fructose-1_6-bisphosphatase
SCO5751	1.749	1.224	1.696		SCO5751	Putative membrane protein
SCO5290	0.439	0.498		1.968	SCO5290	Uncharacterized protein
SCO2161	1.431	1.350	1.082		SCO2161	Uncharacterized protein
SCO6804			0.147		SCO6804	Uncharacterized protein
SCO3651	1.338	1.512	0.612	0.692	SCO3651	Uncharacterized protein
SCO4661	1.351		1.480		SCO4661	Elongation factor G 1
SCO3226	1.529	1.383		1.484	SCO3226	Two component system response regulator
SCO1478	1.365		1.758	1.436	SCO1478	DNA-directed RNA polymerase subunit omega
SCO0681	1.578	1.242			SCO0681	Putative ferredoxin/ferredoxin-NADP reductase protein)
SCO4498				0.470	SCO4498	Putative proton transport protein
SCO5145			1.767	1.570	SCO5145	Uncharacterized protein
SCO3913	1.429		1.529		SCO3913	Uncharacterized protein
SCO3333		0.541		0.730	SCO3333	Putative hydrolase
SCO0923				0.494	SCO0923	Putative reductase flavoprotein subunit
SCO1116	1.600		1.894	1.358	SCO1116	Uncharacterized protein
SCO2067	2.051		2.192	1.240	SCO2067	Putative membrane protein
SCO2388			1.508	1.268	SCO2388	3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 1
SCO4812				0.493	SCO4812	Putative integral membrane protein
SCO4580	0.625	0.648			SCO4580	Putative fumarylacetoacetase
SCO1870		1.671			SCO1870	Uncharacterized protein
SCO1676			1.766	1.172	SCO1676	Putative peptidase

	GlcN-Mann		1447-wt			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO5625	1.542		2.016	1.444	SCO5625	Elongation factor Ts
SCO2322	0.783	0.656			SCO2322	Putative secreted protein
SCO2730				3.135	SCO2730	Putative regulator
SCO4242	0.472			2.290	SCO4242	Putative membrane protein
SCO4648	1.294	0.842	1.519		SCO4648	50S ribosomal protein L11
SCO6041	1.546		1.431		SCO6041	Putative protoporphyrinogen oxidase
SCO4945				0.568	SCO4945	Putative dehydrogenase
SCO5419	1.241		1.341		SCO5419	Putative thioredoxin
SCO3151	0.554	0.726			SCO3151	Uncharacterized protein
SCO5254	2.133	1.559			SCO5254	Superoxide dismutase [Ni]
SCO2619	1.622		1.392		SCO2619	ATP-dependent Clp protease proteolytic subunit 1
SCO5774		0.645		1.260	SCO5774	Glutamate permease
SCO4525	1.239		1.436		SCO4525	Uncharacterized protein
SCO5820	1.214		1.251		SCO5820	RNA polymerase principal sigma factor HrdB
SCO6123	1.912			1.479	SCO6123	Putative quinone binding protein
SCO1814			1.727	1.326	SCO1814	Enoyl-[acyl-carrier-protein] reductase [NADH]
SCO2011		0.615	2.073	1.567	SCO2011	Putative branched chain amino acid transport ATP-binding protein
SCO1480	1.322		1.431		SCO1480	Uncharacterized protein
SCO1514	1.522		1.688	1.209	SCO1514	Adenine phosphoribosyltransferase
SCO2902	1.484		1.593		SCO2902	Non-canonical purine NTP pyrophosphatase
SCO2577				1.234	SCO2577	Ribosomal silencing factor RsfS
SCO5519	1.992		1.349		SCO5519	Uncharacterized protein
SCO1461				0.667	SCO1461	Putative inosine monophosphate dehydrogenase
SCO3122	1.488				SCO3122	Bifunctional protein GlmU
SCO1942	1.475	1.312			SCO1942	Glucose-6-phosphate isomerase 2
SCO2196	1.243		1.363		SCO2196	Putative integral membrane protein
SCO2643			1.369	1.166	SCO2643	Aminopeptidase N
SCO3136	2.048	1.180			SCO3136	Galactokinase
SCO5493	1.434		1.562		SCO5493	Uncharacterized protein
SCO1560	1.331		1.289		SCO1560	Putative phosphatase
SCO1958	1.531			0.906	SCO1958	UvrABC system protein A
SCO4992			1.304	1.253	SCO4992	Uncharacterized protein
SCO6983	1.301	1.244			SCO6983	Uncharacterized protein
SCO2012			1.884	1.414	SCO2012	Putative branched chain amino acid transport ATP-binding protein
SCO1554	1.310	1.217			SCO1554	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
SCO1109				0.542	SCO1109	Putative oxidoreductase
SCO5592	1.166		1.332		SCO5592	UPF0109 protein SCO5592
SCO3127				1.698	SCO3127	Phosphoenolpyruvate carboxylase
SCO4173				0.437	SCO4173	Uncharacterized protein
SCO5102	0.713			1.230	SCO5102	Putative mutT-like protein
SCO1415	2.176			2.554	SCO1415	Putative membrane protein
SCO1898			1.586	1.233	SCO1898	Putative substrate binding protein
SCO0499	2.290	1.624		1.188	SCO0499	Putative formyltransferase
SCO6042	1.373				SCO6042	Uncharacterized protein
SCO4729	2.190				SCO4729	DNA-directed RNA polymerase subunit alpha
SCO1947	1.417			0.849	SCO1947	Glyceraldehyde-3-phosphate dehydrogenase
SCO5385	1.554				SCO5385	Putative 3-hydroxybutyryl-coA dehydrogenase
SCO5281	1.781			1.178	SCO5281	Putative 2-oxoglutarate dehydrogenase
SCO6310			1.183	1.281	SCO6310	Putative cytochrome P450
SCO2076			1.236		SCO2076	Isoleucine--tRNA ligase
SCO4439	1.728				SCO4439	Putative D-alanyl-D-alanine carboxypeptidase
SCO6147		1.337			SCO6147	Probable xylitol oxidase
SCO6835		1.830		1.710	SCO6835	Putative arsenate reductase
SCO4683	1.516			1.132	SCO4683	Glutamate dehydrogenase
SCO5459		0.941	1.270		SCO5459	Putative enoyl-coA hydratase
SCO2267	1.437	1.175			SCO2267	Probable heme oxygenase
SCO3156			1.375	1.245	SCO3156	Putative penicillin-binding protein
SCO5822	1.346		1.205		SCO5822	DNA topoisomerase (ATP-hydrolyzing)
SCO1646	0.745			0.640	SCO1646	Prokaryotic ubiquitin-like protein Pup
SCO5865		0.795			SCO5865	Uncharacterized protein
SCO3399	10.057	5.418			SCO3399	Uncharacterized protein
SCO6743	1.215			0.825	SCO6743	Putative transcriptional accessory protein
SCO1546				1.577	SCO1546	Putative aminotransferase
SCO1871	0.704		0.694		SCO1871	Putative aldehyde dehydrogenase
SCO2771	1.476				SCO2771	Uncharacterized phosphatase SCO2771
SCO5500	1.419				SCO5500	Putative membrane protein
SCO7443	1.942				SCO7443	Phosphoglucomutase
SCO2837		0.767		1.149	SCO2837	Putative secreted protein
SCO5470	1.682			0.704	SCO5470	Serine hydroxymethyltransferase
SCO4199	1.954				SCO4199	Uncharacterized protein
SCO1213	1.294		1.223		SCO1213	Uncharacterized protein
SCO5031	1.206	1.223			SCO5031	Alkyl hydroperoxide reductase AhpD
SCO7102		0.680		1.176	SCO7102	Uncharacterized protein
SCO1848	1.489			1.489	SCO1848	Cobyric acid synthase
SCO3063	1.196		1.243		SCO3063	Putative two-component system reponse regulator
SCO2162			1.345		SCO2162	Quinolinate synthase A
SCO1141	1.403		1.240	0.811	SCO1141	Uncharacterized protein
SCO4587	1.488	1.582			SCO4587	Uncharacterized protein
SCO1815				1.659	SCO1815	Probable 3-oxacyl-(Acyl-carrier-protein) reductase
SCO4584				0.685	SCO4584	Putative membrane protein
SCO0748	1.658	1.764			SCO0748	Putative hydrolase
SCO0525	1.560			1.589	SCO0525	Uncharacterized protein

	GlcN-Mann		**1447-wt**			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO5170				0.512	SCO5170	Putative tetR-family transcriptional regulator
SCO6627				1.678	SCO6627	Uncharacterized protein
SCO2115	1.476				SCO2115	Phospho-2-dehydro-3-deoxyheptonate aldolase
SCO5329	1.271				SCO5329	Uncharacterized protein
SCO2778			1.297	1.120	SCO2778	Hydroxymethylglutaryl-CoA lyase
SCO1490				1.309	SCO1490	N utilization substance protein B homolog
SCO5533	2.035	1.463			SCO5533	Uncharacterized protein
SCO4152			1.764	1.565	SCO4152	Putative secreted 5’-nucleotidase
SCO5477		0.860	1.292		SCO5477	Putative oligopeptide-binding lipoprotein
SCO5260	1.903				SCO5260	Secreted protein
SCO0679	0.388				SCO0679	Uncharacterized protein
SCO3889		1.476		1.478	SCO3889	Thioredoxin-1
SCO4710	1.913			0.797	SCO4710	50S ribosomal protein L29
SCO1852	2.431			1.519	SCO1852	Hydrogenobyrinate a_c-diamide synthase
SCO4366	1.292				SCO4366	Phosphoserine aminotransferase
SCO2168				0.502	SCO2168	Uncharacterized protein
SCO3381	1.484				SCO3381	Nicotinate-nucleotide pyrophophorylase
SCO3074				0.745	SCO3074	Putative integral membrane protein
SCO1705	1.334		1.366		SCO1705	Putative alcohol dehydrogenase (Zinc-binding)
SCO5499				1.326	SCO5499	Glutamyl-tRNA(Gln) amidotransferase subunit A
SCO3958				0.557	SCO3958	ABC transporter ATP-binding protein
SCO0740		1.442			SCO0740	Putative hydrolase
SCO4233				1.104	SCO4233	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
SCO0762		0.307		0.498	SCO0762	Subtilase-type protease inhibitor
SCO4643	1.454		1.305		SCO4643	UDP-N-acetylenolpyruvoylglucosamine reductase
SCO4832				0.000	SCO4832	Putative glycine betaine-binding lipoprotein
SCO5893	0.752			0.660	SCO5893	Oxidoreductase
SCO2597				1.443	SCO2597	50S ribosomal protein L21
SCO6076	1.957	1.398			SCO6076	Putative dipeptidase
SCO1087		0.630		0.910	SCO1087	Putative aldolase
SCO1793		0.808		0.886	SCO1793	Putative secreted protein
SCO1728		0.648	1.466		SCO1728	Putative gntR-family transcriptional regulator
SCO7523	1.353				SCO7523	Putative chaperone
SCO2387			2.035	1.892	SCO2387	Malonyl CoA:acyl carrier protein malonyltransferase
SCO6046		0.773		0.808	SCO6046	Uncharacterized protein
SCO5077				1.308	SCO5077	Uncharacterized protein
SCO3001			1.266		SCO3001	Uncharacterized protein
SCO1081	1.097		1.172		SCO1081	Putative electron transfer flavoprotein_ alpha subunit
SCO7154	1.750				SCO7154	Ketol-acid reductoisomerase 2
SCO1659		0.403		0.481	SCO1659	Probable glycerol uptake facilitator protein
SCO4652	1.455				SCO4652	50S ribosomal protein L10
SCO3673	1.801			1.454	SCO3673	Putative iron-sulphur-binding reductase
SCO3897			1.321		SCO3897	Uncharacterized protein
SCO5225				1.217	SCO5225	Ribonucleoside-diphosphate reductase subunit beta
SCO5813	1.270			1.162	SCO5813	Uncharacterized protein
SCO6199		0.652			SCO6199	Secreted esterase
SCO1864				0.754	SCO1864	L-2_4-diaminobutyric acid acetyltransferase
SCO6564				1.285	SCO6564	3-oxoacyl-[acyl-carrier-protein] synthase 3 protein 4
SCO1640				0.762	SCO1640	Pup--protein ligase
SCO2169			1.395		SCO2169	Putative integral membrane protein
SCO1501				1.203	SCO1501	Alanine--tRNA ligase
SCO1404	1.349				SCO1404	Uncharacterized protein
SCO6216				1.535	SCO6216	Uncharacterized protein
SCO4636				1.167	SCO4636	UPF0336 protein SCO4636
SCO4232	1.264				SCO4232	Putative transcriptional factor regulator
SCO5806				1.387	SCO5806	Uncharacterized protein
SCO7361				1.178	SCO7361	Putative DNA-binding protein
SCO6031	1.557				SCO6031	Uroporphyrinogen decarboxylase
SCO1425	1.807			0.886	SCO1425	Putative AsnC-family transcriptional regulatory protein
SCO2669		0.569		1.222	SCO2669	Uncharacterized protein
SCO3896	2.845				SCO3896	Putative RNA nucleotidyltransferase
SCO6860			1.653	1.426	SCO6860	Uncharacterized protein
SCO1319	1.233		1.387		SCO1319	Putative membrane protein
SCO3187				1.636	SCO3187	Uncharacterized protein
SCO2147	1.306		1.498	1.302	SCO2147	Anthranilate phosphoribosyltransferase 1
SCO5232				2.426	SCO5232	Putative sugar transporter sugar binding protein
SCO1479	1.667				SCO1479	Guanylate kinase
SCO0769				0.776	SCO0769	Putative oxidoreductase
SCO4506	1.517			1.255	SCO4506	Chorismate dehydratase
SCO3977		0.698			SCO3977	Putative protease (Putative secreted protein)
SCO1900				2.255	SCO1900	Putative integral membrane sugar transport protein
SCO4078				1.351	SCO4078	Phosphoribosylformylglycinamidine synthase subunit PurQ
SCO0868			3.562	4.496	SCO0868	Putative regulatory protein
SCO0719	4.043				SCO0719	Uncharacterized protein
SCO4026	0.660				SCO4026	Putative ATP binding protein
SCO3941			1.409	1.290	SCO3941	Putative serine/threonineprotein kinase
SCO1817			1.375		SCO1817	Uncharacterized protein
SCO6776		0.495			SCO6776	Uncharacterized protein
SCO2974				0.783	SCO2974	Serine/threonine-protein kinase PkaA
SCO3617			1.513		SCO3617	Uncharacterized protein
SCO1644				1.652	SCO1644	Proteasome subunit beta
SCO4637	1.532				SCO4637	Uncharacterized protein
SCO5854		1.738			SCO5854	Sulfurtransferase
SCO3884	1.129		1.123		SCO3884	Jag
SCO2075		0.666			SCO2075	Putative DNA-binding protein
SCO3899				1.347	SCO3899	Uncharacterized protein

SCO	GlcN-Mann wt	 1447	1447-wt Mann	 GlcN	SCO	Description
SCO4614				1.326	SCO4614	UPF0234 protein SCO4614
SCO3137	1.401				SCO3137	UDP-glucose 4-epimerase
SCO1088		0.758		0.657	SCO1088	Putative oxidoreductase
SCO2241			0.610		SCO2241	Probable glutamine synthetase (EC 6.3.1.2)
SCO1438	0.785				SCO1438	ATP phosphoribosyltransferase
SCO3862				1.666	SCO3862	Putative membrane protein
SCO3966				1.785	SCO3966	Putative secreted protein
SCO4293				0.755	SCO4293	Putative threonine synthase
SCO3059			1.262		SCO3059	N5-carboxyaminoimidazole ribonucleotide mutase
SCO3197				1.137	SCO3197	Putative 1-phosphofructokinase
SCO4036	1.330	1.218			SCO4036	Uncharacterized protein SCO4036
SCO4814				1.433	SCO4814	Bifunctional purine biosynthesis protein PurH
SCO1602	2.173		5.097	2.120	SCO1602	Uncharacterized protein
SCO2065	1.383				SCO2065	Uncharacterized protein
SCO0641				0.491	SCO0641	Tellurium resistance protein
SCO4493				1.182	SCO4493	Putative asnC-family transcriptional regulator
SCO4394		0.824		1.130	SCO4394	DmdR1 protein
SCO5711				1.502	SCO5711	Riboflavin biosynthesis protein
SCO3815		0.718			SCO3815	Putative dihydrolipoamide acyltransferase component
SCO2951				1.229	SCO2951	Putative malate oxidoreductase
SCO6637		0.736			SCO6637	Uncharacterized protein
SCO3950	1.856			1.150	SCO3950	Uncharacterized protein
SCO4550	1.456				SCO4550	Cyclic dehypoxanthine futalosine synthase
SCO2008		0.623			SCO2008	Putative branched chain amino acid binding protein
SCO6723				1.144	SCO6723	Putative oxidoreductase (Putative secreted protein)
SCO3859				1.210	SCO3859	Putative DNA-binding protein
SCO5396		0.589			SCO5396	Putative cellulose-binding protein
SCO2369		1.843			SCO2369	Putative thiol-specific antioxidant protein
SCO2614	1.574				SCO2614	Folylpolyglutamate synthase
SCO4087	2.446				SCO4087	Phosphoribosylformylglycinamidine cyclo-ligase
SCO6260	1.935				SCO6260	Putative sugar kinase
SCO5738		1.975			SCO5738	Uncharacterized zinc protease SCO5738
SCO3108		0.718			SCO3108	Uncharacterized protein
SCO6658				1.237	SCO6658	6-phosphogluconate dehydrogenase
SCO0736		1.396			SCO0736	Putative secreted protein
SCO6544				1.831	SCO6544	Putative membrane protein
SCO5539	8.098				SCO5539	Uncharacterized protein
SCO4261	1.746			1.073	SCO4261	Putative response regulator
SCO4894				0.374	SCO4894	Uncharacterized protein
SCO3914	3.937				SCO3914	Putative transcriptional regulator
SCO2920		0.446			SCO2920	Putative secreted protease
SCO0730				0.674	SCO0730	Uncharacterized protein
SCO0546	1.138			0.862	SCO0546	Pyruvate carboxylase
SCO4610	4.483				SCO4610	Putative integral membrane protein
SCO7319				0.378	SCO7319	Putative oxidoreductase
SCO5257				1.815	SCO5257	Methyltransferase
SCO4736	0.850		0.799		SCO4736	Phosphoglucosamine mutase
SCO2634	2.203				SCO2634	Uncharacterized protein
SCO4545	5.429				SCO4545	Uncharacterized protein
SCO1244				1.433	SCO1244	Biotin synthase
SCO1718				0.597	SCO1718	Putative regulator
SCO2908	0.833		0.845		SCO2908	Uncharacterized protein
SCO2640	1.216				SCO2640	Aspartate-semialdehyde dehydrogenase
SCO4649				1.132	SCO4649	50S ribosomal protein L1
SCO2044				0.847	SCO2044	Phosphoribosyl-AMP cyclohydrolase
SCO3957				0.550	SCO3957	Possible integral membrane protein
SCO3317				0.815	SCO3317	Putative uroporphyrin-III C-methyltransferase/ uroporphyrinogen-III synthase
SCO5151		0.480	2.143		SCO5151	Uncharacterized protein
SCO6206		2.035			SCO6206	Putative hydroxypyruvate isomerase
SCO1232	1.353				SCO1232	Urease accessory protein UreG
SCO3817				1.319	SCO3817	Putative branched-chain alpha keto acid dehydrogenase E1 alpha subunit
SCO0428		0.717			SCO0428	Putative tetR family transcriptional regulator
SCO0888	2.719			1.394	SCO0888	Putative secreted protein
SCO5136		1.197			SCO5136	Putative aminotransferase
SCO2039		1.079			SCO2039	Indole-3-glycerol phosphate synthase 1
SCO4151				1.178	SCO4151	Mycothiol acetyltransferase
SCO3871		0.282		0.557	SCO3871	Putative decarboxylase
SCO0506		1.393			SCO0506	NH(3)-dependent NAD(+) synthetase
SCO5543				1.144	SCO5543	Uncharacterized protein
SCO3484	3.178			1.661	SCO3484	Putative secreted sugar-binding protein
SCO5172	1.934				SCO5172	Putative hydrolase
SCO3401	2.064				SCO3401	Putative hydroxymethyldihydropteridine pyrophosphokinase
SCO5776		0.765			SCO5776	Glutamate binding protein
SCO5537				1.579	SCO5537	Putative ATP/GTP binding protein
SCO1008	1.725			1.168	SCO1008	Uncharacterized protein
SCO5708		0.732			SCO5708	Ribosome-binding factor A
SCO0884				1.583	SCO0884	Probable oxidoreductase
SCO5859		1.214		1.136	SCO5859	Probable ferrochelatase
SCO7072	1.561				SCO7072	Uncharacterized protein
SCO3343				0.494	SCO3343	Uncharacterized protein
SCO1343	1.226		1.310		SCO1343	Uracil-DNA glycosylase 2
SCO1138		0.750		1.304	SCO1138	Putative secreted protein
SCO1925				1.201	SCO1925	Uncharacterized protein
SCO5178	2.051				SCO5178	Putative sulfurylase

	GlcN-Mann		1447-wt			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO5514	2.174				SCO5514	Ketol-acid reductoisomerase 1
SCO6207	3.318	1.508	2.802		SCO6207	Uncharacterized protein
SCO1556	1.245				SCO1556	Putative acetyltransferase
SCO5240	2.680		4.437	1.908	SCO5240	Transcriptional regulator WhiB
SCO4548	2.104				SCO4548	Putative integral membrane protein
SCO1201				0.555	SCO1201	Putative reductase
SCO3944	1.193			0.900	SCO3944	Putative phenylalanine aminotransferase
SCO3768		0.415	1.819		SCO3768	Putative translocase protein
SCO1706				0.531	SCO1706	Putative aldehyde dehydrogenase
SCO2884	1.990				SCO2884	Putative cytochrome P450
SCO5560	1.210		1.285		SCO5560	D-alanine--D-alanine ligase
SCO2129				1.061	SCO2129	Uncharacterized protein
SCO1598		0.734			SCO1598	50S ribosomal protein L20
SCO1553				1.611	SCO1553	Putative uroporphyrin-III methyltransferase
SCO7585		0.860		0.591	SCO7585	Putative merR-family transcriptional regulator
SCO3302	0.317				SCO3302	Putative integral membrane protein
SCO0494	1.398			0.814	SCO0494	Putative iron-siderophore binding lipoprotein
SCO1254				1.327	SCO1254	Adenylosuccinate lyase
SCO4118				0.763	SCO4118	Putative tetR-family transcriptional regulator
SCO0672	5.067				SCO0672	Anti-sigma factor antagonist
SCO0852				0.822	SCO0852	Putative aldolase
SCO5367	2.630				SCO5367	ATP synthase subunit a
SCO1630			0.592		SCO1630	Putative integral membrane protein
SCO5423	1.431			1.253	SCO5423	Pyruvate kinase
SCO7292	3.041				SCO7292	Putative threonine dehydratase
SCO5701	2.681				SCO5701	Uncharacterized protein
SCO1660				0.710	SCO1660	Glycerol kinase 2
SCO4277				0.445	SCO4277	Putative tellurium resistance protein
SCO1648				0.782	SCO1648	Proteasome-associated ATPase
SCO3669	1.314			0.792	SCO3669	Chaperone protein DnaJ 1
SCO2726	1.335				SCO2726	Methylmalonic acid semialdehyde dehydrogenase
SCO4096	4.368				SCO4096	ATP-dependent RNA helicase
SCO2769	1.974				SCO2769	Putative acetolactate synthase
SCO4734	1.333				SCO4734	50S ribosomal protein L13
SCO1699	1.769				SCO1699	Putative transcriptional regulator
SCO1571	2.873				SCO1571	Uncharacterized protein
SCO5546	1.294				SCO5546	Uncharacterized protein
SCO1639	1.329				SCO1639	Peptidyl-prolyl cis-trans isomerase
SCO3549				1.113	SCO3549	Anti-sigma-B factor antagonist
SCO7468			1.623	1.407	SCO7468	Putative flavin-binding monooxygenase
SCO4704				1.306	SCO4704	50S ribosomal protein L23
SCO6068			3.681	2.048	SCO6068	Uncharacterized protein
SCO2026				1.229	SCO2026	Putative glutamate synthase large subunit
SCO6960		1.343			SCO6960	Uncharacterized protein
SCO7699				1.376	SCO7699	Putative nucleotide-binding protein
SCO5544				1.191	SCO5544	Histidine kinase
SCO5563	4.037		2.940		SCO5563	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase
SCO0427	2.020				SCO0427	Putative hydrolase
SCO4088		0.269			SCO4088	Uncharacterized protein
SCO2582	1.248				SCO2582	Uncharacterized protein
SCO4444	1.729		2.479	1.459	SCO4444	Glutathione peroxidase
SCO5648	3.102			1.204	SCO5648	Fe(3+) ions import ATP-binding protein FbpC
SCO3619	1.567				SCO3619	Nucleoid-associated protein SCO3619
SCO1818	0.787				SCO1818	Tyrosine--tRNA ligase
SCO5140				0.631	SCO5140	Cytokinin riboside 5’-monophosphate phosphoribohydrolase
SCO4932		0.687		0.810	SCO4932	Histidine ammonia-lyase
SCO4651	0.747				SCO4651	Putative lipoprotein SCO4651
SCO3041				0.672	SCO3041	Uncharacterized protein
SCO2579	2.000				SCO2579	Probable nicotinate-nucleotide adenylyltransferase
SCO2774	1.421				SCO2774	Acyl-CoA dehydrogenase
SCO3607				0.828	SCO3607	Putative secreted protein
SCO1511				0.811	SCO1511	Uncharacterized protein
SCO2793				0.784	SCO2793	Oligoribonuclease
SCO6491				2.208	SCO6491	Uncharacterized protein
SCO4585	3.008			0.322	SCO4585	Putative ABC transporter ATP-binding protein
SCO3795				1.235	SCO3795	Aspartate--tRNA ligase
SCO5044				1.167	SCO5044	Fumarate hydratase class I
SCO3060	1.191				SCO3060	N5-carboxyaminoimidazole ribonucleotide synthase
SCO6197		0.547			SCO6197	Putative secreted protein
SCO1223				0.690	SCO1223	Ornithine aminotransferase
SCO4965		0.603			SCO4965	Transcription elongation factor GreA
SCO1174	2.017			0.897	SCO1174	Probable aldehyde dehydrogenase
SCO3614				0.744	SCO3614	Aspartate-semialdehyde dehydrogenase
SCO4020				1.555	SCO4020	Putative two component system response regulator
SCO5788	1.414	0.850	1.718		SCO5788	Uncharacterized protein
SCO2600		0.778			SCO2600	Uncharacterized protein
SCO5501				1.155	SCO5501	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
SCO4556				1.118	SCO4556	Demethylmenaquinone methyltransferase
SCO3009		2.024			SCO3009	Uncharacterized protein
SCO6515		1.665			SCO6515	Putative protease
SCO4708	1.353				SCO4708	30S ribosomal protein S3
SCO2444		0.374	3.884	3.222	SCO2444	Putative fatty acid synthase
SCO1766	3.200				SCO1766	Putative glycohydrolase
SCO3179				2.570	SCO3179	Molybdenum cofactor biosynthesis protein (Putative secreted protein)
SCO5651	1.525				SCO5651	Uncharacterized protein
SCO2054	2.085			1.271	SCO2054	Histidinol dehydrogenase

	GlcN-Mann		1447-wt			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO4296			1.401		SCO4296	60 kDa chaperonin 2
SCO5655	1.301			0.750	SCO5655	Putative aminotransferase
SCO5474		3.186			SCO5474	Uncharacterized protein
SCO2900				0.743	SCO2900	Putative membrane protein
SCO2549	0.786			0.860	SCO2549	Tricorn protease homolog 1
SCO4912		0.684		0.728	SCO4912	Putative aldehyde dehydrogenase
SCO0979				1.396	SCO0979	Uncharacterized protein
SCO1506	2.034				SCO1506	Conserved ATP/GTP binding protein
SCO6456				2.626	SCO6456	Putative hydrolytic protein
SCO1594				1.345	SCO1594	Phenylalanine--tRNA ligase beta subunit
SCO1472	1.822				SCO1472	Conserved hypothetical Sun-family protein SCL6.29c
SCO2923		1.136			SCO2923	Putative membrane protein
SCO2848		0.695			SCO2848	UPF0303 protein SCO2848
SCO4919				0.782	SCO4919	Putative oxidoreductase
SCO1678	4.563				SCO1678	Putative transcriptional regulator
SCO4751				0.744	SCO4751	Putative acetyltransferase
SCO3793				0.863	SCO3793	Uncharacterized protein
SCO1824		0.675		1.197	SCO1824	Secreted subtilisin-like protease
SCO6027	1.312		1.248		SCO6027	Acetyl-coa acetyltransferase (Thiolase)
SCO3878				1.222	SCO3878	DNA polymerase III subunit beta
SCO1428		0.771			SCO1428	Acyl-CoA dehydrogenase
SCO1080				0.666	SCO1080	Uncharacterized protein
SCO4039		1.740			SCO4039	Uncharacterized protein
SCO5775				1.186	SCO5775	Glutamate permease
SCO2301			3.714	1.619	SCO2301	GTP cyclohydrolase 1 type 2 homolog
SCO4159				0.394	SCO4159	Transcriptional regulatory protein GlnR
SCO2590	1.801				SCO2590	Putative glycosyltransferase
SCO4890				3.185	SCO4890	Thymidine phosphorylase
SCO6635	3.426				SCO6635	Bacteriophage (PhiC31) resistance gene pglY
SCO3877	1.413				SCO3877	Putative 6-phosphogluconate dehydrogenase
SCO5388				1.199	SCO5388	Endonuclease NucS
SCO4886				0.720	SCO4886	Putative sugar ABC transporter ATP-binding protein
SCO5258				2.008	SCO5258	ATP-binding protein
SCO6412	1.444		1.639		SCO6412	Putative aminotransferase
SCO0563				1.246	SCO0563	Uncharacterized protein
SCO4295		1.964	0.504		SCO4295	Cold shock protein
SCO1089				0.759	SCO1089	Uncharacterized protein
SCO5583				3.787	SCO5583	Ammonium transporter
SCO5971				0.790	SCO5971	Uncharacterized protein
SCO6660	1.461			0.736	SCO6660	Uncharacterized protein
SCO2150		0.839			SCO2150	Cytochrome C heme-binding subunit
SCO2830	3.162				SCO2830	Probable amino acid ABC transporter protein_ integral membrane component
SCO3049				0.782	SCO3049	Putative acyl-CoA hydrolase
SCO5420				1.456	SCO5420	Cholesterol esterase
SCO5650			0.749		SCO5650	Putative membrane protein
SCO2761				1.675	SCO2761	Putative secreted tripeptidyl aminopeptidase
SCO2266				1.418	SCO2266	Methionine aminopeptidase
SCO5360				0.820	SCO5360	Peptide chain release factor 1
SCO7695				3.516	SCO7695	Uncharacterized protein
SCO1768		0.827		0.832	SCO1768	Pseudouridine synthase
SCO1414				1.251	SCO1414	Putative ankyrin-like protein
SCO2504				1.192	SCO2504	Glycine--tRNA ligase
SCO3115				1.218	SCO3115	Uncharacterized protein
SCO2036				1.257	SCO2036	Tryptophan synthase alpha chain
SCO5038	2.614				SCO5038	F42a
SCO1013				1.141	SCO1013	Putative mut-like protein
SCO3118		1.232		1.306	SCO3118	Uncharacterized protein
SCO2113				0.636	SCO2113	Bacterioferritin
SCO1523				0.858	SCO1523	Pyridoxal 5’-phosphate synthase subunit PdxS
SCO6549	2.435				SCO6549	Uncharacterized protein
SCO4089	1.453				SCO4089	Valine dehydrogenase
SCO2367				0.764	SCO2367	Uncharacterized protein
SCO5389		0.719			SCO5389	Uncharacterized protein
SCO1681		1.290			SCO1681	Putative gluconate dehydrogenase
SCO0204				0.611	SCO0204	Putative luxR family two-component response regulator
SCO3823	1.828				SCO3823	Putative quinone oxidoreductase
SCO2275				1.204	SCO2275	Putative lipoprotein
SCO2999			0.770		SCO2999	Uncharacterized protein
SCO2461		0.526			SCO2461	Putative secreted protein
SCO1262		0.515			SCO1262	Putative gntR-family transcriptional regulator
SCO1563		0.660			SCO1563	Putative acetyltransferase
SCO5289	2.889				SCO5289	Putative two component sensor kinase
SCO1865	1.533			0.741	SCO1865	Diaminobutyrate--2-oxoglutarate transaminase
SCO6169	3.395				SCO6169	Putative regulatory protein
SCO2907	5.545				SCO2907	Putative PTS transmembrane component
SCO6218		0.831	1.351	0.877	SCO6218	Putative phosphatase
SCO4490	2.129				SCO4490	Putative decarboxylase SCD69.10
SCO4577	2.513				SCO4577	Putative helicase
SCO7631	3.538				SCO7631	Putative secreted protein
SCO3026	2.066				SCO3026	Uncharacterized protein
SCO1868				0.803	SCO1868	Uncharacterized protein
SCO1441	2.231				SCO1441	Riboflavin biosynthesis protein RibBA
SCO1945	0.740			1.152	SCO1945	Triosephosphate isomerase
SCO2131				0.791	SCO2131	Putative long chain fatty acid CoA ligase
SCO5337				1.181	SCO5337	Uncharacterized protein

	GlcN-Mann		1447-wt			
SCO	**wt**	**1447**	**Mann**	**GlcN**	**SCO**	**Description**
SCO6590		0.697			SCO6590	Putative secreted esterase
SCO1636		0.748			SCO1636	Uncharacterized protein
SCO2591				1.324	SCO2591	Putative secreted protein
SCO4800	2.358				SCO4800	Isobutiryl CoA mutase_ small subunit
SCO7324	1.151			0.896	SCO7324	Putative regulatory protein
SCO1966				0.522	SCO1966	UvrABC system protein B
SCO0302				1.317	SCO0302	Putative tetR-family transcriptional regulator
SCO7325	2.972	2.777			SCO7325	Anti-sigma factor antagonist
SCO2140	0.765				SCO2140	Putative transcriptional regulator
SCO6663				1.109	SCO6663	Transketolase B
SCO3100	1.737				SCO3100	Uncharacterized protein
SCO3123				0.787	SCO3123	Ribose-phosphate pyrophosphokinase
SCO1853				0.814	SCO1853	Precorrin-2 C20-methyltransferase (EC 2.1.1.130)
SCO3974		0.765			SCO3974	Uncharacterized protein
SCO1840		0.900		0.799	SCO1840	Putative ABC transporter ATP binding protein
SCO5528				2.297	SCO5528	Putative transcriptional regulator
SCO4702		0.712		0.765	SCO4702	50S ribosomal protein L3
SCO5244	3.266				SCO5244	Anti-sigma factor
SCO5901				1.176	SCO5901	Uncharacterized RNA methyltransferase SCO5901
SCO0596				0.707	SCO0596	DpsA
SCO0666				1.428	SCO0666	Catalase
SCO2905		1.795			SCO2905	Uncharacterized protein
SCO2562				1.128	SCO2562	Elongation factor 4
SCO5241				0.716	SCO5241	Uncharacterized protein
SCO4723				1.137	SCO4723	Adenylate kinase
SCO6008				2.106	SCO6008	Probable transcriptional repressor protein
SCO4716	1.305				SCO4716	30S ribosomal protein S8
SCO5652			3.415		SCO5652	Uncharacterized protein
SCO5265		0.647		0.774	SCO5265	Uncharacterized protein
SCO4179		0.722			SCO4179	UPF0678 fatty acid-binding protein-like protein SCO4179
SCO2123	2.837			0.704	SCO2123	Putative esterase/lipase
SCO5393				0.807	SCO5393	Putative ABC transporter ATP-binding subunit
SCO2610				0.902	SCO2610	Rod shape-determining protein
SCO5231			1.258		SCO5231	HTH-type transcriptional repressor DasR
SCO5199	1.241				SCO5199	Uncharacterized protein
SCO1405	1.414				SCO1405	Putative heat shock protein (Hsp90-family)
SCO7463				1.124	SCO7463	Putative sensor histidine kinase
SCO1559				0.639	SCO1559	Methionine import ATP-binding protein MetN
SCO2627		1.344			SCO2627	Putative sugar-phosphate isomerase
SCO2777				1.301	SCO2777	Acetyl/propionyl CoA carboxylase alpha subunit
SCO4687	2.372				SCO4687	Uncharacterized protein
SCO4813	2.186		2.208		SCO4813	Phosphoribosylglycinamide formyltransferase
SCO3960				1.253	SCO3960	Uncharacterized protein
SCO2407	2.045				SCO2407	Aldose 1-epimerase
SCO6979				1.367	SCO6979	Probable solute-binding lipoprotein
SCO6259		0.911			SCO6259	Probable ABC sugar transport ATP binding protein
SCO1758				1.129	SCO1758	GTPase Der
SCO4297	1.203				SCO4297	Putative oxidoreduxtase
SCO2003				0.782	SCO2003	DNA polymerase I
SCO6292	0.749				SCO6292	Putative dihydropicolinate synthase
SCO3018				0.730	SCO3018	Putative regulatory protein
SCO4958	1.676				SCO4958	Cystathionine gamma-synthase
SCO5114		0.860			SCO5114	BldKC_ putative ABC transport system integral membrane protein
SCO2859				0.378	SCO2859	Uncharacterized protein
SCO4830				0.722	SCO4830	Putative glycine betaine ABC transport system ATP-binding protein
SCO7453				1.183	SCO7453	Putative secreted protein
SCO2148		0.880			SCO2148	Ubiquinol-cytochrome c reductase cytochrome b subunit
SCO2917	0.810				SCO2917	Nicotinate phosphoribosyltransferase
SCO0304				2.498	SCO0304	Uncharacterized protein
SCO1453				0.824	SCO1453	Uncharacterized protein
SCO2126				1.099	SCO2126	Glucokinase
SCO5557				0.582	SCO5557	Uncharacterized protein
SCO2828				1.449	SCO2828	Probable amino acid ABC transporter protein_ solute-binding component
SCO0436	2.291				SCO0436	50S ribosomal protein L32-2
SCO3559				1.417	SCO3559	Putative oxidoreductase
SCO2633				0.756	SCO2633	Superoxide dismutase [Fe-Zn] 1
SCO4907		0.716		0.842	SCO4907	Transcriptional regulatory protein AfsQ1
SCO6224				1.272	SCO6224	Putative secreted protein
SCO6714		1.391			SCO6714	Putative hydroxylase
SCO1938				0.833	SCO1938	Uncharacterized protein
SCO5112		0.816			SCO5112	BldKA_ putative ABC transport system integral membrane protein
SCO3951	0.865				SCO3951	Uncharacterized protein
SCO5032		1.233			SCO5032	Alkyl hydroperoxide reductase
SCO1876				0.754	SCO1876	Putative RNA polymerase sigma factor
SCO5185		0.891			SCO5185	Putative peptidase
SCO2015				2.106	SCO2015	Putative nucleotidase
SCO3658				1.549	SCO3658	Putative aspartate aminotransferase
SCO3184	1.255				SCO3184	Putative penicillin acylase (EC 3.5.1.11)
SCO1494				0.735	SCO1494	3-dehydroquinate synthase
SCO5571				1.290	SCO5571	50S ribosomal protein L32-1
SCO4645				0.842	SCO4645	Aspartate aminotransferase
SCO5292				1.274	SCO5292	Putative ATP/GTP-binding protein
SCO1965		0.763			SCO1965	Putative export associated protein
SCO6178				1.269	SCO6178	Putative deacetylase (Putative secreted protein)
SCO6195	1.237				SCO6195	Putative acetyl-coenzyme A synthetase
SCO5196		0.805		1.098	SCO5196	Uncharacterized protein

SCO	GlcN-Mann wt	1447	1447-wt Mann	GlcN	SCO	Description
SCO2180		0.810			SCO2180	Dihydrolipoyl dehydrogenase
SCO3890				0.886	SCO3890	Thioredoxin reductase
SCO2362				1.405	SCO2362	Uncharacterized protein
SCO4091				1.176	SCO4091	Putative DNA-binding protein
SCO1518				1.357	SCO1518	Holliday junction ATP-dependent DNA helicase RuvB
SCO4596				1.586	SCO4596	Putative two-component system response regulator
SCO1655				1.188	SCO1655	Putative lipoprotein oligopeptide binding protein
SCO1953	3.940				SCO1953	UvrABC system protein C
SCO1086		1.985			SCO1086	Uncharacterized protein
SCO3652		0.481	1.804		SCO3652	Putative membrane protein
SCO1827				1.182	SCO1827	Putative DNA polymerase III_ epsilon chain (EC 2.7.7.7)
SCO2396				1.465	SCO2396	Uncharacterized protein
SCO4917				0.722	SCO4917	Purine nucleoside phosphorylase
SCO4470				1.233	SCO4470	Putative phosphoglycerate mutase
SCO2855		2.459			SCO2855	Uncharacterized protein
SCO3066				1.194	SCO3066	Putative regulator of Sig15
SCO6752				1.190	SCO6752	Putative integral membrane transferase
SCO5657				1.165	SCO5657	Aldehyde dehydrogenase
SCO3756	3.634				SCO3756	Putative two component system response regulator
SCO5556				1.158	SCO5556	DNA-binding protein HU 2
SCO3373				0.891	SCO3373	Putative Clp-family ATP-binding protease
SCO4161				1.519	SCO4161	Putative molybdopterin converting factor
SCO5584				0.859	SCO5584	Nitrogen regulatory protein P-II
SCO1502				1.206	SCO1502	Putative secreted protein
SCO1378				0.765	SCO1378	Glycine dehydrogenase (decarboxylating)
SCO4163				0.849	SCO4163	Putative secreted protein
SCO7199				3.320	SCO7199	Putative membrane protein
SCO2048				1.163	SCO2048	Imidazole glycerol phosphate synthase subunit HisF
SCO1805				1.171	SCO1805	Putative membrane protein
SCO2084		0.895			SCO2084	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
SCO5479				1.192	SCO5479	Oligopeptide ABC transporter ATP-binding protein
SCO6060		0.892			SCO6060	UDP-N-acetylmuramate--L-alanine ligase
SCO3659				1.345	SCO3659	Uncharacterized protein
SCO1443				1.162	SCO1443	Putative riboflavin synthase
SCO6756		0.336			SCO6756	Putative glycosyltransferase
SCO6478				2.857	SCO6478	Uncharacterized protein
SCO1082				0.873	SCO1082	Putative electron transfer flavoprotein_ beta subunit
SCO7057				0.849	SCO7057	Putative esterase
SCO5520				1.176	SCO5520	Delta-1-pyrroline-5-carboxylate dehydrogenase
SCO4122				1.767	SCO4122	Putative MarR-family transcriptional regulator
SCO4901				0.600	SCO4901	Adenosine deaminase 1
SCO2034				1.041	SCO2034	Prolipoprotein diacylglyceryl transferase 1
SCO1515				1.189	SCO1515	Protein translocase subunit SecF
SCO1366				0.527	SCO1366	Uncharacterized protein
SCO5595		0.791			SCO5595	50S ribosomal protein L19
SCO4654				0.763	SCO4654	DNA-directed RNA polymerase subunit beta
SCO5805		1.243		1.131	SCO5805	Vitamin B12-dependent ribonucleotide reductase
SCO1922				1.240	SCO1922	Putative ABC transporter ATP-binding subunit
SCO5783		0.846			SCO5783	Uncharacterized protein
SCO1977				0.881	SCO1977	Putative glutamate synthase small subunit
SCO5843				1.273	SCO5843	Uncharacterized protein
SCO6789				1.339	SCO6789	Putative fatty oxidation protein
SCO1210				0.836	SCO1210	Putative transcriptional regulatory protein
SCO5744				1.153	SCO5744	4-hydroxy-tetrahydrodipicolinate synthase 2
SCO6862				1.196	SCO6862	Uncharacterized protein
SCO4660		0.925			SCO4660	30S ribosomal protein S7
SCO4735		0.799			SCO4735	30S ribosomal protein S9
SCO2969				1.119	SCO2969	Cell division ATP-binding protein
SCO6767				1.245	SCO6767	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) 1
SCO5696				1.245	SCO5696	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) 2
SCO4719				1.095	SCO4719	30S ribosomal protein S5
SCO1651				0.801	SCO1651	Uncharacterized protein
SCO3844				0.835	SCO3844	Putative secreted protein
SCO2068		0.812			SCO2068	Putative secreted alkaline phosphatase
SCO5494				1.143	SCO5494	DNA ligase 1
SCO1643				1.234	SCO1643	Proteasome subunit alpha
SCO5837		0.939			SCO5837	Zinc protease
SCO3816				0.842	SCO3816	Putative branched-chain alpha keto acid dehydrogenase E1 beta subunit
SCO0741		0.900			SCO0741	Putative oxidoreductase
SCO3873				1.190	SCO3873	DNA gyrase subunit A
SCO1907				0.856	SCO1907	Uncharacterized protein
SCO6451		0.839			SCO6451	Putative substrate binding protein
SCO5552				0.915	SCO5552	Putative regulator
SCO3906				1.105	SCO3906	30S ribosomal protein S6
SCO2682		1.257			SCO2682	Putative membrane protein
SCO2363				0.907	SCO2363	Putative ATP/GTP-binding protein
SCO4429		0.853			SCO4429	FO synthase
SCO1955				1.142	SCO1955	Putative iron sulphur binding protein
SCO1508				1.072	SCO1508	Histidine--tRNA ligase
SCO5464		1.143		1.282	SCO5464	SCO5464 protein
SCO3885				0.919	SCO3885	Ribosomal RNA small subunit methyltransferase G
SCO3096				1.101	SCO3096	Enolase 1

TABLE S4. Proteomic comparison of *S. coelicolor* M145 and its *rokL6* mutant.

SCO	Description	Sequence	Distance	Score	Region	Co-transcribed SCO
SCO1448	Uncharacterized MFS-type transporter	CTATCAGGCAGGCTCCCTGATAG	-60	28	regulatory	
SCO1447	Putative ROK-family transcriptional regulator	CTATCAGGCAGGCTCCCTGATAG	-75	28	regulatory	
SCO0317	Putative transmembrane transport protein	CTTTCAGACATGGTTCCTGATTG	-72	16.4	regulatory	
SCO4114	sporulation associated protein	TTAAGAGGCATTGTTCCGGATGG	-109	9.2	regulatory	
SCO2657	Putative ROK-family transcriptional regulator	CCAACAGGAAACTTTCCTAACAG	-127	8	regulatory	
SCO1359	Permease of the drug/metabolite transporter (DMT) superfamily	CTACGAGGACGACTGCCTCATCG	5	7.7	regulatory	
SCO7173	Transcriptional regulator	AAATCCGGAACCGTGGCCGATAT	-134	6.1	regulatory	
SCO3732	ATP-dependent RNA helicase	GTATCAAGGAAGGTTCCCCATGA	-19	5.8	regulatory	
Unknown_246	hypothetical protein	GTATCAAGGAAGGTTCCCCATGA	-16	5.8	regulatory	
SCO3250	Integrase	CCATCAGGCAGCCTCCTCGATCT	-19	5.6	regulatory	
SCO4313	Transcriptional regulator%2C AcrR family	CTCCCAGATAATGTTCGTGATAA	-91	5.5	regulatory	SCO4314
SCO4312	hypothetical protein	CTCCCAGATAATGTTCGTGATAA	-32	5.5	regulatory	SCO4311
SCO2089	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase (EC 6.3.2.7)	TCGTCACGGATGGTTCCTGGTGG	-16	5	regulatory	
SCO2956	Integral membrane protein	CGCTCAGGCACGGGCCCGGAAAG	-132	5	regulatory	
SCO2955	hypothetical protein	CGCTCAGGCACGGGCCCGGAAAG	-49	5	regulatory	
SCO5864	hypothetical protein	TGATCATGCACCCTGTCGGAAAG	-279	4.9	regulatory	
SCO4829	Choline oxidase (EC 1.1.3.17)	CGGTACGGCAGGCTCCGTGATCG	44	4.7	regulatory	SCO4830; SCO4831;
SCO0234	Putative oxidoreductase	CTACCTGAGGCGCTGCTTGATAT	-236	3.9	regulatory	
SCO0233	Putative DNA-binding protein	CTACCTGAGGCGCTGCTTGATAT	-186	3.9	regulatory	
SCO5908	hypothetical protein	ATACCAGGCAGGCATCATGACCT	-24	3.9	regulatory	SCO5909; SCO5910
SCO1274	hypothetical protein	CGAACAGGCACGGCTCCGAATGG	-281	3.8	regulatory	
SCO1656	Pseudouridine-5' phosphatase (EC 3.1.3.-)	CGATCAGGCCGGCTCCCACGAAG	-43	3.8	regulatory	
SCO6822	Efflux pump transporter of major facilitator superfamily (MFS)	TTAACAGTGATGACTGTTGATAG	-142	3.8	regulatory	
SCO1755	hypothetical protein	AGACCCGGAACCCTGCCTTCTGG	-62	3.7	regulatory	
SCO1291	hypothetical protein	CTATCGACGACCCTCCGTGCTGG	-16	3.5	regulatory	
SCO2359	Two-component system sensor histidine kinase	CGATCATGCGGTCTTCCTCAGGG	-123	3.5	regulatory	SCO2358
SCO5261	NAD-dependent malic enzyme (EC 1.1.1.38)	TTGTCCGGAAGCCTGGCTATGAG	-272	3.5	regulatory	
SCO5191	hypothetical protein	CTCGCAGGCACCGCGCCTGAAGA	-108	3.4	regulatory	
Unknown_451	hypothetical protein	TGCTCAGGCGAGATGCCCGATAT	5	3.4	regulatory	
SCO5210	Quaternary ammonium compound-resistance protein SugE	TGCTCAGGCTTGGTTCCGGCTTG	-153	3.1	regulatory	
SCO3468	Transposase	CGAGCAGGTCCCCGGGCTGATGG	-130	3	regulatory	
SCO0545	putative secreted protein	CTGTGCGGAGTCTTGCCGGATCG	-125	2.9	regulatory	
SCO2226	Neopullulanase (EC 3.2.1.135) / Maltodextrin glucosidase (EC 3.2.1.20)	TCTTGCGGCAAGGGTCGTGAAAG	-92	2.9	regulatory	
Unknown_408	hypothetical protein	CGCTCACGCACGCTACCTGCTGG	-282	2.9	regulatory	
SCO6806	Phage integrase	GTATTCGGCGAGCTTCATGGTGG	4	2.8	regulatory	
SCO2664	putative sugar-binding protein	CGAGGAGGCAGGACCCGTGAAAG	-79	2.8	regulatory	
SCO2869	Transcriptional regulator%2C Xre family	CGACCAGACAGCCGACCTGATCG	-277	2.8	regulatory	
SCO3256	SpdA protein	CCATCACGGCTCCTTCCTGTCAG	-19	2.8	regulatory	SCO3255; SCO3254;
SCO5919	hypothetical protein	CAGACGGGCGGGGTTCCTGATCA	-95	2.8	regulatory	
SCO6585	Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)	CTTTCAGTCAGGAGCCGAGATGG	-160	2.8	regulatory	SCO6586; SCO6587
SCO6584	Thiamine pyrophosphate-requiring enzymes	CTTTCAGTCAGGAGCCGAGATGG	-126	2.8	regulatory	SCO6583; SCO6582
SCO0083	Mobile element protein	CCATAAGAAACGACGCCTAACAA	-138	2.7	regulatory	
Unknown_17	Mobile element protein	CCATAAGAAACGACGCCTAACAA	-228	2.7	regulatory	
SCO0733	hypothetical protein	ATATCGGACCGTGTTACTGATCA	-83	2.7	regulatory	
SCO0925	Transcriptional regulator%2C LysR family	GTTACGGGGACCATGCCTCATCG	-85	2.7	regulatory	
SCO0924	Succinate dehydrogenase cytochrome b subunit	GTTACGGGGACCATGCCTCATCG	-69	2.7	regulatory	SCO0923; SCO0922
SCO1675	putative small membrane protein	TTCTTGAGCATTGTTCCTCCTAG	-12	2.7	regulatory	
SCO5833	hypothetical protein	CTTATGGGCAAGGTTGCTGGCAG	-33	2.7	regulatory	
SCO5690	Putative large secreted protein	CTGGGAGGACGCCTTCCTGAGCG	50	2.6	regulatory	
SCO2384	hypothetical protein	CTATCGGGCAGACCTCGAGGAAG	-46	2.6	regulatory	
SCO6657	putative membrane protein	CCATCAGGGAGGGACTCTGACCC	-19	2.6	regulatory	
SCO1773	Alanine dehydrogenase (EC 1.4.1.1)	GGATCACGGTCCTTGGCTCAGAG	-25	2.5	regulatory	
SCO4562	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)	AGATCACAAAGCTTGTGTAATAC	-198	2.4	regulatory	SCO4563; SCO4564;
SCO6934	putative secreted protein	CGATCAACAACCCTTTCGCAGAG	-23	2.3	regulatory	
SCO2788	hypothetical protein	ATATCGGGCAGGATTCTTGCGCA	-52	2	regulatory	
SCO0135	hypothetical protein	CGATCATGGACCTCGTCTGTGAC	-201	1.9	regulatory	
SCO0134	hypothetical protein	CGATCATGGACCTCGTCTGTGAC	-209	1.9	regulatory	
SCO3460	Mercuric ion reductase (EC 1.16.1.1)	CCCTCGGGAACCCTGCCGGGCTG	-218	1.9	regulatory	SCO3461; SCO3462;
SCO3459	type 11 methyltransferase	CCCTCGGGAACCCTGCCGGGCTG	-75	1.9	regulatory	
SCO4226	hypothetical protein	GAATCGGCCATGGTTCCTCCTGG	-325	1.9	regulatory	
SCO3507	putative integral membrane efflux protein	CGACCAGGAGGCGAGCCCGATTG	-119	1.8	regulatory	
SCO4616	hypothetical protein	GTATGACGCAGGGTTCGGGTGTG	-133	1.8	regulatory	
SCO7490	Zinc-type alcohol dehydrogenase YcjQ	GCATCAGCAACCCTTCCGGAGCC	-126	1.8	regulatory	SCO7491; SCO7492;
SCO7489	ABC-type sugar transport system%2C periplasmic binding protein YcjN	GCATCAGCAACCCTTCCGGAGCC	-121	1.8	regulatory	
SCO4831	Glycine betaine ABC transport system%2C permease protein OpuAB	CGATCACGGCCACGGCCCGAAAG	7	1.7	regulatory	
SCO4325	Cold shock protein of CSP family %3D> SCO4325	CTATCAAGAGCCGTTTCCGAGCA	-68	1.7	regulatory	
SCO4324	Integral membrane protein	CTATCAAGAGCCGTTTCCGAGCA	-130	1.7	regulatory	
SCO5926	Aconitate hydratase (EC 4.2.1.3)	CGATGCGGCCGGGTCCCTTCGAG	-61	1.7	regulatory	SCO5925

SCO6102	Ferredoxin--sulfite reductase%2C actinobacterial type (EC 1.8.7.1)	CTCTCAGCGGCCCGGACAGATGG	-218	1.7	regulatory	SCO6101; SCO6100;
SCO1094	Transcriptional regulator%2C AcrR family	TCTTGAGCGAGCGATCCAGATAG	-37	1.6	regulatory	
SCO4734	LSU ribosomal protein L13p (L13Ae)	ATGTCAGGACCACTCACTGAAGA	-40	1.6	regulatory	SCO4735
SCO6052	putative membrane protein	ACATGGGGAAACCTTCCTGCTGG	-19	1.6	regulatory	
SCO2448	hypothetical protein	CTATCATGAGCGGTGCCGCGTGG	-5	1.5	regulatory	
SCO0021	hypothetical protein	CTCTGAAGGACGGGTCCTGTTGG	-32	1.5	regulatory	
Unknown_6	hypothetical protein	CTCTGAAGGACGGGTCCTGTTGG	-40	1.5	regulatory	
SCO1383	hypothetical protein	GAAACATGGACCTTCCCTGAAGG	-91	1.5	regulatory	
SCO7015	Putative secreted glycosyl hydrolase	CTTTCACGAGCTACGTCGGATAG	-312	1.5	regulatory	
SCO4232	CarD-like transcriptional regulator	CCATCACGGGGCCGCGCTGATCG	35	1.4	regulatory	
SCO1948	putative zinc-binding carboxypeptidase	GTCTCATGAACCCCCCTAGATGG	-16	1.4	regulatory	
SCO3682	Fatty acid desaturase	TTCTCAGAGAGACGTCCTCATGA	-19	1.4	regulatory	
SCO5107	Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)	ACATCAGAAAGCCTCACTCGTCA	-19	1.4	regulatory	
SCO6855	hypothetical protein	CCGTGATGCAGGCGCGCAGATAG	-131	1.4	regulatory	SCO6854; Unknown_441;
SCO7579	Putative DNA-binding protein	CTGTCAACAACCCTGCGCAACCG	-131	1.4	regulatory	SCO7580
SCO7780	Transcriptional regulator%2C AraC family	CGATCACGTACGCCTGTGGATAG	-223	1.3	regulatory	
SCO6241	hypothetical protein	TCATCTGGCTCCGTGCATGATCG	-193	1.1	regulatory	
SCO6240	hypothetical protein	TCATCTGGCTCCGTGCATGATCG	-273	1.1	regulatory	
SCO0166	Polyphosphate kinase 2 (EC 2.7.4.1)	ATCTCAGGCAAGGTGTACGAGAA	24	1	regulatory	
SCO4524	putative membrane protein	GTGGCAGGCAATTTTCTTGGTTG	-39	1	regulatory	SCO4525; SCO4526;
SCO7600	Alanyl-tRNA synthetase-related protein	TGATCCGGCGATGGCCCTGATCC	44	0.9	regulatory	
SCO2848	hypothetical protein	GGAGCAGGAACGCCGCCTGGTCT	41	0.8	regulatory	
SCO1845	Probable low-affinity inorganic phosphate transporter	CTGCCAGGGACGTCTCCGGAGAG	-156	0.8	regulatory	SCO1846
SCO1844	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	CTGCCAGGGACGTCTCCGGAGAG	-239	0.8	regulatory	
SCO2527	hypothetical protein	CTTTCCGTGACCATCACAGATAT	-112	0.8	regulatory	
SCO5803	SOS-response repressor and protease LexA (EC 3.4.21.88)	CTACCGTGGCGCCTGGCGGACAA	-146	0.8	regulatory	
SCO1374	putative secreted protein	CTAGCCGAAACACAGTCTGAACA	-226	0.7	regulatory	
SCO1725	putative secreted hydrolase	GTCTCATGGAACCTCCCTTAGCA	-16	0.7	regulatory	
SCO3804	Transcriptional regulator%2C AraC family	ATATGTCGCAAGGATCCTCTCAG	-47	0.7	regulatory	SCO3805
SCO3803	Mannose-6-phosphate isomerase	ATATGTCGCAAGGATCCTCTCAG	-72	0.7	regulatory	
SCO4291	putative secreted protein	CGGTCACGGAGCTTGTGTGGGAA	-82	0.7	regulatory	
SCO4290	Alpha%2Calpha-trehalose-phosphate synthase [UDP-forming] (EC	CGGTCACGGAGCTTGTGTGGGAA	-114	0.7	regulatory	
SCO5158	hypothetical protein	TTGTTTGGAGGGGTTCCCCGTAG	-156	0.7	regulatory	
SCO5213	Integral membrane protein	TGTTCGGGGAGGGCTCCTCGTAC	-22	0.7	regulatory	
SCO6027	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	CTCTCCTCCAGGGTGCGGGATGG	-28	0.7	regulatory	SCO6026
SCO7010	Alpha-glucosidase (EC 3.2.1.20)	CTTTCGGGCAGGGTGGATCTTCG	-32	0.7	regulatory	
SCO7257	putative secreted protein	CTGGAAGGCAGGGAGCCTCATGA	-43	0.7	regulatory	
SCO7256	Putative protease	CTGGAAGGCAGGGAGCCTCATGA	-237	0.7	regulatory	
Unknown_157	hypothetical protein	TGAAGGAGCAGGGCTCCTGATGA	-19	0.7	regulatory	
SCO2363	Similar to citrate lyase beta subunit	TGAAGGAGCAGGGCTCCTGATGA	17	0.7	regulatory	
SCO7487	Inner membrane ABC transporter permease protein YcjP	TTGCCACTCACGCTTCCTCCTGG	-12	0.6	regulatory	
SCO7790	putative secreted oxidoreductase	TTGTCCCGTTCGCGTCGTGATAG	41	0.6	regulatory	SCO7789
SCO0763	Lactate 2-monooxygenase (EC 1.13.12.4)	GTTTCGGTAACCTTGCGTATTGA	-246	0.6	regulatory	
SCO1473	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	CGAGCCCGCAAGGTCACGGAAAG	-75	0.6	regulatory	
SCO2074	Lipoprotein signal peptidase (EC 3.4.23.36)	CCCTCAGCCTAGGTCCTTGACTG	-29	0.6	regulatory	
SCO4539	hypothetical protein	TTTTCCGGAACCTTCGGTGGTGA	-193	0.6	regulatory	SCO4538
SCO4866	RNA polymerase ECF-type sigma factor	CGATGAGGAACCACGACGGCGAG	-72	0.6	regulatory	SCO4867
SCO5473	ATP/GTP-binding protein	CGCGCGGTAACGGTGCCTGAGAG	-265	0.6	regulatory	
SCO5472	Aminomethyltransferase (glycine cleavage system T protein) (EC	CGCGCGGTAACGGTGCCTGAGAG	-184	0.6	regulatory	
SCO7337	hypothetical protein	TCAGCGCTCACGCTTCGTGATCG	-96	0.6	regulatory	SCO7338
SCO7336	hypothetical protein	TCAGCGCTCACGCTTCGTGATCG	-231	0.6	regulatory	
SCO2280	Transcriptional regulator%2C AcrR family	CTCGGCGGCGGGGTTCGTGATGC	19	0.5	regulatory	
SCO3926	Sporulation-specific cell division protein SsgA	CGTACAGGCAGAGGTCATGATGA	11	0.5	regulatory	
SCO4831	Glycine betaine ABC transport system%2C permease protein OpuAB	CCACCGAGGAGCCGGTCTGATGG	-19	0.5	regulatory	
SCO6041	Protoporphyrinogen IX oxidase%2C aerobic%2C HemY (EC 1.3.3.4)	GGAACAGGAACCCGGACACGTAG	38	0.5	regulatory	SCO6042
SCO6048	Integral membrane protein	CTACCAGACCGCGCTCCTGCTGC	17	0.5	regulatory	
SCO2292	Endo-1%2C4-beta-xylanase (EC 3.2.1.8)	CACTCACCGTGCCTGCCGGAAAG	-202	0.5	regulatory	SCO2291
SCO2611	Rod shape-determining protein MreB	CTTTCGCGAACACTGCGCGAGGG	-128	0.5	regulatory	
SCO3345	Dihydroxy-acid dehydratase (EC 4.2.1.9)	CGGTCATCCAGGGGTCGGGACAG	-69	0.5	regulatory	
SCO3985	hypothetical protein	CACTCATGGAGCCTGCACGGAAG	-231	0.5	regulatory	
SCO4670	putative serine protease precursor	CGTTATGGAACCCGGCGTTATGG	-143	0.5	regulatory	
SCO4670	putative serine protease precursor	CGTTATGGAACCCGGCGTTATGG	-158	0.5	regulatory	
SCO5190	Transcriptional regulator%2C WhiB family	CGATCAGGCCGGCGCCTTCAGGG	-172	0.5	regulatory	
SCO5805	Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC	CGTACAGGGAGGCGGCATGACAG	-16	0.5	regulatory	
SCO6609	putative secreted protein	CACTCAGGGAGCCGCCGTGTTCG	-16	0.5	regulatory	
SCO1943	hypothetical protein	CACAGACGCAAGCCCCATGATAG	-190	0.4	regulatory	
SCO2351	Integral membrane protein	CGATCACACAAGCCCCCTGTGAA	-131	0.4	regulatory	
SCO5930	possible NTP pyrophosphohydrolase	CTATCGGTCATGGTCGCTCACGA	-54	0.4	regulatory	
SCO5929	Putative oxidoreductase	CTATCGGTCATGGTCGCTCACGA	-83	0.4	regulatory	
SCO6219	Putative serine/threonine protein kinase	ACATTGTGAAGATTGCATGAGAA	-132	0.4	regulatory	
SCO6218	putative phosphoglycerate mutase family protein	ACATTGTGAAGATTGCATGAGAA	-185	0.4	regulatory	

SCO1839	Transcriptional regulator	CCATTCGGCAAGGCTGATGAGAC	-91	0.3	regulatory	
SCO2461	Small hypothetical protein Hyp1	CGAACCAGTAACCTGCCGGTTAA	-275	0.3	regulatory	
SCO2461	Small hypothetical protein Hyp1	CGAACCAGTAACCTGCCGGTTAA	-197	0.3	regulatory	
SCO3644	Putative lipase/esterase	TTATCAGGCCGGTGACGTGCGCG	-93	0.3	regulatory	
SCO7514	Integral membrane protein	CTCGAAGTCAACGTTGCTGACCG	-102	0.3	regulatory	
SCO7513	putative secreted hydrolase	CTCGAAGTCAACGTTGCTGACCG	-102	0.3	regulatory	SCO7512
SCO1390	PTS system%2C N-acetylglucosamine-specific IIA component	CCATCAGACACTGTCCCTGATCC	-4834	7.8	upstream	
SCO1389	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC	CCATCAGACACTGTCCCTGATCC	-997	7.8	upstream	
SCO3334	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	CCATCAGACACTGTCCCTGATCC	-5106	7.8	upstream	
SCO3333	Putative phosphatase YieH	CCATCAGACACTGTCCCTGATCC	-949	7.8	upstream	
SCO5746	pleiotropic regulatory protein	GGATCAGGGACAGTGTCTGATGG	-1002	7.8	upstream	
SCO5335	hypothetical protein	CTATATTGACCCCGGCATGATTA	-3205	4.9	upstream	
SCO5331	Putative DNA methylase	CTATATTGACCCCGGCATGATTA	-2839	4.9	upstream	
SCO0239	hypothetical protein	TGATCATGCCAGGGTCTTGAAAC	-530	3.8	upstream	
SCO1273	Polyketide synthase modules and related proteins	CGAACAGGCACGGCTCCGAATGG	-448	3.8	upstream	
SCO6821	Putative transferase	TTAACAGTGATGACTGTTGATAG	-659	3.8	upstream	
SCO1756	hypothetical protein	AGACCCGGAACCCTGCCTTCTGG	-370	3.7	upstream	
SCO4632	ATP/GTP-binding protein	CTTCCAACAACCCTGCCGGAAGG	-1888	3.7	upstream	
SCO7824	Transcriptional regulator%2C AcrR family	CGATCAGGCGATCTCGCTGCGAG	-1914	3.7	upstream	
SCO5260	Secreted protein	TTGTCCGGAAGCCTGGCTATGAG	-390	3.5	upstream	SCO5259; SCO5258
SCO3445	putative small membrane protein	CCATCACGCAGCACGCCTGCGAA	-693	3.2	upstream	
SCO6945	hypothetical protein	ATTTGAGGGAACTTGCCCGGTAC	-1998	3.1	upstream	
SCO1390	PTS system%2C N-acetylglucosamine-specific IIA component	CCATGAGCAACCGTGCAGGACAT	-2148	2.8	upstream	
SCO1389	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC	CCATGAGCAACCGTGCAGGACAT	-3683	2.8	upstream	
SCO3334	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	CCATGAGCAACCGTGCAGGACAT	-2414	2.8	upstream	
SCO3333	Putative phosphatase YieH	CCATGAGCAACCGTGCAGGACAT	-3641	2.8	upstream	
SCO5746	pleiotropic regulatory protein	ATGTCCTGCACGGTTGCTCATGG	-3691	2.8	upstream	
SCO5335	hypothetical protein	CAATCATGGACACAGCTTGTCAG	-819	2.6	upstream	
SCO5331	Putative DNA methylase	CAATCATGGACACAGCTTGTCAG	-5225	2.6	upstream	
SCO4632	ATP/GTP-binding protein	TGATGAGAAATGCTTCATGAAAC	-4276	2.5	upstream	
SCO4561	putative NLP/P60-family protein	AGATCACAAAGCTTGTGTAATAC	-699	2.4	upstream	
Unknown_466	hypothetical protein	CGGCAACGAACTATGCCTGATTG	-353	1.5	upstream	
SCO0056	Mobile element protein	GTATGAGGAAGCCGCCTTCGAAA	-530	1.4	upstream	
SCO6641	Superfamily I DNA and RNA helicases and helicase subunits	CGATCAGGGAGAGGTCCTCGTCC	-435	1.4	upstream	
SCO7578	hypothetical protein	CTGTCAACAACCCTGCGCAACCG	-386	1.4	upstream	
SCO7779	Putative oxidoreductase	CGATCACGTACGCCTGTGGATAG	-473	1.3	upstream	
SCO6405	Mobile element protein	ATACAGGGCCGGTCTCCTGAAAG	-823	1.1	upstream	
SCO6401	Protein of unknown function DUF664	ATACAGGGCCGGTCTCCTGAAAG	-968	1.1	upstream	
SCO3585	hypothetical protein	TTAGCGGGTCGGGCCCCTGAGTG	-500	1	upstream	
Unknown_300	hypothetical protein	GTGGCAGGCAATTTTCTTGGTTG	-596	1	upstream	
SCO6861	hypothetical protein	CCGTGAGGAATCCGGGCTGGGAA	-1571	0.9	upstream	
SCO5804	Ribonucleotide reductase transcriptional regulator NrdR	CTACCGTGGCGCCTGGCGGACAA	-460	0.8	upstream	
SCO1373	hypothetical protein	CTAGCCGAAACACAGTCTGAACA	-356	0.7	upstream	
SCO5157	Magnesium and cobalt transport protein CorA	TTGTTTGGAGGGGTTCCCCGTAG	-390	0.7	upstream	SCO5156
SCO5335	hypothetical protein	CCATGGGGAACTCAGCGAGATCA	-2419	0.7	upstream	
SCO5331	Putative DNA methylase	CCATGGGGAACTCAGCGAGATCA	-3625	0.7	upstream	
SCO3981	Transcriptional regulator%2C GntR family	CACTCATGGAGCCTGCACGGAAG	-778	0.5	upstream	
SCO1390	PTS system%2C N-acetylglucosamine-specific IIA component	CTCACAGTCAAGCTCCCTTGTGC	-4949	0.4	upstream	
SCO1389	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC	CTCACAGTCAAGCTCCCTTGTGC	-882	0.4	upstream	
SCO3334	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	CTCACAGTCAAGCTCCCTTGTGC	-5221	0.4	upstream	
SCO3333	Putative phosphatase YieH	CTCACAGTCAAGCTCCCTTGTGC	-834	0.4	upstream	
Unknown_285	putative ATP-dependent DNA helicase	CAAACGTCAAGTGTGCCTGATCG	-632	0.4	upstream	
SCO5746	pleiotropic regulatory protein	GCACAAGGGAGCTTGACTGTGAG	-887	0.4	upstream	
SCO3468	Transposase	CTCTCAGTCCGGGTCTGTCAAAC	-489	0.3	upstream	
SCO7179	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	CTATAGGGCGAAGCTGCTTGTAG	-376	0.3	upstream	

CURRICULUM VITAE & LIST OF PUBLICATIONS

CURRICULUM VITAE

Mia Urem was born on the 17th of January 1986 in Split, Croatia. She graduated from the International School Maastricht, The Netherlands, with an International Baccalaureate diploma in 2004. Starting in the autumn of that same year, she followed the joint Life Science & Technology program at Leiden University and TU Delft and obtained her Bachelor's degree in 2007. Her Bachelor's research project, focussed on DNA repair proteins in *E. coli,* was completed in the lab of Dr. Nora Goosen at the Molecular Genetics department of the Leiden Institute of Chemistry. Mia followed this up with a Master's degree, obtained in 2012, in Life Science & Technology with a specialisation in Functional Genomics. During this period, she also worked as a student assistant for Life Science & Technology practical courses and as an KNAW Academy (research) assistant on a project aimed at optimising microfluidic devices at the Chemical Engineering department of TU Delft, under the supervision of Prof. M. Kreutzer, Prof. C. Kleijn, Dr. V. van Steijn and Dr. M. Rosso. She completed her Master's research project with Prof. G. van Wezel at the Leiden Institute of Chemistry, under the supervision of Dr. L. Zhang, on the regulatory role of AfsR in streptomycetes. She also completed an internship in Leeds, in a collaboration between Dr. K. McDowall (University of Leeds) and Evocutis, on the optimalisation of a novel transcriptomics method. Then, Mia began as a PhD student at the Institute of Biology Leiden in the lab of Prof. G. van Wezel at the beginning of 2012; the results of this work are presented in this thesis. During this period, she took part in the John Innes/Rudjer Bošković Summer School in Applied Molecular Microbiology (2014), held poster presentations at a number of (inter)national conferences and was selected to present at NWO CHAINS in 2015 (Veldhoven, The Netherlands) and ISBA18 in 2017 (18th International Symposium on the Biology of Actinomycetes in Jeju, South Korea). Currently, Mia is postdoctoral researcher with Prof. G. van Wezel, continuing on-going projects stemming from this thesis as well as taking up new project focussed on *Streptomyces* development and cell division.

LIST OF PUBLICATIONS

Urem M, Świątek-Połatyńska MA, Rigali S, van Wezel GP. (2016) Intertwining nutrient-sensory networks and the control of antibiotic production in *Streptomyces. Mol Microbiol*. **102:**183-195

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Tenconi E, **Urem M**, Świątek-Połatyńska MA, Titgemeyer F, Muller YA, van Wezel GP, Rigali S. (2015) Multiple allosteric effectors control the affinity of DasR for its target sites. *Biochem Biophys Res Commun.* **464:**324-329

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