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Controlling growth and morphogenesis of the industrial enzyme producer Streptomyces lividans

Mangiameli, G.

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APPENDIX

RNA-Seq DATA

Table S1-A. Genes expessed higher in both *cslA* and *glxA*

Gene # *S. coelicolor*	Gene # *S. lividans*	1326 (RPKM)	cslA (RPKM)	glxA (RPKM)	cslA/1326	glxA/1326	Annotation
SCO0187	SLI0127	6,4	15,5	13,2	2,4	2,1	Phytoene synthase
SCO0188	SLI0128	5,2	13,1	13,0	2,5	2,5	CrtV-methyltransferase-like protein
	SLI0138	9,9	26,5	20,6	2,7	2,1	hypothetical protein
SCO0231	SLI0175	41,8	99,3	97,1	2,4	2,3	small hydrophobic protein
SCO0426	SLI0384	4,9	16,6	10,3	3,4	2,1	hypothetical protein
SCO0508	SLI0468	6,5	14,1	13,3	2,2	2,0	Transcriptional regulator, TetR family
	SLI0944	5,3	11,3	12,4	2,1	2,3	Transcriptional regulator XRE family
	SLI0994	5,7	11,8	13,0	2,1	2,3	CopZ-like Copper chaperone
	SLI1041	3,8	10,0	8,3	2,7	2,2	putative lipoprotein
	SLI1076	4,7	11,5	9,6	2,4	2,0	hypothetical protein
SCO6808	SLI1107	11,9	32,5	29,7	2,7	2,5	ArsR regulator
	SLI1228	4,5	10,1	11,7	2,2	2,6	Non-heme chloroperoxidase
SCO1134	SLI1410	3,1	14,6	8,5	4,7	2,8	Aromatic aldehyde oxidoreductase, YagT
	SLI1425	9,2	27,6	24,6	3,0	2,7	hypothetical protein
SCO1250	SLI1531	4,8	12,8	13,5	2,7	2,8	putative acetyltransferase
	SLI1606	6,4	29,2	19,2	4,5	3,0	hypothetical protein
SCO1620	SLI1923	31,5	193,9	117,3	6,2	3,7	opuABC glycine betaine transport system permease
SCO1621	SLI1924	28,7	153,3	106,7	5,3	3,7	opuAA glycine betaine transport ATP-binding protein
SCO1866	SLI2177	67,7	666,0	139,3	9,8	2,1	L-ectoine synthase, ectC
SCO2631	SLI2974	6,1	14,2	17,4	2,3	2,9	putative amino acid permease
SCO2828	SLI3177	27,1	124,4	62,2	4,6	2,3	amino acid ABC transporter, amino acid-binding protein
SCO2829	SLI3178	17,6	99,8	46,0	5,7	2,6	amino acid ABC transporter, permease
SCO2830	SLI3179	19,6	106,2	52,2	5,4	2,7	amino acid ABC transporter, integral membrane protein
SCO2831	SLI3180	23,7	118,8	54,8	5,0	2,3	amino acid ABC transporter, ATP-binding protein
SCO3121	SLI3478	3,8	9,0	19,2	2,4	5,1	hypothetical protein
SCO3428	SLI3771	2,4	7,5	13,5	3,1	5,6	LSU ribosomal protein L33p, zinc-independent
	SLI3944	4,0	9,2	12,3	2,3	3,1	hypothetical protein
SCO4243	SLI4480	24,9	98,3	60,7	3,9	2,4	secreted protein
SCO4244	SLI4481	39,3	146,7	85,3	3,7	2,2	hypothetical protein
SCO4245	SLI4482	40,4	146,1	87,9	3,6	2,2	hypothetical protein
SCO4246	SLI4483	38,4	165,0	93,3	4,3	2,4	hypothetical protein
SCO4247	SLI4484	56,0	249,4	138,1	4,5	2,5	hypothetical protein
SCO4248	SLI4485	37,2	174,2	94,9	4,7	2,5	hypothetical protein
SCO4252	SLI4488	845,1	4425,2	2045,2	5,2	2,4	hypothetical protein

SCO4255	SLI4491	20,7	73,8	42,5	3,6	2,1	hypothetical protein
SCO4257	SLI4492	73,4	236,8	192,1	3,2	2,6	Hydrolytic protein
SCO4514	SLI4795	29,8	94,3	64,5	3,2	2,2	integral membrane protein
	SLI4831	3,6	10,2	12,0	2,8	3,3	type IV peptidase
SCO4663	SLI4937	1074,9	3617,6	2612,2	3,4	2,4	hypothetical protein
SCO4828	SLI5101	20,9	49,8	48,8	2,4	2,3	Betaine aldehyde dehydrogenase
SCO4829	SLI5102	17,8	62,4	48,6	3,5	2,7	Choline dehydrogenase
SCO4830	SLI5103	8,2	41,1	26,2	5,0	3,2	Glycine betaine ABC transporter, ATP-binding protein
SCO4831	SLI5104	8,1	33,2	22,0	4,1	2,7	Glycine betaine ABC transporter, permease
SCO4832	SLI5105	24,4	67,4	50,1	2,8	2,1	Glycine betaine ABC transporter, substrate binding protein
SCO4947	SLI5222	5,2	11,4	11,2	2,2	2,2	Respiratory nitrate reductase alpha chain
SCO4994	SLI5269	33,4	122,9	70,8	3,7	2,1	hypothetical protein
	SLI5784	83,6	320,1	198,4	3,8	2,4	hypothetical protein
SCO5522	SLI5797	116,8	482,6	242,5	4,1	2,1	3-isopropylmalate dehydrogenase
	SLI6177	26,4	57,4	62,6	2,2	2,4	hypothetical protein
	SLI6330	17,5	40,0	52,9	2,3	3,0	hypothetical protein
SCO6073	SLI6466	3,4	12,0	7,0	3,5	2,0	germacradienol/germacrene D synthase
SCO6509	SLI6857	6,6	22,9	18,9	3,5	2,9	hydrophobic protein
SCO6980	SLI7182	6,0	19,1	12,4	3,2	2,1	Inositol transport system permease
SCO7428	SLI7648	6,2	15,4	14,4	2,5	2,3	Flavohemoprotein, hmpA1
	SLI7822	3,0	36,0	12,0	12,1	4,0	hypothetical protein
	SLI8052	1,1	14,0	16,3	13,0	15,1	hypothetical protein

Table S1-B. Genes expessed higher in *glxA* only

Gene # *S. coelicolor*	**Gene # *S. lividans***	**1326 (RPKM)**	**cslA (RPKM)**	**glxA (RPKM)**	**cslA/1326**	**glxA/1326**	**Annotation**
SCO0569	SLI0532	9,1	13,3	20,4	1,5	2,2	LSU ribosomal protein L36p
SCO0672	SLI0644	8,9	8,1	18,3	0,9	2,1	anti-sigma factor antagonist
	SLI1189	5,7	8,9	13,9	1,6	2,4	hypothetical protein
SCO1423	SLI1720	179,6	136,4	370,5	0,8	2,1	Dolichol-phosphate mannosyltransferase
SCO1700	SLI2004	47,0	33,7	106,1	0,7	2,3	putative membrane protein
SCO1702	SLI2006	5,0	7,4	10,2	1,5	2,0	Transcriptional regulator, TetR family
	SLI2561	14,1	19,6	35,2	1,4	2,5	hypothetical protein
SCO2336	SLI2667	6,7	5,2	14,4	0,8	2,2	L-Proline/Glycine betaine transporter ProP
	SLI2831	7,9	10,2	20,0	1,3	2,6	hypothetical protein
	SLI2934	225,1	284,1	477,1	1,3	2,1	hypothetical protein
SCO2827	SLI3176	7,2	14,1	15,5	2,0	2,2	hypothetical protein
SCO2976	SLI3320	6,1	10,6	12,9	1,8	2,1	hypothetical protein
SCO3167	SLI3521	54,3	63,9	116,0	1,2	2,1	Transcriptional regulator, TetR family
SCO3271	SLI3617	5,3	5,2	16,8	1,0	3,2	dehydrogenase
	SLI4035	17,9	20,4	43,8	1,1	2,4	hypothetical protein
	SLI4041	68,3	129,8	190,7	1,9	2,8	hypothetical protein

	SLI4370	204,9	281,1	424,9	1,4	2,1	hypothetical protein
	SLI4571	37,0	58,8	132,2	1,6	3,6	hypothetical protein
SCO4640	SLI4911	70,0	67,5	159,9	1,0	2,3	Transcriptional regulator, TetR family
SCO4816	SLI5087	5,9	7,7	11,9	1,3	2,0	hypothetical protein
SCO5225	SLI5514	478,0	533,1	967,9	1,1	2,0	Ribonucleotide reductase, beta subunit
SCO5467	SLI5736	4,9	9,5	11,7	1,9	2,4	Zinc D-Ala-D-Ala carboxypeptidase
	SLI5781	13,2	6,2	30,2	0,5	2,3	hypothetical protein
SCO5908	SLI6183	8,1	7,7	20,8	1,0	2,6	hypothetical protein
SCO3525	SLI6348	6,1	5,9	14,2	1,0	2,3	transmembrane protein
	SLI6555	6,3	8,4	14,7	1,3	2,3	hypothetical protein
SCO6259	SLI6648	14,5	16,5	29,1	1,1	2,0	Inositol transport system, ATP-binding protein
SCO6524	SLI6872	7,2	10,8	15,6	1,5	2,2	putative integral membrane protein
SCO6728	SLI7072	34,3	35,6	70,6	1,0	2,1	hypothetical protein
SCO7146	SLI7361	34,8	55,4	84,3	1,6	2,4	Transcriptional regulator, ArsR family
SCO7196	SLI7413	4,7	5,5	10,0	1,2	2,1	possible ion transport integral membrane protein
SCO7271	SLI7489	35,8	57,5	71,9	1,6	2,0	putative ion channel subunit
SCO7506	SLI7727	5,0	7,5	11,0	1,5	2,2	Beta-galactosidase
	SLI7900	4,7	5,5	10,5	1,2	2,2	hypothetical protein
	SLI7991	4,9	9,7	12,0	2,0	2,5	hypothetical protein
SCO7754	SLI7994	7,6	12,1	16,8	1,6	2,2	anti-sigma factor antagonist
SCO7826	SLI8076	4,6	7,5	10,2	1,6	2,2	hypothetical protein

Table S1-C. Genes expessed higher in *cslA* only

Gene # *S. coelicolor*	**Gene # *S. lividans***	**1326 (RPKM)**	**cslA (RPKM)**	**glxA (RPKM)**	**cslA/1326**	**glxA/1326**	**Annotation**
SCO0148	SLI0077	12,6	25,6	23,1	2,0	1,8	Transcriptional regulator, Cro/CI family
SCO0346	SLI0303	4,4	12,9	8,6	2,9	1,9	putative 2-hydroxyhepta-2,4-diene-1,7- dioate isomerase
SCO0379	SLI0337	50,0	122,1	49,8	2,4	1,0	Catalase
SCO0408	SLI0366	11,1	27,0	9,9	2,4	0,9	Methyltransferase
SCO0409	SLI0367	5,6	21,8	7,5	3,9	1,3	Spore-associated protein A precursor
SCO0427	SLI0385	11,4	25,2	15,4	2,2	1,4	Beta-ketoadipate enol-lactone hydrolase
SCO0442	SLI0400	11,0	27,7	14,9	2,5	1,3	Allophanate hydrolase 2 subunit 1
SCO0443	SLI0401	5,9	21,2	10,6	3,6	1,8	Allophanate hydrolase 2 subunit 2
SCO0461	SLI0419	6,8	14,9	8,3	2,2	1,2	putative hydrolase
SCO0484	SLI0443	6,9	19,4	11,4	2,8	1,6	putative monooxygenase
SCO0494	SLI0454	59,7	141,6	53,8	2,4	0,9	iron-siderophore binding lipoprotein
SCO0498	SLI0458	9,8	21,8	7,1	2,2	0,7	Siderophore biosynthesis, monooxygenase
	SLI0487	2624,6	5701,9	3530,0	2,2	1,3	hypothetical protein
SCO0543	SLI0504	6,9	26,7	12,8	3,9	1,9	hypothetical protein
	SLI0587	5,0	13,7	9,8	2,7	2,0	hypothetical protein
SCO0682	SLI0655	46,2	92,3	57,2	2,0	1,2	hypothetical protein

SCO0701	SLI0677	5,2	10,8	6,7	2,1	1,3	hypothetical protein
SCO0760	SLI0741	38,7	98,2	30,6	2,5	0,8	putative methyltransferase
SCO0795	SLI0778	8,3	19,6	7,4	2,4	0,9	hypothetical protein
SCO0825	SLI0809	6,6	14,9	11,0	2,2	1,7	putative transmembrane transport protein
SCO0834	SLI0818	5,4	13,7	7,8	2,6	1,5	hypothetical protein
	SLI0916	8,8	22,5	13,0	2,6	1,5	hypothetical protein
SCO6914	SLI0941	5,4	11,1	8,9	2,1	1,7	hypothetical protein SC1B2.20
SCO3698	SLI1077	7,0	14,2	11,2	2,0	1,6	ArsB heavy metal resistance transport membrane protein
SCO6821	SLI1094	6,3	15,7	5,1	2,5	0,8	hypothetical protein
SCO6819	SLI1096	1,9	10,5	2,6	5,5	1,3	5-Enolpyruvylshikimate-3-phosphate synthase
SCO6818	SLI1097	2,9	11,5	4,0	3,9	1,4	putative phosphoglycerate mutase
SCO6814	SLI1101	3,8	11,2	6,5	2,9	1,7	ABC transporter ATP-binding protein
SCO0912	SLI1141	6,4	13,1	6,8	2,0	1,1	Glutamine amidotransferases class-II
SCO0913	SLI1142	6,4	18,0	9,8	2,8	1,5	ABC transporter ATP-binding protein
SCO0922	SLI1153	2,1	14,1	2,8	6,7	1,3	Succinate dehydrogenase iron-sulfur protein
SCO0923	SLI1154	4,0	23,8	4,0	6,0	1,0	Succinate dehydrogenase flavoprotein subunit
SCO0924	SLI1155	19,8	43,0	17,4	2,2	0,9	Succinate dehydrogenase cytochrome b subunit
SCO1131	SLI1407	6,9	15,9	9,1	2,3	1,3	Xanthine and CO dehydrogenases accessory protein
SCO1132	SLI1408	8,5	19,7	11,0	2,3	1,3	aromatic aldehyde oxidoreductase, YagR
SCO1133	SLI1409	3,2	10,7	4,7	3,3	1,4	aromatic aldehyde oxidoreductase, YagS
SCO1147	SLI1423	7,2	23,8	5,8	3,3	0,8	putative ABC transporter transmembrane subunit
SCO1148	SLI1424	3,2	26,0	6,0	8,1	1,9	putative ABC transporter ATP-binding protein
SCO1293	SLI1575	6,8	15,9	7,5	2,3	1,1	hypothetical protein
SCO1294	SLI1576	2,5	29,9	4,5	12,1	1,8	Methionine gamma-lyase
SCO1357	SLI1649	8,2	17,1	10,9	2,1	1,3	hypothetical protein
SCO1570	SLI1873	32,1	133,9	54,4	4,2	1,7	Argininosuccinate lyase
SCO1577	SLI1880	32,2	116,5	34,3	3,6	1,1	Acetylornithine aminotransferase
SCO1578	SLI1881	17,0	96,9	28,8	5,7	1,7	Acetylglutamate kinase
SCO1579	SLI1882	24,8	100,2	35,6	4,0	1,4	putative glutamate N-acetyltransferase, argJ
SCO1580	SLI1883	26,1	77,1	43,7	3,0	1,7	N-acetyl-gamma-glutamyl-phosphate reductase, argC
SCO1864	SLI2175	32,4	94,2	52,1	2,9	1,6	L-2,4-diaminobutyric acid acetyltransferase
SCO1865	SLI2176	31,3	167,0	61,8	5,3	2,0	Diaminobutyrate-pyruvate aminotransferase
SCO1867	SLI2178	72,5	614,8	125,1	8,5	1,7	Ectoine hydroxylase
SCO1898	SLI2209	14,8	32,7	11,1	2,2	0,8	possible sugar binding protein
SCO1899	SLI2210	8,7	26,5	8,7	3,0	1,0	possible integral membrane sugar transport protein
SCO1900	SLI2211	8,2	40,3	9,5	4,9	1,2	possible integral membrane sugar transport protein
SCO1901	SLI2212	18,2	69,3	18,0	3,8	1,0	Sorbitol dehydrogenase
	SLI2217	29,3	125,6	39,2	4,3	1,3	hypothetical protein
SCO1987	SLI2304	10,5	25,2	10,3	2,4	1,0	Translation initiation inhibitor
SCO1988	SLI2305	22,3	51,7	16,6	2,3	0,7	hypothetical protein
SCO2011	SLI2332	29,2	65,6	32,6	2,2	1,1	Branched-chain amino acid transport ATP-binding protein LivG
SCO2012	SLI2333	39,9	86,9	49,5	2,2	1,2	Branched-chain amino acid transport ATP-binding protein LivF

SCO2025	SLI2346	90,4	235,5	106,5	2,6	1,2	Glutamate synthase (NADPH) small chain
SCO2026	SLI2347	80,5	182,1	104,2	2,3	1,3	Glutamate synthase (NADPH) large chain
SCO2270	SLI2596	7,5	16,6	4,3	2,2	0,6	hypothetical protein
SCO2372	SLI2706	11,7	40,2	21,6	3,4	1,8	Antiholin-like protein LrgA
SCO2449	SLI2785	18,6	46,4	24,6	2,5	1,3	MoxR-like ATPases
SCO2464	SLI2800	19,3	43,3	25,4	2,2	1,3	Lipid A export ATP-binding/permease protein MsbA
SCO2492	SLI2826	57,7	144,7	35,4	2,5	0,6	hypothetical protein
SCO2493	SLI2827	7,8	17,6	10,8	2,3	1,4	hypothetical protein
SCO2591	SLI2930	663,2	1353,8	612,4	2,0	0,9	hypothetical protein
SCO2633	SLI2975	406,1	2553,7	609,1	6,3	1,5	superoxide dismutase, Fe-Zn
SCO2637	SLI2979	59,5	127,2	61,0	2,1	1,0	Serine protease
SCO2776	SLI3123	15,8	198,8	15,1	12,6	1,0	Methylcrotonyl-CoA carboxylase carboxyl transferase
SCO2777	SLI3124	11,6	172,3	9,6	14,8	0,8	Methylcrotonyl-CoA carboxylase biotin-containing
SCO2778	SLI3125	10,6	228,0	8,0	21,6	0,8	Hydroxymethylglutaryl-CoA lyase
SCO2779	SLI3126	16,5	344,2	15,7	20,9	1,0	Isovaleryl-CoA dehydrogenase
SCO2783	SLI3130	11,1	26,8	15,9	2,4	1,4	Desferrioxamine E biosynthesis, monooxygenase, DesB
SCO2785	SLI3132	13,6	28,8	15,1	2,1	1,1	Desferrioxamine E biosynthesis, ligase, DesD
SCO2837	SLI3188	188,4	3460,9	1,1	18,4	0,0	Radical Cu-oxidase, glxA
SCO2838	SLI3189	172,9	529,4	312,0	3,1	1,8	putative secreted endoglucanase
SCO2839	SLI3190	4,7	20,5	8,5	4,3	1,8	lipoprotein
	SLI3212	11,8	24,0	11,1	2,0	0,9	hypothetical protein
	SLI3213	17,2	37,7	25,7	2,2	1,5	hypothetical protein
	SLI3214	92,6	200,2	140,8	2,2	1,5	hypothetical protein
SCO2879	SLI3224	27,8	70,9	21,3	2,5	0,8	conserved hypothetical secreted protein
SCO2880	SLI3225	32,3	83,6	38,2	2,6	1,2	hypothetical protein
SCO2881	SLI3226	29,2	61,8	24,1	2,1	0,8	hypothetical protein
SCO2882	SLI3227	21,1	61,6	21,3	2,9	1,0	conserved ATP/GTP-binding protein
SCO2883	SLI3228	22,1	55,5	24,5	2,5	1,1	cytochrome P450 monooxygenase
SCO2884	SLI3229	41,3	136,1	42,5	3,3	1,0	putative cytochrome P450 hydroxylase
SCO2885	SLI3230	26,4	93,5	31,3	3,5	1,2	hypothetical protein
SCO2920	SLI3264	68,1	264,5	85,4	3,9	1,3	Serine protease 3 precursor
SCO3051	SLI3400	164,9	399,8	190,1	2,4	1,2	Butyryl-CoA dehydrogenase
SCO3160	SLI3514	36,6	75,3	71,6	2,1	2,0	possible integral membrane transport protein, Co transport
SCO3614	SLI3857	219,8	460,1	241,2	2,1	1,1	Aspartate-semialdehyde dehydrogenase
SCO3811	SLI4062	213,3	568,2	197,7	2,7	0,9	D-alanyl-D-alanine carboxypeptidase
SCO3831	SLI4083	5,6	13,8	10,0	2,4	1,8	Branched-chain alpha-keto acid dehydrogenase, E1 alpha subunit, bkdA2
SCO4020	SLI4254	20,3	81,4	20,3	4,0	1,0	putative two-component system response regulator
SCO4021	SLI4255	3,1	32,3	4,5	10,5	1,5	Osmosensitive K+ channel histidine kinase KdpD
SCO4108	SLI4338	100,5	244,1	106,0	2,4	1,1	putative peptidase
SCO4157	SLI4395	6,8	14,7	6,9	2,2	1,0	putative protease
SCO4242	SLI4479	46,5	155,0	80,4	3,3	1,7	hypothetical protein
SCO4249	SLI4486	18,2	57,5	30,0	3,2	1,7	hypothetical protein

SCO4251	SLI4487	575,8	2311,7	1137,6	4,0	2,0	secreted protein
SCO4253	SLI4489	550,1	2388,0	1065,2	4,3	1,9	Phage tail sheath protein FI
SCO4254	SLI4490	12,2	25,2	20,0	2,1	1,6	hypothetical protein
SCO4258	SLI4493	101,4	325,3	193,6	3,2	1,9	hydrolytic protein
SCO4259	SLI4494	29,0	94,4	54,5	3,3	1,9	ATPase, AAA family
SCO4336	SLI4574	236,9	477,1	394,9	2,0	1,7	Transcriptional regulator, MarR family
SCO4512	SLI4793	56,2	122,7	95,3	2,2	1,7	hypothetical protein
SCO4513	SLI4794	35,1	96,4	56,7	2,7	1,6	hypothetical protein
SCO4515	SLI4796	39,5	110,4	63,2	2,8	1,6	hypothetical protein
SCO4683	SLI4956	79,3	168,8	90,5	2,1	1,1	NADP-specific glutamate dehydrogenase
SCO4784	SLI5054	58,4	162,4	70,0	2,8	1,2	Chorismate mutase I
SCO4896	SLI5168	20,9	57,3	32,6	2,7	1,6	putative transport integral membrane protein
SCO4930	SLI5203	12,0	31,2	9,8	2,6	0,8	Methylglutaconyl-CoA hydratase
SCO4931	SLI5204	7,1	23,8	6,3	3,4	0,9	putative secreted protein
SCO4936	SLI5210	7,6	18,6	7,2	2,5	1,0	putative ABC transporter ATP-binding protein
SCO4937	SLI5211	3,8	13,4	3,3	3,5	0,9	hypothetical protein
SCO4951	SLI5223	8,8	18,2	10,3	2,1	1,2	putative oxidoreductase
SCO4995	SLI5270	12,9	35,5	19,9	2,8	1,5	hypothetical protein
SCO5012	SLI5288	9,2	19,9	12,0	2,2	1,3	hypothetical protein
SCO5013	SLI5289	4,6	11,9	7,8	2,6	1,7	secreted protein
SCO5014	SLI5290	4,7	12,6	8,6	2,7	1,8	hypothetical protein
SCO5240	SLI5531	600,9	1401,1	689,7	2,3	1,1	transcription regulator, WhiB-like
SCO5249	SLI5540	5,0	15,6	8,3	3,1	1,7	putative nucleotide-binding protein
SCO5389	SLI5658	185,0	583,3	161,6	3,2	0,9	hypothetical protein
SCO5390	SLI5659	20,3	48,0	16,5	2,4	0,8	putative alkanal monooxygenase (luciferase)
SCO5448	SLI5717	4,7	14,3	7,2	3,0	1,5	putative ABC transporter ATP-binding protein
SCO5449	SLI5718	7,1	18,2	11,1	2,6	1,6	putative ABC transporter transmembrane protein
SCO5450	SLI5719	6,5	22,6	12,0	3,5	1,8	putative ABC transporter ATP-binding protein
	SLI5785	189,0	584,0	315,4	3,1	1,7	hypothetical protein
SCO5512	SLI5786	111,5	311,5	173,7	2,8	1,6	Acetolactate synthase large subunit
SCO5513	SLI5787	51,7	233,3	72,4	4,5	1,4	Acetolactate synthase small subunit
SCO5514	SLI5788	472,1	1735,1	613,3	3,7	1,3	Ketol-acid reductoisomerase
SCO5530	SLI5806	6,4	12,9	9,3	2,0	1,5	putative membrane protein
SCO5553	SLI5830	51,4	141,1	70,9	2,7	1,4	3-isopropylmalate dehydratase large subunit
SCO5554	SLI5831	38,3	137,2	50,7	3,6	1,3	3-isopropylmalate dehydratase small subunit
	SLI6006	104,6	225,4	193,3	2,2	1,8	hypothetical protein
SCO5774	SLI6036	561,1	1300,9	779,6	2,3	1,4	glutamate permease
SCO5776	SLI6038	1414,2	2997,5	1975,9	2,1	1,4	glutamate-binding protein of ABC transporter system
	SLI6109	31,7	75,6	49,8	2,4	1,6	hypothetical protein
SCO5976	SLI6258	25,0	77,2	40,1	3,1	1,6	Ornithine carbamoyltransferase
	SLI6370	5,6	15,2	10,2	2,7	1,8	hypothetical protein
	SLI6371	38,5	82,8	55,1	2,1	1,4	hypothetical protein
	SLI6372	53,9	110,0	80,5	2,0	1,5	hypothetical protein.
	SLI6482	8,9	22,0	16,7	2,5	1,9	hypothetical protein

SCO6090	SLI6484	6,8	18,2	9,5	2,7	1,4	hypothetical protein
SCO6096	SLI6490	5,1	11,6	3,4	2,3	0,7	ABC-transporter, probable sulfate transport
SCO6097	SLI6492	9,8	22,0	7,0	2,3	0,7	Sulfate adenylyltransferase subunit 1
SCO6196	SLI6585	14,5	50,8	19,0	3,5	1,3	putative long-chain-fatty-acid-CoA ligase
SCO6197	SLI6586	272,7	632,1	209,3	2,3	0,8	secreted protein
SCO6198	SLI6587	10,6	51,5	11,8	4,8	1,1	hypothetical protein
SCO6199	SLI6588	14,2	54,1	15,5	3,8	1,1	hypothetical protein
SCO6200	SLI6589	6,4	13,2	3,8	2,1	0,6	hypothetical protein
SCO6243	SLI6631	7,7	15,9	12,3	2,1	1,6	Malate synthase
SCO6295	SLI6688	4,8	14,1	5,8	3,0	1,2	Transport ATP-binding protein CydCD
SCO6298	SLI6690	5,6	14,0	10,6	2,5	1,9	hypothetical protein
	SLI6712	4,5	11,0	5,0	2,4	1,1	hypothetical protein
SCO6344	SLI6741	14,7	29,8	20,3	2,0	1,4	amidotransferase-related protein
SCO6451	SLI6797	45,2	263,1	53,4	5,8	1,2	Nickel ABC transporter, nickel-binding protein, nikA
SCO6452	SLI6798	24,7	192,3	39,3	7,8	1,6	Nickel ABC transporter, permease, nikB
SCO6453	SLI6799	16,7	108,0	22,2	6,4	1,3	Nickel ABC transporter, permease, nikC
SCO6454	SLI6800	11,9	56,9	16,5	4,8	1,4	Nickel ABC transporter, ATP-binding protein, nikD
SCO6455	SLI6801	17,1	65,6	29,0	3,8	1,7	Nickel ABC transporter, ATP-binding protein, nikE
SCO6470	SLI6816	35,2	70,8	51,9	2,0	1,5	Mesaconyl-CoA hydratase
	SLI6822	10,6	27,7	16,8	2,6	1,6	hypothetical protein
SCO6550	SLI6900	6,9	15,6	12,4	2,3	1,8	Short-chain dehydrogenase/reductase SDR
SCO6590	SLI6947	190,0	387,6	107,6	2,0	0,6	hypothetical protein
SCO6644	SLI6989	60,6	141,5	109,2	2,3	1,8	Oligopeptide ABC transporter, solute binding protein
SCO6646	SLI6991	15,4	30,9	21,7	2,0	1,4	putative transport system permease
SCO6658	SLI7003	89,1	223,9	176,2	2,5	2,0	6-phosphogluconate dehydrogenase, decarboxylating
SCO6659	SLI7004	70,9	173,7	131,9	2,5	1,9	Glucose-6-phosphate isomerase
SCO6682	SLI7026	7,4	16,2	7,5	2,2	1,0	Lanthionine precursor peptide LanA
SCO6695	SLI7039	48,5	103,8	55,3	2,1	1,1	hypothetical protein
SCO6715	SLI7059	18,5	59,1	21,6	3,2	1,2	transcriptional regulator, WhiB-type
SCO6717	SLI7061	133,2	405,4	162,9	3,0	1,2	putative acyl-[acyl-carrier protein] desaturase
SCO6766	SLI7114	14,2	31,4	17,2	2,2	1,2	hopanoid biosynthesis associated radical SAM protein HpnH
SCO6767	SLI7115	8,7	23,9	15,7	2,8	1,8	GcpE protein homolog, lipid metabolism
SCO6778	SLI7126	8,8	17,8	15,7	2,0	1,8	hypothetical protein
SCO6981	SLI7183	6,1	14,0	9,7	2,3	1,6	Inositol transport system ATP-binding protein
SCO6982	SLI7184	7,3	16,1	12,6	2,2	1,7	Inosose dehydratase
SCO6989	SLI7191	7,1	18,5	8,0	2,6	1,1	hypothetical protein
SCO6990	SLI7192	12,0	34,5	17,2	2,9	1,4	Sodium-dependent transporter
SCO7002	SLI7204	5,1	12,3	6,5	2,4	1,3	amino acid permease (GABA permease)
SCO7036	SLI7241	36,5	232,4	67,7	6,4	1,9	Argininosuccinate synthase (EC 6.3.4.5)
SCO7040	SLI7245	21,5	50,3	26,9	2,3	1,3	NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase
SCO7047	SLI7252	11,6	35,4	11,4	3,1	1,0	Undecaprenyl-diphosphatase
SCO7251	SLI7467	87,4	201,3	68,5	2,3	0,8	hypothetical protein
SCO7252	SLI7468	69,5	141,1	62,0	2,0	0,9	putative regulatory protein

SCO7253	SLI7469	17,4	40,1	19,4	2,3	1,1	hypothetical protein
	SLI7481	7,5	19,7	9,9	2,6	1,3	hypothetical protein
SCO7399	SLI7618	35,8	76,3	36,8	2,1	1,0	Ferric hydroxamate ABC transporter, substrate binding protein FhuD
SCO7420	SLI7640	27,7	57,2	34,0	2,1	1,2	hypothetical protein
SCO7421	SLI7641	35,7	74,2	47,3	2,1	1,3	hypothetical protein
SCO7467	SLI7684	39,7	122,0	51,0	3,1	1,3	hypothetical protein
SCO7659	SLI7886	58,7	129,5	112,0	2,2	1,9	hypothetical protein
	SLI7935	10,0	20,4	15,8	2,0	1,6	hypothetical protein
SCO7722	SLI7953	3,5	10,0	5,5	2,9	1,6	hypothetical protein
SCO7733	SLI7969	12,9	26,1	21,6	2,0	1,7	hypothetical protein
SCO7772	SLI8015	14,6	33,1	22,9	2,3	1,6	hypothetical protein
	SLI8060	8,7	24,2	15,6	2,8	1,8	hypothetical protein
SCO7814	SLI8061	15,4	35,5	22,0	2,3	1,4	putative oxidoreductase (pseudogene)

Table S2-A. Genes expressed lower in both *cslA* and *glxA*

Gene # *S. coelicolor*	**Gene # *S. lividans***	**1326 (RPKM)**	**cslA (RPKM)**	**glxA (RPKM)**	**cslA/1326**	**glxA/1326**	**Annotation**
	SLI0003	23,0	11,1	11,1	0,5	0,5	hypothetical protein
	SLI0174	37,1	14,6	11,2	0,4	0,3	hypothetical protein
	SLI0229	35,0	15,2	15,1	0,4	0,4	hypothetical protein
SCO0558	SLI0520	40,1	9,5	19,3	0,2	0,5	hypothetical protein
SCO0793	SLI0776	12,4	5,3	5,7	0,4	0,5	hypothetical protein
	SLI1219	13,1	1,9	1,5	0,1	0,1	hypothetical protein
	SLI1372	15,9	4,4	6,9	0,3	0,4	hypothetical protein
	SLI1891	21,9	8,6	10,5	0,4	0,5	Transcriptional regulator, GntR family
SCO1602	SLI1906	144,5	51,5	39,2	0,4	0,3	hypothetical protein
	SLI1910	108,5	43,6	54,2	0,4	0,5	hypothetical protein
	SLI1955	36,7	10,4	8,2	0,3	0,2	hypothetical protein
SCO1708	SLI2012	15,0	6,4	6,4	0,4	0,4	hypothetical protein
SCO1748	SLI2052	77,5	32,7	38,0	0,4	0,5	putative regulator, highly similar to metallo-thionein-like proteins
	SLI2174	94,6	28,3	30,8	0,3	0,3	hypothetical protein
	SLI2277	10,0	3,2	2,5	0,3	0,2	hypothetical protein
	SLI2499	28,1	10,2	12,2	0,4	0,4	hypothetical protein
SCO2185	SLI2512	264,0	76,0	92,6	0,3	0,4	hypothetical protein
SCO2224	SLI2550	168,1	65,7	64,4	0,4	0,4	hypothetical protein
	SLI2615	15,5	7,6	5,2	0,5	0,3	hypothetical protein
SCO2530	SLI2866	11,3	2,5	4,2	0,2	0,4	hypothetical protein
SCO2636	SLI2978	106,0	24,4	50,6	0,2	0,5	hypothetical protein
SCO2887	SLI3232	298,6	101,8	141,8	0,3	0,5	membrane protein
SCO3071	SLI3421	87,9	13,2	33,1	0,1	0,4	Formiminoglutamic iminohydrolase
SCO3072	SLI3422	65,1	6,5	12,2	0,1	0,2	putative amino acid hydrolase
SCO3073	SLI3423	74,5	12,8	10,6	0,2	0,1	Urocanate hydratase

SCO3075	SLI3425	52,3	6,8	8,9	0,1	0,2	Transcriptional regulator, ArsR family
SCO3081	SLI3431	202,7	61,7	101,7	0,3	0,5	hypothetical protein
SCO3088	SLI3440	133,6	19,5	63,5	0,1	0,5	hypothetical protein
SCO3196	SLI3550	45,0	23,4	20,9	0,5	0,5	PTS system, putative fructose-specific permease
SCO3285	SLI3630	30,5	14,0	12,6	0,5	0,4	hypothetical protein
SCO3386	SLI3729	30,8	13,2	7,9	0,4	0,3	hypothetical protein
SCO3431	SLI3775	98,9	26,5	37,2	0,3	0,4	membrane protein
SCO3620	SLI3864	13,8	5,0	6,1	0,4	0,4	putative membrane protein
	SLI3865	78,5	39,0	33,1	0,5	0,4	serine-threonine protein kinase
SCO3657	SLI3904	361,0	61,2	101,4	0,2	0,3	loricrin
SCO3750	SLI3994	28,0	8,0	13,8	0,3	0,5	two-component sensor histidine kinase
SCO3784	SLI4028	130,4	36,7	60,8	0,3	0,5	hypothetical protein
	SLI4074	204,7	81,0	80,2	0,4	0,4	hypothetical protein
SCO3942	SLI4190	23,1	6,2	8,6	0,3	0,4	hypothetical protein
	SLI4248	44,8	7,1	14,8	0,2	0,3	hypothetical protein
	SLI4284	12,9	5,5	5,9	0,4	0,5	penicillin amidase family protein
SCO4174	SLI4415	17,9	7,6	7,5	0,4	0,4	integral membrane protein
	SLI4557	25,5	13,1	12,6	0,5	0,5	probable DNA-binding protein
	SLI4681	33,9	10,0	9,6	0,3	0,3	hypothetical protein
SCO4802	SLI5073	49,8	7,3	21,2	0,1	0,4	hypothetical protein
SCO4803	SLI5075	81,8	13,7	35,4	0,2	0,4	hypothetical protein
SCO4867	SLI5140	20,6	6,3	8,7	0,3	0,4	hypothetical protein
	SLI5201	152,7	65,5	66,8	0,4	0,4	hypothetical protein
SCO4932	SLI5205	499,2	24,5	59,7	0,0	0,1	Histidine ammonia-lyase
	SLI5220	1099,7	498,8	385,4	0,5	0,4	hypothetical protein
	SLI5247	18,8	2,4	5,5	0,1	0,3	hypothetical protein
	SLI5409	287,2	132,4	144,2	0,5	0,5	hypothetical protein
	SLI5426	25,1	10,3	9,4	0,4	0,4	hypothetical protein
SCO5228	SLI5517	55,6	17,4	28,0	0,3	0,5	putative acetyltransferase
SCO5462	SLI5731	12,4	3,3	4,9	0,3	0,4	hypothetical protein
SCO5581	SLI5863	211,7	91,1	96,8	0,4	0,5	hypothetical protein
SCO5680	SLI5940	155,4	14,7	68,4	0,1	0,4	Cytidine deaminase
	SLI6080	459,5	163,8	137,0	0,4	0,3	hypothetical protein
	SLI6081	292,0	141,5	147,4	0,5	0,5	hypothetical protein
SCO5853	SLI6124	29,4	14,7	12,6	0,5	0,4	SgaA homolog
	SLI6195	10,6	2,7	4,8	0,3	0,5	hypothetical protein
SCO6421	SLI6765	13,3	4,7	6,2	0,4	0,5	putative two-component system sensor kinase
SCO6538	SLI6886	20,6	5,7	9,7	0,3	0,5	integral membrane protein
SCO7247	SLI7463	12,6	5,2	5,5	0,4	0,4	Usp-like, universal stress protein family
SCO7284	SLI7502	258,7	86,0	125,4	0,3	0,5	Ribonuclease HI

Table S2-B. Genes expressed lower in *glxA* only

Gene # *S. coelicolor*	Gene # *S. lividans*	1326 (RPKM)	cslA (RPKM)	glxA (RPKM)	cslA/1326	glxA/1326	Annotation
SCO0286	SLI0239	10,7	7,3	4,8	0,7	0,4	secreted peptidoglycan binding protein
SCO0761	SLI0742	281,0	356,8	104,5	1,3	0,4	hypothetical protein
	SLI1233	10,7	6,2	5,3	0,6	0,5	hypothetical protein
	SLI1346	87,5	52,4	43,6	0,6	0,5	hypothetical protein
SCO1682	SLI1987	14,9	9,6	7,5	0,6	0,5	L-idonate 5-dehydrogenase
	SLI2083	78,8	41,5	34,5	0,5	0,4	hypothetical protein
SCO1902	SLI2213	11,4	9,2	4,7	0,8	0,4	hypothetical hydrophilic protein
SCO2038	SLI2360	362,8	334,5	156,1	0,9	0,4	FIG01124547: hypothetical protein
SCO2159	SLI2485	24,7	13,9	11,5	0,6	0,5	SC6G10.32, unknown, len: 69aa
	SLI2771	28,3	24,8	14,1	0,9	0,5	FIG01121890: hypothetical protein
	SLI3141	49,1	34,5	22,8	0,7	0,5	hypothetical protein
SCO2837	SLI3188	188,4	3460,9	1,1	18,4	0,0	Radical Cu-oxidase, glxA
	SLI3223	35,8	57,4	17,8	1,6	0,5	hypothetical protein
SCO3074	SLI3424	149,3	238,5	66,6	1,6	0,4	putative integral membrane protein
SCO3362	SLI3704	19,5	31,1	8,6	1,6	0,4	putative membrane protein
SCO5100	SLI5378	73,7	63,8	35,2	0,9	0,5	Transcriptional regulator, GntR family
SCO6099	SLI6494	20,4	24,1	9,3	1,2	0,5	Adenylylsulfate kinase
SCO6100	SLI6495	36,9	20,1	16,9	0,5	0,5	phosphoadenosine phosphosulfate reductase, cysH
	SLI6946	18,8	13,1	3,9	0,7	0,2	hypothetical protein
	SLI6951	66,5	88,5	32,7	1,3	0,5	hypothetical protein
SCO6716	SLI7060	54,5	93,9	21,4	1,7	0,4	hypothetical protein
	SLI7157	11,8	7,4	5,3	0,6	0,4	hypothetical protein
SCO7257	SLI7473	25,0	14,0	12,1	0,6	0,5	ChpB
SCO7279	SLI7497	32,9	19,2	16,6	0,6	0,5	DNA-binding protein

Table S2-C. Genes expressed lower in *cslA* only. Only hints that are three-fold down or more are shown in the table.

Gene # *S. coelicolor*	Gene # *S. lividans*	1326 (RPKM)	cslA (RPKM)	glxA (RPKM)	cslA/1326	glxA/1326	Annotation
SCO0084	SLI0010	11,3	3,7	6,6	0,3	0,6	hypothetical protein
SCO0536	SLI0496	49,6	14,7	35,3	0,3	0,7	hypothetical protein
SCO0953	SLI1186	158,0	33,1	107,9	0,2	0,7	regulatory protein, LacI
SCO0954	SLI1187	62,8	19,2	44,4	0,3	0,7	putative acetyltransferase
SCO0977	SLI1212	111,1	29,8	94,3	0,3	0,8	hypothetical protein
SCO1000	SLI0872	27,4	1,8	36,3	0,1	1,3	Integrase
SCO1087	SLI1361	469,9	36,9	483,7	0,1	1,0	threonine aldolase
SCO1088	SLI1362	647,8	32,2	697,2	0,0	1,1	putative oxidoreductase
SCO1089	SLI1363	955,2	80,1	947,5	0,1	1,0	hypothetical protein
SCO1090	SLI1364	76,7	17,4	58,6	0,2	0,8	Glycerophosphoryl diester phosphodiesterase
SCO1109	SLI1382	104,9	26,8	91,2	0,3	0,9	2,4-dienoyl-CoA reductase (NADPH)

SCO1377	SLI1670	24,7	6,0	21,6	0,2	0,9	Molybdate-binding domain of ModE
SCO1378	SLI1671	235,7	31,1	229,2	0,1	1,0	putative glycine dehydrogenase
SCO1379	SLI1672	13,1	3,0	8,1	0,2	0,6	hypothetical protein
SCO1454	SLI1752	47,9	14,9	53,6	0,3	1,1	Lysine 2-monooxygenase
SCO1455	SLI1753	73,2	16,5	70,1	0,2	1,0	hydrolase
SCO1459	SLI1756	15,4	4,5	13,2	0,3	0,9	putative amino acid transporter
SCO1541	SLI1842	41,9	11,8	38,8	0,3	0,9	putative regulator
SCO1749	SLI2053	557,5	147,5	507,8	0,3	0,9	hypothetical protein
SCO1788	SLI2096	96,3	31,9	65,1	0,3	0,7	4-nitrophenylphosphatase
SCO1799	SLI2107	22,0	5,8	13,7	0,3	0,6	hypothetical protein
SCO1908	SLI2220	50,6	14,8	33,5	0,3	0,7	putative large secreted protein
SCO1982	SLI2298	83,0	26,1	66,1	0,3	0,8	hypothetical protein
SCO2099	SLI2423	52,8	12,7	27,1	0,2	0,5	hypothetical protein
SCO2107	SLI2431	171,7	53,1	101,2	0,3	0,6	glycine oxidase
SCO2255	SLI2582	107,3	36,7	79,5	0,3	0,7	putative membrane protein
SCO2256	SLI2583	113,1	29,1	109,9	0,3	1,0	3-methyl-2-oxobutanoate hydroxymethyltransferase
SCO2297	SLI2625	64,7	17,6	61,2	0,3	0,9	hypothetical protein
SCO2320	SLI2650	30,0	8,4	19,5	0,3	0,7	hypothetical protein
SCO2352	SLI2683	82,5	25,1	54,0	0,3	0,7	hypothetical protein
SCO2353	SLI2684	121,0	19,2	63,7	0,2	0,5	hypothetical protein
SCO2472	SLI2808	12,2	4,2	6,4	0,3	0,5	SanA protein
SCO2538	SLI2874	318,7	95,8	199,7	0,3	0,6	hypothetical protein
SCO2574	SLI2911	113,7	38,4	102,5	0,3	0,9	hypothetical protein
SCO2939	SLI3283	237,5	71,7	143,9	0,3	0,6	hypothetical protein
SCO2942	SLI3287	459,5	147,5	245,4	0,3	0,5	oxidoreductase
SCO2953	SLI3299	71,8	18,6	37,9	0,3	0,5	putative membrane protein
SCO2954	SLI3300	15,6	5,4	13,7	0,3	0,9	RNA polymerase sigma-70 factor, ECF subfamily
SCO3048	SLI3396	505,7	156,3	435,5	0,3	0,9	putative membrane protein
SCO3070	SLI3420	81,3	14,3	42,5	0,2	0,5	Imidazolonepropionase
SCO3084	SLI3434	13,8	4,0	8,4	0,3	0,6	P-hydroxybenzoate hydroxylase
SCO3086	SLI3437	1554,2	207,9	1456,8	0,1	0,9	putative lipoprotein
SCO3087	SLI3438	981,7	114,2	702,9	0,1	0,7	hypothetical protein
SCO3114	SLI3471	11,7	3,8	10,9	0,3	0,9	putative cellulose-binding protein
SCO3157	SLI3511	210,8	71,4	147,0	0,3	0,7	putative penicillin-binding protein
SCO3194	SLI3548	681,7	198,5	490,6	0,3	0,7	putative lipoprotein
SCO3197	SLI3551	59,1	16,6	44,3	0,3	0,7	Putative sugar kinase
SCO3293	SLI3638	10,1	2,8	7,0	0,3	0,7	hypothetical protein
SCO3330	SLI3673	40,0	10,3	36,9	0,3	0,9	NAD-independent protein deacetylase AcuC
SCO3341	SLI3684	440,5	114,7	258,4	0,3	0,6	hypothetical protein
SCO3342	SLI3685	894,5	129,6	539,8	0,1	0,6	glycine-rich secreted protein
SCO3343	SLI3686	121,6	29,7	71,8	0,2	0,6	hypothetical protein
SCO3356	SLI3698	2083,9	664,0	1835,7	0,3	0,9	ECF sigma factor
SCO3432	SLI3776	41,2	13,0	26,9	0,3	0,7	hypothetical protein
SCO3577	SLI3820	198,4	67,4	144,8	0,3	0,7	Arsenical pump-driving ATPase

SCO3601	SLI3844	240,8	73,4	218,7	0,3	0,9	ligand-binding protein related to C-terminal domains of K+ channels
SCO3621	SLI3866	156,8	28,1	86,5	0,2	0,6	serine-threonine protein kinase
SCO3626	SLI3871	75,5	25,7	53,2	0,3	0,7	putative RNA polymerase sigma factor
SCO3656	SLI3903	67,3	21,0	41,4	0,3	0,6	hypothetical protein
SCO3676	SLI3924	830,2	212,4	502,6	0,3	0,6	hypothetical protein
SCO3686	SLI3934	58,6	16,8	39,3	0,3	0,7	hypothetical protein
SCO3703	SLI3952	70,6	19,6	71,2	0,3	1,0	Molybdate-binding domain of ModE
SCO3710	SLI3959	240,8	67,2	242,8	0,3	1,0	hypothetical protein
SCO3712	SLI3961	719,2	135,4	469,0	0,2	0,7	hydrolase
SCO3772	SLI4016	32,8	8,1	22,3	0,2	0,7	hypothetical protein
SCO3783	SLI4027	46,7	14,9	28,4	0,3	0,6	putative lipoprotein
SCO3786	SLI4030	24,2	6,0	17,8	0,2	0,7	integral membrane protein
SCO3817	SLI4068	617,2	206,3	532,2	0,3	0,9	Branched-chain alpha-keto acid dehydrogenase, E1 alpha subunit
SCO3840	SLI4092	264,3	84,6	209,8	0,3	0,8	hypothetical protein
SCO3866	SLI4120	40,2	14,0	25,8	0,3	0,6	hypothetical protein
SCO3905	SLI4163	158,9	52,1	161,3	0,3	1,0	hypothetical protein
SCO3914	SLI4172	289,6	87,9	264,0	0,3	0,9	Transcriptional regulator, MarR family
SCO3915	SLI4173	261,2	21,9	189,6	0,1	0,7	putative transmembrane efflux protein
SCO3943	SLI4191	21,4	6,6	13,0	0,3	0,6	putative LacI-family transcriptional regulator
SCO3975	SLI4226	208,8	32,0	128,9	0,2	0,6	putative regulatory protein
SCO3976	SLI4227	91,9	26,2	75,1	0,3	0,8	Glycerophosphoryl diester phosphodiesterase
SCO4015	SLI4249	54,5	10,3	30,7	0,2	0,6	hypothetical protein
SCO4038	SLI4272	239,8	80,4	125,6	0,3	0,5	tRNA-specific adenosine-34 deaminase
SCO4039	SLI4273	430,3	121,6	245,9	0,3	0,6	hypothetical protein
SCO4040	SLI4274	31,4	5,5	21,6	0,2	0,7	hypothetical protein
SCO4053	SLI4288	10,7	3,3	8,1	0,3	0,8	Integral membrane protein, CopC & CopD domain
SCO4054	SLI4289	251,1	64,5	279,8	0,3	1,1	hypothetical protein
SCO4055	SLI4290	28,6	8,0	24,6	0,3	0,9	Threonine dehydrogenase and related Zn-dependent dehydrogenases
SCO4069	SLI4297	87,8	25,5	53,8	0,3	0,6	hypothetical protein
SCO4082	SLI4310	109,7	34,9	76,7	0,3	0,7	hypothetical protein
SCO4083	SLI4311	29,8	8,6	22,2	0,3	0,7	hypothetical protein
SCO4084	SLI4312	54,2	17,7	35,0	0,3	0,6	hypothetical protein
SCO4095	SLI4325	83,6	27,1	49,5	0,3	0,6	hypothetical protein
SCO4100	SLI4330	20,5	7,0	14,8	0,3	0,7	hypothetical protein
SCO4113	SLI4344	190,9	63,9	111,3	0,3	0,6	L-2-hydroxyglutarate oxidase
SCO4125	SLI4362	55,1	14,6	36,0	0,3	0,7	acetyltransferase
SCO4142	SLI4381	15,6	5,2	14,5	0,3	0,9	Phosphate ABC transporter, phosphate-binding protein PstS
SCO4167	SLI4408	65,1	21,4	58,6	0,3	0,9	Transcriptional regulator, TetR family
SCO4188	SLI4428	82,8	28,4	59,2	0,3	0,7	Transcriptional regulator, GntR family
SCO4190	SLI4430	298,3	80,4	172,7	0,3	0,6	Transcriptional regulator, GntR family, devA
SCO4234	SLI4472	86,4	29,8	67,4	0,3	0,8	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase

SCO4262	SLI4497	36,1	12,6	37,2	0,3	1,0	hypothetical protein
SCO4268	SLI4503	83,6	24,3	64,7	0,3	0,8	hypothetical protein
SCO4287	SLI4524	138,9	46,9	95,6	0,3	0,7	hypothetical protein
SCO4289	SLI4526	477,5	58,8	299,0	0,1	0,6	secreted protein
SCO4290	SLI4527	190,0	31,6	99,6	0,2	0,5	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15)
SCO4291	SLI4528	26,5	8,7	18,6	0,3	0,7	hypothetical protein
SCO4292	SLI4529	69,9	24,2	51,8	0,3	0,7	putative glucosyl-3-phosphoglycerate synthase
SCO4302	SLI4539	15,7	3,2	10,7	0,2	0,7	secreted protein
SCO4322	SLI4559	86,3	28,7	55,6	0,3	0,6	hypothetical protein
SCO4343	SLI4582	30,4	10,4	21,0	0,3	0,7	Mobile element protein
SCO4386	SLI4620	91,0	30,5	66,7	0,3	0,7	hypothetical protein
SCO4409	SLI4645	101,2	32,4	64,0	0,3	0,6	hypothetical protein
SCO4410	SLI4646	45,3	11,2	44,9	0,2	1,0	putative anti anti sigma factor
SCO4412	SLI4650	31,3	10,2	20,5	0,3	0,7	putative regulatory protein
SCO4422	SLI4659	12,7	3,8	6,9	0,3	0,5	putative hydrolase
SCO4424	SLI4661	353,4	62,4	284,5	0,2	0,8	hypothetical protein
SCO4435	SLI4674	48,9	15,6	28,5	0,3	0,6	putative ADP-ribosylglycohydrolase
SCO4458	SLI4700	89,6	29,0	48,4	0,3	0,5	lipoprotein
SCO4467	SLI4746	283,0	83,6	163,1	0,3	0,6	hypothetical protein
SCO4477	SLI4756	16,4	5,1	14,0	0,3	0,9	Transcriptional regulator, MerR family
SCO4500	SLI4780	43,9	15,0	27,3	0,3	0,6	Acyl dehydratase
SCO4503	SLI4784	15,6	5,1	13,6	0,3	0,9	Long-chain-fatty-acid--CoA ligase
SCO4587	SLI4871	118,0	36,5	97,1	0,3	0,8	Multimeric flavodoxin WrbA
SCO4588	SLI4872	347,5	49,2	197,4	0,1	0,6	hypothetical protein
SCO4633	SLI4904	102,3	34,2	78,9	0,3	0,8	Cytosine deaminase
SCO4696	SLI4967	15,5	5,3	14,4	0,3	0,9	hypothetical protein
SCO4744	SLI5014	31,8	8,1	24,9	0,3	0,8	Holo-[acyl-carrier protein] synthase
SCO4779	SLI5050	158,2	44,9	92,6	0,3	0,6	putative serine/threonine protein kinase
SCO4804	SLI5076	15,4	4,8	8,0	0,3	0,5	hypothetical protein
SCO4818	SLI5089	12,5	3,9	6,5	0,3	0,5	hypothetical protein
SCO4895	SLI5167	192,8	50,5	118,1	0,3	0,6	RNA polymerase sigma-70 factor
SCO4908	SLI5180	2709,8	493,3	1387,1	0,2	0,5	putative RNA polymerase ECF-subfamily sigma factor
SCO4988	SLI5263	56,8	17,4	41,5	0,3	0,7	2-dehydro-3-deoxygluconate kinase
SCO5070	SLI5348	10,9	3,6	5,7	0,3	0,5	hypothetical protein
SCO5138	SLI5420	95,1	25,5	76,1	0,3	0,8	hypothetical protein
SCO5157	SLI5440	301,2	64,1	167,7	0,2	0,6	Magnesium and cobalt transport protein CorA
SCO5158	SLI5441	146,7	48,1	109,9	0,3	0,7	hypothetical protein
SCO5209	SLI5498	50,9	17,6	41,0	0,3	0,8	Transcriptional regulator, TetR family
SCO5254	SLI5545	4185,1	1183,8	3958,7	0,3	0,9	Nickel-dependent superoxide dismutase
SCO5401	SLI5672	83,9	20,3	59,8	0,2	0,7	probable integral membrane protein
SCO5403	SLI5674	116,5	35,7	134,9	0,3	1,2	Two-component response regulator
SCO5415	SLI5684	407,2	135,8	472,5	0,3	1,2	putative isobutyryl-CoA mutase, chain B
SCO5416	SLI5685	148,5	50,7	130,8	0,3	0,9	Transcriptional regulator, AraC family

SCO5417	SLI5686	54,2	16,9	50,0	0,3	0,9	putative zinc-binding oxidoreductase
SCO5437	SLI5705	40,2	13,5	22,6	0,3	0,6	putative MerR-family transcriptional regulator
SCO5469	SLI5738	126,4	34,9	116,4	0,3	0,9	L-serine dehydratase
SCO5472	SLI5741	236,6	49,7	231,1	0,2	1,0	Aminomethyltransferase (glycine cleavage system T protein)
SCO5473	SLI5742	194,1	34,9	148,2	0,2	0,8	putative ATP/GTP binding protein
SCO5483	SLI5753	80,2	26,4	72,3	0,3	0,9	Transcriptional regulator, TetR family
SCO5528	SLI5803	90,1	30,7	74,1	0,3	0,8	Transcriptional regulator, TetR family
SCO5557	SLI5834	212,7	51,9	171,1	0,2	0,8	hypothetical protein
SCO5676	SLI5935	301,3	28,2	213,6	0,1	0,7	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase
SCO5679	SLI5939	192,8	20,7	132,7	0,1	0,7	aldehyde dehydrogenase family protein
SCO5681	SLI5941	26,7	1,6	16,4	0,1	0,6	Dolichol-phosphate mannosyltransferase
SCO5772	SLI6034	109,6	33,0	81,7	0,3	0,7	hypothetical protein
SCO5798	SLI6061	357,9	117,0	245,3	0,3	0,7	putative secreted protein
SCO5807	SLI6073	56,3	19,6	45,0	0,3	0,8	hypothetical protein
SCO5881	SLI6154	181,2	61,1	116,6	0,3	0,6	two-component system response regulator
SCO5915	SLI6190	12,3	3,5	8,3	0,3	0,7	hypothetical protein
SCO5919	SLI6197	27,1	5,8	22,9	0,2	0,8	hypothetical protein
SCO5920	SLI6198	52,6	7,6	63,1	0,1	1,2	ATP-dependent RNA helicase
SCO5985	SLI6267	13,5	2,6	9,7	0,2	0,7	Putative translation initiation inhibitor, yjgF family
SCO5986	SLI6268	116,8	22,5	78,5	0,2	0,7	putative oxidoreductase
SCO5987	SLI6269	144,2	27,5	118,4	0,2	0,8	hypothetical protein
SCO5991	SLI6274	122,1	29,8	71,6	0,2	0,6	secreted protein
SCO6045	SLI6439	198,7	53,9	144,9	0,3	0,7	hypothetical protein
SCO6084	SLI6477	127,2	43,2	87,9	0,3	0,7	putative DNA polymerase III epsilon subunit
SCO6526	SLI6874	13,7	4,0	13,7	0,3	1,0	hypothetical protein
SCO6540	SLI6888	83,3	27,8	43,4	0,3	0,5	Pterin-4-alpha-carbinolamine dehydratase
SCO6621	SLI6980	157,6	36,2	108,6	0,2	0,7	hypothetical protein
SCO6799	SLI7149	127,4	3,5	121,8	0,0	1,0	L-threonine 3-dehydrogenase
SCO6800	SLI7150	138,7	3,7	187,9	0,0	1,4	2-amino-3-ketobutyrate coenzyme A ligase
SCO6801	SLI7151	65,4	19,9	73,3	0,3	1,1	Transcriptional regulator, LysR-family
SCO7248	SLI7464	10,1	3,5	7,1	0,3	0,7	hypothetical protein
SCO7533	SLI7755	11,2	2,7	10,7	0,2	1,0	two-component system response regulator
SCO7597	SLI7819	26,4	9,0	19,2	0,3	0,7	putative N-acetylglucosamine kinase
	SLI5074	20,6	2,7	21,8	0,1	1,1	hypothetical protein
	SLI3439	526,9	107,8	356,3	0,2	0,7	hypothetical protein
	SLI7216	16,5	3,9	14,6	0,2	0,9	Transcriptional regulator, LacI-family
	SLI1383	17,0	4,0	17,4	0,2	1,0	hypothetical protein
	SLI3901	11,5	2,8	7,7	0,2	0,7	hypothetical protein
	SLI4663	69,4	17,7	60,9	0,3	0,9	hypothetical protein
	SLI3397	405,7	112,1	264,6	0,3	0,7	putative membrane protein
	SLI3436	14,1	4,0	11,4	0,3	0,8	hypothetical protein
	SLI0018	88,1	25,5	59,4	0,3	0,7	putative two-component system response regulator

SLI8089	12,1	3,6	8,6	0,3	0,7	hypothetical protein
SLI4844	15,6	4,7	9,7	0,3	0,6	hypothetical protein
SLI4699	25,8	8,0	14,5	0,3	0,6	hypothetical protein
SLI6125	35,3	10,9	27,3	0,3	0,8	hypothetical protein
SLI3499	18,4	5,7	11,7	0,3	0,6	two-component system response regulator
SLI3881	76,2	24,0	42,3	0,3	0,6	hypothetical protein
SLI3774	23,1	7,4	27,0	0,3	1,2	hypothetical protein
SLI7074	9,7	3,1	10,7	0,3	1,1	hypothetical protein
SLI5049	69,6	22,5	78,3	0,3	1,1	hypothetical protein
SLI1401	18,4	6,1	10,2	0,3	0,6	hypothetical protein
SLI5843	53,1	17,9	47,7	0,3	0,9	hypothetical protein
SLI1210	69,1	23,5	39,2	0,3	0,6	hypothetical protein
SLI5857	53,3	18,3	27,0	0,3	0,5	hypothetical protein
SLI2084	19,5	6,7	14,3	0,3	0,7	putative regulatory protein

CURRICULUM VITAE

Giulia Mangiameli was born on the 2nd of May 1984 in Torino, Italy. In 2003, she graduated from Liceo Classico Vincenzo Gioberti, Torino. Between 2003 and 2006, she studied Biotechnology at the University of Torino, obtaining her Bachelor of Science. In 2006, she started her Master's in Industrial Biotechnology at the same university. Between 2007 and 2008, she spent a year abroad at the University of Salamanca, Spain, following an Erasmus project and working on her Master's thesis. She graduated in 2009 with a MSc project on the degradation of textile dyes by the catalytic action of a peroxidase extracted from lentil plants. In the fall of 2009, she joined the group of Molecular Biotechnology at the University of Leiden under the supervision of Dr Erik Vijgenboom and Prof Gilles van Wezel. Her work was funded by the European Research Area for the Industrial Biotechnology (ERA-IB). In early 2014, she moved to London to work as an Executive Editor for the BMC-series at BioMed Central, Springer.

The work done during her PhD is presented in this thesis.