

**List of predicted target sites of the 24 HutC/GntR members of *S. coelicolor***

	<i>orf</i>	+/-	<i>gene</i> , function	#	Sequence
1	SCO0213	-	<i>narK</i> , possible nitrate/nitrite extrusion protein	1	acacgGTGTACACacgac
2	SCO0214	+	Conserved hypothetical protein	1	CggcaGTgTAGACatggG
3	SCO0676	+	Possible integral membrane sensor protein	1	GtttGGTCTAGACCgcgC
4	SCO1117	-	Possible secreted protein	1	cCtccGTGTACACTcgGc
5	SCO1166	-	putative integral membrane protein	1	cCtccGTGTACACTcgGc
6	SCO1167	+	putative helicase (fragment)	1	cCtccGTGTACACTcgGc
7	SCO1373	-	conserved hypothetical oxidoreductase protein	1	atGtcGTaTAaACTcCgc
8	SCO1374	+	putative secreted protein	1	atGtcGTaTAaACTcCgc
9	SCO1390	+	<i>orr</i> , PTS system sugar phosphotransferase component IIA	1	gtGtGGTCTAGACCTcta
10	SCO1517	-	putative secreted protein	1	cGGcgGTGTACACacCCc
11	SCO1547	-	putative anthranilate synthase, chorismate binding enzyme	1	AACCGTgTAGACGGcTT
12	SCO2112	-	conserved hypothetical protein	1	AcTAAGTCTAGACTTAcT
13	SCO2113	+	<i>bfr</i> , probable bacterioferritin	1	AcTAAGTCTAGACTTAcT
14	SCO2182	+	GntR family transcriptional regulator	1	gTattGTcTAaACgtcAg
15	SCO2833	-	<i>chb</i> , secreted chitin binding protein	1	acttGGTCTAGACCTgca
16	SCO2905	-	<i>malX2</i> , PTS enzyme EIIB specific for N-acetyl- glucosamine uptake	1	GTcaACTGGTcTAaACCAGTgtAC
17	SCO2906	+	<i>nagE1</i> , PTS transmembrane and sugar-binding component EIIC	1	GTcaACTGGTcTAaACCAGTgtAC
18	SCO2907	+	<i>nagE2</i> , PTS transmembrane component EIIC	2	aAcaGGTcTAaACCacTg GaGTGGTgTAGACCCaC
19	SCO3207	-	Putative tetR-family transcriptional regulator	1	caCagGTcTAaACggGga
20	SCO3208	+	putative secreted protein	1	caCagGTcTAaACggGga
21	SCO3366	-	putative efflux permease	1	aagtGTcTAaACTggga
22	SCO3367	+	putative tetR-family regulator	1	aagtGTcTAaACTggga
23	SCO3563	+	<i>acsA</i> , acetyl-coenzyme A synthetase	1	AaCaGGTcTAaACCAtTT
24	SCO3655	-	putative spermidine synthase	1	gAaccGTaTAaACCctGtG
25	SCO3711	+	putative small membrane protein	1	CcGtCGTcTAaACGgCcG
26	SCO4285	-	possible sugar kinase	1	cggTGGTgTAGACttaa
27	SCO4286	+	putative solute-binding protein	1	cggTGGTgTAGACttaa
28	SCO4630	-	hypothetical protein	1	taGgCGTcTAaACGgCag
29	SCO5036	-	Unknown ABC transpoter system operon	1	ggtgcGTaTAaACcgtgt
30	SCO5159	-	putative integral membrane transport protein	1	ggtgcGTaTAaACcgtgt
31	SCO5160	+	hypothetical protein	1	ttggcGTaTAaACatagt
32	SCO5231	-	<i>dasR</i> , GntR-family transcriptional regulator	1	tAcTGGTcTAaACCAtTg
33	SCO5232	+	<i>dasA</i> , possible sugar transporter sugar binding protein	1	tAcTGGTcTAaACCAtTg
34	SCO5236	-	<i>nagB</i> , glucosamine phosphate isomerase	1	gATTGGTcTAaACCacATa
35	SCO5240	-	<i>wblE</i> , hypothetical protein	1	cgaaCGTcTAGACcagga
36	SCO5749	+	two-component regulator	1	ggtGTgTAaACggcgg
37	SCO5841	-	<i>ptsH</i> , phosphocarrier protein hpr	1	aAgTtGTCTAGACcAgTc
38	SCO5842	+	conserved hypothetical protein	2	gtCTtGTCTAGACcAGtt
39	SCO5976	+	<i>arcB</i> , ornithine carbamoyltransferase	1	aGttcGTaTAGACTtcCa
40	SCO6032	-	putative hydrolase, possible beta-hexosaminidase	1	tCTTGGTcTAaACCAGg
41	SCO6033	+	hypothetical protein	1	tCTTGGTcTAaACCAGg
42	SCO6062	+	putative ABC transporter ATP-binding subunit	1	cagccGTcTAaACTcgac
43	SCO6178	-	<i>nodB</i> putative chitoooligosaccharide deacetylase	1	tgCGtGTATATACgCGgt
44	SCO6179	+	putative nucleotide-sugar dehydratase	1	tgCGtGTATATACgCGgt
45	SCO6214	+	putative permease	1	CcGaCGTcTAaACGaCcG
46	SCO6222	-	putative aminotransferase class-I	1	AacttGTcTAaACTgcgT
47	SCO6223	+	conserved hypothetical protein	1	AacttGTcTAaACTgcgT
48	SCO6300	-	putative secreted hydrolase, possible beta-hexosaminidase	1	AttttGTCTAGACctctT
49	SCO6344	-	putative secreted amidase	1	ctaAGGTCTAGACCTgca
50	SCO6345	+	possible secreted chitinase	2	CGTAGGTCTAGACCTgCG
51	SCO6445	+	putative inositol monophosphatase	1	caCgcGTGTACACctGat
52	SCO6925	-	putative membrane protein	1	TgCctGTATATACgCgTA
53	SCO6926	+	hypothetical protein	1	TgCctGTATATACgCgTA
54	SCO7017	-	hypothetical protein	1	cgAGCGTGTACACCTgC
55	SCO7018	+	hypothetical protein	1	cgAGCGTGTACACCTgC
56	SCO7056	-	GntR-family transcriptional regulator	1	agcTGGTcTAGACCAatg
57	SCO7224	-	putative integral membrane protein	1	cccTtGTCTAGACcAata
58	SCO7225	+	secreted chitinase	2	cTatGGTCTAGACCTgAa
				3	gtCAGGTCTAGACCTGta
59	SCO7263	+	<i>chiF</i> , chitinase	1	aActGGTcTAaACCctTg
60	SCO7290	-	putative dehydrogenase	1	gCccGTcTAaACCctGt
61	SCO7410	-	putative binding-protein dependent transport protein	1	GGcatGTcTAaACTgCcc
62	SCO7411	+	putative LacI-family transcriptional regulator	1	GGcatGTcTAaACTgCcc