

Position	Strand	Sequence	Score	Downstream ORF
501510	+	CTTGTATGGTCTAGTCCA	83.07	-N(171)- - SCO0481 - - putative secreted chitin binding protein
562712	+	CCTCATTGGTCCATGCCA	81.65	-N(73)- - SCO0531 - - putative sugar transporter sugar binding protein
960415	+	GGATTTTGGTATGGACCA	87.28	-N(68)- - SCO0915 - - hypothetical protein SCM10.03
960421	-	TTGTAATGGTCCATACCA	85.00	-N(129)- - SCO0914 - - putative lipoprotein
1176060	-	CCCGTTTGGTCTAGACCG	85.00	-N(133)- - SCO1117 - - putative secreted protein
1300521	-	TTTGACAGGTCTGGACCA	81.00	-N(190)- - SCO1226 - - putative bifunctional protein
1333748	-	CGGGATTGGTCTTGACCA	89.00	-N(115)- - SCO1262 - - putative gntR-family transcriptional regulator
1474013	-	GGACGGTGGTCAAGAGCA	80.00	-N(5492)- - SCO1389 - - putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase
1474173	+	GGAGTGTGGTCTAGACCT	82.83	-N(100)- - SCO1390 - - putative PTS system sugar phosphotransferase component IIA
1474179	-	GATTAGAGGTCTAGACCA	87.00	-N(5658)- - SCO1389 - - putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase
1524679	+	CAAGAATGGTCCGAACCA	82.01	-N(88)- - SCO1429 - - chitinase (putative secreted protein)
1524685	-	GGTCAATGGTTCGGACCA	84.00	-N(292)- - SCO1428 - - acyl-CoA dehydrogenase
1528646	+	CAATATTGGTGTGCGACCA	89.83	-N(175)- - SCO1433 - - hypothetical protein SC6D7.06c.
1528652	-	AACCAGTGGTTCGACACCA	86.00	-N(88)- - SCO1432 - - putative membrane protein.
1539552	-	GTCAATAGGTATGGACCA	82.00	-N(427)- - SCO1443 - - putative riboflavin synthase
2701155	+	GCCACTTGGTCCAGACCT	82.77	-N(69)- - SCO2503 - - putative chitinase precursor
2701176	+	GACGAAAGGTCTGGACCA	80.38	-N(48)- - SCO2503 - - putative chitinase precursor
2999771	+	GACCGGTGGTCTGGACAA	80.76	-N(90)- - SCO2753 - - putative LacI-family transcriptional regulator.
2999777	-	GCGGTCTTGTCCAGACCA	81.00	-N(129)- - SCO2752 - - putative oxidoreductase
3092623	-	GAGACTTGGTCTAGACCT	84.00	-N(72)- - SCO2833 - - secreted chitin binding protein.
3157678	+	GTCAACTGGTCTACACCA	90.31	-N(11)- - SCO2906 - - putative PTS transmembrane component
3157684	-	GTACACTGGTGTAGACCA	94.00	-N(136)- - SCO2905 - - hypothetical protein
3159192	+	TACAACAGGTCTACACCA	81.08	-N(19)- - SCO2907 - - putative PTS transmembrane component
3159209	+	ACTGAGTGGTGTAGACCA	94.65	-N(2)- - SCO2907 - - putative PTS transmembrane component
3203621	-	ACGAATTGGTTCAGACCT	83.00	-N(114)- - SCO2946 - - putative sugar transporter sugar-binding protein
3941161	+	CAGAACAGGTCTAAACCA	81.20	-N(72)- - SCO3563 - - acetyl-coenzyme A synthetase
4062291	-	CCGAATTGGACTAGACAA	82.00	-N(637)- - SCO3678 - - putative deoxynucleotide triphosphate deaminase
4701620	+	CTGCGGTGGTGTAGACCT	80.96	-N(33)- - SCO4286 - - putative solute-binding protein (putative secreted protein)
4810670	-	CCGCACTGGTCCAGACCG	83.00	-N(57)- - SCO4393 - - conserved hypothetical protein
4864652	+	CGTCATTGGCGTAAACCA	81.08	-N(11)- - SCO4442 - - hypothetical protein SCD6.20
5103047	-	TCCCACTGGTCTGTACCA	85.00	-N(57)- - SCO4671 - - putative lysR-family regulatory protein

5441751	+	ACAAGGTGGTCCAGACCA	91.65	-N(228)-	- SCO5004 - - hypothetical protein SCK15.06
5441757	-	TTCAATTGGTCTGGACCA	93.00	-N(79)-	- SCO5003 - - chitinase A precursor
5691982	+	CACCCTTGGTCTAGTCCA	85.17	-N(292)-	- SCO5232 - - putative sugar transporter sugar binding protein
5691988	-	CACCTATGGACTAGACCA	83.00	-N(152)-	- SCO5231 - - putative gntR-family transcriptional regulator
5692174	+	TCCTATTGGTCTGGGCCA	84.03	-N(100)-	- SCO5232 - - putative sugar transporter sugar binding protein
5692180	-	GGAGCTTGGCCCAGACCA	80.00	-N(344)-	- SCO5231 - - putative gntR-family transcriptional regulator
5692198	+	CCGTAAGTGGTCTACACCA	89.78	-N(76)-	- SCO5232 - - putative sugar transporter sugar binding protein
5692204	-	GACCAATGGTGTAGACCA	93.00	-N(368)-	- SCO5231 - - putative gntR-family transcriptional regulator
5698146	-	TTAGATTGGTCTAAACCA	92.00	-N(70)-	- SCO5236 - - putative glucosamine phosphate isomerase
5699808	+	GGTTAGTGGTCTAGTCCA	86.34	-N(305)-	- SCO5239 - - histidine kinase
5847192	-	CCACATTGGTCCAGACCT	87.00	-N(111)-	- SCO5376 - - chitinase C (putative secreted protein)
6081713	+	GTCCTTTGGTGGAAACCA	82.60	-N(7)-	- SCO5580 - - putative prokaryotic docking protein
6172753	+	CAGAATTGGTCTGGACCA	93.03	-N(33)-	- SCO5673 - - secreted chitinase
6394373	+	TTGAAGTTGTCTAGACCA	88.98	-N(138)-	- SCO5842 - - conserved hypothetical protein SC9B10.09
6394379	-	CAAGACTGGTCTAGACAA	88.00	-N(53)-	- SCO5841 - - phosphocarrier protein hpr
6394388	+	CCAGTCTTGTCTAGACCA	85.84	-N(123)-	- SCO5842 - - conserved hypothetical protein SC9B10.09
6394394	-	GGAAACTGGTCTAGACAA	88.00	-N(68)-	- SCO5841 - - phosphocarrier protein hpr
6524059	+	ACGCATTGGTCCAGACCT	86.13	-N(65)-	- SCO5954 - - chitinase (putative secreted protein)
6594664	+	ACGCAATGGTCTGGACCA	91.25	-N(244)-	- SCO6013 - - probable 1-deoxyxylulose-5-phosphate synthase
6594670	-	CCATTCTGGTCCAGACCA	90.00	-N(113)-	- SCO6012 - - putative secreted chitinase (putative secreted protein)
6594743	-	CCCGGGTGGTCCAGTCCA	80.00	-N(186)-	- SCO6012 - - putative secreted chitinase (putative secreted protein)
6622653	+	GATTCTTGGTATAGACCA	92.70	-N(362)-	- SCO6033 - - hypothetical protein SC1C3.21
6622659	-	CCTCCTTGGTCTATACCA	90.00	-N(42)-	- SCO6032 - - putative hydrolase
6622767	+	CCGCCTTGGTCTAGTCCA	85.63	-N(248)-	- SCO6033 - - hypothetical protein SC1C3.21
6622773	-	TCACAATGGACTAGACCA	88.00	-N(156)-	- SCO6032 - - putative hydrolase
6961928	-	CCTATTTTGTCTAGACCT	80.00	-N(118)-	- SCO6300 - - putative secreted hydrolase
6976834	+	ACGTATTGGTCTGAACCA	87.70	-N(0)-	- SCO6319 - - putative lipoprotein
6976840	-	CCCTCATGGTTCAGACCA	85.00	-N(400)-	- SCO6318 - - conserved hypothetical protein
7178544	+	CTTCAGTGGTCCAGACCA	94.22	-N(41)-	- SCO6486 - - putative transport associated protein
7846353	-	CCCAGCTGGTTTAGACCA	90.00	-N(81)-	- SCO7056 - - putative gntR-family transcriptional regulator
7859573	-	TCATATTGGTCCGGACCT	81.00	-N(63)-	- SCO7069 - - putative secreted hydrolase
8030532	+	CGACCCTTGTCTAGACCA	84.42	-N(138)-	- SCO7225 - - secreted chitinase
8030538	-	CGCTATTGGTCTAGACAA	88.00	-N(161)-	- SCO7224 - - putative integral membrane protein
8030645	+	TCGCTATGGTCTAGACCT	83.78	-N(25)-	- SCO7225 - - secreted chitinase
8030651	-	GACTTCAGGTCTAGACCA	82.00	-N(274)-	- SCO7224 - - putative integral membrane protein

8073122	+	TTGAACTGGTCTACACCC	80.71	-N(142)-	SCO7263	- - chitinase
8073139	+	CTTGACTGGTACAGACCA	90.51	-N(125)-	SCO7263	- - chitinase
8289550	+	GACGATAGGTAGAGACCA	81.36	-N(157)-	SCO7477	- - putative membrane protein

Table 2. Sites in the *Streptomyces coelicolor* genome that match the sequence motif represented by matrix 2083. The non-coding regions of the *S. coelicolor* genome were searched against this matrix to find matches to the corresponding sequence motif. The scanning method assigned a score (maximum 100) to each match site. The minimum score threshold was chosen as 80. The position of the match site is given as the chromosomal sequence coordinate. Descriptions of potential target genes immediately downstream of the motifs were taken from the *S. coelicolor* genome annotation. The distance in nucleotides between the 3' end of the motif and the predicted translational start codon is given in parentheses. The nine genes belonging to functional class 2.1.3 are shown in bold and other genes implicated in carbohydrate transport and catabolism are italicised.