

Position	Strand	Sequence	Score	Downstream ORF
739453	-	GCGGCGCGACAGGCGTAG	82.00	-N(1113)- - SCO0696 - - putative integral membrane protein.
1416427	+	GGCACACTACAGATGTAG	81.38	-N(39)- - SCO1339 - - hypothetical protein
1416433	-	GTGCTACTACATCTGTAG	80.00	-N(52)- - SCO1338 - - putative monooxygenase (putative secreted protein)
1416460	+	ACTGTACTACAGCCGTAG	88.49	-N(6)- - SCO1339 - - hypothetical protein
1416466	-	GTCTCACTACGGCTGTAG	82.00	-N(85)- - SCO1338 - - putative monooxygenase (putative secreted protein)
1846303	+	TAGCAGCTACGCGCGTTG	84.06	-N(114)- - SCO1726 - - putative ATPase
1846309	-	TCCAGTCAACGCGCGTAG	84.00	-N(60)- - SCO1725 - - putative secreted hydrolase
1898465	-	GCGCTGATACGCTGGTAG	81.00	-N(145)- - SCO1776 - - putative CTP synthetase
1898610	-	AGGATACGACGCACGTAG	84.00	-N(290)- - SCO1776 - - putative CTP synthetase
2044349	-	GGGACTCTACGCGCGTCA	81.00	-N(186)- - SCO1907 - - conserved hypothetical protein
2157951	+	CAGAATCTACGCGCGTCG	85.53	-N(21)- - SCO2015 - - putative nucleotidase
2157957	-	CAGTGGCGACGCGCGTAG	82.00	-N(184)- - SCO2014 - - pyruvate kinase
2319655	-	TGGCATCCACCCCGTAG	81.00	-N(205)- - SCO2156 - - putative cytochrome c oxidase subunit II
2325054	-	CCCTTTCTACTCTCGTCG	80.00	-N(330)- - SCO2161 - - conserved hypothetical protein
2550840	+	GCTCGGCTACGCACGGAG	81.57	-N(43)- - SCO2381 - - conserved hypothetical protein SC4A7.09
2735249	-	TACGCACTCCCCCGTAG	80.00	-N(95)- - SCO2536 - - probable transmembrane transport protein.
3171767	+	CGTGCTCAACGCGTGTAG	83.20	-N(333)- - SCO2921 - - putative membrane protein
3324569	+	AGCCCTCTACTCTCGTAG	91.17	-N(43)- - SCO3038 - - conserved hypothetical protein SCE34.20
3487523	+	GAGCCTCTACGCTCATAT	80.24	-N(14)- - SCO3183 - - conserved hypothetical protein SCE87.34
3610608	+	ACCGGGCTACACACCTAG	82.15	-N(250)- - SCO3261 - - putative ATP-binding protein
3739285	-	AAGGTTGTTGCCCCGTAG	80.00	-N(329)- - SCO3373 - - putative Clp-family ATP-binding protease
4128938	-	CGCCCCCTACCGGGGTAG	81.00	-N(169)- - SCO3755 - - putative ABC transport system ATP binding protein
4248192	+	GACGCGCCACGGGCGTAG	83.41	-N(57)- - SCO3863 - - putative secreted protein
4248198	-	GTGGACCTACGCCCGTGG	81.00	-N(117)- - SCO3862 - - putative membrane protein
4333768	+	GCGCTGCTACGACCGTAG	91.81	-N(13)- - SCO3938 - - putative thiamin biosynthesis protein ThiC
4333774	-	CATGAGCTACGGTCGTAG	88.00	-N(127)- - SCO3937 - - putative integrase /recombinase
4470870	+	CCAAGGCTACGCGCGTAG	92.01	-N(41)- - SCO4077 - - hypothetical protein SCD25.13
4470876	-	AAATTTCTACGCGCGTAG	94.00	-N(298)- - SCO4076 - - putative LSR2-like protein
4568729	+	GTCGCGCTACGCGCGTTG	85.65	-N(53)- - SCO4152 - - putative secreted 5'-nucleotidase
4568735	-	TAGAGTCAACGCGCGTAG	85.00	-N(144)- - SCO4151 - - putative acetyltransferase
4748873	+	GGGGGTCTACGCGCGGAG	87.80	-N(109)- - SCO4334 - - putative integral membrane protein
4748879	-	CGCTATCTCCGCGCGTAG	84.00	-N(83)- - SCO4333 - - putative integral membrane protein
5078030	+	GGGCCGGTACGCGCGTAG	89.32	-N(13)- - SCO4654 - - DNA-directed RNA polymerase beta chain

5319626	+	GGGGCGCTACGCGCGTAG	98.32	-N(60)- - SCO4886 - - putative sugar ABC transporter ATP-binding protein
5334528	+	GGCGTTCTACGCGCGTAG	98.68	-N(0)- - SCO4901 - - putative adenosine deaminase
5334534	-	TAATCCTACGCGCGTAG	91.00	-N(124)- - SCO4900 - - conserved hypothetical protein
5348225	+	GCATATCTACGCGCGTAG	93.20	-N(68)- - SCO4915 - - putative integral membrane protein
5348231	-	AGACCGCTACGCGCGTAG	94.00	-N(36)- - SCO4914 - - putative deoxyribose-phosphate aldolase
5351989	-	CACCATCTACGCGCGTAG	94.00	-N(41)- - SCO4917 - - putative purine nucleoside phosphorylase
5616832	-	GCGGGACGACGGACGTAG	80.00	-N(233)- - SCO5168 - - putative integral membrane protein
5760256	+	AAGACTCTACGCACGTAG	95.96	-N(109)- - SCO5287 - - putative MarR-family transcriptional regulator
5760262	-	CCGTTTCTACGTGCGTAG	93.00	-N(128)- - SCO5286 - - putative secreted hydrolase
5961828	+	GGCGATCTTCGCGCGTAG	86.61	-N(249)- - SCO5476 - - oligopeptide transport integral membrane protein
6081642	+	GGGACTCTACGCGCGTTG	88.67	-N(78)- - SCO5580 - - putative prokaryotic docking protein
6081648	-	CCGCATCAACGCGCGTAG	86.00	-N(65)- - SCO5579 - - putative transmembrane protein
6133093	-	CCCACCCTACGCACGTCG	82.00	-N(414)- - SCO5632 - - hypothetical protein SC6A9.35
7077713	+	CCTGCTCTACGGGCGTAG	95.49	-N(15)- - SCO6411 - - putative hydrolase
7542493	+	ACGCTTCTACGTTCTTAG	84.58	-N(48)- - SCO6785 - - probable fatty acid co-A racemase
7542499	-	CGTTCGCTAAGAACGTAG	81.00	-N(186)- - SCO6784 - - putative regulatory protein

Table 8. Sites in the *Streptomyces coelicolor* genome that match the sequence motif represented by matrix 1853. 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 five genes belonging to functional class 3.3.13 are shown in bold.