

Position	Strand	Sequence	Score	Downstream ORF
31472	-	AGAAGAGGACCGGACAGCATGCCGATTTGTGAC	80.00	-N(198)- - SCO0038 - - putative sigma factor
127415	+	CTGTACGGACCGATCATGGACCTCGTCTGTGAC	81.13	-N(123)- - SCO0135 - - conserved hypothetical protein SCJ21.22
140352	-	CGTCGTTGACCACCCAAGCCAGGTAGCCGGGAC	80.00	-N(53)- - SCO0149 - - hypothetical protein SCJ33.13c
282399	+	TGGCCTTGACAGGCCGTGAGCCCGAAACCTAAC	80.51	-N(59)- - SCO0290 - - probable solute-binding protein
333233	+	GAGCGCTGACACCACCGAGGAGATCACCGTGAC	83.77	-N(263)- - SCO0332 - - putative transcriptional regulator
482394	+	ACAACCTGACCTAACCCCTTAAGTGCCTTGAC	82.22	-N(29)- - SCO0461 - - putative hydrolase
482417	+	TGCGCTTGACAGGTTATCTCCGGAGTGCTGGAC	80.01	-N(6)- - SCO0461 - - putative hydrolase
533800	-	TCCTGTTGTCCGAGCCCAGGAGGTCGCCATGAC	81.00	-N(27)- - SCO0500 - - hypothetical protein SCF34.19c
851096	-	GCGGCATGACGGGGGAGCAGGACATGCGGGGAC	80.00	-N(22)- - SCO0803 - - putative RNA polymerase sigma factor.
1007229	-	CGACGGTGACAGGGAACGGCAGCGGCGATGAC	82.00	-N(27)- - SCO0957 - - putative oxidoreductase
1205710	-	CGTCCCTGACGGCATGTCCGAGGGGAGTGGGAC	80.00	-N(41)- - SCO1146 - - putative lipoprotein
1319640	+	GCAACATGACGGGGCCGGCTTCCCGTCCGGGAC	81.57	-N(214)- - SCO1247 - - conserved hypothetical protein
1404617	-	CGATCCTCACCCGCCGCTACCCGTGGCTATGAC	83.00	-N(51)- - SCO1328 - - hypothetical protein
1409816	-	TTCGGGTGACCCGTGCGAGGTCGGTCGTTGAC	82.00	-N(94)- - SCO1332 - - conserved hypothetical protein
1411450	+	AGGTGGTGACAGGCCACCGCCGGCGCCGTGAC	92.00	-N(164)- - SCO1334 - - hypothetical protein
1788546	-	ACCTGTTGCCGCGCCCCCTCGCCGCACTTGAC	80.00	-N(90)- - SCO1668 - - hypothetical protein SCI52.10c
1895944	-	ACGTCTGGCAACTCTCACCGGGCCGGTGTGAC	81.00	-N(145)- - SCO1774 - - putative regulatory protein
1906252	-	GGCCCCGACGGCACAACCCGGCCCGCGTGAC	80.00	-N(94)- - SCO1780 - - putative DNA repair protein
2133025	-	CGGGAATGCCCCACCCGCAAGGGTGTTGTGAC	82.00	-N(61)- - SCO1997 - - conserved hypothetical protein
2192173	-	CCCGGGTGACGGTTCGCCCGGGGTTCCGGTGAT	81.00	-N(33)- - SCO2042 - - putative membrane protein
2257128	+	GGGCCATGACGATCCTCCTGTCTCGTCTCCGTGAC	88.55	-N(126)- - SCO2100 - - putative transcriptional regulator
2270988	+	CCATCCTGACAGACCCGGACCGATGCCCTGAC	88.57	-N(123)- - SCO2113 - - putative bacterioferritin
2283558	-	GGCCATTGACGGTGTCCCGGGATAAGGTCTGAC	84.00	-N(55)- - SCO2122 - - conserved hypothetical protein
2324992	-	TCACTTTGACGATGTTTCATAGTGTCCGGTGTGAC	84.00	-N(268)- - SCO2161 - - conserved hypothetical protein
2517757	+	GTCCCGCGACGGCACTCGTCAAAGTCTGTGAC	81.18	-N(103)- - SCO2348 - - putative secreted protein
2517774	-	GGAGTGCGACGGGACTCGTCACAGGACTTTGAC	81.00	-N(381)- - SCO2347 - - putative integral membrane protein
2524293	+	GCGAACTGACCGGCCCGTGTGTTTCGTCCCTAAC	80.10	-N(16)- - SCO2356 - - putative membrane protein
2691737	-	CAGGCGCGACGGGCACCGCCCCGCGTGCCTGAC	82.00	-N(41)- - SCO2497 - - conserved hypothetical protein SCC82.03c
2789638	-	CCAACCTTGACCTGTGGCGGCGGTTTACGCGAC	80.00	-N(56)- - SCO2583 - - putative membrane protein.
2794370	-	CGGTGGTGACGGAGCGGGGCACGGCGCGGTGGG	80.00	-N(860)- - SCO2587 - - glutamate 5-kinase.
2857099	-	CCCGGGTGACGTCCGCTCACCTGCTCGGTGAC	83.00	-N(27)- - SCO2630 - - putative biotin synthase
2885449	+	CGCCCCTGACCGGCCGATCCCCCTACGCTGAG	81.58	-N(1)- - SCO2654 - - conserved hypothetical protein SC8E4A.24
2943033	+	CCCCCGTGACCCGCTGCGACCGGGTGCGTTGAA	84.48	-N(26)- - SCO2699 - - putative small membrane protein

2989172	+	TGCACGGGACACCGGCCCGGGGTTCTGTGAC	82.93	-N(71)-	SCO2743	- conserved hypothetical protein SCC57A.14
2989218	-	ACCCTGTGACAGGACGCGGACGTGACCCGGGAC	80.00	-N(73)-	SCO2742	- putative sigma factor
3062140	-	CGGCTGTGACGGAGCGGCCACGCGCTGTTTGGC	84.00	-N(179)-	SCO2804	- hypothetical protein
3084207	-	AGGTGTTGACGCGGAAGTTAACCGGCTGTTGAC	83.00	-N(147)-	SCO2823	- putative decarboxylase
3118340	-	TGGCGCTGACGGGCTCGGCGCCGCCCTGCTCAC	81.00	-N(129)-	SCO2862	- hypothetical protein SCE20.36c.
3260550	-	CGCCGCTGATTCAAGTGGGAGGCATGGCTGTGAC	81.00	-N(12)-	SCO2991	- hypothetical protein SCE50.19c
3314528	+	TGCTATGGACCCTGCCGACTGGCCACTTTGAC	83.75	-N(297)-	SCO3031	- hypothetical protein SCE34.12
3357001	+	GACCTGTGGCCGGCCTCACCGCGTGCAGTGAC	82.58	-N(128)-	SCO3064	- putative peptide transporter
3378662	-	GCCCGTTGACAGTGGCGCGGGAGGCCGAGAC	83.00	-N(149)-	SCO3084	- p-hydroxybenzoate hydroxylase
3393063	-	CGGTCATGACCGCTCGCCATCGCGGGCCCCGAC	80.00	-N(246)-	SCO3097	- putative secreted protein
3443180	-	CCCGGGTGACCGTTCCGGCCCCGTCCCTGTGAC	85.00	-N(204)-	SCO3144	- putative two-component system response regulator
3469571	-	CCCACCTGACGTAACCTCCCCACTGCCTTGAA	80.00	-N(112)-	SCO3166	- putative membrane transport protein
3715327	+	CTGAGCTGACGCACAGTCGCCTGCCTCTGTGAC	86.19	-N(244)-	SCO3356	- ECF sigma factor
3827420	+	CGGTGGTGACGGCGCGTGACGGGTTTCGTTGAC	90.93	-N(4)-	SCO3468	- transposase
3906828	-	TTGAACTGTCCTACTAGGGGTGGGTTTCCTTGAC	81.00	-N(27)-	SCO3538	- hypothetical protein
3918008	-	CCCGTTTGACACGGGGCGGGAGGTACCGTCAC	81.00	-N(123)-	SCO3543	- probable DNA topoisomerase I
4080615	+	ACGCCGTGGCCGTACCGTCCCGGGACGGTGAC	82.26	-N(2)-	SCO3703	- putative substrate binding protein
4135323	-	ATCCCGTGACGTAGCCATGTACGCGCCAATGAC	81.00	-N(50)-	SCO3762	- hypothetical protein SCH63.09c
4295722	+	TTGAGGTGAACTTCGGGCGCGGGGTTTTGAC	81.69	-N(460)-	SCO3901	- putative secreted penicillin-binding protein
4701575	+	GGGCGATGACATGTCTCACGGGGACAGTGTGGC	80.31	-N(63)-	SCO4286	- putative solute-binding protein (putative secreted protein)
4876692	+	CGGTCTTGACAGCGGAGGCGGGAAGCCGTTGAC	88.25	-N(82)-	SCO4455	- putative integral membrane protein
4943462	-	TGGCCTTGACGTGTCTCTCCCAAGGACATGAA	80.00	-N(9)-	SCO4522	- hypothetical protein SCD35.29c
5002402	-	CGTGCCTGACGTGACGCACCCCGATCACGTGAC	80.00	-N(149)-	SCO4580	- putative fumarylacetoacetase
5040537	-	ATGCGATGACGCAGCCACGACGCGGACATGAC	83.00	-N(166)-	SCO4616	- excisionase
5043814	-	CGGGTGTGACGCGCCCTCACAGTGTCCCGTCAC	81.00	-N(123)-	SCO4619	- putative integral membrane protein
5234822	+	ATCATGTGACAGGCATCACCGCTCAGGTGTGAC	85.10	-N(138)-	SCO4808	- succinyl-CoA synthetase beta chain
5297444	+	TCGTTGTGACCGGGCCCGCTCCGGGGCTGTGAG	90.57	-N(80)-	SCO4869	- methylmalonyl CoA mutase
5372973	-	CCTCTACGACGCGACGGCGCGGCCGTCTGTGAC	82.00	-N(154)-	SCO4937	- hypothetical protein
5388960	+	ACTGCATGACGGTTCCCTCCAGCGGGGGCATGAC	82.52	-N(87)-	SCO4952	- putative tetR-family transcriptional regulator
5395895	-	AACCCTTGACCGGCGGCCGCCCTGGCCTGAT	80.00	-N(73)-	SCO4960	- putative sigma factor
5462356	-	TCCGGGTGACACGACCCGCACGGCCGGCTTGAC	85.00	-N(406)-	SCO5027	- hypothetical protein SCK15.29c
5542028	+	CGCCTGTGACCGGAGGCATCGGTGTGCGGAGAC	81.28	-N(147)-	SCO5101	- conserved hypothetical protein
5674998	+	TGGGAATGACCGGCGGACGGCCACTGTTGTGCC	81.15	-N(188)-	SCO5216	- RNA polymerase sigma factor
5755914	-	GCGCGGTGACTCCCCGTACGCTGCTGCCCTGAC	82.00	-N(107)-	SCO5283	- putative two-component system response regulator

5922101	+	GGTGGCTGACGAGTGGTGCGTGGCGGGCATGAC	80.51	-N(330)- - SCO5444 - - putative glycogen phosphorylase
6285142	+	GTGTGGCGACAGGCGGGGTGCGGCTACGATGAC	80.82	-N(81)- - SCO5749 - - two-component regulator
6327614	-	GTTACGTGACGGTCCGCGTCCGGGGTTCGTTGCC	82.00	-N(141)- - SCO5790 - - hypothetical protein SC4H2.11c
6357173	+	GATTTCTGACGGTCCCGCTCGCAGGTATGTGCC	83.30	-N(13)- - SCO5813 - - hypothetical protein
6388970	+	CGGCACTGACAGCCACCGACCAGGACCCGTCAC	81.85	-N(213)- - SCO5837 - - zinc protease
6442743	-	GCCCCGCTGACGGCCCCCGTCCGGCGGCCCTGGC	80.00	-N(129)- - SCO5885 - - putative membrane protein
6501234	+	AGGTATTGACGGCGTTTCGCCGTTCTCTATGAT	84.83	-N(69)- - SCO5932 - - arabinofuranosidase
6532321	-	GTGTGATGCCGGTGCGGCCCTCGCCACTGTGAA	80.00	-N(105)- - SCO5961 - - putative cobalt transport protein
6535131	-	GTTAACTGAGCGGCACCCGCGGGTCCCGGTGAC	83.00	-N(118)- - SCO5964 - - putative membrane protein
6589522	+	ACTTCTTGACGTGCGACGTGTGGCCGAGTTGAC	87.57	-N(20)- - SCO6009 - - solute-binding protein
6603579	-	AGCCGGTGACAAGAGAGGACCAGGTGCGATGAC	85.00	-N(27)- - SCO6020 - - putative transcriptional regulator
6674814	+	TGGTGTTGACGTACCCCGCAAGTCGTGACTGAC	84.90	-N(220)- - SCO6080 - - putative dehydrogenase
6829706	+	ATGAAGTGACGCCGGCGTCCCGTGCGGTCTGAC	84.89	-N(278)- - SCO6215 - - hypothetical protein SC9G1.05
6848913	-	TCGTCATGACAGTCGTCGGTCCCGCCGTGAC	86.00	-N(72)- - SCO6226 - - hypothetical protein SC2H4.08c
6864163	+	GCAACATGACGACGACGAGCCGGAAGAATGTGAG	80.66	-N(130)- - SCO6241 - - hypothetical protein SCAH10.06
6898953	-	TGCGCATGACTGTTCCGAACAGGGCGGCGTGAA	80.00	-N(92)- - SCO6271 - - putative acyl-CoA carboxylase complex A subunit
6974845	-	GTCGGCTGACGCGGCTTAGAGCAGCTTTGTGAC	83.00	-N(779)- - SCO6313 - - putative integral membrane protein
7041192	-	CAGAGTTGACCTGCAATGTGAGGACAAAGTGAC	82.00	-N(138)- - SCO6377 - - putative lipoprotein
7045298	-	AGCCTGTGACCAGCCGAGCTGCGCCGCCGTGAC	88.00	-N(231)- - SCO6381 - - putative lipoprotein
7166531	+	GGGCGTGACACGCCCCGCCGGCGGCGCTGTGAC	80.20	-N(179)- - SCO6476 - - hypothetical protein SC9C7.12
7586368	-	CGGCTGTGGCCGGCCGTCGCACGGGGGAATGAC	80.00	-N(704)- - SCO6821 - - putative transferase.
7613224	-	CTCTGGTGGCAGCCCCGCCGGTGCCTTCTCTGAC	80.00	-N(417)- - SCO6840 - - hypothetical protein SC3D9.08c
7766234	-	TGGCGGTGACGACGGCCGGGGCCCGGGCGTGAC	84.00	-N(122)- - SCO6994 - - hypothetical protein SC8F11.20c.
7813892	+	ACGTTTTGAGTCGGCAGCCGCACGGCCATTGAC	81.74	-N(46)- - SCO7028 - - putative sugar-binding lipoprotein.
7880110	+	TCTCGGTGGCGGCCAGGCCCTGGGGGCGGTGAC	82.67	-N(85)- - SCO7092 - - putative secreted protein
7880164	-	CGGTAGAGACCGTGTAGGCCCTCCCGGTGTGAC	82.00	-N(154)- - SCO7091 - - hypothetical protein SC3A4.17c.
7890263	+	CAGAGCAGACCGCACAAAGCGCGGATCATGTGAC	80.34	-N(130)- - SCO7100 - - putative oxidoreductase
7893783	+	TCGCATTGACCCGGACAGTGACCAGCGCTGTGAC	93.80	-N(379)- - SCO7104 - - putative RNA polymerase sigma factor
7896326	-	CCTGGAAGACCCGGACGGTCCGTGCGAATGTGAC	80.00	-N(305)- - SCO7105 - - putative RNA polymerase sigma factor
7900259	-	TCCAGATGACCGGGGACCCCGGCACGGTGTGAC	89.00	-N(110)- - SCO7109 - - putative oxidoreductase
7902455	-	CTGTCCTGACCCGGTGC CGCATCGATCCGTGAC	89.00	-N(199)- - SCO7112 - - putative ECF-family RNA polymerase sigma factor
7908761	-	GACAACTGACTGCGTGTGCCACGCACTTGTGAC	83.00	-N(133)- - SCO7118 - - hypothetical protein SC4B10.19c
7918398	+	TCACCTAGACAGAACGCGAGTCCTTCGTGTGAC	80.83	-N(130)- - SCO7126 - - hypothetical protein SC4B10.27
7918474	-	CCCTCCTGACCCGGACACCGTGC CGCTCTGTGAC	93.00	-N(193)- - SCO7125 - - conserved hypothetical protein

7921856	+	GACCATTGACCGGGTGCCCGCGCGTTCTGTGAC	94.28	-N(208)- - SCO7130 - - conserved hypothetical protein
7928643	+	CCGCAATGACCGAGCGGTGCGGGCGCCTGTGAC	93.91	-N(66)- - SCO7136 - - conserved hypothetical protein
7928702	-	TCCTGGTGACAGGACACGCGCCCCGTCTGTGAC	91.00	-N(147)- - SCO7135 - - hypothetical protein SC4B10.36c
7932367	-	CCCTCTTGATGAGACGGCTCCCCGTTCTGTGAC	87.00	-N(83)- - SCO7137 - - putative regulatory protein
7936527	+	GAGGACCGACCGGCTTGCGGGGGCCCGTGTGAC	82.88	-N(113)- - SCO7143 - - putative transcriptional regulator
7944524	-	AGCGTTTGACCGGACGGGCGGCCGATGTGTGAC	90.00	-N(110)- - SCO7150 - - putative acetyltransferase
7949146	-	CTGCTCTGACCGGCGAAGCCGGACATCTGTGAC	91.00	-N(245)- - SCO7154 - - ketol-acid reductoisomerase
7981456	+	TCTATTCGACAAGCGACGGCTCGCCCCGTGTGAC	81.19	-N(128)- - SCO7181 - - putative branched amino acid transport system ATP-binding protein
7995404	+	AACCAAAGACCGGGCGGGAGCGCCACCTGTGAC	83.10	-N(192)- - SCO7192 - - putative sigma factor
8066389	-	ACCCGCGGACCGGCCCGCCCCGGCCTCTTGAC	84.00	-N(109)- - SCO7254 - - putative myo-inositol dehydrogenase
8195495	+	CCCCGATGGCCGCGCGGTGGCCCGCGTGTGAC	80.96	-N(361)- - SCO7384 - - putative transmembrane transport protein.
8372661	-	GCGCTTTGACACACATCGCCATCGGGCGTTGAC	84.00	-N(106)- - SCO7549 - - hypothetical protein
8461937	-	ACCCACTGACAGTGCCGTCCGGGTCGGGAAGAC	80.00	-N(97)- - SCO7633 - - putative secreted endo-beta-N-acetylglucosaminidase
8563083	+	CGTCCATGACGGCAGTCTAACGAAATCGTTGAC	81.53	-N(94)- - SCO7728 - - conserved hypothetical protein
8607517	-	TCGAGCTGACGCACCGGTCCAAGGCGCCGGGAC	81.00	-N(112)- - SCO7779 - - putative oxidoreductase
8608577	+	GGGGTGTGACGGGGTGTGGCGAGTCTCGTTGAC	88.05	-N(520)- - SCO7782 - - probable IS110 transposase

Table 5. Sites in the *Streptomyces coelicolor* genome that match the sequence motif represented by matrix 46. 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 10 genes belonging to functional class 6.2.1 are shown in bold.