

Position	Strand	Sequence	Score	Downstream ORF
11367	-	GCTGGTCAGTGGCGTGTGTGGGTGAGGA	82.00	-N(7)- - SCO0008 - - hypothetical protein
11616	-	ACGGAGCAGTGATCTTTAGGGGGGTGGA	86.00	-N(256)- - SCO0008 - - hypothetical protein
1327954	-	AATTGTCAGTGGCGGGCGGTTTACTGGA	85.00	-N(30)- - SCO1256 - - hypothetical protein 2SCG18.03c
1577632	-	TGTTGTCAGTGGCCTTTGCGAGAATGCA	83.00	-N(30)- - SCO1475 - - putative primosomal protein n'
1659087	-	GATTGTCAGTGCCCGGCGGAGAGTTGA	86.00	-N(516)- - SCO1550 - - putative small membrane protein
2107230	-	CGTTGTCAGTGCGGGTTCGTACGGTGGA	89.00	-N(31)- - SCO1966 - - ABC excision nuclease subunit B
2263276	-	GACTGTCAGTGCCAGGTGGCAGGCTGGA	82.00	-N(30)- - SCO2105 - - putative transcriptional regulatory protein
2649302	+	GTTAATCGGTTGAGGTAACGCGGGTGGGA	80.15	-N(40)- - SCO2463 - - putative ABC transporter
3328227	-	CATGTCCAGTATCAGGGGCATGCGTGGA	81.00	-N(18)- - SCO3040 - - putative secreted protein
3343007	-	GATTGTCAGTGGTGGGTGAGACGGTGGA	93.00	-N(79)- - SCO3050 - - hypothetical protein
3911591	-	CGTTGTCAGTGCCGCCCGCACAAATGGA	84.00	-N(134)- - SCO3541 - - putative DNA polymerase
4461113	+	CGATGTCAGTGCCGGGTGCCACAGTGGG	80.30	-N(58)- - SCO4069 - - putative integral membrane protein
4492827	-	CAGGACCATTGTCGGGTACGACCGTGGA	80.00	-N(116)- - SCO4093 - - putative integral membrane protein
4513626	-	CATTGTCAGTGGCGCAGTGCACATCGA	81.00	-N(35)- - SCO4113 - - conserved hypothetical protein
4862522	+	ATTTACCAGTGTCTGTGTACGGGTGGA	82.18	-N(92)- - SCO4440 - - hypothetical protein SCD6.18
5033880	+	GTTGACCAGTACGGAAGGGTCCACTGGA	81.24	-N(76)- - SCO4609 - - putative peptidase
5228044	+	GATTGTCAGTGGCGTGGTGCACCGTGGA	92.94	-N(13)- - SCO4803 - - conserved hypothetical protein
6155964	-	CGTGACAGTGAAGCCGTGGCCAGTCGA	83.00	-N(15)- - SCO5656 - - transcriptional regulatory protein
6301295	-	GATTGTCAGTGGCCGGTGCACGATGGA	87.00	-N(30)- - SCO5761 - - putative ATP-dependent DNA helicase
6388951	-	GGCTGTCAGTGCCGAGTCCACAATGGA	81.00	-N(71)- - SCO5836 - - DNA gyrase-like protein
6682703	+	GATTGTCAGTGGCCCGTGGCAGGGTGGA	92.41	-N(14)- - SCO6084 - - putative DNA polymerase
8655917	+	ACGGAGCAGTGATCTTTAGGGGGGTGGA	86.79	-N(203)- - SCO7839 - - hypothetical protein SC8E7.36.

Table 3. Sites in the *Streptomyces coelicolor* genome that match the sequence motif represented by matrix 2318. 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 six genes belonging to functional class 2.1.3 are shown in bold.