

| Position | Strand | Sequence | Score | Downstream ORF |
|----------------|--------|--------------------------------------|--------------|--|
| 745812 | - | ACTGTCTGTCATGCCAGTCCAGTTGG | 82.00 | -N(49)- - SCO0705 - - conserved hypothetical protein |
| 1419746 | - | TCCCGTTGTCAGTGGTCGGCGGTAGG | 84.00 | -N(68)- - SCO1343 - - uracil-DNA glycosylase (EC 3.2.2.-) |
| 1611274 | - | CCGCGTTGTCGGTGCGGTCAATTTAGG | 81.00 | -N(34)- - SCO1506 - - conserved ATP/GTP binding protein |
| 1659090 | - | ACGGATTGTCAGTGCCCGGCGCGAGA | 80.00 | -N(519)- - SCO1550 - - putative small membrane protein |
| 1768129 | + | GGTCGTTGTCAGTGCCCGGCCGTAAG | 84.63 | -N(130)- - SCO1653 - - conserved hypothetical protein SCI41.36 |
| 2089890 | - | CCGGAGTGTGCGGTCCGCGCCAGTAGG | 90.00 | -N(34)- - SCO1953 - - ABC excision nuclease subunit C |
| 2097400 | - | CGGCGTTGTCAGTGGCTCCCCCTAGT | 80.00 | -N(82)- - SCO1958 - - ABC excision nuclease subunit A |
| 2105001 | - | GGGCACTGTCAGTGCCCTGCGTAGG | 84.00 | -N(83)- - SCO1965 - - putative export associated protein |
| 2107233 | - | ACCCGTTGTCAGTGCGGGGTGCTACG | 83.00 | -N(34)- - SCO1966 - - ABC excision nuclease subunit B |
| 2215265 | - | TTTCGAGTGTGTCAGTCCCGAGGCATAGA | 81.00 | -N(89)- - SCO2064 - - DNA polymerase III alpha chain |
| 2348682 | + | CAGCCCTGTCTGCAAAAGACCTAGG | 83.36 | -N(32)- - SCO2183 - - putative pyruvate dehydrogenase E1 component |
| 2521115 | + | ACCCTCTGTACACCCCGGGCGTACG | 80.71 | -N(59)- - SCO2351 - - putative integral membrane protein |
| 3192907 | - | GCGCGTTGTCAGTGGTGCGCGTAGT | 80.00 | -N(10)- - SCO2939 - - hypothetical protein SCE56.03c |
| 3739213 | + | TCTGCATGTGCCCCCTCCACTAGG | 90.76 | -N(159)- - SCO3374 - - hypothetical proline-rich protein |
| 3739244 | - | ATGGAGTGTGTCAGTCCCGCGGGTAAG | 82.00 | -N(288)- - SCO3373 - - putative Clp-family ATP-binding protease |
| 4306806 | + | CTTATTTGTCAGTGCCGTGCCGTAGA | 82.43 | -N(25)- - SCO3911 - - putative replicative DNA helicase |
| 4925661 | - | CCCGGCTGTGTCAGTGGCTGCCACTAGG | 87.00 | -N(33)- - SCO4504 - - putative methyltransferase |
| 5006022 | + | CCTGCGTGTGTCATCCCGCAGGAGTAGG | 91.39 | -N(139)- - SCO4584 - - putative membrane protein |
| 5329505 | - | GGCCATTGTCAGTCCCCTGCGGTAGC | 82.00 | -N(83)- - SCO4895 - - putative ECF sigma factor |
| 5495931 | - | CCGGATTGTCGGACCCGCGGTTACG | 81.00 | -N(34)- - SCO5056 - - putative exoribonuclease large subunit |
| 5937493 | - | GGGCAGTGTGTCAGTGCCAAACCGTAGG | 83.00 | -N(35)- - SCO5451 - - putative ABC transporter |
| 6306607 | + | GCCCATTTGTCAGTGGCAGGCATTAGC | 80.01 | -N(21)- - SCO5769 - - recombinase A |
| 6884090 | + | GCCGATTGTCAGACCCCGCCCGTAGA | 86.95 | -N(22)- - SCO6262 - - putative helicase |
| 8535370 | + | ACCGATTGTCACTGCTTCGGGGTAAG | 81.36 | -N(136)- - SCO7699 - - putative nucleotide-binding protein |

Table 4. Sites in the *Streptomyces coelicolor* genome that match the sequence motif represented by matrix 1744. 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 three genes belonging to functional class 1.2.1 are shown in bold.