

Table 5: Classification of *Streptomyces coelicolor* genes with a putative SFBS $TGTCAGTN_{\{14,15\}}TNG^{m4}$, $TGTCAGTGN_{\{9,12\}}ANG^{m5}$, and/or $TGTCAGTN_{\{12,14\}}TNG^{m6}$ in their upstream region (similar to *recA* promoter). Genes are grouped according to the classification scheme for *S. coelicolor* available on http://www.sanger.ac.uk/Projects/S_coelicolor/classwise.html. Genes without $m4$, $m5$ or $m6$ label own to a possible cluster (with previously cited gene) and are cited because they may be related to DNA damage. Therefore, those genes DO NOT correspond to the classification!!!!

0.0.0	Unknown function, no known homologs (1049)		
SCO0031 ^{m5}	SCJ4.12c	hypothetical protein	tgtcagtgctcgttcatatg
SCO0268 ^{m4m5m6}	SCF1.10	hypothetical protein	tgtcagtggcgtgggcaatggttg
SCO0558 ^{m4m5}	SCF73.05c	hypothetical protein SCF73.05c	tgtcagtggcggatgcgaggccttcg
SCO0679 ^{m4m6}	SCF91.39	hypothetical protein SCF91.39.	tgtcagtgccggaacacgtccttg
SCO1256 ^{m4m6}	2SCG18.03c	hypothetical protein 2SCG18.03c	tgtcagtggcggcgggtttactgg
SCO1291 ^{m5}	SCBAC36F5.02	hypothetical protein SCBAC36F5.02	tgtcagtggcgcctctacg
SCO1334 ^{m4m5m6}	2SCG61.16	hypothetical protein	tgtcagtgcttgcccctaggccttg
SCO2205 ^{m4m6}	SC3H12.13c	hypothetical protein SC3H12.13c	tgtcagtggcggcagtaaaatag
SCO2211 ^{m4m5m6}	SC10B7.06	hypothetical protein SC10B7.06	tgtcagtggcccgtgcgagggtgg
SCO2738 ^{m4m6}	SCC57A.09c	hypothetical protein SCC57A.09c.	tgtcagtccccaccggtaccgtcg
SCO2791 ^{m5m6}	SCC105.22c	hypothetical protein SCC105.22c	tgtcagtggccaatccccgtagg
SCO2975 ^{m5}	SCE50.03	hypothetical protein SCE50.03	tgtcagtggcaggtgcgaggatg
SCO3050 ^{m4m5m6}	SCBAC19G2.05c	hypothetical protein	tgtcagtggcgggtgagacgggtgg
SCO4611 ^{m5}	SCD39.11	hypothetical protein SCD39.11	tgtcagtggcggcctgcatcatg
SCO6674 ^{m4m5m6}	SC5A7.24c	hypothetical protein SC5A7.24c	tgtcagtggcggcggcaagctgg
SCO6735 ^{m4m5m6}	SC5F2A.18	hypothetical protein	tgtcagtggcggcccgtacgggtgg
SCO7634 ^{m4m6}	SC10F4.07	hypothetical protein SC10F4.07	tgtcagtgggtgatggcagcctgg
SCO7723 ^{m5}	SC8D11.14c	hypothetical protein SC8D11.14c	tgtcagtgggtcccggcagg
SCO7787 ^{m5}	SC5E9.35c	hypothetical protein	tgtcagtgttcatggcggacg
0.0.2	Conserved in organism other than Escherichia coli (1322)		
SCO0180 ^{m6}	SCJ1.29c	conserved hypothetical protein SCJ1.29c	tgtcagtgcccccgctgccgtcg

SCO0563 ^{m5} SCF73.10c SCO1653 ^{m5} SCI41.36 SCO1731 ^{m4m5m6} SCI11.20c	conserved hypothetical protein SCF73.10c conserved hypothetical protein SCI41.36 conserved hypothetical protein	tgtcagtgggacctcgtacg tgtcagtgcccgccgtaagg tgtcagtggcggttgtcacg tgtcagtggcgggtgccaccctgg tgtcagtggggctcgggcacgatg tgtcagtggcgcagtgcaactatcg tgtcagtggcgtgggtgcaccgtgg tgtcagtggttactgcaaccatg tgtcagtggcaacaattgtcagg
SCO2204 ^{m5} SC3H12.12 SCO4113 ^{m4m6} SCD17A.05c SCO4803 ^{m4m6} SCD63A.14 SCO6120 ^{m5} SC9B2.07 SCO7098 ^{m5} SC3A4.24c	hypothetical protein SC3H12.12 conserved hypothetical protein conserved hypothetical protein hypothetical protein SC9B2.07 conserved hypothetical protein SC3A4.24c.	
1.2.1	Chromosome replication (8)	
SCO2064 ^{m4} SC4G6.33c dnaE SCO3878 ^{m4m6} dnaN SCH18.15c SCO3877 SCO3876 recF SCH18.13c	DNA polymerase III alpha chain DNA polymerase III, beta chain putative 6-phosphogluconate dehydrogenase DNA replication protein	tgtcagtcccaggcatagacttcg tgtcagtgggggtgcgtcagactgg
1.5.0	Transport/binding proteins (520)	
SCO1965 ^{m5} SCC54.25c SCO2373 ^{m4m6} tcmA SCC8A.31c SC SCO4963 ^{m5} 2SCK31.23 SCO5451 ^{m4m5m6} SC3D11.08c SCO6805 ^{m5} SC1A2.14	putative export associated protein tetracenomycin C efflux protein. tetracenomycin C resistance putative ABC transporter ATP-binding protein putative ABC transporter putative integral membrane efflux protein.	tgtcagtgccctgcgtagg tgtcagtactgactcgtgaattgg tgtcagtggctgcagcctaacg tgtcagtggcaaacctaggctcg tgtcagtggcccgtggcatg
1.6.1	Adaptations, atypical conditions (25)	
SCO4505 ^{m5} scoF2 SCD35.12c	cold shock protein	tgtcagtggctgccactagg
2.1.1	Degradation of DNA (13)	
SCO6341 ^{m5m6} SC3A7.09	putative exonuclease	tgtcagtgcccccggtaggttg
2.2.3	DNA - replication, repair, restr./modific'n (85)	
SCO1343 ^{m5} ung 2SCG61.25c SCO1380 ^{m4m6} SC10A9.22c	uracil-DNA glycosylase (EC 3.2.2.-) putative DNA damage inducible protein, N-terminal region similar to SW:DINP_ECOLI (EMBL:D83536) Escherichia coli DNA-damage-inducible protein P DinP.	tgtcagtggctcggcggtagg tgtcagtggcgtagggcagcatcg

SCO1475 ^{m5} SCL6.32c	putative primosomal protein n', similar to SW:PRIA_ECOLI (EMBL:M33293) Escherichia coli primosomal protein n' (replication factor Y) PriA	tgtcagtggcctttgcgagaatg
SCO1966 ^{m4m5m6} SCC54.26c uvrB SC	ABC excision nuclease subunit B excinuclease ABC subunit B (fragment), highly similar to SW:UVRB_BACSU (EMBL:AF017113) Bacillus subtilis excinuclease ABC subunit B (DinA protein) UvrB or DinA or Uvr aa; fasta scores: opt: 2591 Z-score: 2687.6 bits: 507.5 E(): 4.3e-142; 63.667% identity in 600 aa overlap	tgtcagtgcgggggtcgtacgggtgg
SCO2003 ^{m4m5m6} SC7H2.17c polA	DNA polymerase I	tgtcagtggcacgtggcaggatcg
SCO3351 ^{m4m5} SCE94.02	putative DNA repair protein, similar to many eg. SW:RADA_ECOLI RadA, DNA repair protein (mechanism unknown) from Escherichia coli (460 aa) fasta scores; opt: 1218, z-score: 1309.3, E(): 0, (41.4% identity in 452 aa overlap)	tgtcagtgggggcggttacggttcg
SCO3434 ^{m4m6} SCE36.01 SCE9.41	putative DNA polymerase I hypothetical protein	tgtcagtcccgctgcgacactcg
SCO3541 ^{m4m5m6} SCH5.03c	putative DNA polymerase, len: 401 aa; limited region of similarity to many DNA polymerase III subunits e.g. SW:DP3X_SALTY DNA polymerase III subunits gamma and tau from Salmonella typhimurium (642 aa) fasta scores; opt: 327, z-score: 338.5, E(): 1.5e-11, (32.1% identity in 246 aa overlap)	tgtcagtgccgccccgcacaatgg
SCO3540 SCH5.02c slpD	proteinase (putative secreted protein).	
SCO3874 ^{m5} gyrB SCH18.11c	DNA gyrase subunit B	tgtcagtggtagcggttagaatg
SCO3873 gyrA SCH18.10c	DNA gyrase subunit A	
SCO5761 ^{m4m5m6} SC7C7.16c	putative ATP-dependent DNA helicase, len: 1690 aa; highly similar to e.g. LHR_ECOLI probable atp-dependent helicase lhr (EC 3.6.1.-) (1538 aa), fasta scores; opt: 2361 z-score: 3018.1 E(): 0, 48.6% identity in 1435 aa overlap	tgtcagtggccgggtgcacgatgg
SCO5760	DNA glycosylase involved in DNA repair	

SCO5802 ^{m4m6} SC4H2.23	putative ATP-dependent helicase, probable ATP-dependent helicase, len: 664 aa; similar to e.g. DING_ECOLI P27296 probable ATP-dependent helicase dinG (716 aa), fasta scores opt: 272 z-score: 409.8 E(): 1.3e-15, 26.5% identity in 686 aa overlap	tgtcagtcccgggccgtaggggtgg
SCO5815 ^{m4m5m6}	putative ATP-dependent DNA helicase, similar in N-terminal half to many e.g. RECQ_ECOLIP1 5043 atp-dependent dna helicase recq (607 aa), fasta score s; opt: 546 z-score: 615.9 E(): 4.1e-27, 35.9% identity in 362 aa overlap	tgtcagtgccatcggggttgcattgg
SCO5817	putative DNA hydrolase with mutT domain	
SCO5836 ^{m4m5m6} SC9B10.03c	DNA gyrase-like protein	tgtcagtgccgcagtcacacatgg
SCO6084 ^{m4m5m6} SCBAC1A6.08	putative DNA polymerase, len: 244 aa; similar to SW:DP3E_ECOLI (EMBL:X04027) Escherichia coli DNA polymerase III, epsilon chain (EC 2.7.7.7) DnaQ, 243 aa; fasta scores: opt: 137 z-score: 167.9 E(): 0.089; 26.2% identity in 206 aa overlap,	tgtcagtggcccgtgcgagggtgg
2.2.7	Phospholipids (14)	
SCO6445 ^{m4m5m6} SC9B5.12	putative inositol monophosphatase	tgtcagtggcgcggtgctctcatgg
3.2.6	Heme, porphyrin (16)	
SCO4469 ^{m4m5m6} hemL SCD65.12	glutamate-1-semialdehyde 2,1-aminomutase	tgtcagtgacctccccacgggtcg
SCO4470 SCD65.13	putative phosphoglycerate mutase	
SCO5859 ^{m4m5m6} hemH SC9B10.26	ferrochelatase	tgtcagtgccgggtggcaggatcg
4.1.6	Gram +ve membrane (836)	
SCO4069 ^{m4m6} SCD25.05	putative integral membrane protein	tgtcagtgccgggtgccacagtgg
SCO4811 ^{m5} SCD63A.22	putative integral membrane protein	tgtcagtgcggcggactcacg
SCO6538 ^{m6} SC5C7.23	putative integral membrane protein	tgtcagtctcacaggggtgttcg
SCO6794 ^{m4m5} SC1A2.03 cvnA7	putative membrane protein.	tgtcagtgtccgtcgggacgtag
SCO7763 ^{m4m5m6} SC5E9.11	putative membrane protein	tgtcagtgcctcctgtcagcatgg
4.2.2	Ribosomal proteins - synthesis, modification (62)	
SCO3906 ^{m4m6} SCH24.28 rpsF	putative 30S ribosomal protein S6	tgtcagtgggtcctggtttactcg
SCO3907 SCH24.29 ssb	putative single-strand DNA-binding protein	

SCO3908 SCH24.30 rpsR	putative 30S ribosomal protein S18	
SCO3909 SCH24.31 rplI	50S ribosomal protein L9	
6.3.2	AraC (33)	
SCO0287 ^{m6} SCF85.15	putative regulatory protein	tgtcagtggcgcaccgtcactcg
6.3.6	LysR (38)	
SCO3919 ^{m6} SCQ11.02c abaB	putative lysR-family transcriptional regulator	tgtcagtgtccaatcaccgtag
6.5.0	Others (237)	
SCO2105 ^{m4m5m6} SC2C1A.01c SC4A10	putative transcriptional regulatory protein (fragment). hypothetical protein	tgtcagtgccaggtggcaggctgg
7.0.0	Not classified (included putative assignments) (565)	
SCO0278 ^{m5} SCF85.06 MutT	domain containing protein	tgtcagtggcccctgccaggatg
SCO3000 ^{m5} SCE33.02c	putative phosphatase	tgtcagtggcgccgggtacg
	Not known according to classification	
SCP1.106 ^{m4m6}		tgtcagtcgtccgtcctcgcctcg
SCP1.204c ^{m4m5m6}		tgtcagtgggggttcgtaggggtgg