# Appendix I

## Appendix 1 List of genes of chromomycin biosynthetic cluster from gene bank accession number KC249518.1*

| | | | Closest match to genes of other *Streptomyces* | |
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| **ORF** | **Name of the gene** | **Homology with *Streptomyces griseus* subsp. *griseus*** | **Organism** | **Homology** |
| *sfl*UIII | NDP-4-ketoreductase (*cmm*UIII) | Identities = 157/257 (61%),<br>Positives = 178/257 (69%),<br>Gaps = 4/257 (1%) | *Streptomyces avermitilis* | Identities = 170/272(63%),<br>Positives = 194/272(71%)<br>Gaps = 0/272 (0%) |
| | | | *Streptomyces tsukubensis* | Identities = 177/271(65%),<br>Positives = 200/271(73%)<br>Gaps = 2/271 (0%) |
| *Sfl*C | NDP-C methyl transferase (*cmm*C) | Identities = 317/408 (77%),<br>Positives = 346/408 (84%),<br>Gaps = 0/408 (0%) | *Streptomyces tsukubensis* | Identities = 324/408(79%),<br>Positives = 351/408 (86%)<br>Gaps = 0/408 (0%) |
| | | | *Allokutzneria albata* | Identities = 261/403(65%),<br>Positives = 312/403 (77%)<br>Gaps = 0/403(0%) |
| *Sfl*X | UV repair protein (SfrX) | Identities = 538/701 (76%)<br>Positives = 602/701 (85%)<br>Gaps = 0/701 (0%) | *Streptomyces tsukubensis* | Identities = 541/699 (77%)<br>Positives = 607/699(86%)<br>Gaps = 0/699 (0%) |
| | | | *Streptosporangium canum* | Identities = 524/699 (75%)<br>Positives = 584/699(83%)<br>Gaps = 0/699 (0%) |
| *Sfl*RII | Transcriptional regulator (*cmm*RII) | Identities = 142/185 (76%)<br>Positives = 154/185 (83%)<br>Gaps = 0/185 (0%) | *Streptomyces tsukubensis* | Identities = 140/176 (80%),<br>Positives = 152/176 (86%),<br>Gaps = 0/176 (0%) |
| | | | *Chloroflexi bacterium* 54-19 | Identities = 94/173 (54%),<br>Positives = 119/173 (68%),<br>Gaps = 0/173 (0%) |
| *SfrA* | ATP binding domain | Identities = 238/310 (77%)<br>Positives = 261/310 (84%)<br>Gaps = 0/310 (0%) | *Streptomyces tsukubensis* | Identities = 245/314 (63%),<br>Positives = 240/314(76%),<br>Gaps = 3/314 (0%) |
| | | | *Amycolatopsis balhimycina* | Identities = 198/310 (79%),<br>Positives = 268/310(86%), |

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| | | | | Gaps = 0/310 (0%) |
| *Sfl*B | Membrane protein (SfrB) | Identities = 195/228 (86%)<br>Positives = 212/228 (92%)<br>Gaps = 1/228 (0%) | *Streptomyces tsukubensis* | Identities = 194/227 (85%)<br>Positives = 211/227(92%)<br>Gaps = 1/227 (0%) |
| | | | *Actinomadura madurae* | Identities = 140/248 (56%)<br>Positives = 182/248 (73%)<br>Gaps = 2/248 (0%) |
| *Sfl*LI | Acyl coA ligase (*cmm*LI) | Identities = 275/406 (68%)<br>Positives = 319/406 (78%)<br>Gaps = 0/406 (0%) | *Streptomyces tsukubensis* | Identities = 285/408(70%),<br>Positives = 329/408(80%),<br>Gaps = 0/408 (0%) |
| | | | *Allokutzneria albata* | Identities = 155/409(70%),<br>Positives = 219/409(80%),<br>Gaps = 0/409 (0%) |
| *Sfl*WI | Side chain ketoreductase (*cmm*WI) | Identities = 244/320 (76%)<br>Positives = 270/320 (84%)<br>Gaps = 0/320 (0%) | *Streptomyces tsukubensis* | Identities = 240/320(75%),<br>Positives = 267/320(83%),<br>Gaps = 0/320 (0%) |
| | | | *Streptomyces argillaceus* | Identities = 203/318 (75%),<br>Positives = 244/318 (83%),<br>Gaps = 4/318 (1%) |
| *Sfl*OIV | Oxygenase (*cmm*OIV) | Identities = 372/512 (73%)<br>Positives = 402/512 (78%)<br>Gaps = 7/512 (1%) | *Streptomyces tsukubensis* | Identities = 372/512(73%),<br>Positives = 409/512 (79%),<br>Gaps = 7/512 (1%) |
| | | | *Streptomyces* spp. NRRL F-5630 | Identities = 289/494(59%),<br>Positives = 334/494(67%),<br>Gaps = 13/494 (2%) |
| *Sfl*G | Glycosyl transferase (*cmm*G) | Identities = 295/382 (77%)<br>Positives = 328/382 (85%)<br>Gaps = 1/382(0%) | *Streptomyces tsukubensis* | Identities = 303/391(77%),<br>Positives = 336/391(85%),<br>Gaps = 5/391 (1%) |
| | | | *Streptomyces* spp. MspMP-M5 | Identities = 158/404(39%),<br>Positives = 216/404(53%),<br>Gaps = 30/404 (7%) |
| *Sfl*MI | O-methyltransferase (*cmm*MI) | Identities = 256/357 (72%)<br>Positives = 285/357 (79%) | *Streptomyces tsukubensis* | Identities = 255/358(71%),<br>Positives = 283/358(79%),<br>Gaps = 14/358 (3%) |
| | | | *Streptomyces* spp. | Identities = 173/341(51%), |

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| | | Gaps = 13/357 (3%) | MJM8645 | Positives = 225/341(65%),<br>Gaps = 6/341 (1%) |
| *Sfl*UI | NDP-4-ketoreductase (*cmm*UI) | Identities = 164/249 (66%)<br>Positives = 190/249 (76%)<br>Gaps = 1/249 (0%) | *Streptomyces tsukubensis* | Identities = 167/246(68%),<br>Positives = 193/246(78%),<br>Gaps = 0/246 (0%) |
| | | | *Kibdelosporangium phytohabitans* | Identities = 136/242(56%),<br>Positives = 171/242(70%),<br>Gaps = 0/242 (0%) |
| *sfl*MII | C- Methyl transferase (*cmm*MII) | Identities = 266/374 (71%)<br>Positives = 301/374 (80%)<br>Gaps = 4/374 (1%) | *Streptomyces tsukubensis* | Identities = 255/328 (56%),<br>Positives = 286/328 (72%),<br>Gaps = 3/328 (0%) |
| | | | *Streptomyces* spp. NRRL F-5630 | Identities = 179/327(55%),<br>Positives = 235/327 (71%),<br>Gaps = 1/327(0%) |
| *Sfl*RI | Transcriptional activator (*cmm*R1) | Identities = 166/229 (72%)<br>Positives = 189/229 (82%)<br>Gaps = 1/229 (0%) | *Streptomyces tsukubensis* | Identities = 169/229(73%),<br>Positives = 190/229 (82%),<br>Gaps = 0/229 (0%) |
| | | | *Streptomyces* spp. LaPpAH-108 | Identities = 130/215(60%),<br>Positives = 167/215 (77%),<br>Gaps = 0/215 (0%) |
| *sfl*MIII | O - methyl transferase (*cmm*MIII) | Identities = 193/248 (77%),<br>Positives = 217/248 (87%),<br>Gaps = 0/248 (0%) | *Streptomyces tsukubensis* | Identities = 193/249(78%),<br>Positives = 216/249 (86%),<br>Gaps = 0/249 (0%) |
| | | | *Micromonospora carbonacea* | Identities = 158/248(62%),<br>Positives = 185/248 (75%),<br>Gaps = 3/248 (1%) |
| *Sfl*D | NDP - Glucose synthase (*cmm*D) | Identities = 243/346 (70%),<br>Positives = 286/346 (82%),<br>Gaps = 0/346 (0%) | *Streptomyces tsukubensis* | Identities = 242/346 (70%),<br>Positives = 285/346 (82%),<br>Gaps = 0/346 (0%) |
| | | | *Streptomyces niveus* | Identities = 201/345(58%),<br>Positives = 257/345 (74%),<br>Gaps = 0/345 (0%) |

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| *Sfl*E | NDP 4-6 Dehydratase (*cmm*E) | Identities = 243/326 (75%),<br>Positives = 273/326 (83%),<br>Gaps = 0/326 (0%) | *Streptomyces tsukubensis* | Identities = 246/326 (75%),<br>Positives = 274/326 (84%),<br>Gaps = 0/326 (0%) |
| | | | *Streptomyces rimosus* | Identities = 226/321(70%),<br>Positives = 264/321 (82%),<br>Gaps = 1/321(0%) |
| *Sfl*P | Ketosynthase (*cmm*P) | Identities = 294/340 (86%),<br>Positives = 306/340 (90%),<br>Gaps = 0/340 (3%) | *Streptomyces tsukubensis* | Identities = 314/429 (73%), Positives = 336/429(78%), Gaps = 14/429 (3%) |
| | | | *Actinomadura echinospora* | Identities = 291/427(68%),<br>Positives = 324/427 (75%),<br>Gaps = 14/427 (3%) |
| *Sfl*K | Ketosynthase-chain length factor (*cmm*K) | Identities = 307/402 (76%),<br>Positives = 341/402 (84%),<br>Gaps = 0/402 (0%) | *Streptomyces tsukubensis* | Identities = 302/402(75%),<br>Positives = 339/402 (84%),<br>Gaps = 0/402 (0%) |
| | | | *Streptomyces ravidus* | Identities = 275/401(69%),<br>Positives = 320/401 (79%),<br>Gaps = 3/401 (0%) |
| *Sfl*X | Cyclase | Identities = 97/133 (73%),<br>Positives = 111/133 (83%),<br>Gaps = 0/133 (0%) | *Streptomyces tsukubensis* | Identities = 101/141(72%),<br>Positives = 114/141 (80%),<br>Gaps = 0/141 (0%) |
| | | | *Actinomadura formosensis* | Identities = 81/134(66%),<br>Positives = 94/134 (70%),<br>Gaps = 0/134 (0%) |
| *SflI* | Oxygenase | Identities = 277/418 (66%),<br>Positives = 307/418 (73%),<br>Gaps = 3/418 (0%) | *Streptomyces tsukubensis* | Identities = 296/408(73%),<br>Positives = 327/408 (80%),<br>Gaps = 7/408 (1%) |
| | | | *Streptomyces misionensis* | Identities = 252/407(62%),<br>Positives = 302/407 (74%),<br>Gaps = 5/407 (1%) |
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| *SflUII* | NDP- 4 Ketoreductase (*cmm*UII) | Identities = 163/247 (65%),<br>Positives = 187/247 (75%),<br>Gaps = 7/247 (2%) | *Streptomyces tsukubensis* | Identities = 161/248 (65%), Positives = 187/248 (75%), Gaps = 7/248 (2%) |
|  |  |  | *Kibdelosporangium phytohabitans* | Identities = 143/245 (58%), Positives = 177/245 (72%), Gaps = 3/245 (1%) |
| *SflW* | NDP-3 Ketoreductase (*cmm*W) | Identities = 202/320 (63%),<br>Positives = 237/320 (74%),<br>Gaps = 9/320 (2%) | *Streptomyces tsukubensis* | Identities = 201/326 (62%), Positives = 238/326 (73%), Gaps = 19/326 (5%) |
|  |  |  | *Micromonospora auratinigra* | Identities = 173/315 (55%), Positives = 211/315 (66%), Gaps = 1/315 (0%) |
| *Sfl*V | NDP 2-3-Dehydratase (*cmm*V) | Identities = 222/335 (66%),<br>Positives = 253/335 (75%),<br>Gaps = 5/335 (1%) | *Streptomyces tsukubensis* | Identities = 228/335 (68%),<br>Positives = 258/335 (77%),<br>Gaps = 5/335 (1%) |
|  |  |  | *Streptomyces* spp. TA-0256 | Identities = 194/364(53%),<br>Positives = 235/364 (64%),<br>Gaps = 28/364 (7%) |
| *Sfl*S | Acyl Carrier Protein (*cmm*S) | Identities = 52/81 (64%),<br>Positives = 63/81 (77%),<br>Gaps = 0/81 (0%) | *Streptomyces tsukubensis* | Identities = 50/76 (66%),<br>Positives = 59/76 (77%),<br>Gaps = 0/76 (0%) |
|  |  |  | *Amycolatopsis lurida* NRRL 2430 | Identities = 47/79 (59%),<br>Positives = 61/79 (77%),<br>Gaps = 0/79 (0%) |
| *Sfl*WI | Ketoreductase (*cmm*WI) | Identities = 162/253 (64%),<br>Positives = 181/253 (71%),<br>Gaps = 8/253 (3%) | *Streptomyces tsukubensis* | Identities = 162/257 (63%), Positives = 180/257 (70%), Gaps = 7/257 (2%) |
|  |  |  | *Microbispora sp. NBRC 110460* | Identities = 139/247 (56%), Positives = 166/247 (67%), Gaps = 5/257 (2%) |
| *Sfl*Y | Cyclase (*cmm*Y) | Identities = 196/258 (76%),<br>Positives = 221/258 (85%),<br>Gaps = 0/253 (0%) | *Streptomyces tsukubensis* | Identities = 197/258(76%)<br>Positives = 224/258 (86%)<br>Gaps = 0/258 (0%) |
|  |  |  | *Streptomyces* spp. CS113 | Identities = 185/257(72%)<br>Positives = 211/257 (82%)<br>Gaps = 2/257 (0%) |

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| * Gene Bank Accession Number – Sequence of KC249518.1 is compared to genome sequences of other bacteria available at NCBI. |  |  |  |  |