**Table S2.** Comparison against C-1027 Lidamycin synthetic gene clusters

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C-1027 (Query) | | |  | | TFH56 (subject) | | | Anti-smash results | Protein BLAST coverage | Protein BLAST Identity |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | RASTtk annotation | | Location in pTFSG1 (bp) | strand |
| hypothetical protein | 15468 - 14920 | - | | hypothetical protein | | 105639 - 106187 | + | Additional biosynthetic gene | 100% | 99% |
| 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) | 16703 - 15639 | - | | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) | | 104403 - 015182 | + | Other gene | 24% | 96% |
| 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) | | 105247 - 105468 | + | 45% | 97% |
| hypothetical protein | 17257 - 16841 | - | | possible replication initiation protein | | 103881 - 104267 | + | Other gene | 92% | 98% |
| putative DNA primase/ helicase | 18960 - 17431 | - | | putative DNA primase/helicase | | 102148 - 103677 | + | Other gene | 100% | 99% |
| Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | 20093 - 21469 | + | | Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | | 101064 - 996430 | - | Additional biosynthetic gene | 100% | 97% |
| Excinuclease ABC subunit A paralog of unknown function | 23902 - 21575 | - | | Excinuclease ABC subunit A paralog of unknown function | | 97204 - 99531 | + | Transport-related gene | 100% | 97% |
| hypothetical protein | 25350 - 23983 | - | | hypothetical protein | | 95756 - 97123 | + | Transport-related gene | 100% | 97% |
| FIG022199: FAD-binding protein | 26836 - 25352 | - | | FIG022199: FAD-binding protein | | 94564 - 95754 | + | Core bio synthetic genes | 80% | 99% |
| Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) | 27013 - 28080 | + | | Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) | | 94092 - 93025 | - | Additianl biosynthetic gene | 100% | 98% |
| Continued | | | | | | | | | | |

**Table S2.** (continued)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C-1027 (Query) | | |  | | TFH56 (subject) | | | Anti-smash results | Protein BLAST coverage | Protein BLAST Identity |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | RASTtk annotation | | Location in pTFSG1 (bp) | strand |
| hypothetical protein | 28644 - 28213 | - | | hypothetical protein | | 92463 - 92894 | + | Core biosynthetic genes | 100% | 99% |
| Aminotransferase, DegT/DnrJ/EryC1/StrS family | 29923 - 28691 | - | | Aminotransferase, DegT/DnrJ/EryC1/StrS family | | 91184 - 92416 | + | Core biosynthetic genes | 100% | 99% |
| dTDP-3-amino-3,4,6-trideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.234); dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235) | 30654 - 29920 | - | | dTDP-3-amino-3,4,6-trideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.234); dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235) | | 90453 - 91187 | + | Additional biosynthetic gene | 100% | 99% |
| SAM-dependent methyltransferase | 31925 - 30654 | - | | SAM-dependent methyltransferase | | 89182 - 90453 | + | Additional biosynthetic gene | 100% | 99% |
| Epoxide hydrolase (EC 3.3.2.9) | 33189 - 32032 | - | | Epoxide hydrolase (EC 3.3.2.9) | | 87918 - 89075 | + | Core biosynthetic gene | 100% | 99% |
| Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | 33925 - 33263 | - | | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) @ Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) | | 87524 - 87844 | + | Additional biosynthetic gene | 48% | 97% |
| Anthranilate synthase, aminase component (EC 4.1.3.27) | 35403 - 33922 | - | | Anthranilate synthase, aminase component (EC 4.1.3.27) | | 85703 - 87184 | + | Additional biosynthetic gene | 100% | 99% |
| Coenzyme F390 synthetase | 36874 - 35420 | - | | Coenzyme F390 synthetase | | 84231 - 85685 | + | Core biosynthetic gene | 100% | 99% |
| iron-sulfur flavoprotein | 37542 - 36871 | - | | iron-sulfur flavoprotein | | 83563 - 84234 | + | Other gene | 100% | 99% |
| Continued | | | | | | | | | | |

**Table S2.** (continued)

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C-1027 (Query) | | |  | | TFH56 (subject) | | | Anti-smash results | Protein BLAST coverage | Protein BLAST Identity | |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | RASTtk annotation | | Location in pTFSG1 (bp) | strand |
| hypothetical protein | 38884 - 37562 | - | | hypothetical protein | | 82221 - 83543 | + | Additional biosynthetic gene | 100% | 99% | |
| dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) | 39561 - 38983 | - | | dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) | | 81544 - 82122 | + | Core biosynthetic genes | 100% | 99% | |
| hypothetical protein | 39812 - 41167 | + | | hypothetical protein | | 81293 - 79938 | - | Additional biosynthetic gene | 100% | 100% | |
| Glycosyltransferase IroB | 41211 - 42590 | + | | hypothetical protein | | 79894 - 78515 | - | Core biosynthetic gene | 100% | 98% | |
| dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | 42587 - 43585 | + | | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | | 78518 - 77520 | - | Core biosynthetic gene | 100% | 99% | |
| Uncharacterized MFS-type transporter | 43629 - 45194 | + | | Uncharacterized MFS-type transporter | | 77477 - 75912 | - | Transport-related gene | 100% | 99% | |
| Phenylacetate-coenzyme A ligase (EC 6.2.1.30) | 45277 - 46587 | + | | Phenylacetate-coenzyme A ligase (EC 6.2.1.30) | | 75829 - 74519 | - | Core biosynthetic gene | 100% | 99% | |
| hypothetical protein | 46592 - 46765 | + | | hypothetical protein | | 74514 - 74341 | - | Other gene | 100% | 96% | |
| 4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.14.9) | 46806 - 48389 | + | | 4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.14.9) | | 74300 - 72717 | - | Other gene | 100% | 99% | |
| Hydrolase, alpha/beta fold family | 49299 - 48463 | - | | Hydrolase, alpha/beta fold family | | 71807 - 72643 | + | Core biosynthetic gene | 100% | 100% | |
| hypothetical protein | 50027 - 49521 | - | | hypothetical protein | | 71079 - 71585 | + | Other gene | 100% | 100% | |
| hypothetical protein | 50170 - 51495 | + | | hypothetical protein | | 70936 - 69611 | - | Transport-related gene | 100% | 99% | |
| hypothetical protein | 51564 - 52943 | + | | hypothetical protein | | 69542 - 68163 | - | Core biosynthetic gene | 100% | 99% | |
| Continued | | | | | | | | | | |

**Table S2.** (continued)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C-1027 (Query) | | |  | | | TFH56 (subject) | | | | Anti-smash results | Protein BLAST coverage | | | Protein BLAST Identity |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | | RASTtk annotation | | | Location in pTFSG1 (bp) | strand |
| phosphopantetheine-binding | 52988 - 53269 | + | | | phosphopantetheine-binding | | | 68118 - 67837 | - | Core biosynthetic gene | | 100% | | 99% |
| Tyrosine ammonia-lyase (EC 4.3.1.23) @ Tyrosine 2,3-aminomutase (EC 5.4.3.6) | 54991 - 53372 | - | | | Tyrosine ammonia-lyase (EC 4.3.1.23) @ Tyrosine 2,3-aminomutase (EC 5.4.3.6) | | | 66115 - 67734 | + | Other gene | | 100% | | 99% |
| Putative cytochrome P450 hydroxylase | 61228 - 62484 | + | | | Putative cytochrome P450 hydroxylase | | | 59878 - 58622 | - | Core biosynthetic gene | | 100% | | 99% |
| Acyl-CoA dehydrogenase, type 2-like | 63718 - 62537 | - | | | Acyl-CoA dehydrogenase, type 2-like | | | 57388 - 58569 | + | Additional biosynthetic gene | | 100% | | 99% |
| hypothetical protein | 64022 - 64357 | + | | | hypothetical protein | | | 57085 - 56750 | - | Other gene | | 100% | | 95% |
| alkylhydroperoxidase like protein, AhpD family | 64354 - 65394 | + | | | alkylhydroperoxidase like protein, AhpD family | | | 56753 - 55713 | - | Other gene | | 100% | | 98% |
| Putative oxidoreductase | 66345 - 65425 | - | | | Putative oxidoreductase | | | 54762 - 55682 | + | Additional biosynthetic gene | | 100% | | 99% |
| hypothetical protein | 66921 - 66370 | - | | | hypothetical protein | | | 54186 - 54737 | + | Additional biosynthetic gene | | 100% | | 99% |
| hypothetical protein | 67130 - 66963 | - | | | hypothetical protein | | | 53977 - 54144 | + | Other gene | | 100% | | 100% |
| hypothetical protein | 67888 - 67250 | - | | | hypothetical protein | | | 53240 - 53857 | + | Core biosynthetic gene | | 96% | | 98% |
| hypothetical protein | 68235 - 69383 | + | | | hypothetical protein | | | 52872 - 51724 | - | Other gene | | 100% | | 100% |
| Continued | | | | | | | | | | | | | | | | |
| **Table S2.** (continued) | | | | | | | | | | | | | | |
| C-1027 (Query) | | | |  | | | TFH56 (subject) | | | Anti-smash results | | | Protein BLAST coverage | Protein BLAST Identity | |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | | RASTtk annotation | | | Location in pTFSG1 (bp) | strand |
|  |  |  | | |  | | |  |  |  | |  | |  |
| Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) | 69838 - 70884 | + | | | Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase) | | | 51269 - 50223 | - | Other gene | | 100% | | 99% |
| hypothetical protein | 71734 - 70931 | - | | | hypothetical protein | | | 49373 - 50176 | + | Other gene | | 100% | | 99% |
| 4-hydroxybenzoyl-CoA thioesterase family active site | 72307 - 71837 | - | | | 4-hydroxybenzoyl-CoA thioesterase family active site | | | 48800 - 49270 | + | Other gene | | 100% | | 100% |
| Glucose-methanol-choline (GMC) oxidoreductase:NAD binding site | 74099 - 72444 | - | | | Glucose-methanol-choline (GMC) oxidoreductase:NAD binding site | | | 47008 - 48663 | + | Additional biosynthetic gene | | 100% | | 100% |
| hypothetical protein | 74686 - 74096 | - | | | hypothetical protein | | | 46421 - 47011 | + | Other gene | | 100% | | 99% |
| hypothetical protein | 74944 - 76023 | + | | | hypothetical protein | | | 46163 - 45084 | - | Other gene | | 100% | | 99% |
| antismash: AraC family transcriptional regulator | 76049 - 76903 | + | | | · | | | · | · | Regulatory gene | | · | | · |
| Cytochrome P450 | 78140 - 76791 | - | | | Cytochrome P450 | | | 42966 - 44651 | + | Core biosynthetic gene | | 91% | | 99% |
| Cytochrome P450 | 78140 - 76791 | - | | | Cytochrome P450 | | | 42966 - 44651 | + | Core biosynthetic gene | | 91% | | 99% |
| Putative oxidoreductase | 78685 - 78137 | - | | | Putative oxidoreductase | | | 42421 - 42969 | + | Additional biosynthetic gene | | 100% | | 99% |
| Continued | | | | | | | | | | | | | | | | |

**Table S2.** (continued)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| C-1027 (Query) | | |  | | TFH56 (subject) | | | Anti-smash results | Protein BLAST coverage | Protein BLAST Identity |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | RASTtk annotation | | Location in pTFSG1 (bp) | strand |
| Cytochrome P450 | 78140 - 76791 | - | | Cytochrome P450 | | 42966 - 44651 | + | Core biosynthetic gene | 91% | 99% |
| Putative oxidoreductase | 78685 - 78137 | - | | Putative oxidoreductase | | 42421 - 42969 | + | Additional biosynthetic gene | 100% | 99% |
| Polyketide synthase | 84630 - 78811 | - | | Polyketide synthase | | 36475 - 42294 | + | Core biosynthetic gene | 100% | 99% |
| hypothetical protein | 85751 - 84627 | - | | hypothetical protein | | 35354 - 36478 | + | Other gene | 100% | 98% |
| ASPIC/UnbV domain protein | 87682 - 85754 | - | | ASPIC/UnbV domain protein | | 33423 - 35351 | + | Other gene | 100% | 99% |
| UnbL | 88659 - 87679 | - | | UnbL | | 32446 - 33426 | + | Other gene | 100% | 100% |
| UnbL | 89789 - 88761 | - | | UnbL | | 31316 - 32344 | + | Other gene | 100% | 99% |
| Transcriptional regulator, HxlR family | 90369 - 89926 | - | | Transcriptional regulator, HxlR family | | 30736 - 31179 | + | Regulatory gene | 100% | 100% |
| hypothetical protein | 90516 - 91079 | + | | hypothetical protein | | 30588 - 30025 | - | Other gene | 100% | 98% |
| hypothetical protein | 91117 - 91545 | + | | hypothetical protein | | 30020 - 29559 | - | Other gene | 100% | 96% |
| hypothetical protein | 92822 - 91635 | - | | hypothetical protein | | 28289 - 29476 | + | Other gene | 100% | 99% |
| putative DNA primase /helicase | 94113 - 95537 | + | | putative DNA primase/helicase | | 26995 - 25571 | - | Other gene | 100% | 98% |
| Continued | | | | | | | | | | | |
| **Table S2.** (continued) | | | | | | | | | | |
| C-1027 (Query) | | |  | | TFH56 (subject) | | | Anti-smash results | Protein BLAST coverage | Protein BLAST Identity |
| RASTtk annotation | Location in SGLP 1 (bp) | strand | | RASTtk annotation | | Location in pTFSG1 (bp) | strand |
| possible replication initiation protein | 95908 - 95495 | - | | possible replication initiation protein | | 25200 - 25613 | + | Other gene | 100% | 99% |
| hypothetical protein | 96566 - 97144 | + | | hypothetical protein | | 24542 - 23964 | - | Additional biosynthetic gene | 100% | 99% |
| possible replication initiation protein | 97566 - 97168 | - | | possible replication initiation protein | | 23544 - 23942 | + | Other gene | 100% | 98% |
| putative DNA primase /helicase | 99098 - 97563 | - | | putative DNA primase/helicase | | 22012 - 23547 | + | Other gene | 100% | 99% |