Comparative analysis of secondary metabolite biosynthetic gene clusters and associated P450s in the genera *Streptomyces* and *Mycobacterium*

by

Martin Tjatji

Thesis submitted in fulfilment of the requirements of the degree

Doctor of Health Sciences in Biomedical Technology

Department of Health Sciences

Central University of Technology, Free State

06 August 2019

Supervisor: Prof Khajamohiddin Syed

Co-supervisor: Prof Samson Sitheni Mashele

DECLARATION

I, **MARTIN TJATJI** (SOUTH AFRICAN ID NUMBER:), hereby certify that the thesis submitted by me for the degree DOCTOR OF HEALTH SCIENCES IN BIOMEDICAL TECHNOLOGY is my own independent work; and complies with the Code of Academic Integrity, as well as other relevant policies, procedures, rules and regulations of the Central University of Technology (Free State). I hereby declare that this research project has not previously been submitted to any university or faculty for the attainment of any qualification. I further waive copyright of the dissertation in favour of the Central University of Technology (Free State). I also state that this work is carried out in collaboration with my colleague, Mrs Senate Moshoeshoe.

M.P.Tjatji

18 July 2019

Martin Tjatji

Date

ABSTRACT

Species belonging to the genera *Streptomyces* and *Mycobacterium* are well known for their contrasting lifestyle and impact on humans. *Streptomyces* species produce two-thirds of antibiotics, secondary metabolites, used in the world, whereas mycobacterial species are well known to be the deadliest human pathogens, although a few are environmentally useful. Mycobacterial species also produce secondary metabolites that play a role in pathogenesis. It is a well known fact that genes involved in the synthesis of secondary metabolites form clusters known as biosynthetic gene clusters (BGCs). To date, comparative analysis of secondary metabolite BGCs in species belonging to these two genera has not been reported. Among the genes involved in synthesis of secondary metabolites, cytochrome P450 monooxygenases (CYPs/P450s) play a key role, as these enzymes contribute to the diversity of secondary metabolites owing to their chemo-, stereo- and regio-specific oxidation of substrates. Despite this importance of P450s in the synthesis of secondary metabolites, to date, identification of P450s involved in the synthesis of secondary metabolites in species belonging to these two genera has not been reported. Thus, this study is aimed at addressing these two research gaps by conducting comprehensive comparative analysis of secondary metabolite BGCs and associated P450s in the species belonging to the genera *Streptomyces* (48 species) and *Mycobacterium* (60 species).

Genome-wide analysis revealed the presence of a large and diverse number of secondary metabolite BGCs in *Streptomyces* species compared to mycobacteria species. In total 1 461 secondary metabolite BGCs belonging to 159 types were found in 48 *Streptomyces* species compared to 898 secondary metabolite BGCs belonging to only 18 types found in 60 mycobacterial species. Among *Streptomyces* species, *S. griseochromogenes* has the highest number of secondary metabolite BGCs (49) and *Streptomyces* sp. 4F has the lowest number of

secondary metabolite BGCs (19) in their genomes. *Mycobacterium marinum* has the highest number of secondary metabolite BGCs (29) and two strains of *M. leprae* have the lowest number of secondary metabolite BGCs (five each) in their genomes. Quite a big difference was observed with respect to the types of secondary metabolite BGCs between *Streptomyces* and mycobacterial species. Among 159 types of secondary metabolite BGCs found in *Streptomyces* species, only 13 types of BGCs contributed 80% to the total percentage of BGCs, suggesting that the secondary metabolites produced by these BGCs were highly important in *Streptomyces* species' physiology. The secondary metabolite BGC, terpene, was dominant, followed by siderophores, nonribosomal peptides (Nrps) and Type 1 polyketides (T1pks) in *Streptomyces* species. Among 18 types of secondary metabolite BGCs identified in mycobacterial species, Nrps was the dominant secondary metabolite BGC, followed by 'other', T1pks and T1pks-Nrps. Despite the presence of 15 common types of secondary metabolite BGCs between the genera *Streptomyces* and *Mycobacterium*, large differences were observed in terms of the number of BGCs, indicating that the selective enrichment of particular secondary metabolite BGCs in both genera is possibly due to the different lifestyle, as discussed in the subsequent section.

Comparative analysis of P450s that are part of secondary metabolite BGCs revealed the presence of a large number of diverse P450s as part of these secondary metabolite BGCs in *Streptomyces*, compared to *Mycobacterium*. Not all secondary metabolite BGCs found in *Streptomyces* and *Mycobacterium* have P450s. Among 1 461 *Streptomyces* species, only 554 secondary metabolite BGCs were found to have P450s, whereas in mycobacterial species, among 898 only 204 secondary metabolite BGCs have P450s. Overall, 554 and 204 P450s were found to be part of secondary metabolite BGCs in respectively *Streptomyces* and mycobacterial species. Among 88 P450 families that are part of different secondary metabolite BGCs, some P450 families are highly dominant in *Streptomyces* species, indicating their key role in the synthesis of different secondary metabolites. These P450 families were found to be the same that are highly populated in *Streptomyces* species, with some exceptions. This strongly indicates that these P450 families provide an advantage to *Streptomyces* species by generating diverse secondary metabolites, thus letting these species thrive in nature. Mycobacterial species' secondary metabolite BGC P450 profiles are contrasted with *Streptomyces* species, where the dominant P450 families are not necessarily dominant as part of secondary metabolite BGCs. Ten P450 families, namely CYP51, CYP123, CYP125, CYP130, CYP135, CYP136, CYP138, CYP140, CYP144 and CYP1128, are conserved and highly populated across 60 mycobacterial species. However, none of these P450 families is dominant as part of different secondary metabolite BGCs. The CYP139 P450 family was found to be the dominant family as part of secondary metabolite BGCs. Although eight P450 families, namely CYP124, CYP121, CYP105, CYP125, CYP102, CYP147, CYP136 and CYP161, which are part of secondary metabolite BGCs, were commonly found between the genera *Streptomyces* and *Mycobacterium*, the number of P450s in these families was found to be different.

Based on the above data, it is clear that different lifestyles influenced the gene content in *Streptomyces* and *Mycobacterium*, hence differences in the number and type of secondary metabolite BGCs and P450s that are associated with secondary metabolite BGCs were observed. The saprophytic and symbiotic lifestyle of *Streptomyces* resulted in the highest diversity of secondary metabolite BGCs and P450s, thus helping these organisms to generate chemically diverse secondary metabolites to adapt to different ecological niches. For this reason, *Streptomyces* species have been found to have large and diverse secondary metabolite BGCs and P450s compared to mycobacterial species. Based on the evidence presented in this study, the researcher hereby proposes that lifestyle or ecological niches play a key role in the evolution of secondary metabolite BGCs and associated P450s in species belonging to the genera *Streptomyces* and *Mycobacterium*.

DEDICATION

This work is dedicated to my family: my wife, Maria, and my children, Lebogang and Gausitwe. I would also like to extend the dedication to my parents, Rebecca and Samuel Tjatji, and my sisters, Emily and Damaris.

ACKNOWLEDGEMENT

I would first like to acknowledge the presence of God, for the life and light that were provided to me throughout my life. His protection and guidance is significant and I have grown from strength to strength in my life. I would like to acknowledge that God’s timing is the best.

Secondly, I would like to express my sincere and deepest gratitude to the following people:

1. Prof Khajamohiddin Syed, for his supervision, tolerance and guiding me throughout my study. Thank you so much for your patience and understanding. May God bless you abundantly throughout your great career.

2. Prof Samson Sitheni Mashele, for your co-supervision of my study. You co-operation and understanding in this regard are gratefully acknowledged.

3. Dr Patrick Govender, for mentoring me. It was through your advice that I was encouraged to continue with my studies. Thank you so much for the encouragement.

4. The National Research Foundation, my employer, for allowing me time and the relevant resources to pursue my study.

5. My departmental colleagues, the P450 group, for your continued support during my studies.

RESEARCH OUTPUTS

Title: Similarities, variations, and evolution of cytochrome P450s in *Streptomyces* versus *Mycobacterium*

Authorship: Equal first authorship

Journal: Scientific Reports

Article number: 9:3962

Year: 2019

DOI: 10.1038/s41598-019-40646-y

Journal ISSN number: 2045-2322

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

ABBREVIATIONS

BCG	Bacillus Calmette-Guerin
BGC	Biosynthetic gene cluster
BLAST	Basic Local Alighment Search Tool
CYPs/P450s	Cytochrome P450 monooxygenases
DNA	Deoxyribonucleic acid
KEGG	Kyoto Encyclopedia of Genes and Genomes
MAC	*Mycobacterium avium* complex
MCAC	*Mycobacterium chelonae-abscessus* complex
MCL	Mycobacteria causing leprosy
MTBC	*Mycobacterium tuberculosis* complex
NAD	Nicotinamide adenine dinucleotide
Nrps	Nonribosomal peptides
NTM	Nontuberculous mycobacteria
Pks	Polyketides
RH	Organic substrate with P450 as the catalyst
ROH	Hydroxylated organic product.

CHAPTER 1: INTRODUCTION

1.1. Introduction

Cytochrome P450 monooxygenases (CYPs/P450s) are heme thiolate enzymes that are ubiquitously present in species belonging to all biological kingdoms (Nelson, 2018) and even in non-living entities such as viruses (Lamb *et al.*, 2009). P450s are well-known for their chemo-, regio- and stereo-specific oxidation of substrates with immense catalytic diversity (Sono *et al.*, 1996, Bernhardt, 2006). P450s have been found to be involved in the synthesis of secondary metabolites (Podust and Sherman, 2012, Greule *et al.*, 2018). Secondary metabolites are natural products that are widely used in human and veterinary medicine, agriculture and manufacturing, and are known to mediate a variety of microbe-host and microbe-microbe interactions (Cimermancic *et al.*, 2014, Mthethwa *et al.*, 2018). The genes that produce these metabolites have been found to present as a clusters known as secondary metabolite biosynthesis gene clusters (BGCs) (Medema *et al.*, 2015). According to Medema *et al.* (Medema *et al.*, 2015), a BGC can be defined as a physically clustered group of two or more genes in a particular genome that together encode a biosynthetic pathway for the production of a specialised metabolite (including its chemical variants). Bacteria, fungi and plants are known to possess different types of BGCs producing a variety of secondary metabolites that are beneficial to humans. Among the genes that are part of a BGC, P450s play a key role in contributing to the diversity of secondary metabolites owing to their regio- and stereo-specific oxidation (Greule *et al.*, 2018).

The bacterial phylum *Actinobacteria* encompasses organisms that are adapted to different lifestyles; these may be pathogens (e.g. *Corynebacterium*, *Mycobacterium*, *Nocardia*, *Tropheryma*, and *Propionibacterium*), soil inhabitants (*Streptomyces*), plant commensals (*Leifsonia*), or gastrointestinal commensals (*Bifidobacterium*) (Ventura *et al*., 2007). Organisms belonging to the genera *Mycobacterium* and *Streptomyces* are of particular interest, as the former are well known human pathogens (do Nascimento *et al*., 2016) and the latter are well known for producing most of the antibiotics used in the world (de Lima Procópio *et al*., 2012, Hasani *et al*., 2014).

1.2. Problem statement and rationale of the study

It is well established that the lifestyle of organisms influences their gene content. The genera *Mycobacterium* and *Streptomyces* both belong to the phylum *Actinobacteria*, yet species in these genera are well known for their contrasting lifestyles, despite some similarities (Scherr and Nguyen, 2009). *Mycobacterium tuberculosis* H37Rv, the causative agent of tuberculosis (TB), has been found to produce different secondary metabolites that play a key role in pathogenesis (Quadri, 2014). The secondary metabolites produced by *Streptomyces* are currently used for treating human diseases (de Lima Procópio *et al*., 2012). However, to date, comprehensive comparative analysis of different secondary metabolites' BGCs in both genera, *Mycobacterium* and *Streptomyces*, has not been reported. Furthermore, despite knowing that P450s play a key role in synthesis and attributing the diversity to secondary metabolites (Greule *et al*., 2018), to date, P450s involved in the synthesis of different secondary metabolites in both genera, *Mycobacterium* and *Streptomyces*, are not known. Thus, this study is aimed at addressing both research gaps.

1.3. Aims and objectives of the study

1.3.1. Aim of the study

To perform comparative analysis of secondary metabolite biosynthetic gene clusters and associated P450s in the genera *Mycobacterium* and *Streptomyces.*

1.3.2. Objectives of the study

(i) Genome data-mining and identification of secondary metabolite biosynthetic gene clusters in Mycobacterial species.

(ii) Genome data-mining and identification of secondary metabolite biosynthetic gene clusters in *Streptomyces* species.

(iii) Annotation and comparative analysis of secondary metabolite biosynthetic gene clusters in species belonging to the genera *Mycobacterium* and *Streptomyces*.

(iv) Identification and annotation of P450s involved in the synthesis of secondary metabolites in species belonging to the genera *Mycobacterium* and *Streptomyces*.

(v) Comparative analysis of P450s involved in synthesis of secondary metabolites in species belonging to the genera *Mycobacterium* and *Streptomyces*.

References

BERNHARDT, R. 2006. Cytochromes P450 as versatile biocatalysts. *J Biotechnol,* 124**,** 128-45.

CIMERMANCIC, P., MEDEMA, M. H., CLAESEN, J., KURITA, K., WIELAND BROWN, L. C., MAVROMMATIS, K., PATI, A., GODFREY, P. A., KOEHRSEN, M., CLARDY, J., BIRREN, B. W., TAKANO, E., SALI, A., LININGTON, R. G. & FISCHBACH, M. A. 2014. Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters. *Cell,* 158**,** 412-421.

DE LIMA PROCÓPIO, R. E., DA SILVA, I. R., MARTINS, M. K., DE AZEVEDO, J. L. & DE ARAÚJO, J. M. 2012. Antibiotics produced by *Streptomyces*. *The Brazilian Journal of Infectious Diseases,* 16**,** 466-471.

DO NASCIMENTO, L. V., SAAD, C. F. A., BURDICK, A. E., CAMACHO, I. D., SCOLLARD, D. M., MOTTA, R. N., DA SILVA, G. A. R. & COSENZA, P. P. 2016. *Mycobacteria*. *Tropical Dermatology: Second Edition.* Elsevier Inc.

GREULE, A., STOK, J. E., DE VOSS, J. J. & CRYLE, M. J. 2018. Unrivalled diversity: the many roles and reactions of bacterial cytochromes P450 in secondary metabolism. *Nat Prod Rep,* 35**,** 757-791.

HASANI, A., KARIMINIK, A. & ISSAZADEH, K. 2014. *Streptomycetes*: characteristics and their antimicrobial activities. *Int J Adv Biol Biom Res,* 2**,** 63-75.

LAMB, D. C., LEI, L., WARRILOW, A. G., LEPESHEVA, G. I., MULLINS, J. G., WATERMAN, M. R. & KELLY, S. L. 2009. The first virally encoded cytochrome p450. *J Virol,* 83**,** 8266-9.

MEDEMA, M. H., KOTTMANN, R., YILMAZ, P., CUMMINGS, M., BIGGINS, J. B., BLIN, K., DE BRUIJN, I., CHOOI, Y. H., CLAESEN, J., COATES, R. C., CRUZ-MORALES,

P., DUDDELA, S., DUSTERHUS, S., EDWARDS, D. J., FEWER, D. P., GARG, N., GEIGER, C., GOMEZ-ESCRIBANO, J. P., GREULE, A., HADJITHOMAS, M., HAINES, A. S., HELFRICH, E. J., HILLWIG, M. L., ISHIDA, K., JONES, A. C., JONES, C. S., JUNGMANN, K., KEGLER, C., KIM, H. U., KOTTER, P., KRUG, D., MASSCHELEIN, J., MELNIK, A. V., MANTOVANI, S. M., MONROE, E. A., MOORE, M., MOSS, N., NUTZMANN, H. W., PAN, G., PATI, A., PETRAS, D., REEN, F. J., ROSCONI, F., RUI, Z., TIAN, Z., TOBIAS, N. J., TSUNEMATSU, Y., WIEMANN, P., WYCKOFF, E., YAN, X., YIM, G., YU, F., XIE, Y., AIGLE, B., APEL, A. K., BALIBAR, C. J., BALSKUS, E. P., BARONA-GOMEZ, F., BECHTHOLD, A., BODE, H. B., BORRISS, R., BRADY, S. F., BRAKHAGE, A. A., CAFFREY, P., CHENG, Y. Q., CLARDY, J., COX, R. J., DE MOT, R., DONADIO, S., DONIA, M. S., VAN DER DONK, W. A., DORRESTEIN, P. C., DOYLE, S., DRIESSEN, A. J., EHLING-SCHULZ, M., ENTIAN, K. D., FISCHBACH, M. A., GERWICK, L., GERWICK, W. H., GROSS, H., GUST, B., HERTWECK, C., HOFTE, M., JENSEN, S. E., JU, J., KATZ, L., KAYSSER, L., KLASSEN, J. L., KELLER, N. P., KORMANEC, J., KUIPERS, O. P., KUZUYAMA, T., KYRPIDES, N. C., KWON, H. J., LAUTRU, S., LAVIGNE, R., LEE, C. Y., LINQUAN, B., LIU, X., LIU, W., et al. 2015. Minimum information about a biosynthetic gene cluster. *Nat Chem Biol,* 11**,** 625-31.

MTHETHWA, B. C., CHEN, W., NGWENYA, M. L., KAPPO, A. P., SYED, P. R., KARPOORMATH, R., YU, J. H., NELSON, D. R. & SYED, K. 2018. Comparative analyses of cytochrome P450s and those associated with secondary metabolism in *Bacillus* species. *Int J Mol Sci,* 19.

NELSON, D. R. 2018. Cytochrome P450 diversity in the tree of life. *Biochim Biophys Acta Proteins Proteom*, 1866**,** 141-154.

PODUST, L. M. & SHERMAN, D. H. 2012. Diversity of P450 enzymes in the biosynthesis of natural products. *Nat Prod Rep*, 29**,** 1251-66.

QUADRI, L. E. 2014. Biosynthesis of mycobacterial lipids by polyketide synthases and beyond. *Crit Rev Biochem Mol Biol*, 49**,** 179-211.

SCHERR, N. & NGUYEN, L. 2009. *Mycobacterium* versus *Streptomyces* - we are different, we are the same. *Curr Opin Microbiol*, 12**,** 699-707.

SONO, M., ROACH, M. P., COULTER, E. D. & DAWSON, J. H. 1996. Heme-containing oxygenases. *Chemical Reviews*, 96**,** 2841-2888.

VENTURA, M., CANCHAYA, C., TAUCH, A., CHANDRA, G., FITZGERALD, G. F., CHATER, K. F. & VAN SINDEREN, D. 2007. Genomics of *Actinobacteria*: tracing the evolutionary history of an ancient phylum. *Microbiol Mol Biol Rev*, 71**,** 495-548.

CHAPTER 2: LITERATURE REVIEW

2.1. Secondary metabolites

All living organisms perform biochemical reactions in order to sustain their lives. The sum of all the biochemical reactions carried out by an organism is known as metabolism. The molecules involved in these reactions are known as metabolites. Metabolites are of two types: primary and secondary metabolites. The metabolites that are required for the growth and maintenance of cellular function are called primary metabolites, while metabolites that are not required for the growth and maintenance of the cellular functions and are the end products of primary metabolism are called secondary metabolites. Secondary metabolism produces secondary metabolites and is connected to primary metabolism by using building blocks and biosynthetic enzymes derived from primary metabolism (Figure 2.1).

The term secondary metabolism, first used by plant physiologists more than three decades ago (Campbell, 1985), comprises all parts of metabolism specific to certain organisms. In the ideal case, secondary metabolites correspond to the following criteria:

(i) They appear only in a small, systematically defined, group of organisms (family, genus, species).

(ii) In all chemical groups, one finds large variability. This variability can appear in the same or in different organisms.

(iii) No effect of secondary metabolites on the producing organism is recognisable.

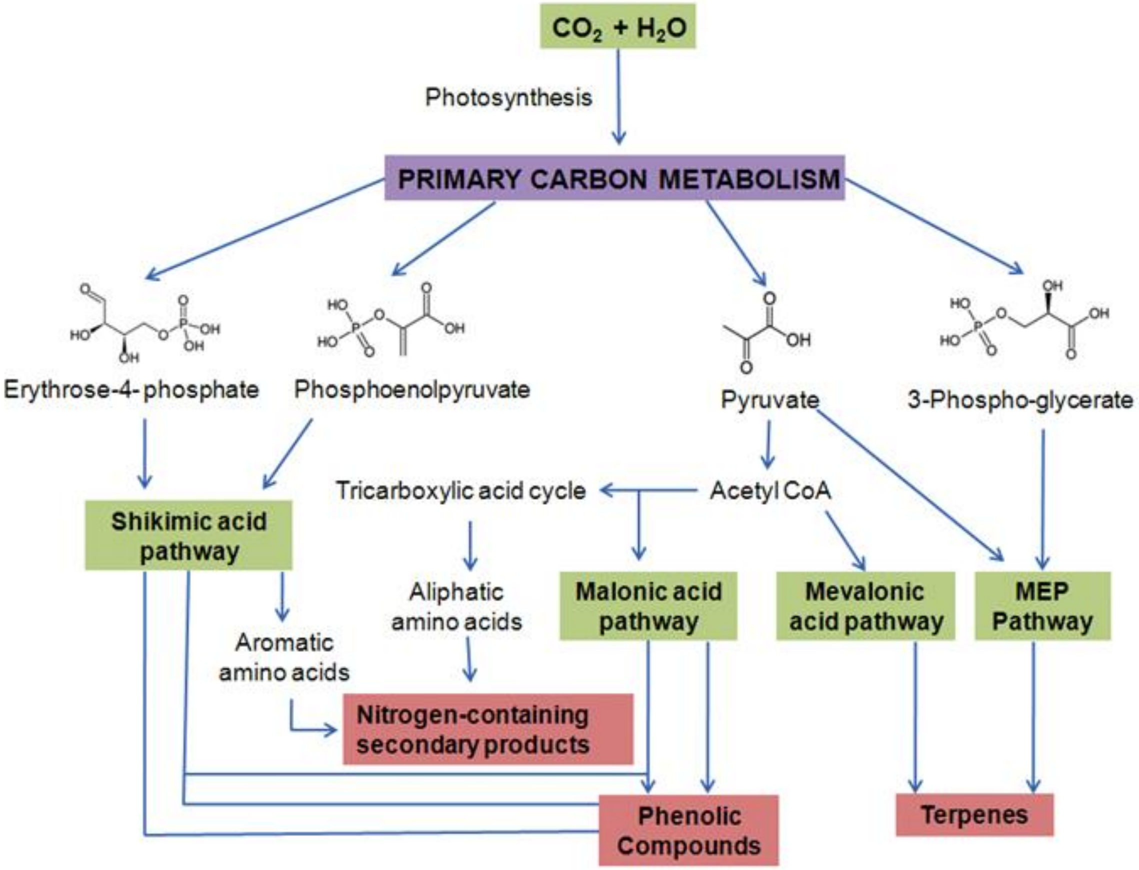


Figure 2. 1 Diagram showing connection between production of secondary metabolites and primary metabolism (taken from https://nptel.ac.in/courses/102103016/module4/lec31/2.html).

2.2. Classification of secondary metabolites

No standard classification is available for secondary metabolites because of their immense diversity in structure, function and biosynthesis (McMurry, 2014). Secondary metabolites can be classified on the basis of chemical structure (for example, having rings, containing a sugar), composition (containing nitrogen or not), their solubility in various solvents, or the pathway by which they are synthesised (e.g., phenylpropanoid, which produces tannins). McMurry (2014) classified secondary metabolites into five main classes: terpenoids and steroids, fatty acid-derived substances and polyketides, alkaloids, non-ribosomal polypeptides, and enzyme cofactors (Figure 2.2).

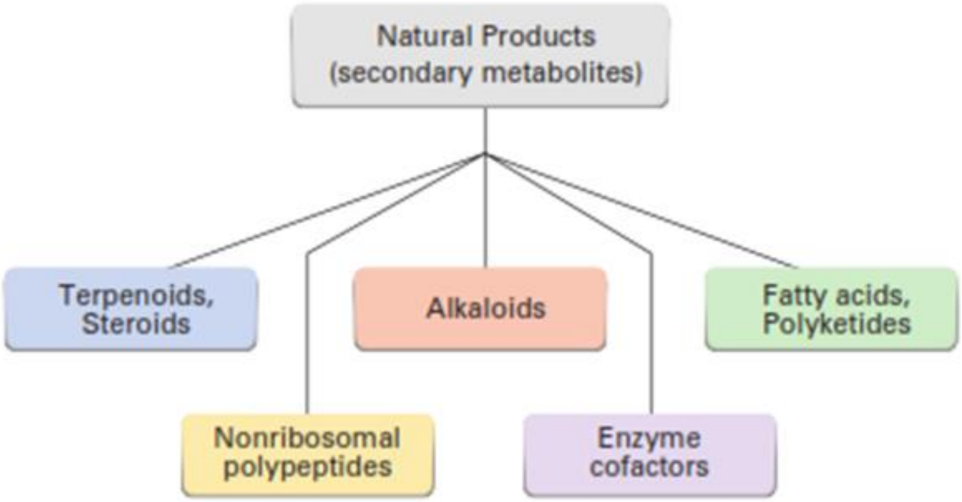


Figure 2. 2 Classification of natural products (McMurry, 2014).

Charactersitics of different groups of secondary metabolites (McMurry, 2014):

- Alkaloids – contain a basic amine group in their structure and are derived biosynthetically from amino acids.
- Fatty acid-derived substances and polyketides – biosynthesised from simple acyl precursors such as acetyl CoA, propionyl CoA, and methylmalonyl CoA. Natural compounds derived from fatty acids generally have most of the oxygen atoms removed but polyketides often have many oxygen substituents remaining.
- Nonribosomal polypeptides - peptidelike compounds that are biosynthesised from amino acids by a multifunctional enzyme complex without direct RNA transcription.
- Enzyme cofactors – do not fit one of the other general categories of natural products and are usually classed separately. One example is pyridoxal phosphate.

Hernández-Alvarado *et al*., (2018) classified secondary metabolites into four main groups: terpenes, phenolic compounds, glycosides and alkaloids (Table 2.1) (Hernández-Alvarado *et al*., 2018). The main function of different groups of secondary metabolites, examples of metabolites, are listed in Table 2.1.

Table 2. 1 Classification of secondary metabolites (Hernández-Alvarado *et al*., 2018).

Group	**Compounds present**	**Main features**
Alkaloids	Hormones, carotenoid pigments, sterols, latex and essential oils.	Group of major importance with more than 40 000 molecules, which are considered of importance for the survival of plants. They are insoluble in water and are derived from the union of isoprene units.
Phenolic compounds	Coumarins, flavonoids, lignin and tannins.	They are derived from a phenol group.
Glycosides	Saponins, cardiac glycosides, cyanogenic glycosides and glucosinolates.	They arise from the condensation of a sugar molecule with another containing a hydroxyl group, thus forming a glycosidic bond. Group with about 15 000 secondary metabolites.
Terpenes	Quinoline, isoquinoline, indole, tropane, quinolizidine, piperidine,	They are soluble in water, contain at least one nitrogen atom and exhibit biological activity. Most are

	purine, pyrrolizidene.	heterocyclic and some are aliphatic compounds.

2.3. Functions of secondary metabolites

Secondary metabolites play a key role in organisms that produce them. Extensive literature is available detailing the functions of secondary metabolites. Demain and Fang (2000) summarised secondary metabolites' functions into five main categories: (i) as competitive weapons used against other bacteria, fungi, amoebae, plants, insects, and large animals; (ii) as metal-transporting agents; (iii) as agents of symbiosis between microbes and plants, nematodes, insects, and higher animals; (iv) as sexual hormones; and (v) as differentiation effectors. In the case of plants, some secondary metabolites (including antibiotics) stimulate spore formation and inhibit or stimulate germination (Demain and Fang, 2000).

2.4. Applications of secondary metabolites

Living organisms produce a range of secondary metabolites with exotic chemical structures and diverse metabolic origins. Many of these secondary metabolites find use as natural products in medicine, agriculture and manufacturing (Medema *et al*., 2015). Secondary metabolites have broad applications; they serve especially as fighting tools against human pathogens and human disease. A summary of applications of different groups of secondary metabolites is listed in Table 2.2.

Table 2. 2 Applications of secondary metabolites (Hernández-Alvarado *et al*., 2018).

Group	**Pharmaceutical properties**
Alkaloids	Anticarcinogenic, antiulcerous, antimalarial, antimicrobial, etc.
Phenolic compounds	Antidiarrhoeals, antitumourals, antibacterials, antivirals and enzyme inhibitors.
Glycosides	Antimicrobials, fungicides, insecticides, anticancer, anti-inflammatory and allelopathic.
Terpenes	At high doses, most are very toxic; however, at low doses they work as muscle relaxants, tranquillizers, antitussives or analgesics.

2.5. Applications of microbial secondary metabolites

Microbes, especially species belonging to the phylum *Actinobacteria*, are well-known producers of different secondary metabolites with properties valuable to humans (Ventura *et al*., 2007). Among the genera in *Actinobacteria*, genus *Streptomyces* species are well known to produce a large number of secondary metabolites applied in most of the antibiotics used today (Table 2.3) (de Lima Procópio *et al*., 2012). The microbial secondary metabolites have a large number of applications in humans to fight human pathogens and human diseases. Thirumurugan and co-workers (Thirumurugan *et al*., 2018) provided extensive information on the application of microbial secondary metabolites. Thus, in brief, microbial secondary metabolites serve as antibioitics, antitumour agents, pharmacological and nutraceutical agents, enzymes and enzyme inhibitors and agricultural and animal health products (Thirumurugan *et al*., 2018).

Table 2. 3 General information on applications of *Streptomyces* species. If information is available, secondary metabolites and their applications are also presented in the table.

Species name	**Specie characteristic or well-known for**	**Reference(s)**
Streptomyces coelicolor	It is involved in breaking down organic material in the soil and responsible for producing most of the antibiotics in use today, as well as some immunosuppressant and anti-tumour agents. It has also been used in genetic engineering studies.	(Bilyk *et al*., 2013)
Streptomyces avermitilis	It produces certain secondary metabolites, namely avermectin, which is a potent agent against a wide array of nematodes and arthropod parasites.	(Witt and Stackebrandt, 1990, Bentley *et al*., 2002)
Streptomyces griseus	It produces streptomycin, a broad-spectrum antibiotic, which has been used for the treatment of various diseases, such as TB and the plague caused by *Yersinia pestis*. The organism has also been reported to contain a gene cluster that includes fredericamycin, an anticancer drug.	(Distler *et al*., 1992, Ohnishi *et al*., 2008, Wendt-

		Pienkowski *et al*., 2005)
Streptomyces globisporus	It produces the antitumour angucyclines landomycin A and landomycin E and enediyne antitumour antibiotic C-1027.	(Rebets *et al*., 2003)
Streptomyces scabiei	It is a plant pathogen causing corky lesions to form on tuber and root crops, as well as decreasing the growth of seedlings. Along with other closely related species it causes potato diseases. It can produce several related toxins, which are mainly responsible for its pathogenicity and moreover, *S. scabiei* produces toxins called thaxtomins, which cause hypertrophy and cell death in host plant tissues and are essential for pathogenicity.	(Beattie, 2007)
Streptomyces sp. *Sirex* AA-E	It is an aerobic microbe that is a prominent member of a bacterial/fungal symbiotic community associated with the invasive pinewood-boring wasp Sirex noctilio. *Streptomyces* sp. *Sirex* AA-E has shown that it secretes a full suite of endo- and exo-cellulases, hemicellulases, pectinases and polysaccharide monooxygenases when grown on biomass.	(Takasuka *et al*., 2013)

Streptomyces violaceusniger	It produces antibiotics that inhibit the growth of other bacteria.	(Gunnelius *et al*., 2014)
Streptomyces cattleya NRRL 8057 = DSM 46488	It produces the antibiotics thienamycin and cephamycin C and is one of the rare bacteria known to synthesise fluorinated metabolites.	(Núñez *et al*., 2003)
Streptomyces pratensis	It shows chemotaxonomic characteristics and also produces antibacterial compounds.	(Rong *et al*., 2013)
Streptomyces bingchenggensis	It is a soil bacterium that produces milbemycins, a family of macrolide antibiotics that is commercially important in crop protection and veterinary medicine. This species has a huge number of protein-coding genes and a huge number of transport proteins, which form systems that are important for metabolism and also enable their adaptation to complex environments.	(Zhou *et al*., 2016)
Streptomyces hygroscopicus subsp. *jinggangensis* 5008	It produces jingangmycin, an aminocyclitol antibiotic, which has been proven to be identical to validamycin. Jingangmycin has been widely used as a prime control reagent against sheath blight disease of rice plants and damping-off of cucumber seedlings in China and many other Eastern Asian countries. Meanwhile, its	(Matsumoto *et al*., 1998)

	transformed product, valienamine, is a pharmaceutically important precursor for the synthesis of voglibose, a highly effective drug for insulin-independent diabetes.	
Streptomyces hygroscopicus subsp. *jinggangensis* TL01	It produces antimycin A, which is widely used as a pesticide in the catfish farming industry and also has potent killing activity against insects, nematodes and fungi.	(Baskaran *et al*., 2014)
Streptomyces venezuelae	It produces chloromyeetin and jadomycin.	(Pullan *et al*., 2011)
Streptomyces davawensis	It produces the riboflavin analogs roseoflavin and 8-demethyl-8-amino-riboflavin. Both compounds show antimicrobial activity against Gram-positive bacteria such as *Bacillus subtilis,* but also against Gram-negative bacteria if uptake systems for flavins/flavin analogs are present.	(Jankowitsch *et al*., 2012)
Streptomyces albus J1074	It is a widely used host for heterogenous expression of bioactive natural products.	(Zaburannyi *et al*., 2014)
Streptomyces albus DSM 41398	It produces salinomycin. Salinomycin has selective activity against cancer. However, it has been widely used as veterinary medicine in animal husbandry as food additive and growth promoter for years.	(Yurkovich *et al*., 2012)

Streptomyces sp. PAMC 26508	This is an endosymbiotic bacterium isolated from the Antarctic lichen *Cladonia borealis*.	(Kim *et al*., 2014)
Streptomyces fulvissimus	It produces the ionophore antibiotic valinomycin. Secretes an antibacterial protein inhibitory to *Micrococcus luteus*, *Bacillus subtillis*, *Bacillus cereus*, and methicillin-resistant *Staphylococcus aureas* strains.	(Myronovskyi *et al*., 2013)
Streptomyces collinus	It produces ansatrienin A2, ansatrienin A3, ansatrienin B, napthomycin A, collinomycine, toromycin, streptocollin, kirromycin (elfamycin-family) and rubromycine. Causes common scab of potato.	(Rückert *et al*., 2013)
Streptomyces rapamycinicus	It produces produce rapamycin (also known as sirolimus) and azalomucin C, a macrodiolide antibiotic used as anthelmintic in animal fodder. Used as an immunosuppressant in renal transplant and for the prevention of restenosis after stent insertion for the treatment of coronary heart disease.	(Baranasic *et al*., 2013)
Streptomyces albulus NK660	It produces ε-Poly-L-lysine (ε-PL). ε-PL exhibits antimicrobial activity against a wide spectrum of microorganisms. Exhibits antiphage activity, and ε -PL has been used as a food preservative.	(Gu *et al*., 2014)

Streptomyces albulus ZPM	This species produces the homopolymer antibiotic, e-poly-lysine (e-PL).	(Wang *et al*., 2015b)
Streptomyces lividans	Used as a host for the synthesis and secretion of homologous and heterologous proteins of industrial interest.	(Rückert *et al*., 2015)
Streptomyces glaucescens	It produces tetracenomycin C, tetracenomycin D and tetracenomycin E. Functions to steer the chemical outcome of cyclization.	(Van Broekhoven *et al*., 2001, Thompson *et al*., 2004)
Streptomyces vietnamensis	It forms a white aerial mycelium and a reddish brown substrate mycelium. It shows antibacterial activity against other bacterial species such as *Escherichia coli*, *Pseudomonas aeruginosa*, *Candida albicans*, *Penicillium citrinum* and *B. subtilis.*	(Zhu *et al*., 2007)
Streptomyces sp. 769	It produces cytotoxic and antibacterial secondary metabolites.	(Song *et al*., 2015)
Streptomyces cyaneogriseus	It is a thermotolerant Streptomyces that produces nemadectin, which is a commercially important antibiotic. This is a macrolide antibiotic widely used as a	(Wang *et al*., 2015a)

	biopesticide. It also produces chitosanase enzyme, which allows it to break down chitosan as a sole carbon source.	
Streptomyces sp. A02	This species produces antifungal metabolites. It is a producer of commercially important polyene macrocylic antibiotic natamycin and potential biocontrol agent to several plant fungal diseases.	(Wu *et al*., 2015)
Streptomyces xiamenensis	It produces an anti-fibrotic benzopyran called xiamenmycin, a compound used for treating fibrotic diseases such as idiopathic pulmonary fibrosis, liver cirrhosis, progressive kidney disease, systemic sclerosis and cardiovascular fibrosis.	(Xu *et al*., 2009)
Streptomyces sp. Mg1	A Streptomyces producing a macrolide antibiotic called chalcomycin A, which takes part in inhibition of *B. subtilis* cell growth in combination by lysis and degradation of *B. subtilis* colonies.	(Barger *et al*., 2012, Hoefler *et al*., 2013)
Streptomyces sp. CNQ-509	It contains 29 putative gene clusters used for biosynthesis of secondary metabolites, which are involved in the formation of meroterpenoid molecules. It produces a variety of terpenoid compounds.	(Leipoldt *et al*., 2015)
Streptomyces ambofaciens	It produces two antibiotics, namely spiramycin, which is a polyketide derivative, and congocidin (netropsin). Reports have indicated that it comprises 23 gene clusters,	(Thibessard *et al*., 2015)

	which produce other secondary compounds such as kinamycins, antimycins and stambomycins.	
Streptomyces pristinaespiralis	This *Streptomyces* produces two antibiotics, namely cyclohexadepsiptide pristinamycin (PI) and polyunsaturated macrolactone pristinamycin II (PII) co-produced at a ratio of 30:70. The PI plays a vital role in synergistic antibacterial activity of a wide range of gram-positive bacteria such as methicillin-resistant *Staphylococci*, drug-resistant *Streptococcus pneumonia* and vancomycin-resistant *Enterococcus faecium* and Gram negative bacteria such as *Haemophilus* sp.	(Tian *et al*., 2015)
Streptomyces sp. CFMR 7	This species was discovered in rubber plantations in Penang Malaysia. It is has been found to degrade rubber.	(Nanthini *et al*., 2015)
Streptomyces sp. CdTB01	It was isolated from soil contaminated with heavy metals. It can tolerate high concentrations of heavy metals such as cadmium.	(Zhou *et al*., 2016)
Streptomyces reticuli	It produces mycelia-associated cellulose, which can degrade crystalline cellulose to cellobiose.	(Wibberg *et al*., 2016)

Streptomyces sp. 4F	Found in the soil in China, it is a fast grower and moderately thermophilic, i.e it grows at temperatures between 30°C and 50°C. It is therefore used for antibiotic expression and DNA assembly.	(Chen and Qin, 2011)
Streptomyces leeuwenhoekii	It was isolated from the hyper-arid high-altitude Atacama Desert in Chile. It produces novel polyketide antibiotics such as the chaxamycins and chaxalactins. Chaxamycins A-D are ansamycin-type polyketides with potential antibacterial activity against MRSA. It is involved in anti-proliferative activity, which results from the inhibition of the ATPase activity of the human Hsp90 protein.	(Gomez-Escribano *et al*., 2015)
Streptomyces rubrolavendulae	It has the potential to produce an anti-methicillin resistant *Staphyloccocus aureus* compound.	(Kannan *et al*., 2014)
Streptomyces parvulus	This streptomyces produces a polypeptide antibiotic called Actinomycin D, which is a potential anti-microbial agent against streptomycin-resistant pathogenic bacteria.	(Shetty *et al*., 2014)
Streptomyces lydicus	It produces actithiazic acid, streptolydigin, lydimycin, natamycin and 1-deoxygalactonojirimycin. It has the ability to be used as an agent against fungal plant pathogens. It has also been reported that the species *S. lydicus* WYEC108 is a strong	(Yuan and Crawford, 1995)

	antagonist against various fungal plant root-rot and white-rot pathogens and a number of wood decay fungi.	
Streptomyces clavuligerus	It produces more than 20 secondary metabolites, which include clavulanic acid that is a beta-lactam antibiotic. Clavulanic acid is a common antibiotic used in combination with *β*-lactam antibiotics (for example, Augmentin) to treat infections caused by *β*-lactamase-producing pathogens. It also synthesises the *β*-lactam antibiotic cephamycin C and numerous antifungal compounds with a clavam structure.	(De la Fuente *et al*., 2002, Paradkar, 2013, Cao *et al*., 2016)
Streptomyces griseochromogenes	It produces blasticidin A, B, C, S. Blasticidin S is a potent antifungal and cytotoxic peptidyl nucleoside antibiotic. It also produces pentalenene and cytomycin.	(Wu *et al*., 2017)
Streptomyces lincolnensis	It produces lincomycin, which is an anti-bacterial antibiotic. It also produces valienol, a C-7 cyclitol similar in structure to valienamine.	(Peschke *et al*., 1995)
Streptomyces noursei	It produces nystatin fungicidin, a polyene antifungal medication.	(Brautaset *et al*., 2000)

In contrast to the *Streptomyces* species, the mycobacterial species are well-known human pathogens, although there are some environmentally useful species in this genus. Table 2.4 below shows the importance of different mycobacterial species.

Table 2. 4 General information on mycobacterial species. Mycobacterial species were grouped into six different categories following the criteria described elsewhere (Parvez *et al*., 2016). The six categories include *Mycobacterium tuberculosis* complex (MTBC), *M. chelonae-abscessus* complex (MCAC), *M. avium* complex (MAC), mycobacteria causing leprosy (MCL), nontuberculous mycobacteria (NTM) and saprophytes (SAP). The criteria for separation of mycobacterial species into six different groups is based on their characteristic features, including ecological niches, as well as the nature and site of infection as described elsewhere (Ventura *et al*., 2007).

Species name	**General information**	**Reference**
	***Mycobacterium tuberculosis* complex**	
Mycobacterium africanum GM041182	Causes TB in humans, especially in West African countries.	(Bentley *et al*., 2012)
Mycobacterium tuberculosis C	Highly transmissible bacteria causing TB in humans. First isolated in New York City, USA and is highly transmitted among humans, causing TB.	(Reddy *et al*., 2008)

Mycobacterium tuberculosis F11	Causes TB in humans. First isolated during a TB epidemic in the Western Cape of South Africa.	(Victor *et al*., 2004)
Mycobacterium tuberculosis H37Rv	Best characterised and first genome sequenced strain causing TB in humans.	(Cole *et al*., 1998)
Mycobacterium tuberculosis H37Ra	An avirulent strain derived from the H37Rv strain. This laboratory strain has since lost its virulence, and has different characteristics from its virulent sibling H37Rv, including decreased ability to survive in macrophages or hypoxic conditions, and loss of virulence in laboratory animals.	(Brosch *et al*., 1999, Reddy *et al*., 2008)
Mycobacterium tuberculosis Haarlem	Human pathogen that causes TB. The first representative of the family was discovered in Haarlem, The Netherlands.	(Brudey *et al*., 2006)
Mycobacterium tuberculosis KZN 1435	Human pathogen that causes TB. It was first isolated in KwaZulu-Natal, South Africa.	(Ioerger *et al*., 2009)
Mycobacterium tuberculosis KZN 605	Human pathogen that causes TB. It was first isolated in KwaZulu-Natal, South Africa.	(Ioerger *et al*., 2009)

Mycobacterium tuberculosis KZN 4207	Human pathogen that causes TB. It was first isolated in KwaZulu-Natal, South Africa.	(Ioerger *et al*., 2009)
Mycobacterium tuberculosis RGTB327	Human pathogen that causes TB. It was first isolated in Kerala, India.	(Madhavilatha *et al*., 2012)
Mycobacterium tuberculosis CDC1551	This strain shows 99% identity at DNA level with *M. tuberculosis H37Rv* but displays phenotypic differences.	(Betts *et al*., 2000)
Mycobacterium tuberculosis strains CCDC5079	Human pathogen that causes TB. It was isolated in Fujian Province, China, in 2004. Sensitive to four first-line drugs.	(Zhang *et al*., 2011a)
Mycobacterium tuberculosis Beijing/NITR203	Human pathogen that causes TB. It was first isolated in the Tamil Nadu state, India.	(Narayanan and Deshpande, 2013)
Mycobacterium tuberculosis CAS/NITR204	Human pathogen that causes TB. It was first isolated in the Tamil Nadu state, India.	(Narayanan and Deshpande, 2013)
Mycobacterium tuberculosis EAI5	Human pathogen that causes TB. It was first isolatedin in Mumbai, India.	(Al Rashdi *et al*., 2014)
Mycobacterium tuberculosis EAI5/NITR206	Human pathogen that causes TB. It was first isolated in the Tamil Nadu state, India.	(Narayanan and Deshpande, 2013)

Mycobacterium tuberculosis Erdman= ATCC 35801	Isolated from human sputum by William H. Feldman in 1945, at Mayo Clinic, Rochester, MN, and deposited with the Trudeau *Mycobacterium* Culture Collection in 1946. It has been widely used as a standard virulent laboratory strain for virulence and immunisation studies. *M. tuberculosis* Erdman has a faster in vivo doubling time than two attenuated strains, *M. tuberculosis* H37Ra and *Mycobacterium bovis* Bacillus Calmette-Guerin (BCG), and a slightly faster in vivo doubling time than the virulent H37Rv strain in mice.	(Miyoshi-Akiyama *et al*., 2012)
Mycobacterium tuberculosis UT205	Human pathogen that causes TB. It was isolated in Colombia.	(Isaza *et al*., 2012)
Mycobacterium canetii CIPT 140010059	Human pathogen that causes TB. However, it exhibits a smooth colony phenotype on culture media compared to *M. tuberculosis* H37Rv.	(Supply *et al*., 2013)
Mycobacterium canetii CIPT 140060008	Human pathogen that causes TB. However, it exhibits a smooth colony phenotype on culture media compared to *M. tuberculosis* H37Rv.	(Supply *et al*., 2013)

Mycobacterium canetii CIPT 140710010	Human pathogen that causes TB. However, it exhibits a smooth colony phenotype on culture media compared to *M. tuberculosis* H37Rv.	(Supply *et al*., 2013)
Mycobacterium bovis AF 2122/97	It is the causative agent of TB in a range of animal species and man. *M. bovis* was also the progenitor for the *M. bovis* BCG vaccine strain, the most widely used human vaccine.	(Garnier *et al*., 2003)
Mycobacterium bovis BCG Pasteur 1173P2	It is the causative agent of TB in cattle and other animals, including buffalo, lions and antelopes. The organism can also cause TB in humans.	(Brosch *et al*., 2007)
Mycobacterium bovis BCG Korea 1168P	Isolated in Korea. The strain that will actually be used in Korea for vaccine production.	(Joung *et al*., 2013)
Mycobacterium bovis BCG Mexico	It was one of the most widely used sub-strains for vaccination in Mexico, BCG Mexico 1931.	(Orduña *et al*., 2011)
Mycobacterium bovis BCG Tokyo 172	Isolated in Tokyo, Japan. The strain used in Japan for vaccine production.	(Seki *et al*., 2009)
Mycobacterium chelonae-abscessus complex		

Mycobacterium abscessus ATCC 19977	Rapidly growing mycobacterium. Causes a pseudotuberculous lung disease to patients with cystic fibrosis. Originally isolated from a human knee infection with subcutaneous abscess-like lesions in 1953.	(Ripoll *et al*., 2009)
Mycobacterium abscessus subsp. *bolletii* 50594	Rapidly growing mycobacterium. Causes nontuberculous mycobacterial infection. Isolated from a Korean patient with a pulmonary infection.	(Kim *et al*., 2013)
***Mycobacterium avium* complex**		
Mycobacterium Avium 104	Opportunistic pathogen causes non-paratuberculosis. Isolated in Southern California, USA.	(Horan *et al*., 2006)
Mycobacterium Avium subsp. *paratuberculosis* K10	The causative agent of Johne's disease in cattle and other ruminants. Clinically isolated from a dairy herd in Wisconsin in the mid-1970s.	(Li *et al*., 2005)
Mycobacterium avium subsp. *paratuberculosis* MAP4	Etiologic agent of Johne's disease in ruminants. Associated with human Crohn's disease. Has a complex cell wall structure containing mycolic acids and several lipids, similar to those of other members of this genus, yet it is the most slowly growing member.	(Bannantine *et al*., 2014)

	Originally isolated from the breast milk of a Crohn's disease patient in 2000.	
Mycobacterium intracellulare ATCC 13950	Slow-growing mycobacteria responsible for opportunistic infections.	(Kim *et al*., 2012c)
Mycobacterium intracellulare MOTT-02	Clinical isolate from Korean patients. Responsible for opportunistic infections (nontuberculous mycobacterial infection).	(Kim *et al*., 2012b)
Mycobacterium intracellulare MOTT-36Y	Clinical isolate from Korean patients. Responsible for opportunistic infections (nontuberculous mycobacterial infection).	(Kim *et al*., 2012a)
Mycobacterium Indicus pranii MTCC 9506	A saprophytic mycobacterial species that is known for its immunomodulatory properties in various human diseases.	(Saini *et al*., 2012)
Mycobacteria causing leprosy		
Mycobacterium leprae Br4923	Originally isolated from a leprosy patient in Brazil. Causes leprosy in humans.	(Monot *et al*., 2009)
Mycobacterium Leprae TN	Isolated from an armadillo experimentally infected with *M. leprae* in biopsy material from a single lepromatous leprosy patient from Tamil Nadu, India. Human and animal pathogen.	(Cole *et al*., 2001)

Nontuberculous mycobacteria		
Mycobacterium sp. JDM601	Causes TB-like disease in humans.	(Zhang *et al*., 2011b)
Mycobacterium liflandii 128FXT	Amphibian pathogen. Originally isolated from infected Xenopus tropicalis at the University of California, Berkeley.	(Tobias *et al*., 2013)
Mycobacterium ulcerans Agy99	Human pathogen. Causes buruli ulcer. Isolated from an ulcerative lesion on the right elbow of a female patient from the Ga district of Ghana in 1999	(Stinear *et al*., 2007)
Mycobacterium Marinum M	Ubiquitous pathogen of fish and amphibia. Shown to be a human pathogen as well. Facultative anaerobe. Unable to reduce nitrate and produces characteristic bright yellow carotenoid pigments when exposed to light. Isolated from a patient with fish tank granuloma in San Francisco in 1992.	(Stinear *et al*., 2008)
Saprophytes		
Mycobacterium sp. JLS	This bacterium was isolated from soil in Libby, Montana, USA. This isolate belongs to a fast-growing group able to degrade high molecular weight PAH, including pyrene.	(Chen *et al*., 2019)

Mycobacterium sp. KMS	This bacterium was isolated from soil in Libby, Montana, USA. This isolate belongs to a fast-growing group able to degrade high molecular weight PAH, including pyrene.	(Chen *et al*., 2019)
Mycobacterium sp. MCS	This bacterium was isolated from soil in Libby, Montana, USA. This isolate belongs to a fast-growing group able to degrade high molecular weight PAH, including pyrene.	(Chen *et al*., 2019)
Mycobacterium smegmatis MC2 155	A nonpathogenic, fast-replicating mycobacterium that is widely used as a model system to study *M. tuberculosis*.	(Mohan *et al*., 2015)
Mycobacterium chubuense NBB4	Isolated on ethane as part of a bioprospecting study searching for novel monooxygenase enzymes. Strain NBB4 was shown to grow on C_2–C_4 alkenes and C_2–C_{16} alkanes.	(Coleman *et al*., 2011)
Mycobacterium gilvum PYR-GCK	Polycyclic aromatic hydrocarbons degradation and N-Acetylnorfloxacin producing strain.	(Badejo *et al*., 2013)
Mycobacterium gilvum Spyr1	Mycobacterium sp. Spyr1 is a newly isolated strain that occurs in a creosote-contaminated site in Greece. It was isolated by an enrichment method using pyrene as sole carbon and energy source	(Kallimanis *et al*., 2011)

	and is capable of degrading a wide range of PAH substrates including pyrene, fluoranthene, fluorene, anthracene and acenapthene.	
Mycobacterium sp. JS623 (formerly named as *Mycobacterium smegmatis* JS623)	Model organism used in bioremediation studies.	(Garcia and Gola, 2016)
Mycobacterium rhodesiae NBB3	Ethane and vinyl chloride-oxidising Mycobacterium strains of significance to bioremediation, biocatalysis and biogeochemistry.	(Chen *et al*., 2019)
Mycobacterium neoaurum VKM Ac-1815D	Fast-growing soil mycobacteria. Used for efficient production of the key steroid intermediates (androst-4-ene-3,17-dione, androsta-1,4-diene-3,17-dione, 9-hydroxy androst-4-ene-3,17-dione) from phytosterol. Originally isolated from soil samples.	(Bragin *et al*., 2013)

2.6 Secondary metabolite biosynthetic gene clusters

It is now well-established that genes involved in the synthesis of secondary metabolites form a cluster known as a biosynthetic gene cluster (BGC) (Medema *et al*., 2015). A BGC can be defined as a physically clustered group of two or more genes in a particular genome that together encode a biosynthetic pathway for the production of a specialised metabolite (including its chemical variants) (Medema *et al*., 2015). Quite a large number of BGCs were reported in bacteria, fungi and plants (Medema, 2018). The availability of a large number of genome sequences enabled the development of novel tools to identify BGCs. A chronological order of tools developed for modelling BGCs, with genome information, is listed in Table 2.5. Using these programs, one can identity different types of secondary metabolite BGCs present in an organism. These programs also give the genes involved in synthesis of the particular secondary metabolite.

Table 2. 5 Software programs available for predicting different secondary metabolite biosynthetic gene clusters (Weber *et al*., 2015).

Software program	**Year of publication**	**Main content and/or function**	**Reference**
Model SEED	2010	First online high-throughput metabolic modeling tool	(Henry *et al*., 2010)
MEMOSys	2011	Allows management, storage and development of metabolic models	(Pabinger *et al*., 2011)
SuBliMinaL Toolbox	2011	Has strengths in managing chemical information for metabolites in a metabolic model	(Swainston *et al*., 2011)
FAME	2012	Allows streamlined analysis of a newly built metabolic model using various simulation methods	(Boele *et al*., 2012)
GEMSiRV	2012	Allows metabolic model reconstruction, simulation and visualisation	(Liao *et al*., 2012)
MetaFlux in Pathway Tools	2012	Provides strong support for predicting, modelling, curating and visualising metabolic pathways	(Latendresse *et al*., 2012)
MicrobesFlux	2012	Allows both flux balance analysis (FBA) and dynamic FBA of a newly generated metabolic model	(Feng *et al*., 2012)

RAVEN Toolbox	2013	Allows metabolic model reconstruction, simulation and visualisation in MATLAB environment	(Agren *et al*., 2013)
CoReCo	2014	Useful for modelling metabolisms of multiple related species	(Pitkanen *et al*., 2014)
merlin	2015	Most recently released metabolic modelling program with comprehensive genome annotation functionalities necessary for model generation	(Dias *et al*., 2015)
antiSMASH	2015	Provides comprehensive genome mining platform for BGCs; currently the only platform offering automated modelling including secondary metabolite-specific reactions	(Weber *et al*., 2015)

2.7. Cytochrome P450 monoxygenases

2.7.1. Introduction

Cytochrome P450 monooxygenases, also known as CYPs/P450s, are heme-thiolate proteins present in species belonging to all domains of life and even in non-living entities such as viruses (Nelson, 2018, Lamb *et al*., 2009). Cytochrome P450 (P450) enzymes have been studied for more than 50 years (Yamazaki, 2014). The origin of P450 enzymes has a historical perspective (Omura, 2011). Two researchers, Garfinkel and Klingenberg, individually identified an enzyme that has a special absorption maximum wavelength of 450 nm as a carbon-monoxide binding pigment in the liver microsomes of rat and pig (Garfinkel, 1958, Klingenberg, 1958). Omura and co-workers then came up with the name ‘cytochrome P450’, which described the coloured substance that was found in a cell (Omura, 2011, Omura and Sato, 1962). This coloured substance produced an uncommon absorption peak at a wavelength of 450 nm when reduced and bound with carbon monoxide in rat liver microsomes (Figure 2.3) (Omura, 2011, Omura and Sato, 1962). There was a contradiction in the name ‘cytochrome’; some people called it an enzyme instead of a true cytochrome. The initial meaning of the term ‘cytochrome P450’ was ‘coloured substance in the cell’ (Omura and Sato, 1962).

2.7.2. Nomenclature

Standard nomenclature set by the International P450 Nomenclature Committee is followed for naming of P450s (Nelson, 1998, Nelson, 2006, Nelson *et al*., 1993). The rules of nomenclature are a CYP prefix, followed by an Arabic numeral, which designates family (all members nominally >40% identity), a capital letter designating the subfamily (all members nominally >55% identity), and an Arabic numeral designating the individual gene (all italics) or message and protein (no italics) (Figure 2.4) (Feyereisen, 2012).

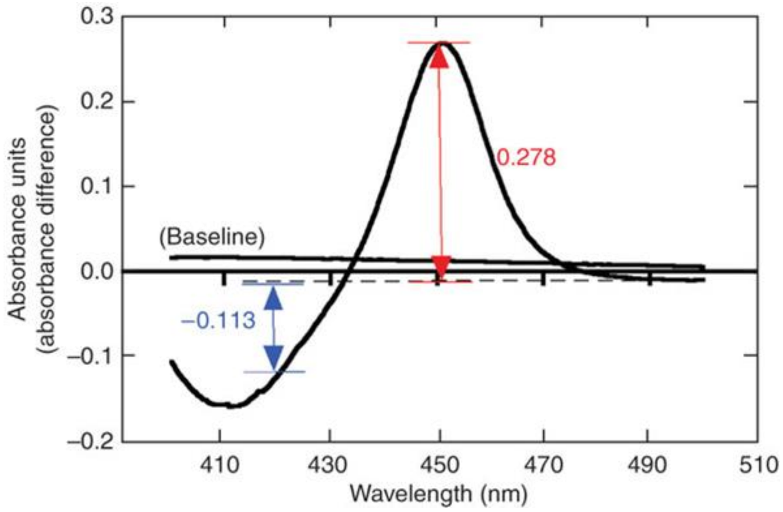


Figure 2. 3 Typical cytochrome P450 monooxygenase ferrous-CO versus ferrous-difference spectrum (Guengerich *et al*., 2009).

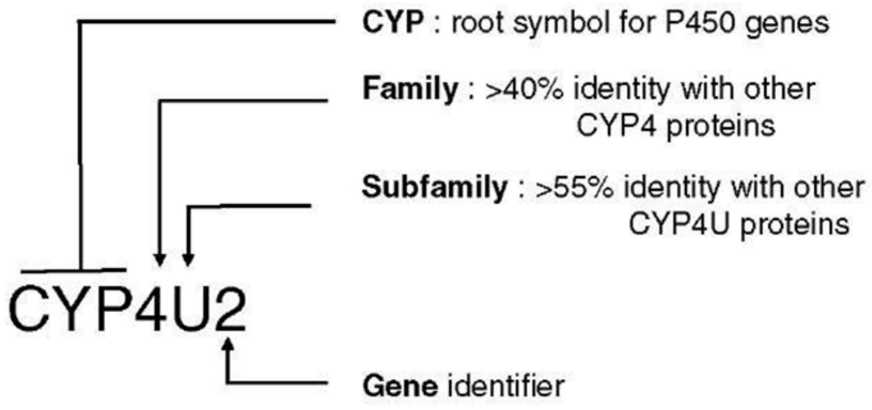


Figure 2. 4 Scheme of P450 nomenclature (Feyereisen, 2012).

2.7.3. Catalytic diversity

P450s were named after their initial reaction of monooxygenation, i.e. inserting one oxygen atom from water into substrate, as shown below:

$$\text{RH} + \text{NAD (P) H} + O_2 + \text{P450} \rightarrow \text{ROH} + H_2O + \text{NAD(P)H}$$

The RH represents an organic substrate with P450 as the catalyst. The oxygen and NAD (P) (reduced nicotinamide adenine dinucleotide phosphate) and ROH constitute the hydroxylated organic product.

However, progress in characterisation of P450s over the years revealed that P450s are catalytically diverse and perform different enzymatic reactions apart from monooxygenation (Figure 2.5).

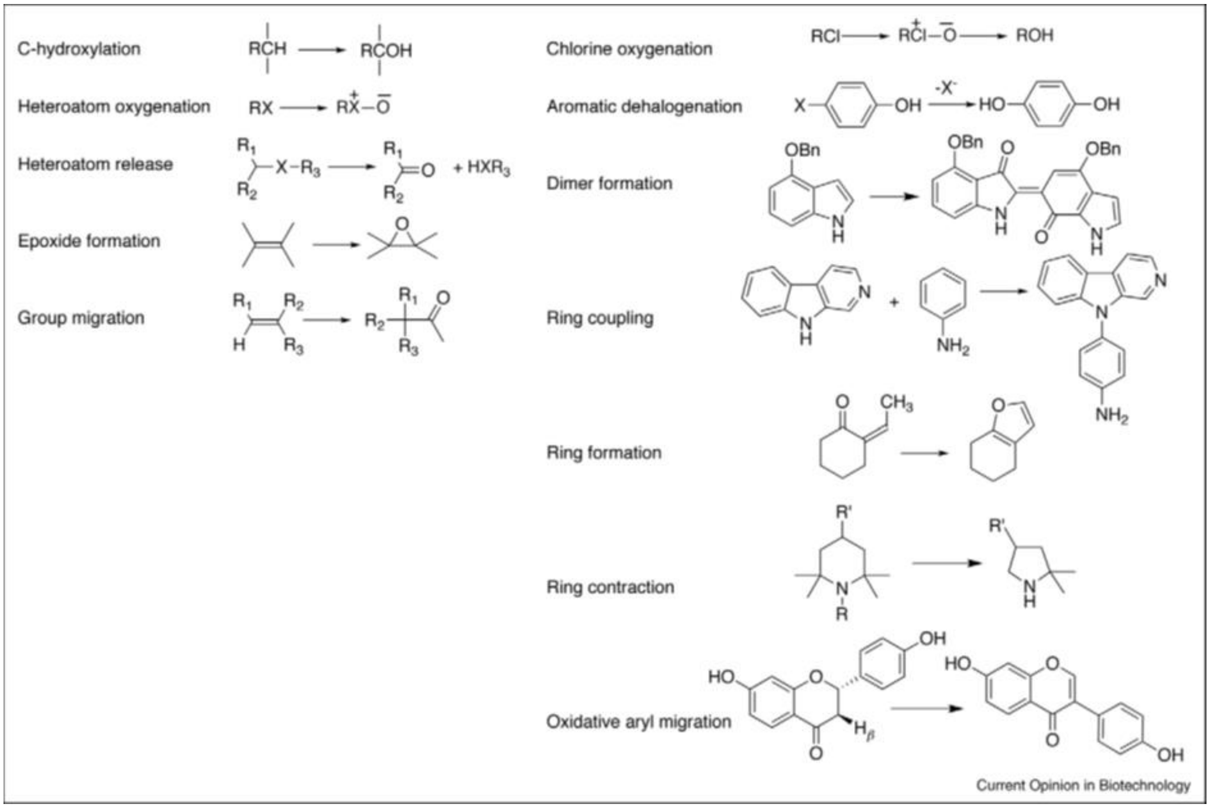
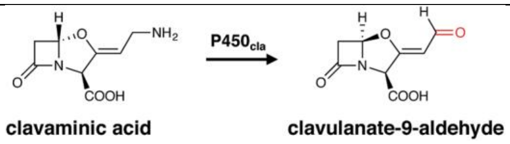
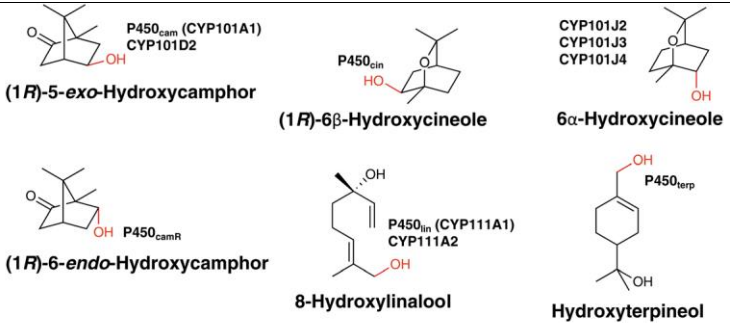


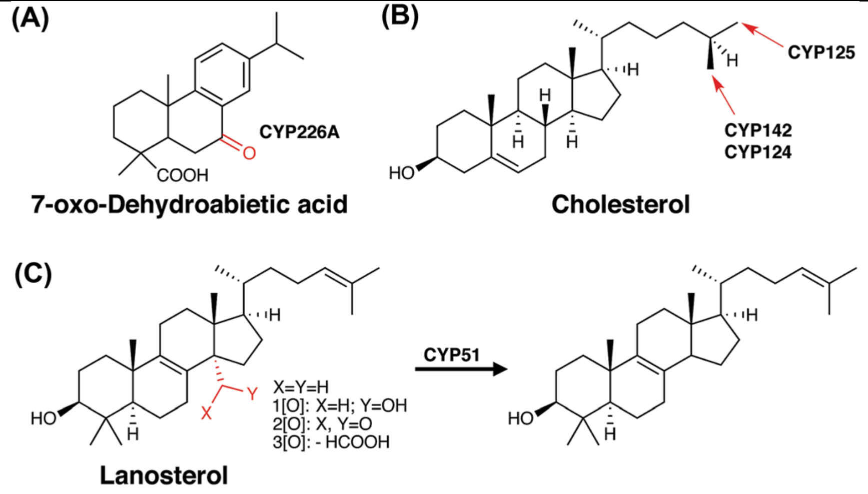
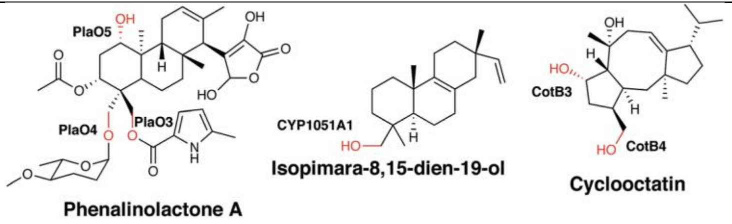
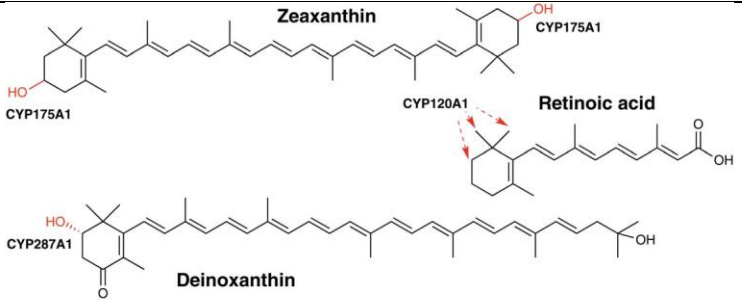
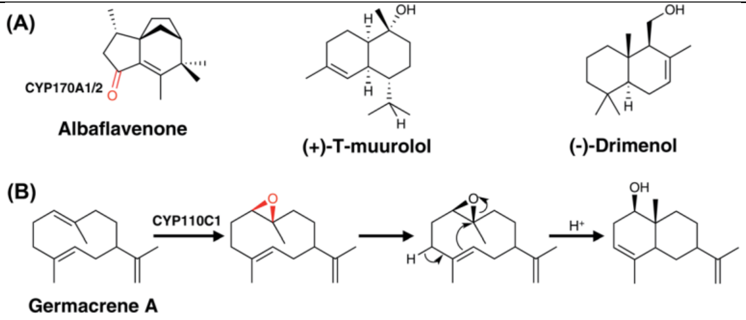
Figure 2. 5 Reactions catalyzed by P450s (Lamb *et al*., 2007).

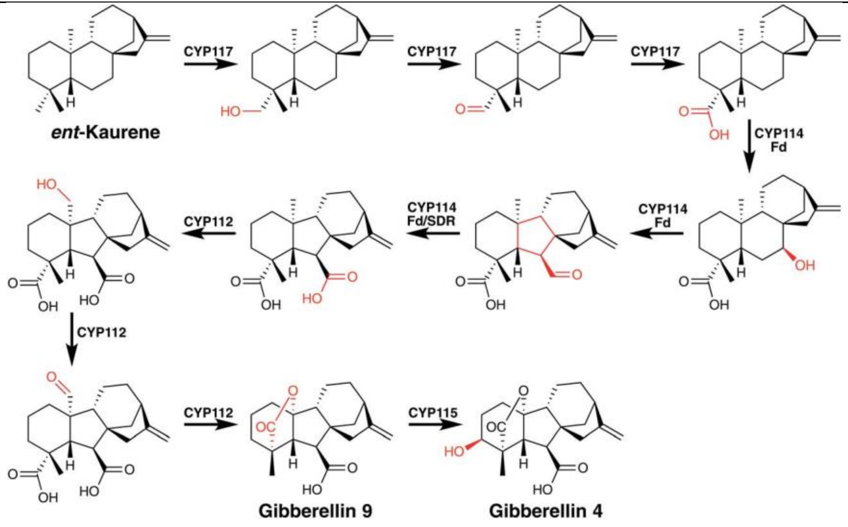
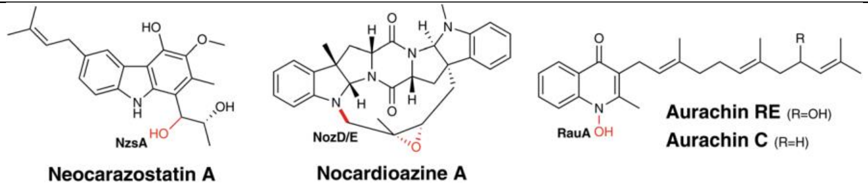
2.7.4. Role of P450s in secondary metabolite synthesis

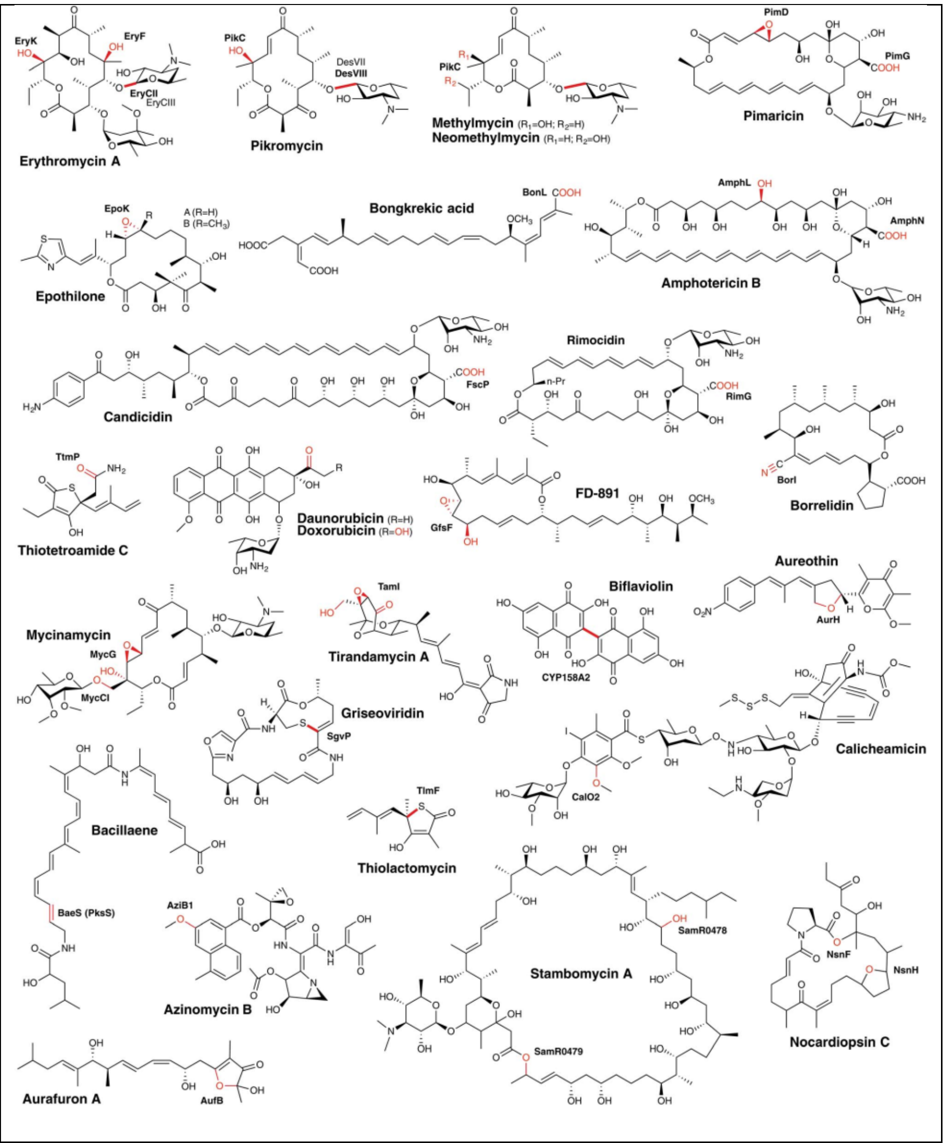
The secondary metabolite biosynthetic gene clusters comprise different genes. Among the genes, cytochrome P450 monooxygenases play a key role contributing to the chemical and structural diversity of secondary metabolites (Rudolf *et al*., 2017, Podust and Sherman, 2012, Greule *et al*., 2018). In *Mycobacterium tuberculosis* H37Rv, P450s were found to be involved in synthesis of polyketides that play a role in virulence (Quadri, 2014). Quite a number of P450s were identified as part of biosynthetic gene clusters in Streptomyces species (Greule *et al*., 2018). Table 2.6 below shows the role of P450s in the synthesis of different groups of secondary metabolites.

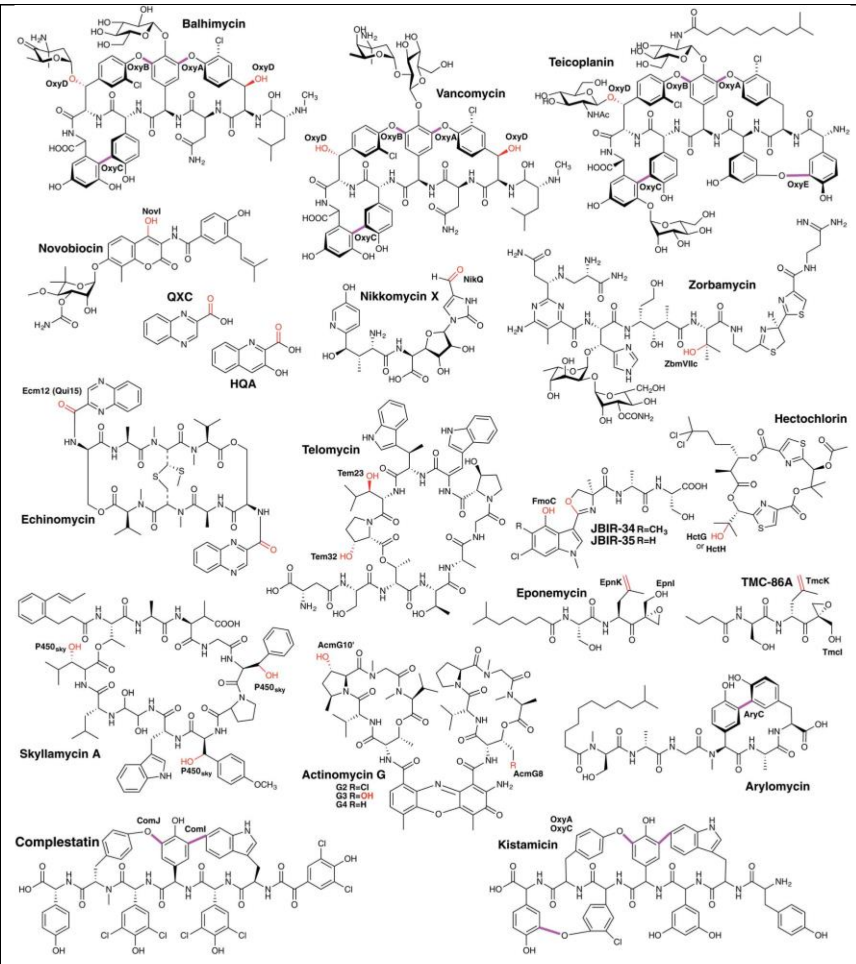
Table 2.6 Role of P450s in synthesis of different secondary metabolites (Greule *et al*., 2018). The oxygen incorporated as a result of this process is indicated in red.

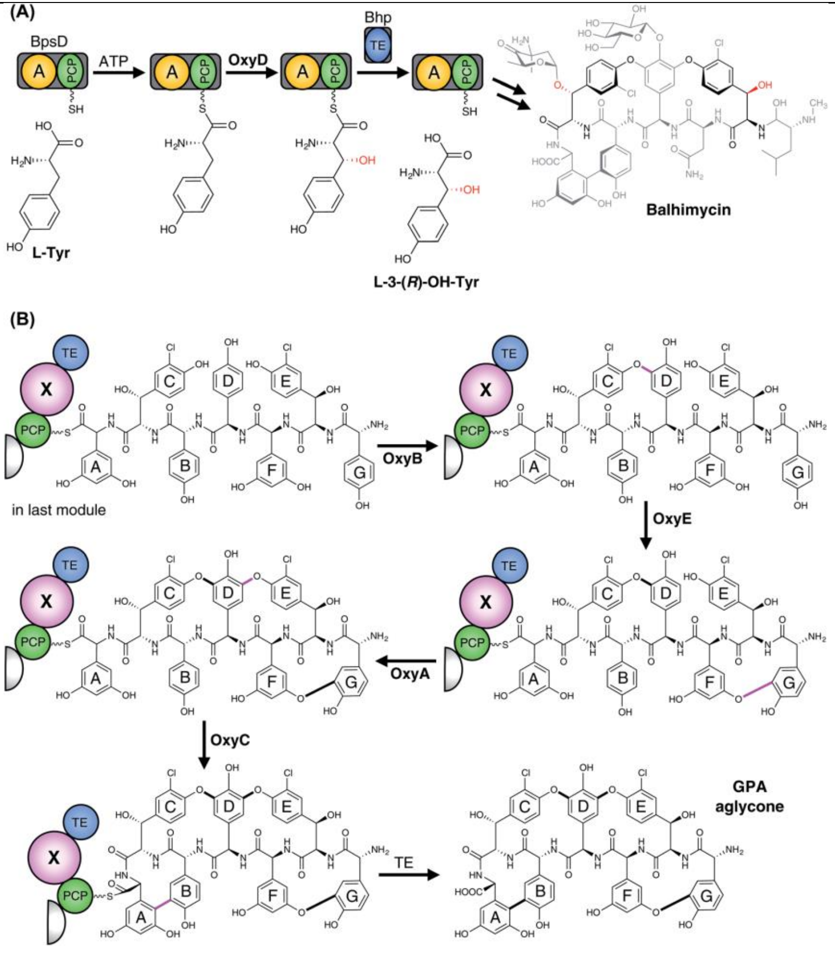
Process	**Schematic diagram**
Clavulanic acid biosynthesis	
Hydroxylation of monoterpenes	

Diterpene and steroid oxidation in bacterial P450 catalysed biodegradation. Example shown for a diterpene is abietic acid (A) and for steroids cholesterol (B) and lanosterol (C).	
Diterpene biosynthesis	
Carotenoid biosynthesis	
Sesquiterpene biosynthesis. (A) modification and (B) oxidative cyclisation.	

P450-mediated transformations found in gibberellin biosynthesis. Fd, gibberellin ferredoxin; SDR, gibberellin short-chain dehydrogenase/ reductase.	
Alkaloid biosynthesis	

Examples of bacterial P450 enzymes involved in polyketide biosynthesis	

P450 enzymes' role in nonribosomal peptide synthesis.	

P450s involved in glycopeptide antibiotic synthesis	

References

AGREN, R., LIU, L., SHOAIE, S., VONGSANGNAK, W., NOOKAEW, I. & NIELSEN, J. 2013. The RAVEN toolbox and its use for generating a genome-scale metabolic model for *Penicillium chrysogenum*. *PLoS Comput Biol,* 9**,** e1002980.

AL RASHDI, A. S. A., JADHAV, B. L., DESHPANDE, T. & DESHPANDE, U. 2014. Whole-genome sequencing and annotation of a clinical isolate of *Mycobacterium tuberculosis* from Mumbai, India. *Genome Announcements,* 2.

BADEJO, A. C., BADEJO, A. O., SHIN, K. H. & CHAI, Y. G. 2013. A gene expression study of the activities of aromatic ring-cleavage dioxygenases in *Mycobacterium gilvum* PYR-GCK to changes in salinity and pH during pyrene degradation. *PLoS One,* 8**,** e58066.

BANNANTINE, J. P., LI, L., MWANGI, M., COTE, R., RAYGOZA GARAY, J. A. & KAPUR, V. 2014. Complete genome sequence of *Mycobacterium avium paratuberculosis*, Isolated from Human Breast Milk. *Genome Announcements*, 2**,** e01252-13.

BARANASIC, D., GACESA, R., STARCEVIC, A., ZUCKO, J., BLAŽIČ, M., HORVAT, M., GJURAČIĆ, K., FUJS, Š., HRANUELI, D. & KOSEC, G. 2013. Draft genome sequence of *Streptomyces rapamycinicus* strain NRRL 5491, the producer of the immunosuppressant rapamycin. *Genome Announcements*, 1**,** e00581-13.

BARGER, S. R., HOEFLER, B. C., CUBILLOS-RUIZ, A., RUSSELL, W. K., RUSSELL, D. H. & STRAIGHT, P. D. 2012. Imaging secondary metabolism of *Streptomyces* sp. Mg1 during cellular lysis and colony degradation of competing Bacillus subtilis. *Antonie Van Leeuwenhoek,* 102**,** 435-445.

BASKARAN, S., CARLSON, L.-A., STJEPANOVIC, G., YOUNG, L. N., GROB, P., STANLEY, R. E., NOGALES, E. & HURLEY, J. H. 2014. Architecture and dynamics of the autophagic phosphatidylinositol 3-kinase complex. *Elife,* 3**,** e05115.

BEATTIE, G. A. 2007. Plant-associated bacteria: survey, molecular phylogeny, genomics and recent advances. *Plant-associated bacteria.* pp. 1-56. Springer, Dordrecht. DOI: https://doi.org/10.1007/978-1-4020-4538-7_1.

BENTLEY, S. D., CHATER, K. F., CERDEÑO-TÁRRAGA, A.-M., CHALLIS, G. L., THOMSON, N., JAMES, K. D., HARRIS, D. E., QUAIL, M. A., KIESER, H. & HARPER, D. 2002. Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3 (2). *Nature,* 417**,** 141.

BENTLEY, S. D., COMAS, I., BRYANT, J. M., WALKER, D., SMITH, N. H., HARRIS, S. R., THURSTON, S., GAGNEUX, S., WOOD, J. & ANTONIO, M. 2012. The genome of *Mycobacterium africanum* West African 2 reveals a lineage-specific locus and genome erosion common to the *M. tuberculosis* complex. *PLoS Neglected Tropical Diseases,* 6**,** e1552.

BETTS, J. C., DODSON, P., QUAN, S., LEWIS, A. P., THOMAS, P. J., DUNCAN, K. & MCADAM, R. A. 2000. Comparison of the proteome of *Mycobacterium tuberculosis* strain H37Rv with clinical isolate CDC 1551. *Microbiology,* 146**,** 3205-3216.

BILYK, B., WEBER, S., MYRONOVSKYI, M., BILYK, O., PETZKE, L. & LUZHETSKYY, A. 2013. In vivo random mutagenesis of *Streptomycetes* using mariner-based transposon Himar1. *Applied Microbiology and Biotechnology,* 97**,** 351-359.

BOELE, J., OLIVIER, B. G. & TEUSINK, B. 2012. FAME, the flux analysis and modeling environment. *BMC Syst Biol,* 6**,** 8.

BRAGIN, E. Y., SHTRATNIKOVA, V. Y., DOVBNYA, D., SCHELKUNOV, M., PEKOV, Y. A., MALAKHO, S., EGOROVA, O., IVASHINA, T., SOKOLOV, S. & ASHAPKIN, V. 2013. Comparative analysis of genes encoding key steroid core oxidation enzymes in fast-growing *Mycobacterium* spp. strains. *The Journal of Steroid Biochemistry and Molecular Biology,* 138**,** 41-53.

BRAUTASET, T., SEKUROVA, O. N., SLETTA, H., ELLINGSEN, T. E., STRLM, A. R., VALLA, S. & ZOTCHEV, S. B. 2000. Biosynthesis of the polyene antifungal antibiotic nystatin in *Streptomyces noursei* ATCC 11455: analysis of the gene cluster and deduction of the biosynthetic pathway. *Chem Biol,* 7**,** 395-403.

BROSCH, R., GORDON, S. V., GARNIER, T., EIGLMEIER, K., FRIGUI, W., VALENTI, P., DOS SANTOS, S., DUTHOY, S., LACROIX, C., GARCIA-PELAYO, C., INWALD, J. K., GOLBY, P., GARCIA, J. N., HEWINSON, R. G., BEHR, M. A., QUAIL, M. A., CHURCHER, C., BARRELL, B. G., PARKHILL, J. & COLE, S. T. 2007. Genome plasticity of BCG and impact on vaccine efficacy. *Proceedings of the National Academy of Sciences,* 104**,** 5596-5601.

BROSCH, R., PHILIPP, W. J., STAVROPOULOS, E., COLSTON, M. J., COLE, S. T. & GORDON, S. V. 1999. Genomic analysis reveals variation between *Mycobacterium tuberculosis* H37Rv and the attenuated *M. tuberculosis* H37Ra strain. *Infection and Immunity,* 67**,** 5768-5774.

BRUDEY, K., DRISCOLL, J. R., RIGOUTS, L., PRODINGER, W. M., GORI, A., AL-HAJOJ, S. A., ALLIX, C., ARISTIMUNO, L., ARORA, J., BAUMANIS, V., BINDER, L., CAFRUNE, P., CATALDI, A., CHEONG, S., DIEL, R., ELLERMEIER, C., EVANS, J. T., FAUVILLE-DUFAUX, M., FERDINAND, S., GARCIA DE VIEDMA, D.,

GARZELLI, C., GAZZOLA, L., GOMES, H. M., GUTTIEREZ, M. C., HAWKEY, P. M., VAN HELDEN, P. D., KADIVAL, G. V., KREISWIRTH, B. N., KREMER, K., KUBIN, M., KULKARNI, S. P., LIENS, B., LILLEBAEK, T., HO, M. L., MARTIN, C., MARTIN, C., MOKROUSOV, I., NARVSKAIA, O., NGEOW, Y. F., NAUMANN, L., NIEMANN, S., PARWATI, I., RAHIM, Z., RASOLOFO-RAZANAMPARANY, V., RASOLONAVALONA, T., ROSSETTI, M. L., RUSCH-GERDES, S., SAJDUDA, A., SAMPER, S., SHEMYAKIN, I. G., SINGH, U. B., SOMOSKOVI, A., SKUCE, R. A., VAN SOOLINGEN, D., STREICHER, E. M., SUFFYS, P. N., TORTOLI, E., TRACEVSKA, T., VINCENT, V., VICTOR, T. C., WARREN, R. M., YAP, S. F., ZAMAN, K., PORTAELS, F., RASTOGI, N. & SOLA, C. 2006. *Mycobacterium tuberculosis* complex genetic diversity: mining the fourth international spoligotyping database (SpolDB4) for classification, population genetics and epidemiology. *BMC Microbiol,* 6**,** 23.

CAMPBELL, I. M. 1985. Secondary metabolism and microbial physiology. *Advances in microbial physiology.* 25, 1-60. Academic Press. https://doi.org/10.1016/S0065-2911(08)60290-8.

CAO, G., ZHONG, C., ZONG, G., FU, J., LIU, Z., ZHANG, G. & QIN, R. 2016. Complete genome sequence of *Streptomyces clavuligerus* F613-1, an industrial producer of clavulanic acid. *Genome Announcements,* 4**,** e01020-16.

CHEN, I. A., CHU, K., PALANIAPPAN, K., PILLAY, M., RATNER, A., HUANG, J., HUNTEMANN, M., VARGHESE, N., WHITE, J. R., SESHADRI, R., SMIRNOVA, T., KIRTON, E., JUNGBLUTH, S. P., WOYKE, T., ELOE-FADROSH, E. A., IVANOVA, N. N. & KYRPIDES, N. C. 2019. IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. *Nucleic Acids Res,* 47**,** D666-d677.

CHEN, W. & QIN, Z. 2011. Development of a gene cloning system in a fast-growing and moderately thermophilic *Streptomyces* species and heterologous expression of Streptomyces antibiotic biosynthetic gene clusters. *BMC Microbiology,* 11**,** 243.

COLE, S., EIGLMEIER, K., PARKHILL, J., JAMES, K., THOMSON, N., WHEELER, P., HONORE, N., GARNIER, T., CHURCHER, C. & HARRIS, D. 2001. Massive gene decay in the leprosy *bacillus*. *Nature,* 409**,** 1007.

COLE, S. T., BROSCH, R., PARKHILL, J., GARNIER, T., CHURCHER, C., HARRIS, D., GORDON, S. V., EIGLMEIER, K., GAS, S., BARRY, C. E., 3RD, TEKAIA, F., BADCOCK, K., BASHAM, D., BROWN, D., CHILLINGWORTH, T., CONNOR, R., DAVIES, R., DEVLIN, K., FELTWELL, T., GENTLES, S., HAMLIN, N., HOLROYD, S., HORNSBY, T., JAGELS, K., KROGH, A., MCLEAN, J., MOULE, S., MURPHY, L., OLIVER, K., OSBORNE, J., QUAIL, M. A., RAJANDREAM, M. A., ROGERS, J., RUTTER, S., SEEGER, K., SKELTON, J., SQUARES, R., SQUARES, S., SULSTON, J. E., TAYLOR, K., WHITEHEAD, S. & BARRELL, B. G. 1998. Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence. *Nature,* 393**,** 537-44.

COLEMAN, N. V., YAU, S., WILSON, N. L., NOLAN, L. M., MIGOCKI, M. D., LY, M. A., CROSSETT, B. & HOLMES, A. J. 2011. Untangling the multiple monooxygenases of *Mycobacterium chubuense* strain NBB4, a versatile hydrocarbon degrader. *Environ Microbiol Rep,* 3**,** 297-307.

DE LA FUENTE, A., LORENZANA, L. M., MARTÍN, J. F. & LIRAS, P. 2002. Mutants of *Streptomyces clavuligerus* with disruptions in different genes for clavulanic acid biosynthesis produce large amounts of holomycin: possible cross-regulation of two unrelated secondary metabolic pathways. *Journal of Bacteriology*, 184**,** 6559-6565.

DE LIMA PROCÓPIO, R. E., DA SILVA, I. R., MARTINS, M. K., DE AZEVEDO, J. L. & DE ARAÚJO, J. M. 2012. Antibiotics produced by *Streptomyces*. *The Brazilian Journal of Infectious Diseases*, 16**,** 466-471.

DEMAIN, A. L. & FANG, A. 2000. The natural functions of secondary metabolites. In *History of modern biotechnology I*. pp. 1-39. Springer, Berlin, Heidelberg. DOI: https://doi.org/10.1007/3-540-44964-7_1.

DIAS, O., ROCHA, M., FERREIRA, E. C. & ROCHA, I. 2015. Reconstructing genome-scale metabolic models with merlin. *Nucleic Acids Res*, 43**,** 3899-910.

DISTLER, J., MANSOURI, K., MAYER, G., STOCKMANN, M. & PIEPERSBERG, W. 1992. Streptomycin biosynthesis and its regulation in *Streptomycetes*. *Gene*, 115**,** 105-111.

FENG, X., XU, Y., CHEN, Y. & TANG, Y. J. 2012. MicrobesFlux: a web platform for drafting metabolic models from the KEGG database. *BMC Syst Biol*, 6**,** 94.

FEYEREISEN, R. 2012. Insect CYP genes and P450 enzymes. In *Insect Molecular Biology and Biochemistry*. pp. 236-316. Academic Press.

GARCIA, M. J. & GOLA, S. 2016. Gene and whole genome analyses reveal that the mycobacterial strain JS623 is not a member of the species *Mycobacterium smegmatis*. *Microb Biotechnol*, 9**,** 269-74.

GARFINKEL, D. 1958. Studies on pig liver microsomes. I. Enzymic and pigment composition of different microsomal fractions. *Archives of Biochemistry and Biophysics*, 77**,** 493-509.

GARNIER, T., EIGLMEIER, K., CAMUS, J.-C., MEDINA, N., MANSOOR, H., PRYOR, M., DUTHOY, S., GRONDIN, S., LACROIX, C., MONSEMPE, C., SIMON, S., HARRIS,

B., ATKIN, R., DOGGETT, J., MAYES, R., KEATING, L., WHEELER, P. R., PARKHILL, J., BARRELL, B. G., COLE, S. T., GORDON, S. V. & HEWINSON, R. G. 2003. The complete genome sequence of *Mycobacterium bovis*. *Proceedings of the National Academy of Sciences,* 100**,** 7877-7882.

GOMEZ-ESCRIBANO, J. P., CASTRO, J. F., RAZMILIC, V., CHANDRA, G., ANDREWS, B., ASENJO, J. A. & BIBB, M. J. 2015. The *Streptomyces leeuwenhoekii* genome: de novo sequencing and assembly in single contigs of the chromosome, circular plasmid pSLE1 and linear plasmid pSLE2. *BMC Genomics,* 16**,** 485.

GREULE, A., STOK, J. E., DE VOSS, J. J. & CRYLE, M. J. 2018. Unrivalled diversity: the many roles and reactions of bacterial cytochromes P450 in secondary metabolism. *Nat Prod Rep,* 35**,** 757-791.

GU, Y., YANG, C., WANG, X., GENG, W., SUN, Y., FENG, J., WANG, Y., QUAN, Y., CHE, Y. & ZHANG, C. 2014. Genome sequence of the ε-poly-L-lysine-producing strain *Streptomyces albulus* NK660, isolated from soil in Gutian, Fujian Province, China. *Genome Announcements,* 2**,** e00532-14.

GUENGERICH, F. P., MARTIN, M. V., SOHL, C. D. & CHENG, Q. 2009. Measurement of cytochrome P450 and NADPH-cytochrome P450 reductase. *Nat Protoc,* 4**,** 1245-51.

GUNNELIUS, L., KURKELA, J., HAKKILA, K., KOSKINEN, S., PARIKAINEN, M. & TYYSTJÄRVI, T. 2014. The ω subunit of RNA polymerase is essential for thermal acclimation of the cyanobacterium *Synechocystis* sp. PCC 6803. *PloS One,* 9**,** e112599.

HENRY, C. S., DEJONGH, M., BEST, A. A., FRYBARGER, P. M., LINSAY, B. & STEVENS, R. L. 2010. High-throughput generation, optimization and analysis of genome-scale metabolic models. *Nature Biotechnology,* 28**,** 977.

HERNÁNDEZ-ALVARADO, J., ZARAGOZA-BASTIDA, A., LÓPEZ-RODRÍGUEZ, G., PELÁEZ-ACERO, A., OLMEDO-JUÁREZ, A. & RIVERO-PEREZ, N. 2018. Actividad antibacteriana y sobre nematodos gastrointestinales de metabolitos secundarios vegetales: enfoque en Medicina Veterinaria. *Abanico Veterinario,* 8**,** 14-27.

HOEFLER, B. C., KONGANTI, K. & STRAIGHT, P. D. 2013. De novo assembly of the *Streptomyces* sp. strain Mg1 genome using PacBio single-molecule sequencing. *Genome Announcements,* 1.

HORAN, K. L., FREEMAN, R., WEIGEL, K., SEMRET, M., PFALLER, S., COVERT, T. C., VAN SOOLINGEN, D., LEAO, S. C., BEHR, M. A. & CANGELOSI, G. A. 2006. Isolation of the genome sequence strain *Mycobacterium avium* 104 from multiple patients over a 17-year period. *J Clin Microbiol,* 44**,** 783-9.

IOERGER, T. R., KOO, S., NO, E.-G., CHEN, X., LARSEN, M. H., JACOBS JR, W. R., PILLAY, M., STURM, A. W. & SACCHETTINI, J. C. 2009. Genome analysis of multi- and extensively-drug-resistant tuberculosis from KwaZulu-Natal, South Africa. *PloS One,* 4**,** e7778.

ISAZA, J. P., DUQUE, C., GOMEZ, V., ROBLEDO, J., BARRERA, L. F. & ALZATE, J. F. 2012. Whole genome shotgun sequencing of one Colombian clinical isolate of *Mycobacterium tuberculosis* reveals DosR regulon gene deletions. *FEMS Microbiology Letters,* 330**,** 113-120.

JANKOWITSCH, F., SCHWARZ, J., RÜCKERT, C., GUST, B., SZCZEPANOWSKI, R., BLOM, J., PELZER, S., KALINOWSKI, J. & MACK, M. 2012. Genome sequence of the bacterium *Streptomyces davawensis* JCM 4913 and heterologous production of the unique antibiotic roseoflavin. *Journal of Bacteriology,* 194**,** 6818-6827.

JOUNG, S. M., JEON, S. J., LIM, Y. J., LIM, J.-S., CHOI, B.-S., CHOI, I.-Y., YU, J. H., NA, K.-I., CHO, E.-H., SHIN, S.-S., PARK, Y. K., KIM, C.-K., KIM, H.-J. & RYOO, S. W. 2013. Complete genome sequence of *Mycobacterium bovis* BCG Korea, the Korean vaccine strain for substantial production. *Genome Announcements*, 1**,** e00069-13.

KALLIMANIS, A., KARABIKA, E., MAVROMATIS, K., LAPIDUS, A., LABUTTI, K. M., LIOLIOS, K., IVANOVA, N., GOODWIN, L., WOYKE, T. & VELENTZAS, A. D. 2011. Complete genome sequence of *Mycobacterium* sp. strain (Spyr1) and reclassification to *Mycobacterium gilvum* Spyr1. *Standards in Genomic Sciences*, 5**,** 144.

KANNAN, R. R., INIYAN, A. M. & VINCENT, S. G. P. 2014. Production of a compound against methicillin resistant *Staphylococcus aureus* (MRSA) from *Streptomyces rubrolavendulae* ICN3 and its evaluation in zebrafish embryos. *The Indian Journal of Medical Research*, 139**,** 913.

KIM, B.-J., CHOI, B.-S., CHOI, I.-Y., LEE, J.-H., CHUN, J., HONG, S.-H., KOOK, Y.-H. & KIM, B.-J. 2012a. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-36Y, belonging to the INT5 genotype. *Journal of Bacteriology*, 194**,** 4141-4142.

KIM, B.-J., CHOI, B.-S., LIM, J.-S., CHOI, I.-Y., LEE, J.-H., CHUN, J., KOOK, Y.-H. & KIM, B.-J. 2012b. Complete genome sequence of *Mycobacterium intracellulare* clinical strain MOTT-02. *Journal of Bacteriology*, 194**,** 2771-2771.

KIM, B.-J., CHOI, B.-S., LIM, J.-S., CHOI, I.-Y., LEE, J.-H., CHUN, J., KOOK, Y.-H. & KIM, B.-J. 2012c. Complete genome sequence of *Mycobacterium intracellulare* strain ATCC 13950T. *Journal of Bacteriology*, 194**,** 2750-2750.

KIM, B.-J., KIM, B.-R., HONG, S.-H., SEOK, S.-H., KOOK, Y.-H. & KIM, B.-J. 2013. Complete genome sequence of *Mycobacterium massiliense* clinical strain Asan 50594, belonging to the Type II genotype. *Genome Announcements,* 1**,** e00429-13.

KIM, M.-K., PARK, H. & OH, T.-J. 2014. Antibacterial and antioxidant potential of polar microorganisms isolated from Antarctic lichen *Psoroma* sp. *African Journal of Microbiology Research,* 8**,** 3529-3535.

KLINGENBERG, M. 1958. Pigments of rat liver microsomes. *Arch Biochem Biophys,* 75**,** 376-86.

LAMB, D. C., LEI, L., WARRILOW, A. G., LEPESHEVA, G. I., MULLINS, J. G., WATERMAN, M. R. & KELLY, S. L. 2009. The first virally encoded cytochrome p450. *J Virol*, 83**,** 8266-9.

LAMB, D. C., WATERMAN, M. R., KELLY, S. L. & GUENGERICH, F. P. 2007. Cytochromes P450 and drug discovery. *Current Oopinion in Biotechnology,* 18**,** 504-512.

LATENDRESSE, M., KRUMMENACKER, M., TRUPP, M. & KARP, P. D. 2012. Construction and completion of flux balance models from pathway databases. *Bioinformatics,* 28**,** 388-96.

LEIPOLDT, F., ZEYHLE, P., KULIK, A., KALINOWSKI, J., HEIDE, L. & KAYSSER, L. 2015. Diversity of ABBA prenyltransferases in marine *Streptomyces* sp. CNQ-509: promiscuous enzymes for the biosynthesis of mixed terpenoid compounds. *PLoS One,* 10**,** e0143237.

LI, L., BANNANTINE, J. P., ZHANG, Q., AMONSIN, A., MAY, B. J., ALT, D., BANERJI, N., KANJILAL, S. & KAPUR, V. 2005. The complete genome sequence of *Mycobacterium avium* subspecies *paratuberculosis*. *Proceedings of the National Academy of Sciences of the United States of America,* 102**,** 12344-12349.

LIAO, Y. C., TSAI, M. H., CHEN, F. C. & HSIUNG, C. A. 2012. GEMSiRV: a software platform for GEnome-scale metabolic model simulation, reconstruction and visualization. *Bioinformatics,* 28**,** 1752-8.

MADHAVILATHA, G., JOSEPH, B. V., PAUL, L. K., KUMAR, R. A., HARIHARAN, R. & MUNDAYOOR, S. 2012. Whole-genome sequences of two clinical isolates of *Mycobacterium tuberculosis* from Kerala, South India. *Journal of Bacteriology,* 194**,** 4430.

MATSUMOTO, S., KOUCHI, M., FUKUI, H. & UEDA, Y. Phylogenetic analyses of the subgenus Eurosa using the ITS nrDNA sequence. *XXV International Horticultural Congress, Part 11: Application of Biotechnology and Molecular Biology and Breeding-Gene 521*, 1998. 193-202.

MCMURRY, J. E. 2014. Organic chemistry with biological applications. *In: Secondary metabolites: An introduction to natural products chemistry,* Stamford, USA: Cengage Learning. https://www.cengage.com/resource_uploads/downloads/0495015253_60174.pdf.

MEDEMA, M. H. 2018. Computational genomics of specialized metabolism: from natural product discovery to microbiome ecology. *mSystems,* 3**,** e00182-17.

MEDEMA, M. H., KOTTMANN, R., YILMAZ, P., CUMMINGS, M., BIGGINS, J. B., BLIN, K., DE BRUIJN, I., CHOOI, Y. H., CLAESEN, J., COATES, R. C., CRUZ-MORALES, P., DUDDELA, S., DUSTERHUS, S., EDWARDS, D. J., FEWER, D. P., GARG, N., GEIGER, C., GOMEZ-ESCRIBANO, J. P., GREULE, A., HADJITHOMAS, M., HAINES, A. S., HELFRICH, E. J., HILLWIG, M. L., ISHIDA, K., JONES, A. C., JONES, C. S., JUNGMANN, K., KEGLER, C., KIM, H. U., KOTTER, P., KRUG, D., MASSCHELEIN, J., MELNIK, A. V., MANTOVANI, S. M., MONROE, E. A., MOORE,

M., MOSS, N., NUTZMANN, H. W., PAN, G., PATI, A., PETRAS, D., REEN, F. J., ROSCONI, F., RUI, Z., TIAN, Z., TOBIAS, N. J., TSUNEMATSU, Y., WIEMANN, P., WYCKOFF, E., YAN, X., YIM, G., YU, F., XIE, Y., AIGLE, B., APEL, A. K., BALIBAR, C. J., BALSKUS, E. P., BARONA-GOMEZ, F., BECHTHOLD, A., BODE, H. B., BORRISS, R., BRADY, S. F., BRAKHAGE, A. A., CAFFREY, P., CHENG, Y. Q., CLARDY, J., COX, R. J., DE MOT, R., DONADIO, S., DONIA, M. S., VAN DER DONK, W. A., DORRESTEIN, P. C., DOYLE, S., DRIESSEN, A. J., EHLING-SCHULZ, M., ENTIAN, K. D., FISCHBACH, M. A., GERWICK, L., GERWICK, W. H., GROSS, H., GUST, B., HERTWECK, C., HOFTE, M., JENSEN, S. E., JU, J., KATZ, L., KAYSSER, L., KLASSEN, J. L., KELLER, N. P., KORMANEC, J., KUIPERS, O. P., KUZUYAMA, T., KYRPIDES, N. C., KWON, H. J., LAUTRU, S., LAVIGNE, R., LEE, C. Y., LINQUAN, B., LIU, X., LIU, W., *et al*. 2015. Minimum information about a biosynthetic gene cluster. *Nat Chem Biol,* 11**,** 625-31.

MIYOSHI-AKIYAMA, T., MATSUMURA, K., IWAI, H., FUNATOGAWA, K. & KIRIKAE, T. 2012. Complete annotated genome sequence of *Mycobacterium tuberculosis* Erdman. *Journal of Bacteriology,* 194**,** 2770.

MOHAN, A., PADIADPU, J., BALONI, P. & CHANDRA, N. 2015. Complete genome sequences of a *Mycobacterium smegmatis* laboratory strain (MC² 155) and Isoniazid-resistant (4XR1/R2) mutant strains. *Genome Announcements,* 3**,** e01520-14.

MONOT, M., HONORÉ, N., GARNIER, T., ZIDANE, N., SHERAFI, D., PANIZ-MONDOLFI, A., MATSUOKA, M., TAYLOR, G. M., DONOGHUE, H. D. & BOUWMAN, A. 2009.

Comparative genomic and phylogeographic analysis of *Mycobacterium leprae*. *Nature Genetics,* 41**,** 1282.

MYRONOVSKYI, M., TOKOVENKO, B., MANDERSCHEID, N., PETZKE, L. & LUZHETSKYY, A. 2013. Complete genome sequence of *Streptomyces fulvissimus*. *Journal of Biotechnology,* 168**,** 117-118.

NANTHINI, J., CHIA, K.-H., THOTTATHIL, G. P., TAYLOR, T. D., KONDO, S., NAJIMUDIN, N., BAYBAYAN, P., SINGH, S. & SUDESH, K. 2015. Complete genome sequence of *Streptomyces* sp. strain CFMR 7, a natural rubber degrading actinomycete isolated from Penang, Malaysia. *Journal of Biotechnology,* 214**,** 47-48.

NARAYANAN, S. & DESHPANDE, U. 2013. Whole-genome sequences of four clinical isolates of *Mycobacterium tuberculosis* from Tamil Nadu, south India. *Genome Announcements,* 1.

NELSON, D. R. 1998. Cytochrome P450 nomenclature. *Methods Mol Biol,* 107**,** 15-24.

NELSON, D. R. 2006. Cytochrome P450 nomenclature, 2004. *Methods Mol Biol,* 320**,** 1-10.

NELSON, D. R. 2018. Cytochrome P450 diversity in the tree of life. *Biochim Biophys Acta Proteins Proteom,* 1866**,** 141-154.

NELSON, D. R., KAMATAKI, T., WAXMAN, D. J., GUENGERICH, F. P., ESTABROOK, R. W., FEYEREISEN, R., GONZALEZ, F. J., COON, M. J., GUNSALUS, I. C., GOTOH, O. & ET AL. 1993. The P450 superfamily: update on new sequences, gene mapping, accession numbers, early trivial names of enzymes, and nomenclature. *DNA Cell Biol,* 12**,** 1-51.

NÚÑEZ, L. E., MÉNDEZ, C., BRAÑA, A. F., BLANCO, G. & SALAS, J. A. 2003. The biosynthetic gene cluster for the β-lactam carbapenem thienamycin in *Streptomyces cattleya*. *Chemistry & Biology,* 10**,** 301-311.

OHNISHI, Y., ISHIKAWA, J., HARA, H., SUZUKI, H., IKENOYA, M., IKEDA, H., YAMASHITA, A., HATTORI, M. & HORINOUCHI, S. 2008. Genome sequence of the streptomycin-producing microorganism *Streptomyces griseus* IFO 13350. *Journal of Bacteriology,* 190**,** 4050-4060.

OMURA, T. 2011. Recollection of the early years of the research on cytochrome P450. *Proc Jpn Acad Ser B Phys Biol Sci,* 87**,** 617-40.

OMURA, T. & SATO, R. 1962. A new cytochrome in liver microsomes. *J Biol Chem,* 237**,** 1375-6.

ORDUÑA, P., CEVALLOS, M. A., DE LEÓN, S. P., ARVIZU, A., HERNÁNDEZ-GONZÁLEZ, I. L., MENDOZA-HERNÁNDEZ, G. & LÓPEZ-VIDAL, Y. 2011. Genomic and proteomic analyses of *Mycobacterium bovis* BCG Mexico 1931 reveal a diverse immunogenic repertoire against tuberculosis infection. *BMC Genomics,* 12**,** 493.

PABINGER, S., RADER, R., AGREN, R., NIELSEN, J. & TRAJANOSKI, Z. 2011. MEMOSys: Bioinformatics platform for genome-scale metabolic models. *BMC Systems Biology,* 5**,** 20.

PARADKAR, A. 2013. Clavulanic acid production by *Streptomyces clavuligerus*: biogenesis, regulation and strain improvement. *The Journal of Antibiotics,* 66**,** 411.

PARVEZ, M., QHANYA, L. B., MTHAKATHI, N. T., KGOSIEMANG, I. K., BAMAL, H. D., PAGADALA, N. S., XIE, T., YANG, H., CHEN, H., THERON, C. W., MONYAKI, R., RASELEMANE, S. C., SALEWE, V., MONGALE, B. L., MATOWANE, R. G., ABDALLA, S. M., BOOI, W. I., VAN WYK, M., OLIVIER, D., BOUCHER, C. E.,

NELSON, D. R., TUSZYNSKI, J. A., BLACKBURN, J. M., YU, J. H., MASHELE, S. S., CHEN, W. & SYED, K. 2016. Molecular evolutionary dynamics of cytochrome P450 monooxygenases across kingdoms: Special focus on mycobacterial P450s. *Sci Rep,* 6**,** 33099.

PESCHKE, U., SCHMIDT, H., ZHANG, H. Z. & PIEPERSBERG, W. 1995. Molecular characterization of the lincomycin-production gene cluster of *Streptomyces lincolnensis* 78-11. *Molecular Microbiology,* 16**,** 1137-1156.

PITKANEN, E., JOUHTEN, P., HOU, J., SYED, M. F., BLOMBERG, P., KLUDAS, J., OJA, M., HOLM, L., PENTTILA, M., ROUSU, J. & ARVAS, M. 2014. Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. *PLoS Comput Biol,* 10**,** e1003465.

PODUST, L. M. & SHERMAN, D. H. 2012. Diversity of P450 enzymes in the biosynthesis of natural products. *Nat Prod Rep,* 29**,** 1251-66.

PULLAN, S. T., CHANDRA, G., BIBB, M. J. & MERRICK, M. 2011. Genome-wide analysis of the role of GlnR in *Streptomyces venezuelae* provides new insights into global nitrogen regulation in actinomycetes. *BMC Genomics,* 12**,** 175.

QUADRI, L. E. 2014. Biosynthesis of mycobacterial lipids by polyketide synthases and beyond. *Crit Rev Biochem Mol Biol,* 49**,** 179-211.

REBETS, Y., OSTASH, B., LUZHETSKYY, A., HOFFMEISTER, D., BRAŇA, A., MENDEZ, C., SALAS, J., BECHTHOLD, A. & FEDORENKO, V. 2003. Production of landomycins in *Streptomyces globisporus* 1912 and S. cyanogenus S136 is regulated by genes encoding putative transcriptional activators. *FEMS Microbiology Letters,* 222**,** 149-153.

REDDY, T., RILEY, R., WYMORE, F., MONTGOMERY, P., DECAPRIO, D., ENGELS, R., GELLESCH, M., HUBBLE, J., JEN, D. & JIN, H. 2008. TB database: an integrated platform for tuberculosis research. *Nucleic Acids Research*, 37**,** D499-D508.

RIPOLL, F., PASEK, S., SCHENOWITZ, C., DOSSAT, C., BARBE, V., ROTTMAN, M., MACHERAS, E., HEYM, B., HERRMANN, J.-L. & DAFFÉ, M. 2009. Non mycobacterial virulence genes in the genome of the emerging pathogen *Mycobacterium abscessus*. *PloS One*, 4**,** e5660.

RONG, X., DOROGHAZI, J. R., CHENG, K., ZHANG, L., BUCKLEY, D. H. & HUANG, Y. 2013. Classification of *Streptomyces* phylogroup pratensis (Doroghazi and Buckley, 2010) based on genetic and phenotypic evidence, and proposal of *Streptomyces pratensis* sp. nov. *Systematic and Applied Microbiology*, 36**,** 401-407.

RÜCKERT, C., ALBERSMEIER, A., BUSCHE, T., JAENICKE, S., WINKLER, A., FRIÐJÓNSSON, Ó. H., HREGGVIÐSSON, G. Ó., LAMBERT, C., BADCOCK, D. & BERNAERTS, K. 2015. Complete genome sequence of *Streptomyces lividans* TK24. *Journal of Biotechnology*, 199**,** 21-22.

RÜCKERT, C., SZCZEPANOWSKI, R., ALBERSMEIER, A., GOESMANN, A., IFTIME, D., MUSIOL, E. M., BLIN, K., WOHLLEBEN, W., PÜHLER, A. & KALINOWSKI, J. 2013. Complete genome sequence of the kirromycin producer *Streptomyces collinus* Tü 365 consisting of a linear chromosome and two linear plasmids. *Journal of Biotechnology*, 168**,** 739-740.

RUDOLF, J. D., CHANG, C.-Y., MA, M. & SHEN, B. 2017. Cytochromes P450 for natural product biosynthesis in *Streptomyces*: sequence, structure, and function. *Natural Product Reports*, 34**,** 1141-1172.

SAINI, V., RAGHUVANSHI, S., KHURANA, J. P., AHMED, N., HASNAIN, S. E., TYAGI, A. K. & TYAGI, A. K. 2012. Massive gene acquisitions in *Mycobacterium indicus pranii* provide a perspective on mycobacterial evolution. *Nucleic Acids Research,* 40**,** 10832-10850.

SEKI, M., HONDA, I., FUJITA, I., YANO, I., YAMAMOTO, S. & KOYAMA, A. 2009. Whole genome sequence analysis of *Mycobacterium bovis bacillus* Calmette–Guerin (BCG) Tokyo 172: A comparative study of BCG vaccine substrains. *Vaccine,* 27**,** 1710-1716.

SHETTY, P. R., BUDDANA, S. K., TATIPAMULA, V. B., NAGA, Y. V. V. & AHMAD, J. 2014. Production of polypeptide antibiotic from *Streptomyces parvulus* and its antibacterial activity. *Brazilian Journal of Microbiology,* 45**,** 303-312.

SONG, Y., LIU, G., LI, J., HUANG, H., ZHANG, X., ZHANG, H. & JU, J. 2015. Cytotoxic and antibacterial angucycline-and prodigiosin-analogues from the deep-sea derived *Streptomyce*s sp. SCSIO 11594. *Marine Drugs,* 13**,** 1304-1316.

STINEAR, T. P., SEEMANN, T., HARRISON, P. F., JENKIN, G. A., DAVIES, J. K., JOHNSON, P. D., ABDELLAH, Z., ARROWSMITH, C., CHILLINGWORTH, T. & CHURCHER, C. 2008. Insights from the complete genome sequence of *Mycobacterium marinum* on the evolution of *Mycobacterium tuberculosis*. *Genome Research,* 18**,** 729-741.

STINEAR, T. P., SEEMANN, T., PIDOT, S., FRIGUI, W., REYSSET, G., GARNIER, T., MEURICE, G., SIMON, D., BOUCHIER, C. & MA, L. 2007. Reductive evolution and niche adaptation inferred from the genome of *Mycobacterium ulcerans*, the causative agent of *Buruli ulcer*. *Genome Research,* 17**,** 192-200.

SUPPLY, P., MARCEAU, M., MANGENOT, S., ROCHE, D., ROUANET, C., KHANNA, V., MAJLESSI, L., CRISCUOLO, A., TAP, J. & PAWLIK, A. 2013. Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of *Mycobacterium tuberculosis*. *Nature Genetics,* 45**,** 172.

SWAINSTON, N., SMALLBONE, K., MENDES, P., KELL, D. & PATON, N. 2011. The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. *J Integr Bioinform,* 8**,** 186.

TAKASUKA, T. E., BOOK, A. J., LEWIN, G. R., CURRIE, C. R. & FOX, B. G. 2013. Aerobic deconstruction of cellulosic biomass by an insect-associated *Streptomyces*. *Scientific Reports,* 3**,** 1030.

THIBESSARD, A., HAAS, D., GERBAUD, C., AIGLE, B., LAUTRU, S., PERNODET, J.-L. & LEBLOND, P. 2015. Complete genome sequence of *Streptomyces ambofaciens* ATCC 23877, the spiramycin producer. *Journal of Biotechnology,* 214**,** 117-118.

THIRUMURUGAN, D., CHOLARAJAN, A., RAJA, S. S. & VIJAYAKUMAR, R. 2018. An introductory hapter: Secondary metabolites. *Secondary Metabolites - Sources and Applications.* IntechOpen.DOI: 10.5772/intechopen.79766.

THOMPSON, T. B., KATAYAMA, K., WATANABE, K., HUTCHINSON, C. R. & RAYMENT, I. 2004. Structural and functional analysis of Tetracenomycin F2 Cyclase from *Streptomyces glaucescens* a type II polyketide cyclase. *Journal of Biological Chemistry,* 279**,** 37956-37963.

TIAN, J., YANG, J., LI, L., RUAN, L., WEI, W., ZHENG, G., ZHAO, W., CHEN, J., JIANG, W. & GE, M. 2015. The complete genome sequence of a high pristinamycin-producing strain *Streptomyces pristinaespiralis* HCCB10218. *Journal of Biotechnology,* 214**,** 45-46.

TOBIAS, N. J., DOIG, K. D., MEDEMA, M. H., CHEN, H., HARING, V., MOORE, R., SEEMANN, T. & STINEAR, T. P. 2013. Complete genome sequence of the frog pathogen

Mycobacterium ulcerans Ecovar Liflandii. *Journal of Bacteriology*, 195**,** 556-564.

VAN BROEKHOVEN, A., SHAPIRO, F. & ANNÉ, J. 2001. *Novel frontiers in the production of compounds for biomedical use*, Springer Science & Business Media.

VENTURA, M., CANCHAYA, C., TAUCH, A., CHANDRA, G., FITZGERALD, G. F., CHATER, K. F. & VAN SINDEREN, D. 2007. Genomics of *Actinobacteria*: tracing the evolutionary history of an ancient phylum. *Microbiol Mol Biol Rev*, 71**,** 495-548.

VICTOR, T. C., DE HAAS, P. E., JORDAAN, A. M., VAN DER SPUY, G. D., RICHARDSON, M., VAN SOOLINGEN, D., VAN HELDEN, P. D. & WARREN, R. 2004. Molecular characteristics and global spread of *Mycobacterium tuberculosis* with a western cape F11 genotype. *Journal of Clinical Microbiology*, 42**,** 769-772.

WANG, H., LI, C., ZHANG, B., HE, H., JIN, P., WANG, J., ZHANG, J., WANG, X. & XIANG, W. 2015a. Complete genome sequence of *Streptomyces cyaneogriseus* ssp. noncyanogenus, the thermotolerant producer of commercial antibiotics nemadectin. *Journal of Biotechnology*, 204**,** 1-2.

WANG, L., GAO, C., TANG, N., HU, S. & WU, Q. 2015b. Identification of genetic variations associated with epsilon-poly-lysine biosynthesis in *Streptomyces albulus* ZPM by genome sequencing. *Scientific Reports*, 5**,** 9201.

WEBER, T., BLIN, K., DUDDELA, S., KRUG, D., KIM, H. U., BRUCCOLERI, R., LEE, S. Y., FISCHBACH, M. A., MULLER, R., WOHLLEBEN, W., BREITLING, R., TAKANO, E. & MEDEMA, M. H. 2015. antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res*, 43**,** W237-43.

WENDT-PIENKOWSKI, E., HUANG, Y., ZHANG, J., LI, B., JIANG, H., KWON, H., HUTCHINSON, C. R. & SHEN, B. 2005. Cloning, sequencing, analysis, and heterologous expression of the Fredericamycin biosynthetic gene cluster from *Streptomyces g riseus*. *Journal of the American Chemical Society,* 127**,** 16442-16452.

WIBBERG, D., AL-DILAIMI, A., BUSCHE, T., WEDDERHOFF, I., SCHREMPF, H., KALINOWSKI, J. & DE ORUÉ LUCANA, D. O. 2016. Complete genome sequence of *Streptomyces reticuli*, an efficient degrader of crystalline cellulose. *Journal of Biotechnology,* 222**,** 13-14.

WITT, D. & STACKEBRANDT, E. 1990. Unification of the genera *Streptoverticillum* and *Streptomyces*, and amendation of *Streptomyces Waksman* and *Henrici* 1943, 339AL. *Systematic and Applied Microbiology,* 13**,** 361-371.

WU, H., LI, J., DONG, D., LIU, T., ZHANG, T., ZHANG, D. & LIU, W. 2015. Heterologous coexpression of *Vitreoscilla* hemoglobin and *Bacillus* megaterium glucanase in *Streptomyces lydicus* A02 enhanced its production of antifungal metabolites. *Enzyme and Microbial Technology,* 81**,** 80-87.

WU, L., CHEN, G. & FENG, G. 2017. Complete genome sequence of *Streptomyces griseochromogenes* ATCC 14511T, a producer of nucleoside compounds and diverse secondary metabolites. *Journal of Biotechnology,* 249**,** 16-19.

XU, J., WANG, Y., XIE, S.-J., XU, J., XIAO, J. & RUAN, J.-S. 2009. *Streptomyces xiamenensis* sp. nov., isolated from mangrove sediment. *International Journal of Systematic and Evolutionary Microbiology,* 59**,** 472-476.

YAMAZAKI, H. 2014. *Fifty years of Cytochrome P450 research,* Japan, Springer Japan.

YUAN, W. M. & CRAWFORD, D. L. 1995. Characterization of *Streptomyces lydicus* WYEC108 as a potential biocontrol agent against fungal root and seed rots. *Appl. Environ. Microbiol.*, 61**,** 3119-3128.

YURKOVICH, M. E., TYRAKIS, P. A., HONG, H., SUN, Y., SAMBORSKYY, M., KAMIYA, K. & LEADLAY, P. F. 2012. A late-stage intermediate in salinomycin biosynthesis is revealed by specific mutation in the biosynthetic gene cluster. *ChemBioChem,* 13**,** 66-71.

ZABURANNYI, N., RABYK, M., OSTASH, B., FEDORENKO, V. & LUZHETSKYY, A. 2014. Insights into naturally minimised *Streptomyces albus* J1074 genome. *BMC genomics,* 15**,** 97.

ZHANG, Y., CHEN, C., LIU, J., DENG, H., PAN, A., ZHANG, L., ZHAO, X., HUANG, M., LU, B. & DONG, H. 2011a. Complete genome sequences of *Mycobacterium tuberculosis* strains CCDC5079 and CCDC5080, which belong to the Beijing family. *Journal of Bacteriology,* 193**,** 5591-2.

ZHANG, Z.-Y., SUN, Z.-Q., WANG, Z.-L., WEN, Z.-L., SUN, Q.-W., ZHU, Z.-Q., SONG, Y.-Z., ZHAO, J.-W., WANG, H.-H., ZHANG, S.-L. & GUO, X.-K. 2011b. Complete genome sequence of a novel clinical isolate, the nontuberculous *Mycobacterium* strain JDM601. *Journal of Bacteriology,* 193**,** 4300-4301.

ZHOU, G., YANG, H., ZHOU, H., WANG, C., FU, F., YU, Y., LU, X. & TIAN, Y. 2016. Complete genome sequence of the *Streptomyces* sp. strain CdTB01, a bacterium tolerant to cadmium. *Journal of Biotechnology,* 229**,** 42-43.

ZHU, H.-H., GUO, J., YAO, Q., YANG, S.-Z., DENG, M.-R., HANH, V. T. & RYAN, M. J. 2007. *Streptomyces vietnamensis* sp. nov., a *Streptomycete* with violet–blue diffusible pigment isolated from soil in Vietnam. *International Journal of Systematic and Evolutionary Microbiology*, 57**,** 1770-1774.

CHAPTER 3: METHODOLOGY

3.1. Species and database

In total 60 *Mycobacterial* species and 48 *Streptomyces* species' genomes available for public use from the Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa *et al*., 2016) were used in this study (Table 3.1). *Mycobacterial* species and *Streptomyces* species used in this study, along with their names, species codes and individual genome IDs, were presented in Table 3.1.

Table 3. 1 Information on mycobacterial species and *Streptomyces* species used in the study. Species names, codes, and genome IDs (from NCBI) were listed in the table.

Species name	**Species code**	**Genome ID**
Mycobacterial species		
Mycobacterium africanum GM041182	maf	FR878060
Mycobacterium tuberculosis C	mto	CP002992
Mycobacterium tuberculosis F11	mtf	CP000717
Mycobacterium tuberculosis H37Ra	mra	CP000611
Mycobacterium tuberculosis H37Rv	mtu	NC_000962
Mycobacterium tuberculosis Haarlem	mtul	CP001664
Mycobacterium tuberculosis KZN 1435	mtb	CP001658
Mycobacterium tuberculosis KZN 605	mtz	CP001976
Mycobacterium tuberculosis KZN 4207	mtk	CP001662

Mycobacterium tuberculosis RGTB327	mtg	CP003233
Mycobacterium tuberculosis CDC1551	mtc	AE000516
Mycobacterium tuberculosis strains CCDC5079	mte	CP001641
Mycobacterium tuberculosis 7199-99	mtub	HE663067
Mycobacterium tuberculosis Beijing/NITR203	mtj	CP005082
Mycobacterium tuberculosis CAS/NITR204	mtuc	CP005386
Mycobacterium tuberculosis EAI5	mtx	CP006578
Mycobacterium tuberculosis EAI5/NITR206	mtuh	CP004886
Mycobacterium tuberculosis Erdman=ATCC 35801	mtn	AP012340
Mycobacterium tuberculosis UT205	mtd	HE608151
Mycobacterium canetti CIPT 140010059	mce	HE572590
Mycobacterium canetti CIPT 140060008	mcq	FO203507
Mycobacterium canetti CIPT 140710010	mcx	FO203509
Mycobacterium bovis AF 2122/97	mbo	NC_002945
Mycobacterium bovis BCG Pasteur 1173P2	mbb	AM408590
Mycobacterium bovis BCG Korea 1168P	mbk	CP003900
Mycobacterium bovis BCG Mexico	mbm	CP002095
Mycobacterium bovis BCG Toyko 172	mbt	AP010918
Mycobacterium abscessus ATCC 19977	mab	NC_010397
Mycobacterium abscessus subsp.*bolletti* 50594	mabb	CP004374
Mycobacterium abscessus 47J26	mabl	AP014547
Mycobacterium abscessus 103	maz	CP009408
Mycobacterium abscessus subsp.*bolletti* MA 1948	may	CP009408

Mycobacterium abscessus VO6705	mys	CP009615
Mycobacterium Avium 104	mav	CP000479
Mycobacterium Avium subsp.*paratuberculosis* K10	mpa	AE016958
Mycobacterium avium subsp.*paratuberculosis* MAP4	mao	CP005928
Mycobacterium intracellulare ATCC 13950	mia	CP003322
Mycobacterium intracellulare MOTT-02	mit	CP003323
Mycobacterium intracellulare MOTT-64	mie	CP009499
Mycobacterium intracellulare MOTT-36Y	mmm	CP003491
Mycobacterium indicus pranii MTCC 9506	mid	CP002275
Mycobacterium sp.JDM601	myv	CP009914
Mycobacterium liflandi 128FXT	mli	CP003899
Mycobacterium marinum	mmae	HG917972
Mycobacterium massiliense	mmal	CP023147
Mycobacterium kansassi ATCC 12478	mmv	CP003699
Mycobacterium vanbaalenii PYR-1	mva	CP000511
Mycobacterium smegmatis MC2 155	msb	CP009494
Mycobacterium chubuense NBB4	mcb	CP003053
Mycobacterium gilvum PYR-GCK	mgi	CP000656
Mycobacterium gilvum Spyr1	msp	CP002385
Mycobacterium smegmatis JS623	msa	CP003078
Mycobacterium rhodesiae	mrh	CP003169
Mycobacterium neoaurum VKM Ac-18150	mne	CP006936

***Streptomyces* species**		
Streptomyces coelicolor	sco	NC_003888
Streptomyces avermitilis MA-4680	sma	BA000030
*Streptomyces griseus*_NBRC_13350	sgr	AP009493
Streptomyces globisporus	sgb	CP013738
Streptomyces scabiei 87.22	scb	FN554889
Streptomyces sp. Sirex AA-E	ssx	CP002993
Streptomyces violaceusniger Tu 4113	svl	CP002994
Streptomyces cattleya NRRL 8057	sct	FQ859185
Streptomyces cattleya NRRL 8058 = DSM 46488	scy	CP003219
Streptomyces pratensis/flavogriseus IAF 45	sfa	CP002475
Streptomyces bingchenggensis	sbh	CP002047
Streptomyces hygroscopicus subsp. jinggangensis 5008	shy	CP003275
Streptomyces hygroscopicus subsp. jinggangensis TL01	sho	CP003720
Streptomyces venezuelae	sve	FR845719

Streptomyces davawensis	sdv	HE971709
Streptomyces albus J1074	salb	CP004370
Streptomyces albus DSM 41398	sals	CP010519
Streptomyces sp. PAMC 26508	strp	CP003990
Streptomyces fulvissimus	sfi	CP005080
Streptomyces collinus	sci	CP006259
Streptomyces rapamycinicus	src	CP006567
Streptomyces albulus NK660	salu	CP007574
Streptomyces albus ZPM	sall	CP006871
Streptomyces lividans	slv	CP009124
Streptomyces glaucescens	sgu	CP009438
Streptomyces vietnamensis	svt	CP010407
Streptomyces sp. 769	stre	CP003987
Streptomyces cyaneogriseus	scw	CP010849
Streptomyces lydicus A02	sld	CP007699
Streptomyces xiamenensis 318	sxi	CP009922

Streptomyces sp. Mg1	strm	CP011664
Streptomyces sp. CNQ-509	strc	CP011492
Streptomyces ambofaciens	samb	CP012382
Streptomyces pristinaespiralis HCCB 10218	spri	CP011340
Streptomyces sp. CFMR 7	scz	CP011522
Streptomyces sp. CdTB01	scx	CP013743
Streptomyces reticuli	srw	LN997842
Streptomyces sp. 4F	strf	CP013142
Streptomyces leeuwenhoekii C34(2013)	sle	LN831790
Streptomyces rubrolavendulae	srn	CP017316
Streptomyces parvulus	spav	CP015866
Streptomyces lydicus 103	slc	CP017157
Streptomyces sp. SAT1	strt	CP015849
Streptomyces clavuligerus	sclf	CP016559
Streptomyces griseochromogenes	sgs	CP016279
Streptomyces sp. S10(2016)	stsi	CP015098

Streptomyces lincolnensis	sls	CP016438
Streptomyces noursei	snr	CP011533

3.2. Secondary metabolite biosynthetic gene clusters analysis

Secondary metabolite BGCs analysis was carried out following the method described elsewhere (Mthethwa *et al*., 2018). Briefly, individual *Streptomyces* species' and mycobacterial species' genome IDs from NCBI (Table 3.1) were submitted to antibiotics and Secondary Metabolite Analysis Shell (anti-SMASH) (Weber *et al*., 2015) for identification of secondary metabolite BGCs. Results from anti-SMASH were downloaded both in the form of gene cluster sequences and Excel spreadsheets representing species-wise cluster information. Standard gene cluster abbreviation terminology available on the anti-SMASH database (Weber *et al*., 2015) was maintained in this study.

3.3. Identification of P450s in biosynthetic gene clusters

Individual gene-cluster sequences were manually checked for the presence of P450s. Once a P450 had been identified, the sequence was selected and BLAST analysis was performed at the P450 BLAST server (https://ksyed.weebly.com/p450-blast.html) to identify its name as annotated by the International P450 nomenclature committee (Nelson, 1998, Nelson, 2006). Based on the percentage identity to the named homolog P450, i.e. >40% amino acid identity and >55% amino acid identity, P450s were grouped under the same family and the same subfamily (Nelson, 1998, Nelson, 2006). P450s that had less than 40% and 55% amino acid identity to the named homolog P450s were assigned to new P450 families and new P450 subfamilies. Some mycobacterial species and *Streptomyces* species P450s were annotated and made available at the P450 BLAST server (https://ksyed.weebly.com/p450-blast.html). In this case, the same nomenclature for P450s was continued.

References

KANEHISA, M., SATO, Y., KAWASHIMA, M., FURUMICHI, M. & TANABE, M. 2016. KEGG as a reference resource for gene and protein annotation. *Nucleic Acids Res,* 44**,** D457-62.

MTHETHWA, B. C., CHEN, W., NGWENYA, M. L., KAPPO, A. P., SYED, P. R., KARPOORMATH, R., YU, J. H., NELSON, D. R. & SYED, K. 2018. Comparative analyses of Cytochrome P450s and those associated with secondary metabolism in *Bacillus* species. *Int J Mol Sci,* 19.

NELSON, D. R. 1998. Cytochrome P450 nomenclature. *Methods Mol Biol,* 107**,** 15-24.

NELSON, D. R. 2006. Cytochrome P450 nomenclature, 2004. *Methods Mol Biol,* 320**,** 1-10.

WEBER, T., BLIN, K., DUDDELA, S., KRUG, D., KIM, H. U., BRUCCOLERI, R., LEE, S. Y., FISCHBACH, M. A., MULLER, R., WOHLLEBEN, W., BREITLING, R., TAKANO, E. & MEDEMA, M. H. 2015. antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res,* 43**,** W237-43.

CHAPTER 4: RESULTS AND DISCUSSION

4.1. *Streptomyces* species have a large and diverse number of secondary metabolite biosynthetic gene clusters

Streptomyces species are well known for producing chemically diverse secondary metabolites (Hwang *et al*., 2014) Because of this ability one can expect the presence of a large number of secondary metabolite BGCs in *Streptomyces* species. As anticipated, genome-wide analysis revealed the presence of a large and diverse number of secondary metabolite BGCs in *Streptomyces* species compared to mycobacteria species (Figures 4.1-4.3). Almost double the number of secondary metabolite BGCs and eight times the types of BGCs were found in 48 *Streptomyces* species compared to mycobacterial species (Figure 4.1). In total 1 461 secondary metabolite BGCs belonging to 159 types were found in 48 *Streptomyces* species compared to 898 secondary metabolite BGCs belonging to only 18 types found in 60 mycobacterial species (Figure 4.1). The average number of secondary metabolite BGCs was found to be double in *Streptomyces* species (30) compared to mycobacterial species (15) (Figure 4.2). Among *Streptomyces* species, *S. griseochromogenes* has the highest number of secondary metabolite BGCs (49) and *Streptomyces* sp. 4F has the lowest number of secondary metabolite BGCs (19) in their genomes (Figure 4.2A). *M. marinum* has the highest number of secondary metabolite BGCs (29) and two strains of *M. leprae* have the lowest number of secondary metabolite BGCs (five each) in their genomes (Figure 4.2B). Detailed information on secondary metabolite BGCs found in each of the species belonging to the genera *Streptomyces* and *Mycobacterium* is presented in Table 4.1.

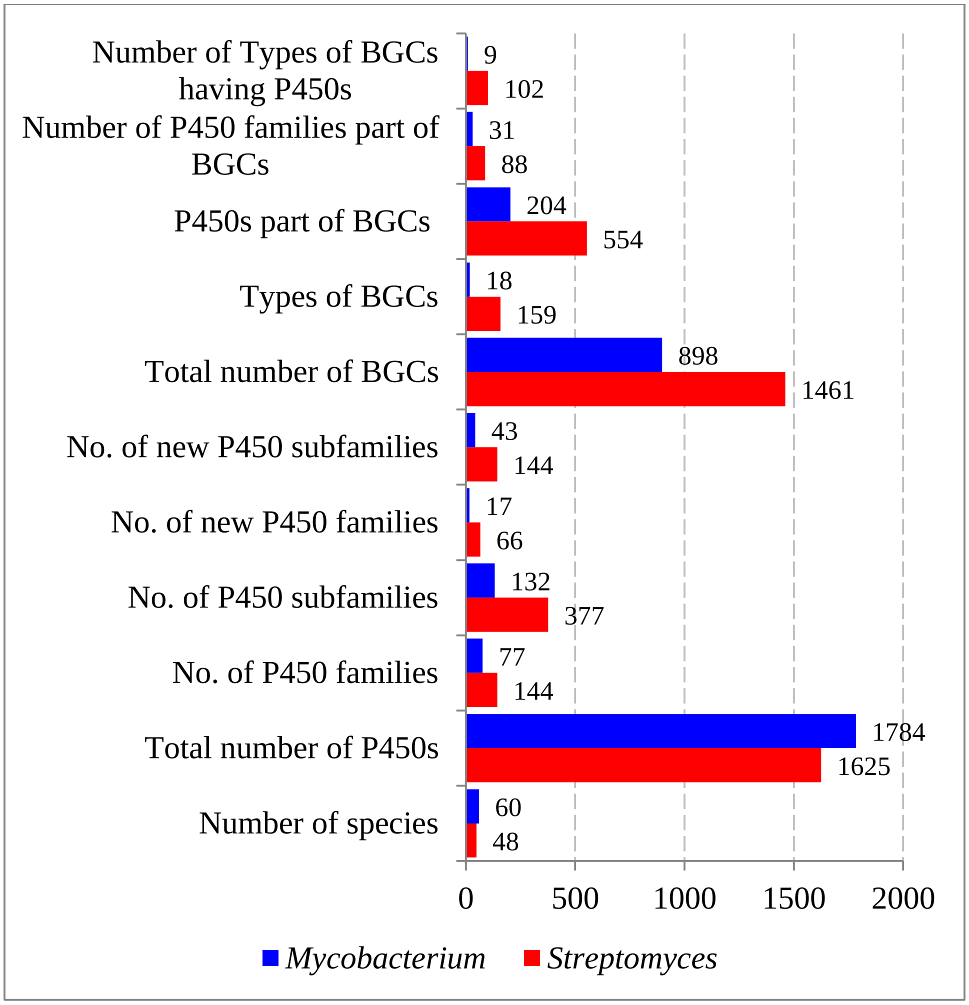


Figure 4. 1 Comparative analysis of key features of P450s between the genera *Streptomyces* and *Mycobacterium*. Y-axis indicates the count for each of the key features

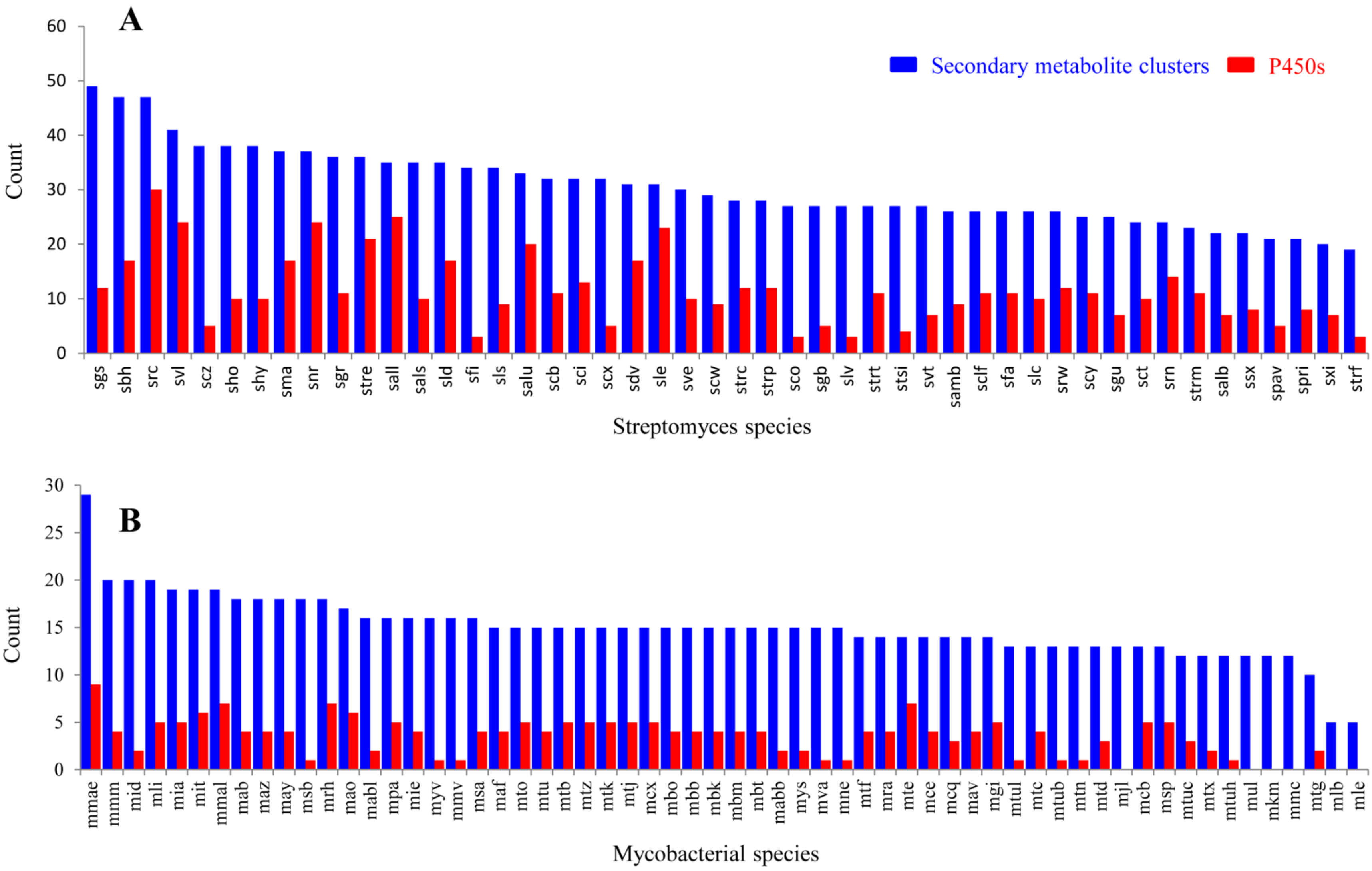

A
Count
60
50
40
30
20
10
0
Secondary metabolite clusters
P450s
sgs
sbh
src
svl
scz
sho
shy
sma
snr
sgr
stre
sall
sals
sld
sfi
sls
salu
scb
sci
scx
sdv
sle
sve
scw
strc
strp
sco
sgb
slv
strt
stsi
svt
samb
sclf
sfa
slc
srw
scy
sgu
sct
srn
strm
salb
ssx
spav
spri
sxi
strf
Streptomyces species
B
Count
30
25
20
15
10
5
0
mmae
mmm
mid
mli
mia
mit
mmal
mab
maz
may
msb
mrh
mao
mabl
mpa
mie
myv
mmv
msa
maf
mto
mtu
mtb
mtz
mtk
mtj
mcx
mbo
mbb
mbk
mbm
mbt
mabb
mys
mva
mne
mtf
mra
mte
mce
mcq
mav
mgi
mtul
mtc
mtub
mtn
mtd
mjl
mcb
msp
mtuc
mtx
mtuh
mul
mkm
mmc
mtg
mlb
mle
Mycobacterial species

Figure 4. 2 Comparative analysis of secondary metabolite BGCs and P450s associated with secondary metabolite BGCs in Streptomyces species (A) and mycobacterial species (B). Detailed information on secondary metabolite BGCs in Streptomyces species and mycobacterial species is presented in Table 4.1.

Table 4. 1 Secondary metabolite biosynthetic gene clusters and P450 analysis in 48 *Streptomyces* species and 60 mycobacterial species. The number of P450s that formed part of each cluster and their corresponding P450 names (in parenthesis) were also presented in the table. Standard gene cluster abbreviation terminology available on the anti-SMASH database (Weber *et al*., 2015) was used in the table.

***Streptomyces* species**

Streptomyces coelicolor

Cluster	**Type**	**Frrom**	**To**	**Most similar known cluster**	**MIBiG BGC-ID**	**P450s**	**Name of the P450**
Cluster 1	T1pks-Otherks	86637	139654	Leinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001101_c1		
Cluster 2	Terpene	166501	192038	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 3	Lantipeptide	235986	271084	Sanglifehrin_A_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001042_c1		
Cluster 4	Nrps	493989	544920	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 5	Bacteriocin	791584	801799	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 6	T3pks	1257625	1298749	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A2
Cluster 7	Ectoine	1995500	2005898	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Melanin	2939306	2949875	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 9	Siderophore	3033895	3045682	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 10	Nrps	3523335	3603988	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000315_c1		
Cluster 11	T2pks	5509801	5552424	Actinorhodin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000194_c1		
Cluster 12	Terpene	5671016	5692101	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A1
Cluster 13	T2pks	5766945	5809487	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1		
Cluster 14	Siderophore	6335587	6347533	-	-		
Cluster 15	T1pks	6429549	6476442	Undecylprodigiosin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001063_c1		

Cluster 16	Bacteriocin	6632343	6643659	-	-		
Cluster 17	Terpene	6656219	6678399	-	-		
Cluster 18	Siderophore	6842315	6855522	Enduracidin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000341_c1		
Cluster 19	T1pks-Butyrolactone	6871293	6951959	Coelimycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000038_c1		
Cluster 20	Nrps	7088264	7136089	Nogalamycin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0000249_c1		
Cluster 21	Lantipeptide	7409664	7432456	SAL-2242_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000546_c1		
Cluster 22	Terpene	7506017	7532758	Hopene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000663_c1		
Cluster 23	T1pks-Otherks	7570412	7618555	Arsenopolyketides_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001283_c1		
Cluster 24	Lantipeptide	7685016	7709795	-	-		
Cluster 25	Other	7973470	8014357	-	-		
Cluster 26	Indole	8269637	8290764	Ravidomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000263_c1		
Cluster 27	T3pks-Terpene-Nrps	8475102	8558352	Coelibactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000324_c1	1	CYP105N1
***Streptomyces avermitilis* MA-4680**							
Cluster 1	Terpene	76073	97080	-	-		
Cluster 2	Lassopeptide	290466	313052	SSV-2083_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000579_c1		
Cluster 3	T1pks	478846	587017	Filipin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000059_c1	2	CYP105D6; CYP105P1
Cluster 4	Nrps	734376	780552	Herbimycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000074_c1	1	CYP147B1
Cluster 5	Nrps-T1pks-Otherks	958292	1062269	Landepoxcin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0001202_c1	2	CYP178A1; CYP178A3P
Cluster 6	T1pks	1117817	1222573	Avermectin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000025_c1	1	CYP171A1
Cluster 7	Terpene	1277518	1302828	Carotenoid_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000633_c1		
Cluster 8	Melanin	1419869	1430225	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000908_c1		
Cluster 9	T1pks-Nrps	1875828	1932282	Daptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000336_c1		
Cluster 10	Terpene	2010191	2036846	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 11	Siderophore	2436883	2449994	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 12	Terpene	2625583	2647760	-	-	1	CYP180A1
Cluster 13	Lassopeptide	2660814	2683259	-	-		
Cluster 14	Bacteriocin	2692334	2703797	-	-		
Cluster 15	T1pks-Butyrolactone-Otherks	2746968	2811733	Chlorizidine_A_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0001172_c1		
Cluster 16	T2pks-T1pks-Otherks	2859868	2921483	Mannopeptimycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000388_c1	2	CYP107Y1; CYP181A1
Cluster 17	Siderophore	3004049	3016109	-	-		
Cluster 18	T2pks	3464232	3506747	Spore_pigment_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000271_c1		
Cluster 19	T1pks	3516766	3646347	Oligomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000117_c1	2	CYP107W1; CYP105B23

Cluster 20	Terpene	3744725	3765735	Pentalenolactone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000678_c1	1	CYP183A1
Cluster 21	Terpene	3780128	3801219	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A2
Cluster 22	Nrps	3910306	3957489	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 23	Nrps	3960213	4012310	Naphthomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000106_c1		
Cluster 24	Butyrolactone-Otherks	4335459	4381172	Herboxidiene_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001065_c1	2	CYP107V1; CYP107U2
Cluster 25	Ladderane-Arylpolyene-Nrps	4480084	4560161	WS9326_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0001297_c1		
Cluster 26	Terpene	4831782	4852768	-	-		
Cluster 27	Siderophore	6378181	6389953	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 28	Melanin	6495109	6505495	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000909_c1		
Cluster 29	Lassopeptide	6869386	6891873	Pimaricin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000125_c1		
Cluster 30	Nrps	6903259	6953329	SCO-2138_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000595_c1		
Cluster 31	Ectoine	7666129	7676533	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 32	Other	7913326	7957201	Pristinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000952_c3		
Cluster 33	T3pks	8471426	8512484	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A3
Cluster 34	T1pks	8533602	8578155	Kirromycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001070_c1	1	CYP105R1
Cluster 35	Siderophore	8727144	8740816	-	-		
Cluster 36	T1pks-Otherks	8758095	8809766	Herboxidiene_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001065_c1		
Cluster 37	Bacteriocin-Lantipeptide	8921460	8953908	Informatipeptin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000518_c1		
***Streptomyces griseus*_NBRC_13350**							
Cluster 1	Terpene	47111	72706	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 2	Lantipeptide	149896	172562	-	-		
Cluster 3	T1pks-Nrps	274490	327047	Daptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000336_c1	1	CYP105D1
Cluster 4	T3pks-Nrps	463570	571330	Tetronasin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000163_c1		
Cluster 5	Melanin	603389	613793	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G2
Cluster 6	T1pks-Nrps	640959	793028	Sporolide_biosynthetic_gene_cluster (53% of genes show similarity)	BGC0000150_c1	3	CYP162C1; CYP208A1; CYP154M2
Cluster 7	Bacteriocin	899922	910719	Tetronasin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000163_c1		
Cluster 8	T1pks-Nrps	936042	985512	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX5
Cluster 9	Nrps	1040073	1091469	Nucleocidin_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0001387_c1	1	CYP107BY1
Cluster 10	Terpene	1127168	1153741	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 11	Terpene	1481583	1502896	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 12	Bacteriocin	1704704	1716146	-	-		
Cluster 13	Linaridin	1766706	1787314	Legonaridin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0001188_c1		
Cluster 14	Siderophore	2025368	2040162	-	-		

Cluster 15	Terpene	2450742	2471749	-	-		
Cluster 16	Lantipeptide	2816830	2839457	AmfS_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000496_c1		
Cluster 17	Melanin	2879832	2890254	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000912_c1		
Cluster 18	T1pks-Nrps	2907245	2961895	Enduracidin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000341_c1		
Cluster 19	Nrps	3029350	3094603	Arixanthomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000200_c1		
Cluster 20	Ladderane-Arylpolyene-Nrps	3747228	3873950	Skyllamycin_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000429_c1	2	CYP163B5; CYP107BZ1
Cluster 21	Lantipeptide	4496390	4520962	-	-		
Cluster 22	Melanin	4960832	4971221	Grixazone_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000662_c1		
Cluster 23	Thiopeptide	5142038	5174689	-	-		
Cluster 24	Siderophore	5573822	5585600	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 25	Lantipeptide	5645167	5668604	-	-		
Cluster 26	Otherks	6216239	6257198	Salinilactam_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000142_c1		
Cluster 27	Ectoine	6603626	6614024	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 28	Amglyccycl	6935101	6958692	Streptomycin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000717_c1		
Cluster 29	T1pks-Terpene	7069072	7191428	BE-7585A_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000203_c1		
Cluster 30	T1pks	7270248	7372684	Tautomycin_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000159_c1		
Cluster 31	T1pks-Linaridin	7552138	7639551	Grisemycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000583_c1		
Cluster 32	T3pks	7888518	7929636	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1	1	CYP107F4
Cluster 33	Transatpks-T1pks-Otherks-Nrps	7995928	8182236	Griseobactin_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000368_c1	1	CYP107CA2
Cluster 34	Terpene	8196573	8236655	Carotenoid_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000649_c1		
Cluster 35	Butyrolactone	8268444	8279388	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1		
Cluster 36	Terpene	8473224	8498819	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
***Streptomyces globisporus* C-1027**							
Cluster 1	Terpene	104229	125263	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Cluster 2	Butyrolactone	177217	188161	Coelimycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000038_c1		
Cluster 3	Terpene	222188	244401	-	-		
Cluster 4	Terpene-Nrps	284764	451409	Griseobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000368_c1		
Cluster 5	T3pks	472394	513512	Lasalocid_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000087_c1	1	CYP107F4
Cluster 6	Terpene-Nrps	844594	917380	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1		
Cluster 7	Terpene	1181612	1202688	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		
Cluster 8	Ectoine	1631082	1641480	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	Lantipeptide	2652852	2675896	-	-		
Cluster 10	Siderophore	2742719	2754497	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		

Cluster 11	Thiopeptide	3122859	3151721	-	-		
Cluster 12	Nrps	3335176	3400695	Oxazolomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001106_c1		
Cluster 13	Lassopeptide	4463970	4486667	SRO15-2005_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000578_c1		
Cluster 14	Lantipeptide	4552589	4594559	Labyrinthopeptin_A1,A3_/_labyrinthopeptin_A2_biosynthetic_gene (40% of genes show similarity)	BGC0000519_c1		
Cluster 15	T1pks-Nrps	5167813	5222510	Leinamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001101_c1		
Cluster 16	Lantipeptide	5299671	5322418	AmfS_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000496_c1		
Cluster 17	Ectoine	5532667	5543041	Pristinamycin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000952_c2		
Cluster 18	Terpene	5664830	5685807	-	-		
Cluster 19	Siderophore	6082612	6097344	-	-		
Cluster 20	Bacteriocin	6331423	6342799	-	-		
Cluster 21	Ectoine	6564225	6574599	Kosinostatin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0001073_c1		
Cluster 22	Arylpolyene-Ladderane	6765985	6819639	Skyllamycin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0000429_c1	1	CYP1373A2
Cluster 23	Terpene	6959815	6986388	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 24	Bacteriocin-T1pks-Nrps	7040610	7115186	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX10
Cluster 25	Melanin	7287746	7298213	Istamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000700_c1	1	CYP124G14
Cluster 26	T3pks	7337452	7378504	Tetronasin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000163_c1		
Cluster 27	T1pks-Nrps	7483759	7536082	Daptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000336_c1	1	CYP105D30
Streptomyces scabiei **87.22**							
Cluster 1	Nrps	121440	196006	Coelibactin_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000324_c1		
Cluster 2	Nrps	331163	401309	Enduracidin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000341_c1		
Cluster 3	Lantipeptide	401538	424192	Labyrinthopeptin_A1,A3_/_labyrinthopeptin_A2_biosynthetic_gene (60% of genes show similarity)	BGC0000519_c1		
Cluster 4	Terpene	560917	582239	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 5	Terpene	601915	628277	Carotenoid_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000633_c1		
Cluster 6	Bacteriocin-Lantipeptide	958478	990742	Informatipeptin_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000518_c1		
Cluster 7	Butyrolactone	1354264	1365265	Calcimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000032_c1		
Cluster 8	Terpene	1443175	1469862	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 9	Siderophore	2066419	2079787	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 10	Other	2213586	2256048	Medermycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000245_c1		
Cluster 11	Terpene	2272242	2294449	Meridamycin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0001012_c1	1	CYP154A4
Cluster 12	Bacteriocin	2343619	2354977	-	-		
Cluster 13	Terpene	2615765	2637636	FD-594_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000222_c1		
Cluster 14	Siderophore	2788855	2800942	-	-		

Cluster 15	Lantipeptide-Nrps	3580343	3663950	Thaxtomin_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000444_c1	4	CYP246A1; CYP1048A1; CYP156D1; CYP154L1
Cluster 16	T2pks	4846105	4888608	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 17	T1pks-Nrps	4907380	4959979	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1	1	CYP107AM1
Cluster 18	Lantipeptide	5327449	5350019	-	-		
Cluster 19	Bacteriocin-Bottromycin	6296673	6328951	Bottromycin_A2_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000469_c1	1	CYP283A1
Cluster 20	Siderophore	6440872	6452644	Desferrioxamine_B_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000940_c1		
Cluster 21	Melanin	6583132	6593572	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000909_c1		
Cluster 22	Butyrolactone-T1pks-Otherks	6948618	7031953	RK-682_biosynthetic_gene_cluster (45% of genes show similarity)	BGC0000140_c1	1	CYP107AL1
Cluster 23	Ectoine	7828037	7838435	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 24	Other	8049774	8093640	Pristinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000952_c3		
Cluster 25	Terpene	8145730	8166746	-	-	1	CYP157C5
Cluster 26	Indole-T1pks	8700511	8773617	Fortimicin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000695_c1	1	CYP156B2
Cluster 27	T1pks	8793133	8848674	Lasalocid_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000087_c1	1	CYP107AK1
Cluster 28	Terpene	9109494	9130543	Oxazolomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001106_c1		
Cluster 29	T1pks-Linaridin	9288856	9423896	Concanamycin_A_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000040_c1		
Cluster 30	Siderophore	9430375	9443981	-	-		
Cluster 31	Melanin-Nrps	9526250	9606840	Scabichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000423_c1		
Cluster 32	Terpene	9618596	9639636	-	-		
***Streptomyces sp.* SirexAA-E**							
Cluster 1	Nrps	183422	233810	Thiocoraline_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000445_c1		
Cluster 2	T2pks-Terpene	248129	297390	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 3	Melanin	333103	343633	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G3
Cluster 4	Nrps	689835	740721	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 5	Nrps	809951	864046	Coelibactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000324_c1	1	CYP105N1
Cluster 6	Terpene	989127	1010161	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		
Cluster 7	Ectoine	1441158	1451556	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Otherks	1930630	1983417	Nataxazole_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0001213_c1		
Cluster 9	Otherks	2409002	2449961	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 10	Lantipeptide	2462308	2485445	-	-		
Cluster 11	Butyrolactone	3534233	3545165	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 12	Terpene	5143473	5164480	Carbapenem_MM_4550_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000842_c1		
Cluster 13	Siderophore	5511501	5526094	-	-		

Cluster 14	Nrps	5617605	5679551	WAP-8294A2_(lotilibcin)_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000461_c1		
Cluster 15	Terpene	5745560	5771085	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 16	T2pks-T1pks-Otherks	5841512	5903128	Hedamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000233_c1	2	CYP181A1; CYP107Y1
Cluster 17	Bacteriocin	5953056	5964366	-	-		
Cluster 18	T1pks	6260096	6354741	Vicenistatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000167_c1	2	CYP105AZ1; CYP105AZ2
Cluster 19	Terpene	6577011	6599080	Leinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001101_c1		
Cluster 20	Terpene	6730096	6756683	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 21	T1pks-Nrps	6922336	6971791	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX4
Cluster 22	T2pks-Butyrolactone-Nrps	7145734	7230746	Auricin_biosynthetic_gene_cluster (41% of genes show similarity)	BGC0000201_c1	1	CYP105A4
***Streptomyces violaceusniger* Tu 4113**							
Cluster 1	Siderophore	886115	897905	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 2	Lantipeptide	1145837	1170458	-	-		
Cluster 3	Other	1450857	1493703	Echosides_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000340_c1		
Cluster 4	Siderophore	2078339	2090252	-	-		
Cluster 5	Bacteriocin	2301044	2312369	-	-		
Cluster 6	T2pks	2543707	2586222	Spore_pigment_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000271_c1		
Cluster 7	Terpene	2936974	2963422	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1	2	CYP107BW1; CYP1013A2
Cluster 8	Lantipeptide	3160291	3199125	BE-7585A_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000203_c1		
Cluster 9	Nrps	3219941	3299320	Lipopeptide_8D1-1_/_lipopeptide_8D1-2_biosynthetic_gene_clus... (6% of genes show similarity)	BGC0001370_c1	2	CYP162A3; CYP107CK1
Cluster 10	Lassopeptide	3364827	3387368	SSV-2083_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000579_c1		
Cluster 11	T1pks	3419279	3467405	-	-		
Cluster 12	Butyrolactone	3770063	3780995	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 13	Hserlactone	3791483	3812241	Daptomycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000336_c1		
Cluster 14	T1pks	3977601	4057790	Elaiophylin_biosynthetic_gene_cluster (87% of genes show similarity)	BGC0000053_c1		
Cluster 15	T1pks	4154756	4201139	Salinomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000144_c1		
Cluster 16	T1pks	4202037	4333901	Nigericin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000114_c1	1	CYP124B3
Cluster 17	T1pks	4514441	4670396	ECO-02301_biosynthetic_gene_cluster (39% of genes show similarity)	BGC0000052_c1	2	CYP107BW1; CYP105AX1
Cluster 18	T1pks-Nrps	5128359	5213730	Actinomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000296_c1		
Cluster 19	T1pks-Nrps	5224048	5312355	Naphthomycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000106_c1		
Cluster 20	Other	5434110	5476848	Echosides_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000340_c1		
Cluster 21	Otherks	5520939	5561958	Galbonolides_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000065_c1	2	CYP183F2; CYP105AV1
Cluster 22	Terpene	5684250	5706013	Brasilicardin_A_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000632_c1		

Cluster 23	Bacteriocin-Lantipeptide-T1pks-Otherks-Nrps	5741925	5876020	Leinamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001101_c1	4	CYP105AQ2; CYP155A5; CYP107E9; CYP105AN3
Cluster 24	Other	5927077	5968123	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1		
Cluster 25	T1pks	6014424	6098236	Hygrocin_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000075_c1	1	CYP107AD1
Cluster 26	Lantipeptide-T1pks-Nrps	6091811	6215900	Meridamycin_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0001011_c1	1	CYP105AY1
Cluster 27	Terpene	6421015	6442313	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 28	Terpene	6555062	6576216	-	-		
Cluster 29	T1pks	6675986	6758493	Herbimycin_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000074_c1	1	CYP105U1
Cluster 30	T1pks-Otherks	7181560	7243764	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 31	T1pks	7437179	7552962	Reveromycin_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000135_c1		
Cluster 32	T1pks-Siderophore	7736179	7814751	Apoptolidin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000021_c1		
Cluster 33	Ectoine	7966340	7976744	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 34	Terpene	8459184	8480494	-	-	2	CYP156C9; CYP125A20
Cluster 35	Lantipeptide	8814684	8837881	Actagardine_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000495_c1		
Cluster 36	T1pks	9065094	9247443	ECO-02301_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000052_c1		
Cluster 37	Ladderane	9434566	9475807	WS9326_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0001297_c1		
Cluster 38	Nrps	9526467	9570633	Ochronotic_pigment_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000918_c1		
Cluster 39	Indole	9805824	9826966	7-prenylisatin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0001294_c1	2	CYP107U9; CYP156B6
Cluster 40	Ladderane-Arylpolyene-Nrps	10111293	10214141	Skyllamycin_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000429_c1	3	CYP163B4; CYP107CF1; CYP107CE1
Cluster 41	Terpene	10465383	10487659	Desotamide_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001196_c1	1	CYP147F5
***Streptomyces cattleya* NRRL 8057**							
Cluster 1	Butyrolactone	1	6680	-	-		
Cluster 2	T1pks-Lassopeptide	32796	99728	Mannopeptimycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000388_c1		
Cluster 3	T1pks	129575	276643	Akaeolide_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0001199_c1	2	CYP107AS; CYP107CR1
Cluster 4	Terpene	570378	591112	-	-		
Cluster 5	Lantipeptide	626485	651045	-	-		
Cluster 6	Other	968655	1009491	Pyrrolomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000130_c1		
Cluster 7	Ectoine	1153014	1163418	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Lantipeptide	1527378	1550026	AmfS_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000496_c1		
Cluster 9	Butyrolactone	2315622	2326407	Rabelomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000262_c1		
Cluster 10	T3pks	2334065	2375096	-	-		
Cluster 11	Nrps	2784016	2856738	Salinosporamide_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0001041_c1		

Cluster 12	Lantipeptide	2936415	2965706	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1	1	CYP107AE6
Cluster 13	Terpene	3092166	3114391	-	-		
Cluster 14	T1pks-Nrps	3416953	3486060	Akaeolide_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001199_c1	1	CYP184A4
Cluster 15	Transatpks-T1pks-Nrps	3784857	3878760	Kirromycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001070_c1	2	CYP107CS1; CYP107W2
Cluster 16	Other	4554858	4595580	Oviedomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000253_c1		
Cluster 17	Siderophore	4913457	4928849	-	-		
Cluster 18	Bacteriocin	5057506	5068354	-	-		
Cluster 19	Terpene	5321497	5348209	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1		
Cluster 20	T3pks-Terpene	5403543	5473532	R1128_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000261_c1	1	CYP158A13
Cluster 21	Other	5972017	6015850	Paromomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000712_c1		
Cluster 22	Nrps-Otherks	6074191	6141816	Cephamycin_C_biosynthetic_gene_cluster (73% of genes show similarity)	BGC0000319_c1		
Cluster 23	Lantipeptide	6142053	6171709	-	-	1	CYP105AA10
Cluster 24	T1pks-Butyrolactone-Nrps	6163651	6250787	U-68204_biosynthetic_gene_cluster (64% of genes show similarity)	BGC0001355_c1	2	CYP107CT1; CYP105B25
***Streptomyces cattleya* NRRL 8058 = DSM 46488**							
Cluster 1	Butyrolactone	1	6681	Chrysomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000211_c1		
Cluster 2	T1pks-Lassopeptide	32797	99729	Mannopeptimycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000388_c1		
Cluster 3	T1pks	129576	276592	Hygrocin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000075_c1	3	CYP107AS; CYP1274A1; CYP107CR1
Cluster 4	Terpene	570471	591205	-	-		
Cluster 5	Lantipeptide	626578	651138	-	-		
Cluster 6	Other	968747	1009583	Pyrrolomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000130_c1		
Cluster 7	Ectoine	1152703	1163107	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Lantipeptide	1526812	1549460	AmfS_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000496_c1		
Cluster 9	Butyrolactone	2315078	2326091	Rabelomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000262_c1		
Cluster 10	T3pks	2333868	2374899	-	-		
Cluster 11	Nrps	2783826	2856549	Stenothricin_biosynthetic_gene_cluster (31% of genes show similarity)	BGC0000431_c1		
Cluster 12	Lantipeptide	2936367	2965589	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1	1	CYP107AE6
Cluster 13	Terpene	3092046	3114271	-	-		
Cluster 14	T1pks-Nrps	3416761	3485868	Akaeolide_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001199_c1	1	CYP184A4
Cluster 15	Transatpks-T1pks-Nrps	3784664	3878568	Kirromycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001070_c1	2	CYP107CS1; CYP107W2
Cluster 16	Bacteriocin	4006188	4016460	-	-		
Cluster 17	Other	4554666	4595388	Oviedomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000253_c1		
Cluster 18	Siderophore	4913334	4928699	-	-		
Cluster 19	Bacteriocin	5057400	5068248	-	-		

Cluster 20	Terpene	5321391	5348103	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1		
Cluster 21	T3pks-Terpene	5403437	5473426	R1128_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000261_c1	1	CYP158A13
Cluster 22	Other	5972016	6015924	Paromomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000712_c1		
Cluster 23	Nrps-Otherks	6074210	6141835	Cephamycin_C_biosynthetic_gene_cluster (73% of genes show similarity)	BGC0000319_c1		
Cluster 24	Lantipeptide	6142071	6171727	-	-	1	CYP105AA10
Cluster 25	T1pks-Butyrolactone-Nrps	6163675	6251650	U-68204_biosynthetic_gene_cluster (64% of genes show similarity)	BGC0001355_c1	2	CYP107CT1; CYP105B25
***Streptomyces pratensis/flavogriseus* IAF 45**							
Cluster 1	Blactam-T1pks-Nrps	70873	221343	Carbapenem_MM_4550_biosynthetic_gene_cluster (65% of genes show similarity)	BGC0000842_c1	2	CYP247A3; CYP107BX5
Cluster 2	Nrps	327693	378596	Coelichelin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000325_c1		
Cluster 3	Terpene	393138	418630	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 4	Blactam	634715	658209	Clavulanic_acid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000845_c1		
Cluster 5	Terpene	738599	765184	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 6	T1pks	1104244	1198984	Vicenistatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000167_c1	2	CYP105AZ2; CYP105AZ1
Cluster 7	Bacteriocin	1409256	1420548	-	-		
Cluster 8	Nrps	1560425	1622443	Arylomycin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000306_c1		
Cluster 9	Siderophore	1894420	1909004	-	-		
Cluster 10	Terpene	1973589	1994659	-	-		
Cluster 11	Bacteriocin	2151745	2161966	-	-		
Cluster 12	Butyrolactone	3819031	3829957	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 13	T1pks-Nrps	4023172	4080102	Istamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000700_c1	3	CYP1029A2; CYP1423A2; CYP285A2
Cluster 14	Siderophore	4727646	4739427	Desferrioxamine_B_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000940_c1		
Cluster 15	Lantipeptide	4792335	4815403	-	-		
Cluster 16	Terpene	5226078	5247109	-	-	1	CYP157K1
Cluster 17	Ectoine	5705549	5715947	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 18	T2pks-Otherks	6079056	6136319	Cinerubin_B_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000212_c1		
Cluster 19	Terpene	6181067	6202113	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		
Cluster 20	Ectoine-Terpene	6482662	6509101	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 21	Bacteriocin	6532212	6542439	-	-		
Cluster 22	T3pks	6695745	6736803	Tetronasin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000163_c1		
Cluster 23	Melanin	6830784	6841248	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G4
Cluster 24	T2pks-Terpene	6882032	6931236	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 25	Nrps	7082613	7132319	Zorbamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001058_c1	2	CYP1035A4; CYP156B9
Cluster 26	Butyrolactone	7211688	7222623	-	-		

Streptomyces bingchenggensis							
Cluster 1	Bacteriocin-T1pks-Nrps	115407	214376	Leinamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001101_c1	2	CYP183C1; CYP183D1
Cluster 2	Terpene	229745	251688	Actinomycin_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000296_c1	1	CYP183E1
Cluster 3	Transatpks-Otherks-Nrps	330056	401421	Heterocyst_glycolipids_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000869_c1		
Cluster 4	Bacteriocin-Lantipeptide-T1pks	583067	635091	Tetronasin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000163_c1	1	CYP1039A1
Cluster 5	Transatpks-T1pks-Nrps	766606	1101234	Meilingmycin_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000093_c1	3	CYP105H6; CYP107BK1; CYP171A2
Cluster 6	T1pks	1126684	1179715	Meilingmycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000093_c1		
Cluster 7	Nrps	1181504	1228730	Chloroeremomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000322_c2	2	CYP107BM3; CYP157B13
Cluster 8	Nrps-Furan-T1pks-Otherks	1336592	1514066	Lipopeptide_8D1-1_/_lipopeptide_8D1-2_biosynthetic_gene_clus... (11% of genes show similarity)	BGC0001370_c1		
Cluster 9	Terpene	1545363	1566433	-	-		
Cluster 10	Other	1572192	1632869	Stenothricin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000431_c1		
Cluster 11	T1pks-Nrps	1820646	1956768	Lasalocid_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0000087_c1	1	CYP113G1
Cluster 12	T1pks-Otherks	2057881	2122132	Cremimycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000042_c1		
Cluster 13	Terpene	2182414	2203337	Kinamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000236_c1		
Cluster 14	Other	2477371	2520403	Piericidin_A1_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001169_c1	1	CYP154P1
Cluster 15	T1pks	2625076	2746943	Amphotericin_biosynthetic_gene_cluster (35% of genes show similarity)	BGC0000015_c1		
Cluster 16	Terpene	2813692	2835947	Geosmin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000661_c1		
Cluster 17	T1pks-Nrps	2969559	3026953	Clarexpoxcin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0001203_c1		
Cluster 18	Thiopeptide	3030559	3059514	-	-		
Cluster 19	Terpene	3417796	3444497	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1		
Cluster 20	Lassopeptide	3518110	3545015	Chaxapeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0001307_c1		
Cluster 21	T2pks	3622902	3665426	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 22	Nrps	3880299	3933590	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000315_c1		
Cluster 23	Bacteriocin	4012751	4024121	-	-		
Cluster 24	Nrps	4052289	4100532	Enduracidin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000341_c1		
Cluster 25	T1pks	4124810	4172660	Borrelidin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000031_c1		
Cluster 26	Siderophore	4305798	4317810	-	-		
Cluster 27	Other	4995984	5038752	Echosides_biosynthetic_gene_cluster (88% of genes show similarity)	BGC0000340_c1		
Cluster 28	T1pks-Nrps	7330156	7378757	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1	1	CYP1037A1
Cluster 29	Siderophore-Nrps	7742586	7808875	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 30	Arylpolyene-Ladderane	8061655	8104092	Skyllamycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000429_c1		

Cluster 31	Nrps	8115580	8170587	Skyllamycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000429_c1		
Cluster 32	T2pks-Oligosaccharide-Otherks	8166510	8248974	Saquayamycin_Z_/_galtamycin_B_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0000267_c1		
Cluster 33	Lantipeptide	8306880	8331657	-	-		
Cluster 34	Lantipeptide	8346685	8375315	SBI_06990_alpha_/_SBI_06989_beta_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001229_c1		
Cluster 35	Otherks	9124966	9166030	Chlortetracycline_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000209_c1	1	CYP268A4
Cluster 36	Ectoine	9613076	9623480	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 37	Siderophore	9790988	9804831	-	-		
Cluster 38	T1pks	9898279	10029213	Nanchangmycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000105_c1	1	CYP124B2
Cluster 39	Butyrolactone	10562794	10573729	-	-		
Cluster 40	Terpene	10597183	10618109	Oxazolomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001106_c1		
Cluster 41	Other	10715172	10757925	Echosides_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000340_c1		
Cluster 42	Lantipeptide	10862642	10886007	-	-		
Cluster 43	T1pks-Nrps	10895566	10951243	Herboxidiene_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001065_c1		
Cluster 44	Otherks-Nrps	10975893	11048987	Himastatin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001117_c1	1	CYP163C1
Cluster 45	Other	11070003	11112945	-	-		
Cluster 46	Transatpks-Terpene-Nrps	11442027	11575518	Oxazolomycin_biosynthetic_gene_cluster (45% of genes show similarity)	BGC0001106_c1	2	CYP161C1; CYP183A2
Cluster 47	T1pks	11900331	11936683	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Streptomyces hygroscopicus **subsp.** ***jinggangensis*** **5008**							
Cluster 1	Amglyccycl	358721	379965	Validamycin_biosynthetic_gene_cluster (59% of genes show similarity)	BGC0000722_c1		
Cluster 2	T1pks	392106	450957	Validamycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000722_c1	1	CYP105B22
Cluster 3	Bacteriocin	702612	713424	-	-		
Cluster 4	Nrps	725003	785737	Laspartomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000379_c1		
Cluster 5	T3pks	869601	910647	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000315_c1		
Cluster 6	Terpene	996365	1017102	Kedarcidin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000081_c1	1	CYP107X1
Cluster 7	Terpene	1059813	1080706	-	-		
Cluster 8	Siderophore	1105331	1118637	-	-		
Cluster 9	Phenazine-Nrps	1334791	1396137	Azinomycin_B_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000960_c1		
Cluster 10	T2pks	1404229	1446738	Dactylocycline_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000216_c1		
Cluster 11	T1pks-Nrps	1489978	1547401	Antimycin_biosynthetic_gene_cluster (93% of genes show similarity)	BGC0000958_c1		
Cluster 12	Nrps	1622283	1695049	Laspartomycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000379_c1	1	CYP163B6
Cluster 13	T1pks	1811332	1857499	Ansatrienin_(mycotrienin)_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000957_c1		
Cluster 14	Lantipeptide-Terpene-Nrps	1971071	2064317	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		

Cluster 15	Nrps	2205659	2262627	Zorbamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001058_c1	1	CYP285B1
Cluster 16	T1pks	2293648	2404726	Vicenistatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000167_c1	2	CYP105AZ2; CYP105AZ1
Cluster 17	T3pks	3138718	3179740	Herboxidiene_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001065_c1	1	CYP158A14
Cluster 18	Ectoine	3881676	3892080	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 19	T2pks	4251729	4294228	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 20	Butyrolactone	4609696	4620709	Methylenomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000914_c1		
Cluster 21	Melanin	4830523	4841017	Istamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000700_c1		
Cluster 22	Siderophore	4931971	4943740	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 23	Nrps	6457264	6510229	Arginomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000883_c1		
Cluster 24	T2pks-Ladderane-Nrps	6727130	6796406	Skyllamycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000429_c1		
Cluster 25	Terpene	7197859	7218872	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A10
Cluster 26	Siderophore	7848002	7860050	-	-		
Cluster 27	Bacteriocin-Nrps	7996885	8075186	Meilingmycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000093_c1		
Cluster 28	Bacteriocin	8112492	8123820	-	-		
Cluster 29	Terpene	8147354	8169507	-	-	1	CYP180A6
Cluster 30	Siderophore	8310258	8323412	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 31	Butyrolactone	8344332	8355243	Methylenomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000914_c1		
Cluster 32	Terpene	8696575	8723398	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 33	Lantipeptide	9016982	9041437	-	-		
Cluster 34	Bacteriocin-Nrps	9252598	9340733	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1	1	CYP113K3
Cluster 35	T3pks	9689376	9730512	Yatakemycin_biosynthetic_gene_cluster (48% of genes show similarity)	BGC0000466_c1		
Cluster 36	Lassopeptide	9750195	9772223	-	-		
Cluster 37	Butyrolactone	9868256	9936950	A-500359s_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000949_c1		
Cluster 38	Thiopeptide	10075365	10100043	Cyclothiazomycin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000603_c1		
***Streptomyces hygroscopicus* subsp. *jinggangensis* TL01**							
Cluster 1	Amglyccycl	132410	153654	Validamycin_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0000722_c1		
Cluster 2	T1pks	165795	224646	Validamycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000722_c1	1	CYP105B22
Cluster 3	Bacteriocin	476341	487153	-	-		
Cluster 4	Nrps	498732	559466	Laspartomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000379_c1		
Cluster 5	T3pks	643330	684376	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000315_c1		
Cluster 6	Terpene	770094	790831	Kedarcidin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000081_c1	1	CYP107X1
Cluster 7	Terpene	833542	854435	-	-		
Cluster 8	Siderophore	879060	892366	-	-		

Cluster 9	Phenazine-Nrps	1108524	1169870	Azinomycin_B_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000960_c1		
Cluster 10	T2pks	1177962	1220471	Dactylocycline_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000216_c1		
Cluster 11	T1pks-Nrps	1263711	1321134	Antimycin_biosynthetic_gene_cluster (93% of genes show similarity)	BGC0000958_c1		
Cluster 12	Nrps	1396016	1468782	Laspartomycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000379_c1	1	CYP163B6
Cluster 13	T1pks	1585065	1631232	Ansatrienin_(mycotrienin)_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000957_c1		
Cluster 14	Lantipeptide-Terpene-Nrps	1664585	1757831	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		
Cluster 15	Nrps	1899173	1956141	Zorbamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001058_c1	1	CYP285B1
Cluster 16	T1pks	1987162	2098240	Vicenistatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000167_c1	2	CYP105AZ2; CYP105AZ1
Cluster 17	T3pks	2832233	2873255	Herboxidiene_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001065_c1	1	CYP158A14
Cluster 18	Ectoine	3575399	3585803	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 19	T2pks	3945338	3987837	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 20	Butyrolactone	4303305	4314318	Methylenomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000914_c1		
Cluster 21	Melanin	4524132	4534626	Istamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000700_c1		
Cluster 22	Siderophore	4625580	4637349	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 23	Nrps	6150956	6203921	Arginomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000883_c1		
Cluster 24	T2pks-Ladderane-Nrps	6420822	6490098	Skyllamycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000429_c1		
Cluster 25	Terpene	6891676	6912689	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A10
Cluster 26	Siderophore	7541947	7553995	-	-		
Cluster 27	Bacteriocin-Nrps	7690830	7769131	Meilingmycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000093_c1		
Cluster 28	Bacteriocin	7806437	7817765	-	-		
Cluster 29	Terpene	7841299	7863452	-	-	1	CYP180A6
Cluster 30	Siderophore	8004203	8017357	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 31	Butyrolactone	8038418	8049329	Methylenomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000914_c1		
Cluster 32	Terpene	8390775	8417598	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 33	Lantipeptide	8711185	8735640	-	-		
Cluster 34	Bacteriocin-Nrps	8946801	9034936	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1	1	CYP113K3
Cluster 35	T3pks	9383644	9424780	Yatakemycin_biosynthetic_gene_cluster (48% of genes show similarity)	BGC0000466_c1		
Cluster 36	Lassopeptide	9444463	9466491	-	-		
Cluster 37	Butyrolactone	9562524	9631218	A-500359s_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000949_c1		
Cluster 38	Thiopeptide	9769634	9794312	Cyclothiazomycin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000603_c1		
Streptomyces venezuelae							
Cluster 1	Ectoine	237842	248258	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 2	Terpene	274553	296739	-	-		

Cluster 3	T3pks-T1pks-Nrps	504136	604067	Thiotetronate_Tu_3010_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0001352_c1		
Cluster 4	Lantipeptide-Terpene	614220	645285	Chrysomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000211_c1	1	CYP157C14
Cluster 5	Lantipeptide	707463	730315	Venezuelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000563_c1		
Cluster 6	Indole	867489	890695	Rebeccamycin_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000823_c1	1	CYP245A3
Cluster 7	Other	1031023	1073914	Chloramphenicol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000893_c1		
Cluster 8	Other	2055965	2096690	-	-	1	CYP121A2
Cluster 9	Siderophore	2794973	2806751	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 10	Lassopeptide	3408328	3430687	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 11	Other	4408196	4451900	Lactonamycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000238_c1		
Cluster 12	Butyrolactone	4522134	4533171	-	-		
Cluster 13	Melanin	5003818	5014228	Istamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000700_c1		
Cluster 14	Butyrolactone	5462370	5517716	A-503083_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000288_c1		
Cluster 15	Thiopeptide	5531076	5557501	BD-12_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001379_c1		
Cluster 16	T3pks	5785193	5826323	K-252a_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000814_c1	1	CYP158A5
Cluster 17	Siderophore	5869901	5883169	-	-		
Cluster 18	Siderophore	5935668	5950407	-	-		
Cluster 19	Bacteriocin	6350466	6361866	-	-		
Cluster 20	T2pks-Butyrolactone	6479470	6531416	Rabelomycin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000262_c1		
Cluster 21	Other	6672467	6716369	Herbimycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000074_c1	2	CYP105AC2; CYP180A5
Cluster 22	Ladderane-Nrps	6720590	6855167	Skyllamycin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0000429_c1	4	CYP1056A1; CYP107CL1; CYP162A4; CYP163B5
Cluster 23	Terpene	7021575	7048100	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 24	Bacteriocin	7128838	7139692	-	-		
Cluster 25	T2pks	7421589	7464101	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 26	Melanin	7484949	7495338	Melanin_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000908_c1		
Cluster 27	Nrps	7706602	7760938	Albachelin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001211_c1		
Cluster 28	Terpene	7788497	7809951	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1		
Cluster 29	T3pks	7946080	7987237	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 30	Terpene-Nrps	8179935	8226158	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Streptomyces davawensis							
Cluster 1	Lassopeptide	298906	321414	-	-		
Cluster 2	T1pks-Nrps	699548	770346	Lasalocid_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000087_c1	1	CYP105BA1
Cluster 3	Other	886131	928683	Meridamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001011_c1	1	CYP1005B2

Cluster 4	Bacteriocin-Lantipeptide	1091732	1132429	Informatipeptin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000518_c1	1	CYP179B1
Cluster 5	Lassopeptide	1361367	1383943	-	-		
Cluster 6	T1pks	1456468	1499518	RK-682_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000140_c1		
Cluster 7	Terpene	1551356	1572273	-	-	1	CYP183K1
Cluster 8	Terpene	1719195	1745819	Hopene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000663_c1		
Cluster 9	T3pks	2207909	2248970	-	-		
Cluster 10	Siderophore	2297883	2311023	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 11	Lantipeptide-T1pks-Nrps	2350589	2428901	Jerangolid_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000080_c1	1	CYP179A3
Cluster 12	Butyrolactone-Terpene	2547059	2574343	Gamma-butyrolactone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000850_c1	1	CYP180A6
Cluster 13	Bacteriocin-Oligosaccharide	2613657	2675880	Meilingmycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000093_c1	2	CYP107CN1; CYP107CP1
Cluster 14	T2pks-T1pks	2749113	2852588	Pyrrolomycin_biosynthetic_gene_cluster (45% of genes show similarity)	BGC0000130_c1		
Cluster 15	Siderophore	2995354	3007165	-	-		
Cluster 16	Terpene-Nrps	3556587	3614866	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A9
Cluster 17	Phosphonate	4565919	4606854	Rhizocticin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000926_c1		
Cluster 18	Butyrolactone	4950501	4961502	-	-		
Cluster 19	Siderophore	6101969	6113741	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 20	Melanin-Nrps	6185869	6254487	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000909_c1		
Cluster 21	T1pks-Nrps	6539485	6608235	SCO-2138_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000595_c1	3	CYP113J1; CYP113J2; CYP162A5
Cluster 22	T3pks	6619324	6660409	SWA-2138_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000597_c1		
Cluster 23	Otherks-Nrps	6741355	6816556	Taromycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000439_c1	2	CYP125A22; CYP163C2
Cluster 24	Ectoine	7452784	7463182	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 25	Other	7566704	7610435	Gobichelin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000366_c1		
Cluster 26	Other	7715214	7759068	-	-		
Cluster 27	T3pks	8237578	8278642	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A7
Cluster 28	Nrps	8403464	8462129	Scabichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000423_c1		
Cluster 29	Lantipeptide	8666789	8691350	-	-		
Cluster 30	Terpene-T3pks-Cyanobactin-Nrps	8866036	8983549	Furaquinocin_A_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001078_c1	2	CYP1041A2; CYP1058A1
Cluster 31	Melanin-Terpene	9217881	9244553	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Streptomyces albus **J1074**							
Cluster 1	T1pks-Nrps	3011	61711	-	-		
Cluster 2	T1pks-Nrps	224752	274162	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX2
Cluster 3	Terpene	308626	335190	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1		

Cluster 4	Bacteriocin	415688	425903	-	-		
Cluster 5	Otherks	669953	711002	Avermectin_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000025_c1	1	CYP1420A1
Cluster 6	Bacteriocin	879961	891289	-	-		
Cluster 7	Nrps	1136316	1199422	Tetronasin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000163_c1	1	CYP146A3
Cluster 8	Siderophore	1268164	1283196	-	-		
Cluster 9	Terpene	1531774	1554059	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1		
Cluster 10	Terpene	1865241	1886293	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170B5
Cluster 11	Thiopeptide	2376688	2409159	-	-		
Cluster 12	Bacteriocin	2560714	2571226	Goadsporin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000565_c1		
Cluster 13	Lantipeptide	2694944	2735867	SAL-2242_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000546_c1	1	CYP154A1
Cluster 14	Nrps	3553726	3604015	Scabichelin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0000423_c1		
Cluster 15	Nrps	3877105	3982798	Herboxidiene_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001065_c1		
Cluster 16	Nrps	4469477	4513826	-	-		
Cluster 17	Siderophore	4740450	4752270	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 18	Ectoine	5635346	5645744	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 19	Other	6337383	6381213	Auricin_deoxysugar_moieties_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000727_c1		
Cluster 20	Bacteriocin-Terpene	6396161	6430092	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		
Cluster 21	T3pks	6520374	6561471	Herboxidiene_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001065_c1	1	CYP107F4
Cluster 22	Lantipeptide-T1pks-Nrps	6566423	6838639	Candicidin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000034_c1	1	CYP105H3
***Streptomyces albus* DSM 41398**							
Cluster 1	Nrps	117650	166226	Incednine_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000078_c1	1	CYP105BK3
Cluster 2	Nrps	183666	273577	Cahuitamycins_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0001351_c1		
Cluster 3	T1pks-Butyrolactone-Nrps	284628	428617	Salinomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000144_c1	1	CYP107EJ1
Cluster 4	Amglyccycl	746865	768097	Pyralomicin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0001038_c1		
Cluster 5	T1pks-Otherks	843887	1009285	PM100117_/_PM100118_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0001359_c2	2	CYP113Y1; CYP105DB1
Cluster 6	Bacteriocin-Terpene	1051608	1089082	-	-		
Cluster 7	T1pks	1174261	1276844	Oligomycin_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0000117_c1	1	CYP107DU1
Cluster 8	Thiopeptide	1281647	1316387	-	-		
Cluster 9	Terpene-T1pks	1416484	1519438	Lasalocid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000087_c1		
Cluster 10	Lantipeptide-Terpene-Nrps	1512526	1617897	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1		
Cluster 11	Lantipeptide	1622376	1645752	-	-		
Cluster 12	Siderophore	1912797	1924731	-	-		
Cluster 13	Other	2456612	2498069	Arginomycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000883_c1		

Cluster 14	Terpene	2586173	2607264	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170B5
Cluster 15	T1pks	2726842	2791263	Streptazone_E_biosynthetic_gene_cluster (58% of genes show similarity)	BGC0001296_c1		
Cluster 16	Lassopeptide	2823976	2846376	-	-		
Cluster 17	Butyrolactone	3380027	3391028	-	-		
Cluster 18	Melanin	3764392	3775000	Istamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000700_c1		
Cluster 19	T1pks-Otherks	3889534	3937675	Arsenopolyketides_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0001283_c1		
Cluster 20	Arylpolyene-Nrps	4012866	4110187	Albachelin_biosynthetic_gene_cluster (70% of genes show similarity)	BGC0001211_c1	1	CYP107T3
Cluster 21	Other	4614979	4658800	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 22	Other	5088621	5131383	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 23	Butyrolactone-Otherks	5451890	5493951	Macrotetrolide_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000243_c1		
Cluster 24	Lantipeptide	5665895	5688501	SAL-2242_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000546_c1		
Cluster 25	Arylpolyene	5725897	5794495	Svaricin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001382_c1	1	CYP107KW1
Cluster 26	T2pks-Otherks	5913570	6003941	Kinamycin_biosynthetic_gene_cluster (48% of genes show similarity)	BGC0000236_c1	1	CYP1193A1
Cluster 27	T1pks	6434045	6478607	-	-		
Cluster 28	Bacteriocin	6561595	6572500	-	-		
Cluster 29	Melanin-Arylpolyene-Ladderane	6572744	6632562	Salinilactam_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000142_c1		
Cluster 30	Ectoine	6947249	6957647	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 31	Terpene	7787708	7814387	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 32	Nucleoside	7841287	7861661	-	-		
Cluster 33	T1pks-Nrps	7925460	8051064	Undecylprodigiosin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001063_c1	1	CYP1194A1
Cluster 34	Siderophore	8262822	8276665	-	-		
Cluster 35	T1pks-Phenazine	8302435	8384669	Elaiophylin_biosynthetic_gene_cluster (79% of genes show similarity)	BGC0000053_c1		
***Streptomyces* sp. PAMC 26508**							
Cluster 1	Butyrolactone	207520	218455	-	-		
Cluster 2	Nrps	289719	343175	Zorbamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001058_c1	2	CYP156B9; CYP1035A4
Cluster 3	T2pks-Terpene	491367	540556	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 4	Melanin	581362	591826	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G4
Cluster 5	T3pks	688185	729243	Tetronasin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000163_c1		
Cluster 6	Bacteriocin	882331	892558	-	-		
Cluster 7	Terpene-Ectoine	915537	941976	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Terpene	1222262	1243308	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		
Cluster 9	T2pks-Otherks	1288058	1345321	Cinerubin_B_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0000212_c1		
Cluster 10	Ectoine	1758238	1768636	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		

Cluster 11	Terpene	2220628	2241659	-	-	1	CYP157K1
Cluster 12	Lantipeptide	2650699	2673779	-	-		
Cluster 13	Siderophore	2726161	2737942	Desferrioxamine_B_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000940_c1		
Cluster 14	T1pks-Nrps	3360869	3417772	Istamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000700_c1	3	CYP285A2, CYP1423A2, CYP1029A2
Cluster 15	Butyrolactone	3618213	3629124	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 16	Bacteriocin	5270198	5280419	-	-		
Cluster 17	Terpene	5440267	5461337	-	-		
Cluster 18	Siderophore	5525938	5540522	-	-		
Cluster 19	Nrps	5813270	5875303	Arylomycin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000306_c1		
Cluster 20	Bacteriocin	5954424	5965716	-	-		
Cluster 21	T1pks	6177678	6272426	Vicenistatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000167_c1	2	CYP105AZ1; CYP105AZ2
Cluster 22	Terpene	6622210	6648795	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 23	Blactam	6729751	6753170	Clavulanic_acid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000845_c1		
Cluster 24	Nrps	6809052	6859494	BE-14106_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000029_c1		
Cluster 25	Bacteriocin-Otherks	6902116	6963314	A54145_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000291_c1	1	CYP1057A1
Cluster 26	Terpene	7090034	7115526	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 27	Nrps	7129534	7180438	Coelichelin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000325_c1		
Cluster 28	Blactam-T1pks-Nrps	7287163	7437851	Carbapenem_MM_4550_biosynthetic_gene_cluster (65% of genes show similarity)	BGC0000842_c1	2	CYP107BX5; CYP247A3
Streptomyces fulvissimus							
Cluster 1	Terpene	24365	49959	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 2	Nrps	117602	164831	A-500359s_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000949_c1		
Cluster 3	Ectoine	192433	202834	-	-		
Cluster 4	Butyrolactone	290337	301287	Coelimycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000038_c1		
Cluster 5	Terpene	330914	353127	-	-		
Cluster 6	Nrps-Transatpks-T1pks-Otherks	362798	478874	Griseobactin_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000368_c1		
Cluster 7	Nrps	483517	534421	Coelichelin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000325_c1		
Cluster 8	T1pks-Nrps	540366	590843	Arsenopolyketides_biosynthetic_gene_cluster (45% of genes show similarity)	BGC0001283_c1		
Cluster 9	T3pks	601562	642680	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1	1	CYP107F4
Cluster 10	Terpene	1114958	1136052	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		
Cluster 11	Ectoine	1612719	1623117	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 12	Lantipeptide	2590811	2614077	-	-		
Cluster 13	Siderophore	2685518	2697296	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 14	Other	2783366	2827199	Bottromycin_A2_biosynthetic_gene_cluster (39% of genes show similarity)	BGC0000469_c1		

Cluster 15	Thiopeptide	3079000	3111360	-	-		
Cluster 16	Nrps	3311019	3375870	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 17	T2pks	4454092	4496646	Auricin_biosynthetic_gene_cluster (44% of genes show similarity)	BGC0000201_c1		
Cluster 18	Lassopeptide	4558373	4580998	SRO15-2005_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000578_c1		
Cluster 19	T1pks	5106090	5171059	Streptazone_E_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0001296_c1		
Cluster 20	Lantipeptide	5444394	5467015	AmfS_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000496_c1		
Cluster 21	Terpene	5812728	5842233	Calcimycin_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000032_c1		
Cluster 22	Siderophore	6318303	6333008	-	-		
Cluster 23	Lantipeptide	6520512	6545133	Nataxazole_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001213_c1		
Cluster 24	Other	6603133	6647134	Lomofungin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001302_c1		
Cluster 25	Bacteriocin	6707089	6718420	-	-		
Cluster 26	Nrps	6852653	6913175	Salinomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000144_c1		
Cluster 27	Arylpolyene	6967295	7010476	Hexaricin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001376_c1		
Cluster 28	T2pks	7029570	7070850	Nonactin_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000252_c1		
Cluster 29	Terpene	7318585	7345177	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 30	T1pks-Nrps	7412328	7461708	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX3
Cluster 31	Bacteriocin	7500970	7511770	Tetronasin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000163_c1		
Cluster 32	Nrps	7648530	7706884	Valinomycin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000453_c1		
Cluster 33	Melanin	7712879	7723352	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G2
Cluster 34	T3pks	7755934	7796986	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Streptomyces collinus							
Cluster 1	Lantipeptide	175267	198335	Streptocollin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001226_c1		
Cluster 2	Lassopeptide-Nrps	195828	265307	Azicemicin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000202_c1		
Cluster 3	Transatpks-T1pks-Nrps	341018	503094	Kirromycin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0001070_c1	2	CYP107CQ1; CYP105AJ2
Cluster 4	Terpene	688085	713347	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001227_c1		
Cluster 5	Other	749234	793100	Lasalocid_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000087_c1		
Cluster 6	Melanin-Terpene	1068125	1093783	Melanin_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000908_c1		
Cluster 7	T1pks-Nrps	1113779	1169492	Piericidin_A1_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000124_c1		
Cluster 8	Bacteriocin	1176893	1188815	-	-	2	CYP1059A1; CYP105B21
Cluster 9	Other	1456613	1499876	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 10	T3pks	1500891	1541931	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1	1	CYP158A2
Cluster 11	T1pks-Otherks	1600538	1653105	Cinnamycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000503_c1		
Cluster 12	Ectoine	2273646	2284050	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 13	Thiopeptide-T2pks-	3030814	3123812	Sch47554_/_Sch47555_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000268_c1		

	Otherks-Nrps						
Cluster 14	Melanin	3299612	3310022	Istamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000700_c1		
Cluster 15	Siderophore	3392488	3404257	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 16	T2pks	4049256	4091753	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 17	T1pks-Nrps	4541482	4597772	Chalcomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000035_c1		
Cluster 18	Nrps	4902691	4957721	PM100117_/_PM100118_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001359_c2		
Cluster 19	Nrps-Ladderane	5425623	5484284	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (27% of genes show similarity)	BGC0000315_c1		
Cluster 20	Terpene	5642053	5663066	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A10
Cluster 21	Siderophore	6264134	6276302	-	-		
Cluster 22	Bacteriocin	6405006	6417150	Lipopeptide_8D1-1_/_lipopeptide_8D1-2_biosynthetic_gene_clus... (4% of genes show similarity)	BGC0001370_c1		
Cluster 23	T1pks	6430389	6483375	Tetronasin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000163_c1	2	CYP105BC1; CYP105AH2
Cluster 24	Bacteriocin	6548725	6560143	-	-		
Cluster 25	Terpene	6578041	6600203	-	-	1	CYP180A6
Cluster 26	Siderophore	6758341	6771498	-	-		
Cluster 27	Terpene	6862292	6883302	Pentalenolactone_biosynthetic_gene_cluster (58% of genes show similarity)	BGC0000653_c1	1	CYP183A4
Cluster 28	Terpene	7118021	7144778	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 29	Other	7416924	7458297	A-503083_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000288_c1		
Cluster 30	Bacteriocin-Nrps	7527490	7616173	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1	1	CYP113K3
Cluster 31	Transatpks-T1pks-Nrps	7769831	7931907	Kirromycin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0001070_c1	2	CYP105AJ2; CYP107CQ1
Cluster 32	Lantipeptide-Lassopeptide-Nrps	8007618	8107658	Streptocollin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001226_c1		
Streptomyces rapamycinicus							
Cluster 1	T3pks-T1pks-Nrps	38640	150103	Lobophorin_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0001183_c1		
Cluster 2	Nrps	532970	583958	Coelichelin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000325_c1		
Cluster 3	Butyrolactone	900466	911455	-	-		
Cluster 4	T1pks	1067818	1206134	ECO-02301_biosynthetic_gene_cluster (39% of genes show similarity)	BGC0000052_c1	1	CYP105AX1
Cluster 5	T1pks	1392961	1533488	Nigericin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000114_c1	1	CYP124B3
Cluster 6	T1pks	1536114	1579959	Salinomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000144_c1		
Cluster 7	T1pks	1680321	1757212	Elaiophylin_biosynthetic_gene_cluster (87% of genes show similarity)	BGC0000053_c1		
Cluster 8	Hserlactone	1933809	1954564	Daptomycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000336_c1		
Cluster 9	Butyrolactone	1965192	1976124	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 10	T1pks-Nrps	2182193	2235170	Meilingmycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000093_c1		
Cluster 11	T3pks-Nrps	2292584	2394338	Feglymycin_biosynthetic_gene_cluster (78% of genes show similarity)	BGC0001233_c1		

Cluster 12	T1pks-Nrps	2500404	2707075	Neocarzilin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000111_c1	3	CYP161D1; CYP105AT1; CYP107L12
Cluster 13	Lantipeptide	2709760	2747820	BE-7585A_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000203_c1		
Cluster 14	Lassopeptide	2873655	2896097	Streptomycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000717_c1		
Cluster 15	Terpene	2934213	2960877	Hopene_biosynthetic_gene_cluster (76% of genes show similarity)	BGC0000663_c1	1	CYP1013A2
Cluster 16	T2pks	3350102	3392617	Spore_pigment_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000271_c1		
Cluster 17	Bacteriocin	3679519	3690859	-	-		
Cluster 18	Siderophore	3859558	3871444	-	-		
Cluster 19	Other	4448217	4490991	Echosides_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000340_c1		
Cluster 20	Siderophore	5052198	5063985	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 21	T1pks-Nrps	5362278	5478116	TP-1161_biosynthetic_gene_cluster (41% of genes show similarity)	BGC0000615_c1	1	CYP105AU1
Cluster 22	Terpene	6406844	6429246	-	-	1	CYP147F5
Cluster 23	Nrps-Arylpolyene-Ladderane	6723014	6828195	Skyllamycin_biosynthetic_gene_cluster (44% of genes show similarity)	BGC0000429_c1	3	CYP107CE1; CYP107CF1; CYP163B4
Cluster 24	Indole	7126202	7147344	7-prenylisatin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0001294_c1	2	CYP156B6; CYP107U9
Cluster 25	Nrps	7363926	7407936	Ochronotic_pigment_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000918_c1		
Cluster 26	Arylpolyene-Ladderane	7459089	7501424	WS9326_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0001297_c1		
Cluster 27	T1pks	7670799	7852915	ECO-02301_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000052_c1		
Cluster 28	Terpene	8356513	8377778	-	-	2	CYP125A20; CYP156C8
Cluster 29	Ectoine	9039123	9049527	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 30	T1pks-Siderophore	9207893	9280685	Apoptolidin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000021_c1		
Cluster 31	Terpene	9291107	9312180	Xiamycin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000665_c1		
Cluster 32	T1pks	9618433	9752874	Oligomycin_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000117_c1	3	CYP194B3; CYP194B4; CYP107BS2
Cluster 33	Other	9825530	9867362	BD-12_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001379_c1		
Cluster 34	T1pks-Nrps	9905472	10151658	Rapamycin_biosynthetic_gene_cluster (96% of genes show similarity)	BGC0001040_c1	3	CYP105AW1; CYP122A4; CYP107G2
Cluster 35	Otherks	10231970	10272998	Galbonolides_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000065_c1	1	CYP183F1
Cluster 36	Terpene	10275433	10296563	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 37	Terpene	10714282	10735382	-	-		
Cluster 38	T1pks-Arylpolyene-Ladderane	10828170	10879625	Skyllamycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000429_c1	1	CYP107B3
Cluster 39	T1pks-Nrps	11126450	11244528	Meridamycin_biosynthetic_gene_cluster (73% of genes show similarity)	BGC0001011_c1	1	CYP105AY1
Cluster 40	T1pks	11250323	11334466	Hygrocin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000075_c1	1	CYP107AD1

Cluster 41	Bacteriocin-Nrps-Lantipeptide-T1pks-Otherks	11489476	11707824	Bafilomycin_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000028_c1	3	CYP105AN3; CYP107E9; CYP155A5
Cluster 42	Terpene	11918860	11939768	-	-	1	CYP105AV1
Cluster 43	Other	11989963	12032665	Herboxidiene_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001065_c1		
Cluster 44	T1pks	12189709	12284210	Concanamycin_A_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000040_c1	1	CYP107CD1
Cluster 45	Nrps	12397424	12450754	-	-		
Cluster 46	T1pks	12467081	12520518	Geldanamycin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000066_c1		
Cluster 47	Terpene	12663104	12688864	Carotenoid_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000633_c1		
***Streptomyces albulus* NK660**							
Cluster 1	Butyrolactone	191856	202725	Chalcomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000035_c1	1	CYP107L43
Cluster 2	T1pks	223312	268246	Ansamitocin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000020_c1		
Cluster 3	Other	293048	333884	Guadinomine_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000998_c1	1	CYP1190A1
Cluster 4	T1pks-Nrps	384583	440308	Sporolide_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000150_c1		
Cluster 5	Other	455350	498610	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 6	Other	729299	772400	-	-	1	CYP1192A1
Cluster 7	Lantipeptide	802532	826984	Himastatin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001117_c1		
Cluster 8	T1pks-Nrps	956162	1047337	Siomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000611_c1	1	CYP1191A1
Cluster 9	Nrps	1251461	1315374	Laspartomycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000379_c1	1	CYP107EB1
Cluster 10	Transatpks-T1pks-Nrps	1323278	1373000	Cinnabaramide_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000971_c1	2	CYP163B9; CYP105AA13
Cluster 11	T1pks	1518010	1626108	Nystatin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000115_c1	2	CYP105H9; CYP161A7
Cluster 12	Bacteriocin	1681644	1691859	-	-		
Cluster 13	T2pks	1739194	1781709	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 14	Lantipeptide-Lassopeptide	2314663	2344101	Streptomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000717_c1		
Cluster 15	Siderophore	2603121	2614923	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 16	Ectoine	2689910	2700320	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 17	Terpene	5036219	5058516	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 18	Transatpks-Nrps	6189940	6292793	Oxazolomycin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0001106_c1	3	CYP107B6; CYP1189A1; CYP1189A2
Cluster 19	Siderophore	6726080	6740335	-	-		
Cluster 20	T3pks-Otherks-Butyrolactone-Nrps	6807354	6922217	Svaricin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001382_c1	2	CYP107F9; CYP163C3
Cluster 21	Lantipeptide	7171814	7196375	-	-		
Cluster 22	T2pks-Oligosaccharide-	7502025	7608293	Rabelomycin_biosynthetic_gene_cluster (39% of genes show similarity)	BGC0000262_c1	2	CYP113D6; CYP157C28

	Nucleoside-Nrps						
Cluster 23	Terpene	7715089	7741766	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 24	Butyrolactone	7992340	8048938	Oxazolomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001106_c1		
Cluster 25	Butyrolactone	8290273	8301271	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1	1	CYP107AE9
Cluster 26	Nrps	8435386	8490322	Azicemicin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000202_c1		
Cluster 27	Lantipeptide	8499891	8561229	SAL-2242_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000546_c1	1	CYP251G1
Cluster 28	Butyrolactone	8599016	8609951	Lactonamycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000238_c1		
Cluster 29	Other	8842091	8884604	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 30	Terpene-T1pks	8946818	9103383	Nystatin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000115_c1	2	CYP161A6; CYP105H1
Cluster 31	T1pks	9157043	9240750	Kedarcidin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000081_c1		
Cluster 32	Lantipeptide	9260281	9288895	9-methylstreptimidone_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000171_c1		
Cluster 33	T1pks	9330879	9360281	-	-		
***Streptomyces albus* ZPM**							
Cluster 1	Nrps	17026	109753	Himastatin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0001117_c1	3	CYP107EL1; CYP163B8; CYP107EA2
Cluster 2	Butyrolactone	330907	341776	Chalcomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000035_c1	1	CYP107L43
Cluster 3	Other	433815	474639	Guadinomine_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000998_c1	1	CYP1190A1
Cluster 4	T1pks-Nrps	526610	582304	Sporolide_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000150_c1		
Cluster 5	Other	596797	640057	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 6	Other	883066	926167	Tetarimycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000274_c1	3	CYP147F21; CYP1060A2; CYP1192A1
Cluster 7	Lantipeptide	954336	978788	Himastatin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001117_c1		
Cluster 8	T1pks	1103165	1150568	Hygrocin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000075_c1	1	CYP1191A1
Cluster 9	Nrps	1413155	1468194	Carbapenem_MM_4550_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000842_c1		
Cluster 10	Transatpks-T1pks-Nrps	1476172	1525894	Cinnabaramide_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000971_c1	2	CYP163B9; CYP105AA13
Cluster 11	T1pks	1670952	1716162	Rimocidin_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000138_c1	1	CYP105H9
Cluster 12	Bacteriocin	1838897	1849112	-	-		
Cluster 13	T2pks	1896764	1939279	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 14	Siderophore	2770965	2782767	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 15	Siderophore	2865668	2880351	-	-		
Cluster 16	Ectoine	3021273	3031683	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 17	Terpene	5358147	5380444	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 18	Other	6045012	6089226	Meridamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001011_c1		
Cluster 19	Transatpks-Nrps	6554322	6638419	Oxazolomycin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0001106_c1	2	CYP1189A1; CYP1189A2
Cluster 20	T3pks	7015396	7056448	FD-594_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000222_c1	1	CYP107F9

Cluster 21	Otherks-Butyrolactone-Nrps	7041728	7131800	FD-594_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000222_c1	1	CYP163C3
Cluster 22	Lantipeptide	7528854	7553415	-	-		
Cluster 23	T2pks-Oligosaccharide-Nucleoside-Nrps	7788124	7894680	Rabelomycin_biosynthetic_gene_cluster (39% of genes show similarity)	BGC0000262_c1	2	CYP113D6; CYP157C28
Cluster 24	Terpene	8001771	8028454	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 25	Butyrolactone	8283727	8340249	Oxazolomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001106_c1		
Cluster 26	Butyrolactone	8585464	8596462	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1	1	CYP107AE9
Cluster 27	Nrps	8706076	8762919	Azicemicin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000202_c1		
Cluster 28	Lantipeptide	8771860	8833243	SapB_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000551_c1	1	CYP251G1
Cluster 29	Butyrolactone	8870590	8881525	Lactonamycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000238_c1		
Cluster 30	Other	9116811	9160601	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 31	T1pks	9240892	9287062	Nystatin_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000115_c1	2	CYP161A6; CYP105H1
Cluster 32	Terpene	9358138	9379196	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 33	Other	9444178	9526669	Toxoflavin_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000929_c1		
Cluster 34	Lantipeptide	9545426	9574041	9-methylstreptimidone_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000171_c1		
Cluster 35	Nrps	9674825	9767552	Himastatin_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0001117_c1	3	CYP107EA2; CYP163B8; CYP107EL1
Streptomyces lividans							
Cluster 1	Terpene	16436	37485	A54145_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000291_c1		
Cluster 2	T3pks-Terpene-Nrps	135815	218933	Coelibactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000324_c1	1	CYP105N1
Cluster 3	Indole	408329	429456	Ravidomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000263_c1		
Cluster 4	Other	683230	724117	-	-		
Cluster 5	Terpene	1013200	1039941	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 6	Lantipeptide	1112999	1135713	SapB_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000551_c1		
Cluster 7	Nrps	1379776	1427601	Nogalamycin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0000249_c1		
Cluster 8	Butyrolactone-T1pks	1504046	1584720	Coelimycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000038_c1		
Cluster 9	Siderophore	1600479	1613686	Enduracidin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000341_c1		
Cluster 10	Terpene	1777516	1799696	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 11	Bacteriocin	1811789	1823105	-	-		
Cluster 12	T1pks	2069522	2116415	Undecylprodigiosin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001063_c1		
Cluster 13	Siderophore	2198321	2210267	-	-		
Cluster 14	T2pks	2687566	2730108	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1		
Cluster 15	Terpene	2804079	2825092	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A1

Cluster 16	T2pks	2943724	2986218	Actinorhodin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000194_c1		
Cluster 17	Nrps	4737916	4818557	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000315_c1		
Cluster 18	Siderophore	5290107	5301891	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 19	Melanin	5384385	5394954	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 20	Ectoine	6336408	6346806	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 21	T3pks	7041742	7082866	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A2
Cluster 22	Bacteriocin	7570510	7580725	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 23	Nrps	7826445	7877382	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 24	Lantipeptide	8100785	8135884	Sanglifehrin_A_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001042_c1		
Cluster 25	Terpene	8180092	8205599	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 26	T1pks-Otherks	8241896	8294872	Leinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001101_c1		
Cluster 27	Terpene	8307799	8328848	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000362_c1		
Streptomyces glaucescens							
Cluster 1	Thiopeptide	154073	181725	Lactazole_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0000606_c1		
Cluster 2	Other	193911	235617	Acarviostatin_biosynthetic_gene_cluster (37% of genes show similarity)	BGC0000804_c1	1	CYP178B1
Cluster 3	Amglyccycl	273980	300700	5'-hydroxystreptomycin_biosynthetic_gene_cluster (95% of genes show similarity)	BGC0000690_c1		
Cluster 4	Terpene	365767	391614	Carotenoid_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000633_c1		
Cluster 5	Melanin	622415	632819	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 6	Nrps	994531	1107137	SW-163_biosynthetic_gene_cluster (32% of genes show similarity)	BGC0000434_c1	1	CYP163B10
Cluster 7	Other	1120487	1161569	BE-14106_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000029_c1		
Cluster 8	T1pks-Otherks	1613939	1668625	Xantholipin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000279_c1		
Cluster 9	Ectoine	1897008	1907412	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 10	Melanin	2820776	2831324	Melanin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000909_c1		
Cluster 11	Siderophore	2914060	2925829	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 12	Terpene	5085549	5106472	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A22
Cluster 13	Siderophore	5682914	5694878	-	-		
Cluster 14	Lassopeptide	5766933	5789727	-	-		
Cluster 15	Butyrolactone	5802942	5813874	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1		
Cluster 16	Bacteriocin	5903335	5914678	-	-		
Cluster 17	Terpene	5942344	5964521	-	-	1	CYP180A9
Cluster 18	T2pks	5992056	6034562	Tetracenomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000275_c1		
Cluster 19	Siderophore	6106223	6119335	Grincamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000229_c1		
Cluster 20	Terpene	6451173	6478211	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		

Cluster 21	T2pks	6563775	6640031	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1	1	CYP107AH4
Cluster 22	Terpene	6811706	6832737	-	-	1	CYP157K3
Cluster 23	Bacteriocin	6851421	6861636	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 24	Lassopeptide	7061912	7084480	-	-		
Cluster 25	Nrps	7094980	7173584	Zorbamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001058_c1	1	CYP113K5
Streptomyces vietnamensis							
Cluster 1	Lantipeptide	346045	373904	Venezuelin_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000563_c1		
Cluster 2	Nrps	399968	455320	Streptolydigin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0001046_c1		
Cluster 3	Ectoine	566113	576529	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 4	Terpene	641540	663738	-	-		
Cluster 5	Butyrolactone	690180	701109	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1		
Cluster 6	Butyrolactone-T1pks-Nrps	742368	867912	Lankamycin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000085_c1		
Cluster 7	Other	2414787	2455359	Lomofungin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001302_c1	1	CYP121A2
Cluster 8	Siderophore	3014427	3025998	-	-		
Cluster 9	Siderophore	3104104	3115873	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 10	T2pks	4190266	4232787	Granaticin_biosynthetic_gene_cluster (64% of genes show similarity)	BGC0000227_c1		
Cluster 11	Other	4692700	4736419	Saframycin_A_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000422_c1		
Cluster 12	Melanin	5341238	5351639	Istamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000700_c1		
Cluster 13	Other	5791545	5832648	Stambomycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000151_c1		
Cluster 14	Thiopeptide	5844801	5871088	BD-12_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001379_c1		
Cluster 15	Siderophore	6229349	6241184	-	-		
Cluster 16	T2pks-Nrps	6341578	6422345	Kinamycin_biosynthetic_gene_cluster (51% of genes show similarity)	BGC0000236_c1	3	CYP1029A3; CYP1423A1; CYP285A5
Cluster 17	Bacteriocin	6509824	6521212	-	-		
Cluster 18	Butyrolactone	6646523	6657473	Griseoviridin_/_viridogrisein_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000459_c1		
Cluster 19	Terpene	7009307	7036249	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 20	Bacteriocin	7087107	7097922	-	-		
Cluster 21	Other	7175741	7217552	Enduracidin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000341_c1		
Cluster 22	Terpene	7297687	7319081	Griseobactin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000368_c1		
Cluster 23	Lantipeptide	7778604	7802417	-	-	1	CYP107LD1
Cluster 24	T2pks-Lantipeptide-Terpene	7912992	7991337	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1	2	CYP154C11; CYP157A19
Cluster 25	Other	8287563	8331471	-	-		
Cluster 26	T1pks-Nrps	8367712	8417038	Heat-stable_antifungal_factor_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000999_c1		

Cluster 27	Lantipeptide	8457714	8484769	A54145_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000291_c1		
***Streptomyces* sp. 769**							
Cluster 1	Butyrolactone-T1pks-Nrps	37787	174548	Coelimycin_biosynthetic_gene_cluster (29% of genes show similarity)	BGC0000038_c1	1	CYP105BA3
Cluster 2	T1pks-Arylpolyene	205753	287809	Ansamitocin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000020_c1	3	CYP107EM1; CYP1198A1; CYP105BV1
Cluster 3	Terpene	390343	411401	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 4	Lantipeptide-Nrps	462632	544432	A-503083_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000288_c1		
Cluster 5	Terpene	605351	626247	-	-		
Cluster 6	Terpene	705884	726852	-	-	1	CYP157C31
Cluster 7	T1pks	796740	940715	Nystatin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000115_c1	2	CYP105H1; CYP161A6
Cluster 8	Butyrolactone	1390494	1401339	Coelimycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000038_c1	1	CYP107AE10
Cluster 9	Bacteriocin-Butyrolactone	1650849	1758890	Sch47554_/_Sch47555_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000268_c1		
Cluster 10	Terpene	2074720	2101403	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 11	Lassopeptide	2283178	2305712	-	-		
Cluster 12	T3pks	2967642	3008706	FD-594_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000222_c1	1	CYP107F9
Cluster 13	Nrps	3068017	3130113	Desotamide_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0001196_c1		
Cluster 14	Siderophore	3136814	3151493	-	-		
Cluster 15	Other	3470479	3511162	Albonoursin_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000851_c1		
Cluster 16	T1pks	3951761	4057662	Aldgamycin_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0001396_c1	3	CYP105DE1; CYP105BS1; CYP1197A1
Cluster 17	Other	4149655	4193803	-	-		
Cluster 18	Linaridin	4625017	4645924	Legonaridin_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0001188_c1		
Cluster 19	Terpene	4789780	4812017	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 20	Lantipeptide	6168869	6193334	Melanin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0000909_c1		
Cluster 21	Ectoine	7150807	7161211	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 22	Siderophore	7239980	7251785	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 23	Thiopeptide-T1pks	7382358	7445646	Virginiamycin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0001116_c1	1	CYP184A8
Cluster 24	Lantipeptide	7631682	7669877	Streptomycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000717_c1		
Cluster 25	Nrps	7834376	7918670	Streptolydigin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001046_c1	1	CYP1196A1
Cluster 26	T2pks	8232006	8274521	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 27	Bacteriocin	8327176	8337427	-	-		
Cluster 28	T1pks	8699010	8746527	Zorbamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001058_c1		
Cluster 29	Transatpks-Nrps	8764353	8873800	Cycloheximide_/_actiphenol_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000175_c1	2	CYP107CA2; CYP154D14
Cluster 30	Nrps	8897613	8945199	A54145_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000291_c1		

Cluster 31	Lantipeptide	8994980	9034826	Hygrocin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000075_c1	1	CYP107L42
Cluster 32	Terpene-T3pks-T1pks-Nrps	9424609	9517486	Friulimicin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000354_c1		
Cluster 33	T1pks-Otherks	9531023	9582274	-	-		
Cluster 34	Lantipeptide-Nrps	9598330	9713563	Zorbamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001058_c1	2	CYP163B; CYP1278B1
Cluster 35	Terpene-T1pks	9773372	9896021	Natamycin_biosynthetic_gene_cluster (68% of genes show similarity)	BGC0000108_c1	1	CYP105H8
Cluster 36	T1pks-Butyrolactone-Nrps	9926227	10062988	Coelimycin_biosynthetic_gene_cluster (29% of genes show similarity)	BGC0000038_c1	1	CYP105BA3
				Streptomyces cyaneogriseus			
Cluster 1	T1pks	181794	235227	Pristinamycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000952_c3	2	CYP107L35; CYP105BT1
Cluster 2	Terpene	343990	368554	Carotenoid_biosynthetic_gene_cluster (45% of genes show similarity)	BGC0000633_c1		
Cluster 3	T2pks	511967	554485	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 4	Transatpks-T1pks-Nrps	751250	905378	Tautomycin_biosynthetic_gene_cluster (27% of genes show similarity)	BGC0000159_c1		
Cluster 5	Nrps	1136002	1186077	Azicemicin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000202_c1		
Cluster 6	T3pks	1300604	1341668	BE-14106_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000029_c1		
Cluster 7	Other	1422519	1464243	Kirromycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001070_c1		
Cluster 8	Ectoine	1984280	1994678	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	Butyrolactone	2792194	2803150	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 10	Melanin	2865688	2876242	Melanin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000909_c1		
Cluster 11	Siderophore	2968691	2980460	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 12	Lassopeptide	4593899	4616468	TP-1161_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000615_c1		
Cluster 13	Terpene	5096111	5117199	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A17
Cluster 14	T1pks	5255104	5335576	Oligomycin_biosynthetic_gene_cluster (44% of genes show similarity)	BGC0000117_c1	1	CYP107W3
Cluster 15	Other	5447763	5489730	BD-12_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001379_c1		
Cluster 16	Siderophore	5842192	5854036	-	-		
Cluster 17	Bacteriocin	6155544	6166959	-	-		
Cluster 18	Terpene	6194937	6217144	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 19	Siderophore	6382826	6396032	-	-	1	CYP105AC8
Cluster 20	Terpene	6517415	6538428	Pentalenolactone_biosynthetic_gene_cluster (58% of genes show similarity)	BGC0000653_c1	2	CYP161C4; CYP183A4
Cluster 21	T1pks	6613280	6660692	-	-		
Cluster 22	Terpene	6884308	6910993	Hopene_biosynthetic_gene_cluster (84% of genes show similarity)	BGC0000663_c1		
Cluster 23	Terpene	6974573	6995385	Isorenieratene_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001227_c1		
Cluster 24	Transatpks-Nrps	7022565	7087583	Reveromycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000135_c1		
Cluster 25	Otherks-Nrps	7273843	7389100	Taromycin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000439_c1		
Cluster 26	Terpene	7480737	7501765	-	-	1	CYP157K4

Cluster 27	Bacteriocin	7518472	7528687	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 28	T2pks	7575898	7618389	Enterocin_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0000220_c1		
Cluster 29	T3pks-Fused-Nrps	7679429	7762396	Pheganomycin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001148_c1	1	CYP105AC17

Streptomyces lydicus **A02**

Cluster 1	T2pks	1	36695	Xantholipin_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000279_c1	1	CYP105BW1
Cluster 2	Melanin	105776	116342	-	-		
Cluster 3	Thiopeptide	155035	187474	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Cluster 4	Transatpks	215263	294994	Dorrigocin_/_migrastatin_biosynthetic_gene_cluster (72% of genes show similarity)	BGC0000177_c1	2	CYP147K2; CYP1038A7
Cluster 5	Terpene	366916	388229	2-methylisoborneol_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000657_c1	1	CYP147F28P
Cluster 6	Butyrolactone	514149	525132	Meilingmycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000093_c1	1	CYP107AE8
Cluster 7	Ladderane	697287	738447	Chloramphenicol_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000893_c1		
Cluster 8	Other	942629	983345	Streptomycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000717_c1	1	CYP1469A2
Cluster 9	Terpene	1000786	1022123	Frankiamicin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0001197_c1		
Cluster 10	T2pks-Terpene	1213663	1277337	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 11	Lantipeptide	1349036	1373093	-	-		
Cluster 12	Terpene	1435606	1495524	Siomycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000655_c1	1	CYP157C29
Cluster 13	Cyanobactin-T1pks-Nrps	1582697	1669681	BE-14106_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000029_c1		
Cluster 14	T3pks-Nrps	1677418	1775435	Kanamycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000703_c1	2	CYP107F8; CYP105D25
Cluster 15	Lantipeptide	1792777	1817670	Planosporicin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000544_c1		
Cluster 16	Bacteriocin-Nrps	2117695	2188684	Enduracidin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000341_c1		
Cluster 17	Butyrolactone	2305530	2316477	Neocarzinostatin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000112_c1		
Cluster 18	Siderophore	2460921	2475144	-	-		
Cluster 19	Terpene	4148488	4170725	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 20	Terpene	5784113	5805222	-	-	1	CYP157C42
Cluster 21	Lassopeptide	6126895	6149273	Chaxapeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0001307_c1		
Cluster 22	Lassopeptide	6229829	6252047	-	-		
Cluster 23	Ectoine	6717405	6727821	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 24	Siderophore	6806328	6818127	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 25	T1pks	6896429	6976696	ECO-02301_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000052_c1		
Cluster 26	T2pks-Oligosaccharide	7320728	7395690	Grincamycin_biosynthetic_gene_cluster (58% of genes show similarity)	BGC0000229_c1	1	CYP113D5
Cluster 27	Siderophore	7657288	7672394	Scabichelin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000423_c1		
Cluster 28	Bacteriocin-Lantipeptide	7921105	7949889	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1		
Cluster 29	Lassopeptide-Nrps	8201080	8256818	Streptomycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000717_c1	2	CYP1278B2; CYP163B11

Cluster 30	Nrps	8258692	8317893	Friulimicin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000354_c1		
Cluster 31	Other	8473783	8514496	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1	1	CYP121A3
Cluster 32	T1pks	8525251	8643939	Natamycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000108_c1	2	CYP161A5; CYP105H3
Cluster 33	T1pks	8655758	8700065	-	-	1	CYP186D1
Cluster 34	Lantipeptide	8785297	8808044	SAL-2242_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000546_c1		
Cluster 35	Lantipeptide-Lassopeptide	9136656	9205488	A-503083_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000288_c1		
***Streptomyces xiamenensis* 318**							
Cluster 1	Lantipeptide-T1pks	186123	258027	Xiamenmycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000933_c1		
Cluster 2	Siderophore	856962	868779	Desferrioxamine_B_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000941_c1		
Cluster 3	Ectoine	910771	921175	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 4	Terpene	1252926	1273975	Chlortetracycline_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000209_c1	1	CYP157C32
Cluster 5	Butyrolactone	1925564	1936604	-	-		
Cluster 6	T1pks-Nrps	2569761	2618819	Thioviridamide_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000625_c1	2	CYP1029A4; CYP285A6
Cluster 7	Other	2649340	2690476	Simocyclinone_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000270_c1		
Cluster 8	Butyrolactone	3050670	3061389	Methylenomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000914_c1		
Cluster 9	T2pks	3777683	3820216	Lomaiviticin_biosynthetic_gene_cluster (38% of genes show similarity)	BGC0000240_c1		
Cluster 10	Lantipeptide-Linaridin	3913176	3941259	-	-	1	CYP1223B1
Cluster 11	Linaridin-T1pks-Lassopeptide-Nrps	4332894	4397384	Heat-stable_antifungal_factor_biosynthetic_gene_cluster (37% of genes show similarity)	BGC0000999_c1	1	CYP107LF1
Cluster 12	Terpene	4494948	4515865	-	-	1	CYP183W1
Cluster 13	Thiopeptide	4549081	4583346	-	-		
Cluster 14	Siderophore	4879386	4893738	-	-		
Cluster 15	Nrps	5106208	5164444	Valinomycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000453_c1		
Cluster 16	T1pks-Nrps	5264533	5315551	Carotenoid_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000633_c1		
Cluster 17	Terpene	5429897	5451770	Hopene_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000663_c1		
Cluster 18	T3pks-Terpene-Nrps	5469251	5606895	Herboxidiene_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001065_c1	1	CYP107F11
Cluster 19	T1pks-Nrps	5621426	5672095	Akaeolide_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001199_c1		
Cluster 20	Nrps	5686309	5752451	WS9326_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001297_c1		
***Streptomyces* sp. Mg1**							
Cluster 1	Terpene	127319	152797	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1		
Cluster 2	T1pks	501941	550367	Maklamicin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001288_c1		
Cluster 3	Terpene-Nrps	554730	625429	Xantholipin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000279_c1	1	CYP154Q2
Cluster 4	Lantipeptide-Terpene	745744	780037	-	-	2	CYP157C26; CYP134A3

Cluster 5	Other	949375	993295	Divergolide_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0001119_c1	1	CYP105DF1
Cluster 6	Terpene	1027112	1048392	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 7	T1pks	1057302	1248586	ECO-02301_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000052_c1		
Cluster 8	Thiopeptide	1270469	1302825	Thaxtomin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000444_c1	2	CYP2238A1; CYP1048A3
Cluster 9	Terpene-Otherks	1637598	1706261	A201A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001138_c1	2	CYP154D15; CYP157C27
Cluster 10	Siderophore	3145817	3157598	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 11	Lantipeptide	4292765	4317277	-	-		
Cluster 12	Lantipeptide	5106228	5130687	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 13	Siderophore	5851645	5863480	-	-		
Cluster 14	Bacteriocin	6103526	6114881	-	-		
Cluster 15	Terpene	6180567	6202783	-	-		
Cluster 16	Terpene	6479912	6506775	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 17	Lantipeptide	6634722	6657028	-	-		
Cluster 18	T1pks	6892260	6958618	Aldgamycin_biosynthetic_gene_cluster (44% of genes show similarity)	BGC0001396_c1	2	CYP105L3; CYP1995C1
Cluster 19	Lantipeptide	6975153	7013297	SapB_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000551_c1		
Cluster 20	Melanin	7093620	7121271	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1		
Cluster 21	Siderophore	7189328	7202508	-	-		
Cluster 22	T2pks-T3pks	7208586	7277065	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1		
Cluster 23	Terpene	7293753	7314790	-	-	1	CYP251F1
***Streptomyces* sp. CNQ-509**							
Cluster 1	T1pks-Transatpks-Terpene	114915	263143	Tetronomycin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000164_c1	1	CYP105AC15
Cluster 2	Terpene	506604	528829	Laspartomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000379_c1		
Cluster 3	Nrps	1031663	1082217	Taromycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000439_c1	2	CYP107LC1; CYP105BK2
Cluster 4	Ectoine	1297153	1307551	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 5	Terpene	1840979	1861968	-	-		
Cluster 6	Bacteriocin	2037173	2047970	Arginomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000883_c1		
Cluster 7	Siderophore	2496813	2509146	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 8	Nrps	2913716	2970785	-	-		
Cluster 9	Other	3012179	3056803	Sporolide_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000150_c1		
Cluster 10	Terpene	3438020	3459228	Fosfazinomycin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000937_c1		
Cluster 11	T2pks	3511946	3554521	Tetracenomycin_biosynthetic_gene_cluster (41% of genes show similarity)	BGC0000275_c1	1	CYP1064A5
Cluster 12	Lantipeptide	3683952	3708270	-	-		
Cluster 13	Terpene	4340279	4383600	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 14	Fused	4512434	4536010	-	-	1	CYP1341E2

Cluster 15	Thiopeptide	4563155	4597839	-	-		
Cluster 16	T3pks	4639896	4680939	Pactamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000119_c1	2	CYP157A20; CYP154C13
Cluster 17	T1pks	4837274	4883564	Laspartomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000379_c1		
Cluster 18	T3pks-Terpene-Otherks	5581524	5655064	Merochlorin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0001083_c1	1	CYP123D1
Cluster 19	Terpene	5674860	5699525	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1		
Cluster 20	Siderophore	6179666	6194253	-	-		
Cluster 21	T1pks-Nrps	6797099	6869660	Arsenopolyketides_biosynthetic_gene_cluster (37% of genes show similarity)	BGC0001283_c1	1	CYP105BA2
Cluster 22	T2pks	7072594	7145146	Fluostatin_biosynthetic_gene_cluster (35% of genes show similarity)	BGC0000223_c1		
Cluster 23	Phenazine	7178028	7223783	Marinophenazines_biosynthetic_gene_cluster (88% of genes show similarity)	BGC0001221_c1		
Cluster 24	T3pks-Nrps	7442803	7539290	A47934_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000290_c1	2	CYP165E2; CYP165B8
Cluster 25	Terpene	7568186	7609590	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1	1	CYP157C32
Cluster 26	T3pks	7613012	7654100	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 27	Nrps	7676692	7724338	Oxazolomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001106_c1		
Cluster 28	Siderophore	7759755	7773368	-	-		
***Streptomyces ambofaciens* ATCC 23877**							
Cluster 1	T2pks-Butyrolactone	142506	222698	Fluostatin_biosynthetic_gene_cluster (29% of genes show similarity)	BGC0000223_c1	1	CYP154K2
Cluster 2	T1pks-Terpene-Nrps	340601	411878	Antimycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000958_c1		
Cluster 3	Indole	706084	727211	-	-	1	CYP156B15
Cluster 4	Terpene	783854	815417	Carotenoid_biosynthetic_gene_cluster (27% of genes show similarity)	BGC0000633_c1		
Cluster 5	Ectoine	2000972	2011370	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 6	Melanin	2873096	2883623	Melanin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000909_c1		
Cluster 7	Siderophore	2980232	2992004	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 8	Butyrolactone	3468493	3478867	-	-		
Cluster 9	Nrps	4538916	4580316	Zorbamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001058_c1		
Cluster 10	Terpene	5302337	5323356	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A1
Cluster 11	T2pks	5372707	5415255	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1		
Cluster 12	Siderophore	5867408	5879165	-	-		
Cluster 13	Oligosaccharide-T1pks-Nrps	5942161	6143480	Midecamycin_biosynthetic_gene_cluster (41% of genes show similarity)	BGC0000096_c1	2	CYP107EP1; CYP113B4
Cluster 14	Bacteriocin	6235154	6246572	-	-		
Cluster 15	Terpene	6259614	6281794	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 16	Siderophore	6452952	6466082	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 17	Terpene	6901163	6927934	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		

Cluster 18	Nrps	7171867	7240586	Congocidine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000327_c1		
Cluster 19	Terpene	7277128	7298159	-	-	1	CYP157K5
Cluster 20	Bacteriocin	7314194	7324409	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 21	Nrps	7565299	7616302	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 22	Terpene	7629726	7650940	Isorenieratene_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000664_c1		
Cluster 23	T1pks	7665382	7835031	Stambomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000151_c1	2	CYP107EF1, CYP107EP1
Cluster 24	Lantipeptide-Terpene	7921717	7968985	Tetronasin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000163_c1		
Cluster 25	T1pks	8007437	8054819	Clavams_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000843_c1		
Cluster 26	T2pks-Butyrolactone	8081268	8161435	Fluostatin_biosynthetic_gene_cluster (29% of genes show similarity)	BGC0000223_c1	1	CYP154K2
***Streptomyces pristinaespiralis* HCCB 10218**							
Cluster 1	Oligosaccharide-Ectoine-T2pks-Nrps-T1pks-Otherks	136600	410171	Pristinamycin_biosynthetic_gene_cluster (93% of genes show similarity)	BGC0000952_c3	3	CYP154A22; CYP107EH1; CYP113C2
Cluster 2	T3pks	668742	709860	Lasalocid_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000087_c1		
Cluster 3	Thiopeptide-Nrps	1072428	1148005	Albachelin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001211_c1		
Cluster 4	Terpene	1167008	1193675	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 5	Lassopeptide	1363490	1386215	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1		
Cluster 6	Bacteriocin	2055619	2066929	-	-		
Cluster 7	Thiopeptide-T2pks	2205468	2274572	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 8	Terpene	2311778	2337445	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1		
Cluster 9	Siderophore	2467192	2482043	-	-		
Cluster 10	Lantipeptide	2837152	2859773	SapB_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000551_c1		
Cluster 11	Melanin	3390526	3401059	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G6
Cluster 12	T1pks-Otherks	4034744	4089572	R1128_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000261_c1		
Cluster 13	Siderophore	5528888	5540660	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 14	Terpene	5662970	5684067	-	-		
Cluster 15	Ectoine	6550882	6606667	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 16	Terpene	7528164	7549282	-	-		
Cluster 17	Bacteriocin	7675340	7685558	Sch47554_/_Sch47555_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000268_c1		
Cluster 18	Terpene	8034955	8057159	-	-		
Cluster 19	T2pks-Oligosaccharide-Nrps-Otherks	8110148	8245788	Pristinamycin_biosynthetic_gene_cluster (97% of genes show similarity)	BGC0000952_c3	3	CYP154B6; CYP113C2, CYP107EH1
Cluster 20	Ectoine-Nrps	8233370	8340124	Pristinamycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000952_c1		

Cluster 21	T1pks-Ectoine-Otherks	8335201	8395993	Kosinostatin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001073_c1	1	CYP154A22
***Streptomyces* sp. CFMR 7**							
Cluster 1	Thiopeptide-T1pks-Nrps	58429	118641	Daptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000336_c1		
Cluster 2	Terpene	123726	149324	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 3	T3pks-Nrps	258620	375779	Herboxidiene_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001065_c1		
Cluster 4	Melanin	410995	421465	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G2
Cluster 5	Nrps	428038	486263	Valinomycin_biosynthetic_gene_cluster (22% of genes show similarity)	BGC0000453_c1		
Cluster 6	Nrps	557485	624704	Tallysomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001048_c1		
Cluster 7	Bacteriocin-T1pks-Nrps	651520	718561	SGR_PTMs_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001043_c1	1	CYP107BX7
Cluster 8	T1pks	755925	855340	Bafilomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000028_c1		
Cluster 9	Nrps	877606	932660	A201A_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001138_c1	1	CYP154A18
Cluster 10	Terpene	955342	981915	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 11	Nrps	1423338	1482428	Asukamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000187_c1		
Cluster 12	Bacteriocin	1611798	1623204	-	-		
Cluster 13	Nrps	1723980	1767063	FD-594_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000222_c1		
Cluster 14	Nrps	1868317	1911696	Marformycins_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001214_c1		
Cluster 15	Siderophore	2160199	2174961	-	-		
Cluster 16	Amglyccycl	2552447	2573640	Neocarzilin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000111_c1		
Cluster 17	Terpene	2584713	2605690	-	-		
Cluster 18	Lantipeptide	2947152	2969935	AmfS_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000496_c1		
Cluster 19	Lantipeptide	3663589	3683780	-	-		
Cluster 20	Lassopeptide	3813538	3836280	SRO15-2005_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000578_c1		
Cluster 21	T2pks	3890875	3933366	Rabelomycin_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000262_c1		
Cluster 22	Ectoine-Butyrolactone	4682870	4698288	Skyllamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000429_c1		
Cluster 23	Other	4842524	4883618	-	-		
Cluster 24	Nrps	5023924	5090780	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 25	Otherks	5155943	5196989	-	-		
Cluster 26	Thiopeptide	5320375	5352933	-	-		
Cluster 27	Other	5591139	5635029	Bottromycin_A2_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000469_c1		
Cluster 28	Siderophore	5714230	5726008	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 29	Lantipeptide	5832437	5866769	-	-		
Cluster 30	Ectoine	6815095	6825493	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 31	Terpene	7283944	7305038	Steffimycin_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0000273_c1		

Cluster 32	T3pks	7787378	7828496	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1	1	CYP107F4
Cluster 33	Terpene	7878228	7899235	-	-		
Cluster 34	Melanin-Nrps	7892226	7956790	Coelichelin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000325_c1		
Cluster 35	Transatpks-T1pks-Otherks-Nrps	7970068	8086862	Griseobactin_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000368_c1		
Cluster 36	Terpene	8091617	8113830	-	-		
Cluster 37	Butyrolactone	8140824	8151774	Coelimycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000038_c1		
Cluster 38	Arylpolyene	8160105	8203268	A-500359s_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000949_c1	1	CYP105D20
***Streptomyces* sp. CdTB01**							
Cluster 1	T2pks-Nrps	203006	302123	Friulimicin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000354_c1		
Cluster 2	Other	316900	357316	Lomaiviticin_biosynthetic_gene_cluster (35% of genes show similarity)	BGC0000240_c1		
Cluster 3	T3pks	448018	489094	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1		
Cluster 4	Nrps	600355	704555	Azicemicin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000202_c1		
Cluster 5	Indole	962291	983421	-	-	1	CYP145C3
Cluster 6	Lassopeptide	1077842	1100421	Carbapenem_MM_4550_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000842_c1		
Cluster 7	Bacteriocin-Lantipeptide	1408106	1438334	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1		
Cluster 8	Terpene	2019582	2046239	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 9	Siderophore	2557703	2570808	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 10	Terpene	2703518	2725674	-	-	1	CYP180A29
Cluster 11	Bacteriocin	2777155	2788468	-	-		
Cluster 12	Bacteriocin	2856792	2868627	Lipopeptide_8D1-1_/_lipopeptide_8D1-2_biosynthetic_gene_clus... (4% of genes show similarity)	BGC0001370_c1		
Cluster 13	Siderophore	2978195	2990246	-	-		
Cluster 14	Other	3311789	3352478	-	-		
Cluster 15	Other	3415999	3456520	-	-		
Cluster 16	Other	3840003	3880713	-	-		
Cluster 17	Terpene	3987144	4008067	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A19
Cluster 18	T2pks	4156435	4198941	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 19	Butyrolactone	4903660	4914622	Gilvocarcin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000226_c1		
Cluster 20	Butyrolactone	5451362	5462285	Pactamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000119_c1		
Cluster 21	Bacteriocin-Lassopeptide-Nrps	5563100	5662606	Chaxapeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0001307_c1		
Cluster 22	Siderophore	6377594	6389363	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 23	Melanin	6480146	6490643	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000909_c1		
Cluster 24	Ectoine	7604852	7615256	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		

Cluster 25	Other	7842280	7886146	-	-		
Cluster 26	Terpene	7938794	7959870	Pradimicin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000256_c1	2	CYP157C39; CYP183B5
Cluster 27	T1pks	8789168	8833130	Maduropeptin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001008_c1		
Cluster 28	Melanin	9121961	9132335	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 29	Terpene	9309416	9335435	Carotenoid_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000633_c1		
Cluster 30	T3pks-T1pks-Nrps	9576854	9677125	Antimycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000958_c1		
Cluster 31	Thiopeptide	9678619	9723583	ECO-02301_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000052_c1		
Cluster 32	Butyrolactone	9877671	9888660	Merochlorin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001083_c1		
Streptomyces reticuli							
Cluster 1	T1pks	58809	169393	Naphthomycin_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000106_c1	1	CYP166A3
Cluster 2	Bacteriocin-Nrps	436777	524492	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1	1	CYP113K6
Cluster 3	Other	782580	824268	Tambromycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001368_c1	1	CYP162B2
Cluster 4	Terpene	956043	980632	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		
Cluster 5	Other	996598	1037308	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1	2	CYP121A5; CYP154U7
Cluster 6	Melanin	1135647	1146024	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 7	Nrps-T1pks-Otherks	1309947	1435677	Sanglifehrin_A_biosynthetic_gene_cluster (43% of genes show similarity)	BGC0001042_c1		
Cluster 8	T2pks-T1pks-Otherks	1583764	1641835	Hedamycin_biosynthetic_gene_cluster (31% of genes show similarity)	BGC0000233_c1		
Cluster 9	T2pks-T3pks-Otherks	1910507	1979532	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A14
Cluster 10	Ectoine-T1pks-Otherks	2033920	2093478	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 11	Lassopeptide	2310021	2332519	Chaxapeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0001307_c1		
Cluster 12	Ectoine	2761145	2771549	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 13	T2pks	3172003	3214516	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 14	Nrps	3313387	3364223	Laspartomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000379_c1	2	CYP107LB1; CYP105BK2
Cluster 15	Melanin	3838744	3849271	Istamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000700_c1		
Cluster 16	Siderophore	3940015	3951784	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 17	Butyrolactone-Amglyccycl-T1pks-Nrps	5652600	5761564	Pyralomicin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001038_c1	1	CYP1037A2
Cluster 18	Terpene	6427916	6448839	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A23
Cluster 19	Siderophore	7100383	7112428	-	-		
Cluster 20	Nrps	7197457	7312041	Friulimicin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000354_c1	1	CYP2045A1
Cluster 21	Bacteriocin-Nrps	7368052	7446646	Meilingmycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000093_c1		
Cluster 22	Bacteriocin	7495248	7506561	-	-		

Cluster 23	Terpene	7535955	7558117	-	-	1	CYP180A28
Cluster 24	Siderophore	7728182	7741322	-	-		
Cluster 25	Terpene	8260062	8286833	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 26	Lassopeptide	8302751	8325328	Rifamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000136_c1		
***Streptomyces* sp. 4F**							
Cluster 1	Lantipeptide	141260	165398	-	-		
Cluster 2	Nrps-T2pks-Otherks-T1pks-Phenazine	266514	406568	Antimycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000958_c1	1	CYP105DD1
Cluster 3	Lantipeptide	577739	609900	-	-		
Cluster 4	T3pks	656707	697780	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 5	Terpene	916010	940106	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		
Cluster 6	T2pks	1143767	1186276	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 7	Ectoine	2042040	2052438	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Nrps	2648339	2697721	SCO-2138_biosynthetic_gene_cluster (64% of genes show similarity)	BGC0000595_c1		
Cluster 9	Siderophore	3056286	3068058	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 10	Terpene	5286843	5307928	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A16
Cluster 11	Nrps	5920868	6005627	Friulimicin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000354_c1		
Cluster 12	Bacteriocin	6205199	6216509	-	-		
Cluster 13	Terpene	6254217	6276373	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1		
Cluster 14	T1pks-Nrps	6330111	6379887	Althiomycin_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000955_c1		
Cluster 15	Siderophore	6456557	6469796	Grincamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000229_c1		
Cluster 16	Terpene	6897309	6924002	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 17	Bacteriocin	7347393	7357608	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1		
Cluster 18	T2pks-Otherks	7710378	7781259	Hedamycin_biosynthetic_gene_cluster (34% of genes show similarity)	BGC0000233_c1	1	CYP105DD1
Cluster 19	Lantipeptide	7882374	7906512	-	-		
***Streptomyces leeuwenhoekii* C34(2013)**							
Cluster 1	T1pks	99264	143430	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Cluster 2	T1pks	191701	240196	Cremimycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000042_c1		
Cluster 3	T3pks-T1pks-Nrps	324784	458084	Pristinamycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000952_c3	3	CYP107L35; CYP105BT1; CYP154B4
Cluster 4	Bacteriocin	572464	582679	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 5	Terpene	598795	619823	-	-	1	CYP157K4
Cluster 6	Lassopeptide	642180	664830	Labyrinthopeptin_A1,A3_/_labyrinthopeptin_A2_biosynthetic_gene (40% of genes show similarity)	BGC0000519_c1	1	CYP102B20
Cluster 7	Nrps	714060	794426	Rishirilide_B_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001179_c1	1	CYP113K3

Cluster 8	Nrps-Transatpks-Terpene-Otherks	1046004	1155931	Leinamycin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001101_c1	2	CYP107EG1; CYP105BR1
Cluster 9	Terpene-T1pks	1211564	1331006	Chaxamycin_A_/_chaxamycin_B_/_chaxamycin_C_/_chaxamycin_D (96% of genes show similarity)	BGC0001287_c1	3	CYP107Q3; CYP105D28; CYP166A2
Cluster 10	T1pks	1497127	1544539	-	-	3	CYP154Z1; CYP1416A1; CYP2266A2
Cluster 11	Terpene	1624097	1645110	Pentalenolactone_biosynthetic_gene_cluster (58% of genes show similarity)	BGC0000653_c1	2	CYP183A4; CYP161C4
Cluster 12	T1pks-Siderophore	1776281	1833813	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1	2	CYP107L33; CYP105AC8
Cluster 13	Terpene	1972277	1994487	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 14	Bacteriocin	2013690	2025087	-	-		
Cluster 15	Siderophore	2293580	2305424	-	-		
Cluster 16	T1pks-Nrps	2668194	2719415	BD-12_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001379_c1		
Cluster 17	T3pks	2937137	2978264	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1	1	CYP107F10
Cluster 18	Terpene	3047731	3068819	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A17
Cluster 19	Lassopeptide	3552136	3574705	TP-1161_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000615_c1		
Cluster 20	Bacteriocin	3683199	3693399	Arginomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000883_c1		
Cluster 21	Siderophore	5232176	5243945	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 22	Melanin	5330379	5340933	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000910_c1		
Cluster 23	Butyrolactone-Amglyccycl	5385171	5417416	Neocarzilin_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000111_c1		
Cluster 24	Ectoine	6176293	6186691	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 25	Other	6710095	6751819	Kirromycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001070_c1		
Cluster 26	T3pks	6822979	6864043	BE-14106_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000029_c1		
Cluster 27	T1pks	7141058	7240871	Brasilinolide_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001381_c1	1	CYP1418A1
Cluster 28	T1pks	7355977	7439461	JBIR-100_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0001348_c1	1	CYP1031A3
Cluster 29	Other	7486047	7529121	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1	1	CYP107AM11
Cluster 30	T2pks-Terpene	7530162	7588405	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 31	Terpene	7744176	7768730	Carotenoid_biosynthetic_gene_cluster (54% of genes show similarity)	BGC0000633_c1		
Streptomyces rubrolavendulae							
Cluster 1	Terpene	137572	159833	-	-		
Cluster 2	Terpene	301875	322972	-	-	3	CYP251A3; CYP157C21; CYP158A20
Cluster 3	Other	488022	530907	Desotamide_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001196_c1		
Cluster 4	Lantipeptide	608457	633367	Akaeolide_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001199_c1		
Cluster 5	Indole	654870	678301	Staurosporine_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000825_c1	2	CYP245A6; CYP244A3
Cluster 6	Lassopeptide	1093159	1115588	-	-		

Cluster 7	Ectoine	1271932	1282330	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Siderophore	2154239	2166161	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 9	Melanin	3552050	3562661	Istamycin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000700_c1		
Cluster 10	Bacteriocin	3689684	3700145	-	-		
Cluster 11	Nrps	5063839	5170579	Viomycin_biosynthetic_gene_cluster (95% of genes show similarity)	BGC0000458_c1	2	CYP159A23; CYP157B32
Cluster 12	T1pks	5199891	5265457	Bleomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000963_c1		
Cluster 13	Thiopeptide	5298877	5374556	Cyclooctatin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000677_c1	2	CYP183H3; CYP183G3
Cluster 14	Bacteriocin	5488275	5499714	-	-		
Cluster 15	Other	5563360	5607193	Auricin_deoxysugar_moieties_biosynthetic_gene_cluster (24% of genes show similarity)	BGC0000727_c1		
Cluster 16	Siderophore	5623819	5639364	Macrotetrolide_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000244_c1		
Cluster 17	Nrps	5676095	5774369	Kanamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000703_c1		
Cluster 18	Terpene	5934523	5961241	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 19	Terpene	5978656	6004547	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 20	Amglyccycl	6026409	6060840	Neomycin_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000709_c1		
Cluster 21	Terpene	6213351	6234451	Herbimycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000074_c1	1	CYP251F2
Cluster 22	Lantipeptide-Nrps	6258519	6316171	-	-	1	CYP1207A10
Cluster 23	T3pks-Butyrolactone	6387947	6471130	Lomofungin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0001302_c1	1	CYP158A19
Cluster 24	Nrps	6479692	6532273	Daptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000336_c1	2	CYP107E12; CYP285D1
Streptomyces parvulus							
Cluster 1	Terpene	90078	111136	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Cluster 2	Terpene	132842	201970	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 3	Indole	313179	334306	Ravidomycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000263_c1	2	CYP156B15; CYP183J3
Cluster 4	Nrps	556539	624553	Actinomycin_biosynthetic_gene_cluster (82% of genes show similarity)	BGC0000296_c1		
Cluster 5	Ectoine	1603590	1613988	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 6	Melanin	2492824	2503330	Melanin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000909_c1		
Cluster 7	Siderophore	2584513	2596282	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 8	Nrps	4119934	4178843	Borrelidin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000031_c1		
Cluster 9	Terpene	4829070	4850155	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A1
Cluster 10	T2pks	4896168	4938716	Spore_pigment_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000271_c1		
Cluster 11	Other	5248686	5289795	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000315_c1		
Cluster 12	Siderophore	5414789	5426603	-	-		
Cluster 13	Bacteriocin	5626803	5638137	-	-		
Cluster 14	Terpene	5655570	5677768	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		

Cluster 15	Siderophore	5827742	5840921	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1		
Cluster 16	Lantipeptide	6160164	6182773	SAL-2242_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000546_c1		
Cluster 17	Terpene	6248979	6275723	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 18	Terpene	6617669	6638700	Versipelostatin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001204_c1	2	CYP157K6; CYP105D33
Cluster 19	Bacteriocin	6649380	6659595	Informatipeptin_biosynthetic_gene_cluster (42% of genes show similarity)	BGC0000518_c1		
Cluster 20	Nrps	6874609	6925528	Coelichelin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000325_c1		
Cluster 21	T3pks	6973951	7015135	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1		
***Streptomyces lydicus* 103**							
Cluster 1	Lantipeptide	140498	176168	Svaricin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001382_c1		
Cluster 2	T1pks	632618	678779	Laspartomycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000379_c1	1	CYP147F26
Cluster 3	T1pks-Nrps	679298	735222	Antalid_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001235_c1		
Cluster 4	Lassopeptide	1043432	1066034	-	-		
Cluster 5	Ectoine	2288692	2299108	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 6	Siderophore	2381075	2392883	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 7	Terpene-T1pks-Nrps	2855513	2966648	Streptolydigin_biosynthetic_gene_cluster (97% of genes show similarity)	BGC0001046_c1	2	CYP107FH2; CYP107B26
Cluster 8	T2pks	3269571	3312086	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 9	Bacteriocin	3367107	3377340	-	-		
Cluster 10	Lantipeptide	3656937	3679549	SapB_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000551_c1		
Cluster 11	T1pks-Nrps	3761430	3831019	SW-163_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000434_c1	1	CYP163G1
Cluster 12	Thiopeptide	3985879	4047327	Cyclothiazomycin_biosynthetic_gene_cluster (38% of genes show similarity)	BGC0000603_c1	1	CYP147F27
Cluster 13	Terpene-Nrps	4476045	4560849	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 14	Bacteriocin	4574348	4586282	-	-		
Cluster 15	Butyrolactone	4723978	4734838	Hygrocin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000075_c1	1	CYP107AE12
Cluster 16	Melanin-Nrps	4933655	4994238	WS9326_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0001297_c1	1	CYP107FV4
Cluster 17	Other	5056238	5097611	A-503083_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000288_c1	1	CYP1005B7
Cluster 18	Nucleoside-Lassopeptide-Nrps	5141027	5208382	Rapamycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001040_c1	1	CYP157C36
Cluster 19	Terpene	5409855	5436452	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 20	Terpene	5579689	5600747	Kanamycin_biosynthetic_gene_cluster (53% of genes show similarity)	BGC0000706_c1		
Cluster 21	Bacteriocin	5993231	6004689	-	-		
Cluster 22	Butyrolactone	6060071	6071060	Griseoviridin_/_viridogrisein_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000459_c1		
Cluster 23	T3pks-Nrps	6090851	6154344	Feglymycin_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0001233_c1	1	CYP107F15
Cluster 24	Siderophore	6256819	6271591	-	-		
Cluster 25	Nrps	7791714	7850912	Mannopeptimycin_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000388_c1		
Cluster 26	Terpene	7923764	7946001	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		

***Streptomyces* sp. SAT1**							
Cluster 1	Lantipeptide	1	24200	Herboxidiene_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001065_c1		
Cluster 2	Phosphonate-Nrps	74302	148960	Scabichelin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000423_c1	1	CYP1618A1
Cluster 3	Thiopeptide-Terpene	215878	265579	Isorenieratene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000664_c1	1	CYP180B6
Cluster 4	Butyrolactone	285579	296460	U-68204_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001354_c1	1	CYP105B73
Cluster 5	T1pks	354232	403174	Herboxidiene_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001065_c1		
Cluster 6	Other	708904	752167	Stenothricin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000431_c1		
Cluster 7	Terpene	868664	889695	Oxazolomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001106_c1	1	CYP183X4
Cluster 8	T3pks	922781	963839	Herboxidiene_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0001065_c1	1	CYP158A25
Cluster 9	Ectoine	1573240	1583644	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 10	Melanin	2467228	2477665	Melanin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000909_c1		
Cluster 11	T2pks	3223020	3265538	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 12	Other	3883484	3925397	Salinosporamide_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0001041_c1	1	CYP107P31
Cluster 13	Terpene	4852785	4873798	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A18
Cluster 14	Siderophore	5500156	5512363	-	-		
Cluster 15	Nrps-T1pks-Otherks	5556590	5645890	Nataxazole_biosynthetic_gene_cluster (77% of genes show similarity)	BGC0001213_c1		
Cluster 16	Bacteriocin	5864472	5875941	-	-		
Cluster 17	Terpene	5883559	5905742	-	-		
Cluster 18	Siderophore	6064359	6077546	Grincamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000229_c1		
Cluster 19	Terpene	6367454	6394225	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		
Cluster 20	Bacteriocin-T1pks	6551532	6664649	Bafilomycin_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000028_c1	1	CYP158A24
Cluster 21	Nrps	6783735	6830197	Griseobactin_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0000368_c1		
Cluster 22	Lantipeptide	6903694	6926321	Informatipeptin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000518_c1		
Cluster 23	Phosphoglycolipid	7099434	7124720	Teichomycin_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0001395_c1	1	CYP107E32
Cluster 24	Lantipeptide	7146616	7187284	-	-		
Cluster 25	Other	7191528	7243622	-	-		
Cluster 26	Bacteriocin-Terpene-Nrps	7252610	7427729	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1	2	CYP1722A3; CYP1618A2
Cluster 27	Terpene	7437496	7458770	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Streptomyces clavuligerus							
Cluster 1	Siderophore	10562	24130	-	-		
Cluster 2	Terpene-T1pks-Nrps	76329	184101	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	3	CYP105BG1; CYP163B7; CYP251E1
Cluster 3	T3pks	276819	317874	Naringenin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001310_c1	1	CYP107F7
Cluster 4	Indole-Terpene-Nrps	531915	645805	Nucleocidin_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0001387_c1	2	CYP107NSF1; CYP107BY2

Cluster 5	Nrps	657794	707790	Holomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000373_c1		
Cluster 6	Terpene	715154	741936	Hopene_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000663_c1		
Cluster 7	Nrps	821138	866647	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000315_c1		
Cluster 8	Lantipeptide	1047480	1085758	AmfS_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000496_c1		
Cluster 9	T2pks	1098934	1141500	Spore_pigment_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000271_c1		
Cluster 10	Bacteriocin	1178193	1189566	-	-		
Cluster 11	Nrps	1300723	1379478	A201A_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000873_c1		
Cluster 12	Siderophore	1428060	1440111	-	-		
Cluster 13	T1pks-Nrps	1680579	1735743	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1	1	CYP136E1
Cluster 14	Lantipeptide	1791838	1816396	-	-		
Cluster 15	Nucleoside	1918425	1939396	Tunicamycin_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000880_c1		
Cluster 16	Blactam-Nrps	1997030	2057025	Clavulanic_acid_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000845_c1	1	CYP105M1
Cluster 17	Melanin	2367325	2377759	Melanin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000911_c1	1	CYP124G5
Cluster 18	Blactam	3437138	3458112	Clavams_biosynthetic_gene_cluster (81% of genes show similarity)	BGC0000843_c1		
Cluster 19	Lantipeptide	3971117	3995628	-	-		
Cluster 20	Butyrolactone	4147482	4158450	Lactonamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000238_c1		
Cluster 21	Nrps	4164716	4212044	-	-		
Cluster 22	Siderophore	4567319	4579139	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000941_c1		
Cluster 23	Ectoine	5558823	5569248	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 24	T1pks-Butyrolactone-Otherks	6201299	6288439	Daptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000336_c1	1	CYP107AL2
Cluster 25	Terpene	6639864	6662038	-	-		
Cluster 26	T1pks	6788964	6883702	Bafilomycin_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000028_c1	1	CYP154A14
Streptomyces griseochromogenes							
Cluster 1	T2pks-Butyrolactone	122962	169387	Skyllamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000429_c1		
Cluster 2	Thiopeptide-Bacteriocin	257601	305335	GE37468_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000605_c1	1	CYP113V2
Cluster 3	Phosphonate-Bacteriocin	525563	578114	Thioviridamide_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000625_c1		
Cluster 4	Terpene	1454562	1475575	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A10
Cluster 5	T1pks	1534283	1580330	Tiancimycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0001378_c1		
Cluster 6	Nrps-T1pks-Otherks	1759065	1815292	Caerulomycin_A_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000966_c1		
Cluster 7	Siderophore-T1pks-Nrps	2196713	2380559	Apoptolidin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000021_c1		
Cluster 8	T1pks-Nrps	2485653	2611697	Polyoxypeptin_biosynthetic_gene_cluster (51% of genes show similarity)	BGC0001036_c1	1	CYP247A3_ortholog

Cluster 9	Bacteriocin	2620971	2632827	Lipopeptide_8D1-1_/_lipopeptide_8D1-2_biosynthetic_gene_clus... (4% of genes show similarity)	BGC0001370_c1		
Cluster 10	T1pks	2638274	2691239	Meilingmycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000093_c1	1	CYP105BC2
Cluster 11	Lassopeptide	2696145	2718685	Nanchangmycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000105_c1		
Cluster 12	Bacteriocin	2761295	2772596	-	-		
Cluster 13	Terpene	2797534	2819723	-	-	1	CYP180A26
Cluster 14	Phosphonate-Terpene	2914963	2978479	FR900098_biosynthetic_gene_cluster (27% of genes show similarity)	BGC0000904_c1		
Cluster 15	Siderophore	3069319	3082416	Marineosin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000091_c1		
Cluster 16	Terpene	3525277	3551973	Hopene_biosynthetic_gene_cluster (84% of genes show similarity)	BGC0000663_c1		
Cluster 17	T1pks-Nrps	3577665	3670783	Filipin_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000059_c1		
Cluster 18	Nrps	3857540	3912587	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000026_c1		
Cluster 19	Other	3937513	3978886	A-503083_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000288_c1		
Cluster 20	Bacteriocin-Lantipeptide	4145274	4177698	Informatipeptin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000518_c1		
Cluster 21	Lantipeptide-T1pks-Nrps	4509770	4638651	Meilingmycin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000093_c1	2	CYP208A9; CYP107BK3
Cluster 22	Bacteriocin-T1pks	4660365	4727894	Blasticidin_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000874_c1		
Cluster 23	Lantipeptide	4734648	4757377	Blasticidin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000874_c1		
Cluster 24	Thiopeptide	4867845	4896118	Lactazole_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000606_c1		
Cluster 25	Lantipeptide-T1pks-Otherks	5181716	5260298	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Cluster 26	Nrps	5367740	5446027	Napsamycin_biosynthetic_gene_cluster (82% of genes show similarity)	BGC0000950_c1	1	CYP107KX1
Cluster 27	Ladderane	5670509	5712983	Metatricycloene_biosynthetic_gene_cluster (32% of genes show similarity)	BGC0001369_c1		
Cluster 28	Bacteriocin	5821912	5832472	Streptothricin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000432_c1		
Cluster 29	Lantipeptide	5857594	5887006	-	-		
Cluster 30	Other	6211240	6251734	Kanamycin_biosynthetic_gene_cluster (1% of genes show similarity)	BGC0000703_c1	2	CYP121A4; CYP154U6
Cluster 31	Lassopeptide	6260073	6282641	-	-		
Cluster 32	Melanin-Terpene	6357273	6382845	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 33	T1pks-Nrps	6415636	6471337	-	-		
Cluster 34	Terpene	6484659	6505666	-	-	1	CYP183X2
Cluster 35	Lantipeptide	6664388	6702945	-	-		
Cluster 36	Nucleoside	6780943	6801308	Toyocamycin_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000881_c1		
Cluster 37	Terpene	6813225	6834391	2-methylisoborneol_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000657_c1		
Cluster 38	Siderophore	6843831	6857240	-	-		
Cluster 39	Siderophore	7263646	7276995	-	-		
Cluster 40	Phosphonate-T3pks-	7289629	7395040	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A21

	Nrps-Ladderane						
Cluster 41	T1pks-Otherks	7616533	7668101	Cinnamycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000503_c1		
Cluster 42	Other	8072352	8116209	-	-		
Cluster 43	Ectoine	8338442	8348846	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 44	Lassopeptide	8845999	8868499	Chaxapeptin_biosynthetic_gene_cluster (28% of genes show similarity)	BGC0001307_c1		
Cluster 45	Terpene	8994774	9016135	Kanamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000703_c1		
Cluster 46	Melanin-Nrps	9444124	9491130	Melanin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000909_c1		
Cluster 47	Siderophore	9562300	9574069	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 48	T2pks-T1pks	10278621	10365301	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 49	T2pks-Oligosaccharide-Nrps-Otherks	10485649	10561348	Saquayamycin_Z_/_galtamycin_B_biosynthetic_gene_cluster (41% of genes show similarity)	BGC0000267_c1		
***Streptomyces* sp. S10(2016)**							
Cluster 1	Other	224145	266760	A-500359s_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000949_c1		
Cluster 2	Other	343674	387549	-	-		
Cluster 3	Melanin	544336	554704	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 4	T3pks-Nrps	924883	1081396	Feglymycin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0001233_c1		
Cluster 5	Ectoine	2149543	2159941	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 6	Terpene-Nrps	2878958	2945938	SCO-2138_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000595_c1		
Cluster 7	Melanin	3247945	3258424	Istamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000700_c1		
Cluster 8	Siderophore	3354794	3366563	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 9	Thiopeptide	3912000	3938554	Platencin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001156_c1		
Cluster 10	Butyrolactone	4637521	4648519	Pristinamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000952_c3	1	CYP154K3
Cluster 11	Butyrolactone	4778184	4789218	Methylenomycin_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000914_c1		
Cluster 12	Nrps	4941976	4998990	A54145_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000291_c1		
Cluster 13	Terpene	5837066	5862615	Isorenieratene_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000664_c1		
Cluster 14	Terpene	6000626	6021549	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A15
Cluster 15	T2pks	6221507	6264022	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 16	Siderophore	6648574	6660568	-	-		
Cluster 17	T1pks	6803083	6866736	Streptazone_E_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001296_c1		
Cluster 18	Bacteriocin	6993517	7005028	-	-		
Cluster 19	Terpene	7037519	7059687	-	-		
Cluster 20	Siderophore	7289433	7302563	Lividomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000708_c1		
Cluster 21	Nrps	7374569	7511121	Telomycin_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0001406_c1	2	CYP163B15; CYP113Z1
Cluster 22	Terpene	7918247	7944944	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		

Cluster 23	Nrps	8045066	8095973	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 24	Bacteriocin-Lantipeptide	8623448	8655847	Informatipeptin_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0000518_c1		
Cluster 25	T1pks	8723410	8767378	Oxazolomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001106_c1		
Cluster 26	Indole-T3pks	8857041	8900715	7-prenylisatin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0001294_c1		
Cluster 27	Terpene	8976981	8998324	2-methylisoborneol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000658_c1		
Streptomyces lincolnensis							
Cluster 1	Other	249090	291954	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1		
Cluster 2	Other	299197	339826	Lincomycin_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000907_c1		
Cluster 3	Ladderane	451428	492678	Skyllamycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000429_c1	1	CYP105B41
Cluster 4	Melanin-Terpene	576129	602496	Melanin_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000908_c1		
Cluster 5	Nrps	863441	922947	Pristinamycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000952_c1	1	CYP163A5
Cluster 6	Nrps	1585396	1641767	Coelibactin_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0000324_c1	1	CYP1424A1
Cluster 7	T3pks	1646746	1687819	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1	1	CYP158A15
Cluster 8	Terpene	2183010	2204059	-	-	2	CYP183Y1; CYP157C22
Cluster 9	Other	2262790	2306653	Pristinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000952_c3		
Cluster 10	Ectoine	2542017	2552421	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 11	Butyrolactone	3105357	3115644	-	-		
Cluster 12	Melanin	3706522	3716998	Istamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000700_c1		
Cluster 13	Siderophore	3814323	3826095	Desferrioxamine_B_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000940_c1		
Cluster 14	Ladderane	5253351	5294520	Colabomycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000213_c1		
Cluster 15	Amglyccycl-Butyrolactone	6047626	6079735	Pyralomicin_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001038_c1		
Cluster 16	Terpene	6671108	6692193	Albaflavenone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000660_c1	1	CYP170A20
Cluster 17	T1pks-Nrps	6978487	7040117	BD-12_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001379_c1		
Cluster 18	Siderophore	7415509	7427461	-	-		
Cluster 19	Phosphoglycolipid	7574317	7603039	Teichomycin_biosynthetic_gene_cluster (88% of genes show similarity)	BGC0001395_c1		
Cluster 20	Bacteriocin-T2pks	7704225	7765020	Pamamycin_biosynthetic_gene_cluster (95% of genes show similarity)	BGC0001150_c1		
Cluster 21	Terpene-Butyrolactone	7842166	7872226	Gamma-butyrolactone_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000850_c1		
Cluster 22	Other	7902702	7944810	Medermycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000245_c1		
Cluster 23	Nrps-Siderophore	8091854	8156922	Grincamycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000229_c1	1	CYP107L32
Cluster 24	T2pks	8254465	8296926	Kanamycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000703_c1	1	CYP105B41
Cluster 25	Nrps	8404510	8455426	Coelichelin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000325_c1		
Cluster 26	Terpene	8628322	8654989	Hopene_biosynthetic_gene_cluster (92% of genes show similarity)	BGC0000663_c1		

Cluster 27	T1pks	8690932	8739022	Meilingmycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000093_c1		
Cluster 28	Terpene	9074027	9095814	Ansatrienin_(mycotrienin)_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000957_c1		
Cluster 29	Bacteriocin-Lantipeptide	9254500	9284511	Informatipeptin_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000518_c1		
Cluster 30	Siderophore	9308354	9323052	Scabichelin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000423_c1		
Cluster 31	T1pks	9567580	9611593	Daptomycin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000336_c1		
Cluster 32	Nrps	9921582	9972122	Incednine_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000078_c1		
Cluster 33	T1pks-Nrps	10025162	10106144	Antimycin_biosynthetic_gene_cluster (93% of genes show similarity)	BGC0000958_c1		
Cluster 34	T1pks	10167404	10211375	Lomofungin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001302_c1		
Streptomyces noursei							
Cluster 1	Lassopeptide	116803	139284	A54145_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000291_c1		
Cluster 2	Terpene	222311	243384	2-methylisoborneol_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000657_c1		
Cluster 3	T1pks	349984	410183	Ebelactone_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000051_c1	5	CYP105BV1; CYP1198A1; CYP107EM1; CYP1060A2; CYP147F29
Cluster 4	Terpene	584083	604979	-	-		
Cluster 5	Terpene	688002	708970	-	-	1	CYP157C31
Cluster 6	T1pks	768290	912056	Nystatin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000115_c1	2	CYP105H1; CYP161A1
Cluster 7	Terpene	1064783	1085721	-	-		
Cluster 8	Butyrolactone	1243689	1254624	Merochlorin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001083_c1	1	CYP107AE10
Cluster 9	Butyrolactone	1473958	1530565	Sch47554_/_Sch47555_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000268_c1		
Cluster 10	Other	1573019	1616555	4-hydroxy-3-nitrosobenzamide_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000885_c1	1	CYP1248A3
Cluster 11	T1pks	1644455	1691954	Actinomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000296_c1	1	CYP107EQ1
Cluster 12	Terpene	1957660	1984391	Hopene_biosynthetic_gene_cluster (61% of genes show similarity)	BGC0000663_c1		
Cluster 13	Lassopeptide	2156897	2179430	Echosides_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000340_c1		
Cluster 14	T1pks	2213917	2292303	Erythromycin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000055_c1	3	CYP107KZ1; CYP1420A1; CYP107A3
Cluster 15	Bacteriocin	2670339	2681181	-	-		
Cluster 16	T3pks	2741982	2783037	FD-594_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000222_c1	1	CYP107F9
Cluster 17	Nrps	2853066	2915225	Desotamide_biosynthetic_gene_cluster (63% of genes show similarity)	BGC0001196_c1		
Cluster 18	Siderophore	2921611	2936270	-	-		
Cluster 19	Other	3248238	3288957	Albonoursin_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000851_c1		
Cluster 20	Other	3884567	3928700	Meridamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001011_c1		
Cluster 21	Linaridin	4361283	4382173	Legonaridin_biosynthetic_gene_cluster (55% of genes show similarity)	BGC0001188_c1		
Cluster 22	Thiopeptide-Bacteriocin	4401731	4437294	TP-1161_biosynthetic_gene_cluster (37% of genes show similarity)	BGC0000615_c1	1	CYP113D4

Cluster 23	Terpene	4523671	4545989	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 24	Lantipeptide	6032833	6057286	-	-		
Cluster 25	T1pks	6511142	6554210	Collismycin_A_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000973_c1	1	CYP105AB15
Cluster 26	Ectoine	6984258	6994662	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 27	Siderophore	7075833	7087638	Desferrioxamine_B_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0000941_c1		
Cluster 28	Lantipeptide	7331458	7356001	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1		
Cluster 29	T2pks	7864563	7907078	Spore_pigment_biosynthetic_gene_cluster (83% of genes show similarity)	BGC0000271_c1		
Cluster 30	Bacteriocin	7950154	7960369	-	-		
Cluster 31	Transatpks-Nrps	8270365	8375658	Cycloheximide_/_actiphenol_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000175_c1	3	CYP107CA2; CYP154D14; CYP105AC16
Cluster 32	Nrps	8386157	8448082	Friulimicin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000354_c1		
Cluster 33	Terpene	8910362	8931330	Filipin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000059_c1	1	CYP105A7
Cluster 34	Terpene-T3pks-T1pks-Nrps	9016679	9111228	Leinamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0001101_c1		
Cluster 35	Lantipeptide-Nrps	9139090	9243844	Zorbamycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001058_c1	2	CYP163B; CYP1278B1
Cluster 36	Terpene-T1pks	9247044	9370657	Nystatin_biosynthetic_gene_cluster (72% of genes show similarity)	BGC0000115_c1	1	CYP105H8
Cluster 37	Lassopeptide	9676601	9699082	A54145_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000291_c1		

Mycobacterial species

***Mycobacterium africanum* GM041182**							
Cluster	Type	From	To	Most similar known cluster	MIBiG BGC-ID	P450s	Name of the P450
Cluster 1	Nrps	88242	137625	-	-		
Cluster 2	T1pks	462468	506676	-	-		
Cluster 3	Bacteriocin	882527	893324	-	-		
Cluster 4	Nrps	1298767	1355947	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1528107	1569288	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1705714	1752040	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1850834	1904620	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1950426	1992024	-	-		

Cluster 9	T1pks	2267339	2319794	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2514759	2555628	-	-	3	CYP124A1 ; CYP128A1 ; CYP121A1
Cluster 11	Nrps	2625730	2685663	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2885311	2928817	-	-		
Cluster 13	T1pks-Nrps	3203861	3298599	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3787393	3808301	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4213486	4299107	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c		
				***Mycobacterium tuberculosis* C**			
Cluster 1	Nrps	88185	137568	-	-		
Cluster 2	T1pks	465451	509659	-	-		
Cluster 3	Bacteriocin	885597	896394	-	-		
Cluster 4	T1pks-Nrps	1294041	1347876	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1523766	1564947	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1702580	1748906	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1845411	1904899	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1950635	2006069	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	1	CYP144A1
Cluster 9	T1pks	2274453	2326911	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2523905	2564774	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP124A1 ; CYP128A1 ; CYP121A1
Cluster 11	Nrps	2633986	2693919	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2892773	2936279	-	-		
Cluster 13	T1pks-Nrps	3221603	3316055	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3801146	3822054	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4222934	4308555	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* F11**			
Cluster 1	Nrps	88290	137673	-	-		
Cluster 2	T1pks	468901	513109	-	-		
Cluster 3	Bacteriocin	888983	899780	-	-		
Cluster 4	T1pks-Nrps	1297442	1360980	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1529166	1570347	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1706720	1753046	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1849550	1907677	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1

Cluster 8	T1pks	2289143	2341598	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Other	2539029	2579898	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 10	Nrps	2650995	2710928	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 11	Other	2911188	2954694	-	-		
Cluster 12	T1pks-Nrps	3236918	3331427	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 13	Terpene	3815207	3836115	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 14	T1pks-Nrps	4248946	4334567	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* H37Ra**			
Cluster 1	Nrps	89514	138897	-	-		
Cluster 2	T1pks	467041	511249	-	-		
Cluster 3	Bacteriocin	887778	898575	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 4	T1pks-Nrps	1295036	1358526	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1526135	1567316	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1703600	1749926	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1855678	1913805	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2284431	2336886	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1	1	CYP139A1
Cluster 9	Other	2536787	2577656	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	2	CYP124A1; CYP128A1
Cluster 10	Nrps	2649668	2709601	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 11	Other	2909839	2953345	-	-		
Cluster 12	T1pks-Nrps	3237437	3331946	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 13	Terpene	3812768	3833676	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 14	T1pks-Nrps	4244391	4330012	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* H37Rv**			
Cluster 1	Nrps	88156	137539	-	-		
Cluster 2	T1pks	465731	509939	-	-		
Cluster 3	Bacteriocin	886472	897269	-	-		
Cluster 4	Nrps	1300035	1357215	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1524825	1566006	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1702083	1748409	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1854160	1912287	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1957969	2014661	-	-	1	CYP144A1
Cluster 9	T1pks	2274531	2326986	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		

Cluster 10	Other	2526883	2567752	-	-	2	CYP124A1; CYP128A1
Cluster 11	Nrps	2637700	2697633	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2897871	2941377	-	-		
Cluster 13	T1pks-Nrps	3225445	3319954	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3804090	3824998	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4235945	4321566	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* Haarlem**			
Cluster 1	Nrps	88292	137675	-	-		
Cluster 2	T1pks	470237	514445	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 3	Bacteriocin	890036	900833	-	-		
Cluster 4	T1pks-Nrps	1298849	1362387	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1525449	1566630	BE-7585A_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1704363	1750689	Glycopeptidolipid_biosynthetic_gene_cluster (38% of genes show similarity)	BGC0000362_c1		
Cluster 7	T3pks-T1pks	1847252	1905379	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2279163	2331618	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2633645	2693578	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	2893131	2936637	-	-		
Cluster 11	T1pks-Nrps	3221367	3315876	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 12	Terpene	3797784	3818692	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 13	T1pks-Nrps	4232784	4318405	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* KZN 1435**			
Cluster 1	Nrps	88287	137670	-	-		
Cluster 2	T1pks	465990	510198	-	-		
Cluster 3	Bacteriocin	886314	897111	-	-		
Cluster 4	T1pks-Nrps	1093650	1188160	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	Other	1472438	1515944	-	-		
Cluster 6	Nrps	1716070	1776003	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 7	Other	1848840	1889373	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP121A1; CYP128A1; CYP124A1
Cluster 8	T1pks	2089725	2142183	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2409168	2464677	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	1	CYP144A1
Cluster 10	T3pks-T1pks	2510425	2568552	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 11	T1pks	2665057	2711383	Glycopeptidolipid_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000362_c1		

Cluster 12	T3pks	2847698	2888879	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 13	T1pks-Nrps	3055078	3118618	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3798602	3819510	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4222891	4308512	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* KZN 605**			
Cluster 1	Nrps	88285	137668	-	-		
Cluster 2	T1pks	465991	510199	-	-		
Cluster 3	Bacteriocin	886319	897116	-	-		
Cluster 4	T1pks-Nrps	1093652	1188160	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	Other	1472550	1516056	-	-		
Cluster 6	Nrps	1716185	1776118	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 7	Other	1848956	1889489	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP121A1; CYP128A1; CYP124A1
Cluster 8	T1pks	2089602	2142061	Piericidin_A1_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000124_c1		
Cluster 9	Nrps	2409049	2464558	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	1	CYP144A1
Cluster 10	T3pks-T1pks	2510307	2568434	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 11	T1pks	2664940	2711266	Glycopeptidolipid_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000362_c1		
Cluster 12	T3pks	2847469	2888650	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 13	T1pks-Nrps	3054850	3118361	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3799712	3820620	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4223760	4309381	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* KZN 4207**			
Cluster 1	Nrps	88286	137669	-	-		
Cluster 2	T1pks	465990	510198	-	-		
Cluster 3	Bacteriocin	886317	897114	-	-		
Cluster 4	T1pks-Nrps	1093650	1188158	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	Other	1472382	1515888	-	-		
Cluster 6	Nrps	1715957	1775890	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 7	Other	1848727	1889260	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP121A1; CYP128A1; CYP124A1
Cluster 8	T1pks	2087814	2140272	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2405898	2461407	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	1	CYP144A1
Cluster 10	T3pks-T1pks	2507098	2565225	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1

Cluster 11	T1pks	2661730	2708056	Glycopeptidolipid_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000362_c1		
Cluster 12	T3pks	2844371	2885552	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 13	T1pks-Nrps	3051750	3115288	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3795336	3816244	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4219495	4305116	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* RGTB327**			
Cluster 1	Nrps	90060	137277	Glycopeptidolipid_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000362_c1		
Cluster 2	Bacteriocin	887005	897802	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 3	Nrps	1300846	1358039	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 4	T3pks	1525759	1566940	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 5	T3pks-T1pks	1850431	1907434	Streptomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000717_c1		
Cluster 6	Other	2520687	2561202	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	2	CYP124A1; CYP102B25
Cluster 7	Other	2891575	2935081	-	-		
Cluster 8	T1pks-Nrps	3226347	3313899	Candicidin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000034_c1		
Cluster 9	Terpene	3773355	3794263	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 10	Nrps	4232920	4290071	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* CDC1551**			
Cluster 1	Nrps	88146	137529	-	-		
Cluster 2	T1pks	467180	511388	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 3	Bacteriocin	886381	897178	-	-		
Cluster 4	T1pks-Nrps	1293164	1356702	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1524683	1565864	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T3pks-T1pks	1845066	1903193	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 7	T1pks	2276864	2329319	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 8	Other	2524087	2564956	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 9	Nrps	2635031	2694964	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	2894015	2937521	-	-		
Cluster 11	T1pks-Nrps	3219766	3314275	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 12	Terpene	3794965	3815873	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 13	T1pks-Nrps	4228268	4313889	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		

				***Mycobacterium tuberculosis* strains CCDC5079**			
Cluster 1	Nrps	85821	135158	-	-		
Cluster 2	T1pks	464327	507521	Glycopeptidolipid_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000362_c1		
Cluster 3	Bacteriocin	882693	893490	-	-		
Cluster 4	T1pks-Nrps	1291321	1354813	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1524046	1565227	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1701368	1747631	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1844222	1902349	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2267794	2314201	Hygrocin_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000075_c1	3	CYP124A1; CYP128A1; CYP121A1
Cluster 9	Other	2513369	2554229	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 10	Nrps	2621067	2680998	Mycobactin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0001021_c1		
Cluster 11	Other	2879665	2923171	-	-		
Cluster 12	T1pks-Nrps	3200387	3294904	Cremimycin_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000042_c1		
Cluster 13	Terpene	3788074	3808982	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 14	T1pks-Nrps	4223124	4308749	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* 7199-99**			
Cluster 1	Nrps	88193	137576	-	-		
Cluster 2	T1pks	469987	514195	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 3	Bacteriocin	889733	900530	-	-		
Cluster 4	T1pks-Nrps	1298263	1361753	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1529729	1570910	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1707228	1753554	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1850116	1909601	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2283970	2336425	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2639653	2699586	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	2898468	2941974	-	-		
Cluster 11	T1pks-Nrps	3223580	3318089	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 12	Terpene	3801540	3822448	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 13	T1pks-Nrps	4245655	4331276	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* Beijing/NITR203**			

Cluster 1	Nrps	88147	137530	-			
Cluster 2	T1pks	467006	509918	Rubradirin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000141_c1		
Cluster 3	Bacteriocin	886390	897187	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 4	T1pks-Nrps	1293600	1357090	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1524696	1565877	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1701947	1748273	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1854013	1912140	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1957816	2014457	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	1	CYP144A1
Cluster 9	T1pks	2274341	2326796	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2526666	2567535	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2637478	2697396	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2897602	2941108	-			
Cluster 13	T1pks-Nrps	3225133	3319641	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3803713	3824621	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4235544	4321162	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* CAS/NITR204**			
Cluster 1	T1pks	465362	506675	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 2	Bacteriocin	883770	894567	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 3	T1pks-Nrps	1289949	1353397	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 4	T3pks	1520441	1561622	BE-7585A_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000203_c1		
Cluster 5	T3pks	1848672	1889733	Streptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 6	T1pks	2271732	2316264	Monensin_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000100_c1		
Cluster 7	Other	2519374	2560243	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	2	CYP124A1; CYP128A1
Cluster 8	Nrps	2633125	2684309	Mycobactin_biosynthetic_gene_cluster (40% of genes show similarity)	BGC0001021_c1		
Cluster 9	Other	2888395	2931373	-	-		
Cluster 10	T1pks-Nrps	3231109	3308740	Epothilone_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000990_c1		
Cluster 11	Terpene	3788576	3809484	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 12	Nrps	4245982	4303122	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* EAI5**			
Cluster 1	Nrps	88158	137541	-	-		
Cluster 2	T1pks	466282	509950	-	-		
Cluster 3	Bacteriocin	885125	895922	-	-		

Cluster 4	T1pks-Nrps	1292378	1355868	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1522123	1563304	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T3pks-T1pks	1852601	1909584	Streptomycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 7	Nrps	1955266	2010597	-	-	1	CYP144A1
Cluster 8	Nrps	2626850	2686783	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 9	Other	2885657	2929163	-	-		
Cluster 10	T1pks-Nrps	3211874	3306382	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 11	Terpene	3785088	3806008	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 12	T1pks-Nrps	4215580	4301200	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				Mycobacterium tuberculosis EAI5/NITR206			
Cluster 1	Nrps	88410	134359	-			
Cluster 2	T1pks	467755	509074	Cremimycin_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0000042_c1		
Cluster 3	Bacteriocin	888488	899285	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 4	Nrps	1302990	1360183	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1527541	1568029	BE-7585A_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1707794	1750760	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks	1857101	1897934	Streptomycin_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2286023	2329235	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2635271	2695268	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	3274152	3316209	Piericidin_A1_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0001169_c1		
Cluster 11	Terpene	3796074	3816985	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 12	T1pks	4229489	4312569	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
				Mycobacterium tuberculosis Erdman=ATCC 35801			
Cluster 1	Nrps	87332	136670	-			
Cluster 2	T1pks	468741	511653	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 3	Bacteriocin	885438	896235	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1		
Cluster 4	T1pks-Nrps	1292243	1355731	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1518963	1560144	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1694913	1741176	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1837801	1895928	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2270605	2323060	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2626627	2686560	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	2886112	2929618	-	-		

Cluster 11	T1pks-Nrps	3214209	3308717	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 12	Terpene	3785902	3806810	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 13	T1pks-Nrps	4216853	4302474	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium tuberculosis* UT205**			
Cluster 1	Nrps	88255	137638	-	-		
Cluster 2	T1pks	467045	511253	-	-		
Cluster 3	Bacteriocin	888533	899330	-	-		
Cluster 4	T1pks-Nrps	1296390	1359880	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1527789	1568970	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1705146	1751472	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1857379	1915506	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Other	2532570	2573439	-	-	2	CYP124A1; CYP128A1
Cluster 9	Nrps	2642431	2702364	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 10	Other	2902700	2946206	-	-		
Cluster 11	T1pks-Nrps	3230570	3325079	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 12	Terpene	3810044	3830952	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 13	T1pks-Nrps	4242395	4328016	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium canetti* CIPT 140010059**			
Cluster 1	Nrps	91719	141102	-	-		
Cluster 2	T1pks	473020	520252	Rubradirin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000141_c1		
Cluster 3	Bacteriocin	894179	904976	-	-		
Cluster 4	Nrps	1320091	1377271	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1548166	1589347	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1726309	1780572	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1880898	1939026	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2324305	2376769	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Other	2582707	2623576	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	3	CYP124A1; CYP128A1; CYP121A1
Cluster 10	Nrps	2696313	2756246	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 11	Other	2967557	3011063	-	-		
Cluster 12	T1pks-Nrps	3284106	3376575	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 13	Terpene	3871405	3892313	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 14	T1pks-Nrps	4303115	4388651	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		

				***Mycobacterium canetti* CIPT 140060008**			
Cluster 1	Nrps	93492	142875	-	-		
Cluster 2	T1pks	472069	516271	-	-		
Cluster 3	Bacteriocin	880676	891473	-	-		
Cluster 4	T1pks-Nrps	1289683	1353176	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1525644	1566825	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1706894	1753157	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1855101	1913229	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	T1pks	2296179	2348634	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Other	2558631	2599491	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000362_c1	2	CYP124A1; CYP128A1
Cluster 10	Nrps	2667576	2727509	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 11	Other	2935556	2979062	-	-		
Cluster 12	T1pks-Nrps	3248529	3340884	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 13	Terpene	3831892	3852800	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 14	T1pks-Nrps	4254850	4340471	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium canetti* CIPT 140710010**			
Cluster 1	Nrps	104157	153540	-	-		
Cluster 2	T1pks	478749	522951	-	-		
Cluster 3	Bacteriocin	900411	911208	-	-		
Cluster 4	T1pks-Nrps	1350891	1414367	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1599811	1640992	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1780717	1826980	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1927571	1985699	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	2039070	2098936	Oxazolomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001106_c1	1	CYP144A1
Cluster 9	T1pks	2391616	2444071	Chartreusin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000206_c2		
Cluster 10	Other	2642997	2683866	-	-	3	CYP124A1; CYP128A; CYP121A1
Cluster 11	Nrps	2758943	2818861	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	3030055	3073561	-	-		
Cluster 13	T1pks-Nrps	3349860	3445383	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3918921	3939829	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4350509	4440905	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium bovis* AF 2122/97**			

Cluster 1	Nrps	88192	137575	-	-		
Cluster 2	T1pks	468118	510958	Nigericin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000114_c1		
Cluster 3	Bacteriocin	887302	898099	-	-		
Cluster 4	T1pks-Nrps	1295003	1358493	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1525912	1567093	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1690505	1736831	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1843955	1902082	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1947776	1989374	-	-		
Cluster 9	T1pks	2262855	2315310	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2510248	2551117	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2610182	2670115	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2869730	2913236	-	-		
Cluster 13	T1pks-Nrps	3186430	3281054	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3760840	3781748	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4176630	4262251	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium bovis* BCG Pasteur 1173P2**			
Cluster 1	Nrps	117898	167281	-	-		
Cluster 2	T1pks	497914	540754	Nigericin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000114_c1		
Cluster 3	Bacteriocin	916894	927691	-	-		
Cluster 4	T1pks-Nrps	1325009	1386951	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1549982	1591163	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1714424	1760750	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1859427	1917551	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1963129	2004727	-	-		
Cluster 9	T1pks	2258183	2310638	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2505335	2546204	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2602722	2662655	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2862318	2905824	-	-		
Cluster 13	T1pks-Nrps	3179434	3274115	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3790354	3811262	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		

Cluster 15	T1pks-Nrps	4208348	4293968	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium bovis* BCG Korea 1168P**			
Cluster 1	Nrps	88231	137614	-	-		
Cluster 2	T1pks	468247	511087	Nigericin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000114_c1		
Cluster 3	Bacteriocin	887227	898024	-	-		
Cluster 4	T1pks-Nrps	1295342	1357284	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1520315	1561496	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1684653	1730979	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1829654	1887778	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1933356	1974954	-	-		
Cluster 9	T1pks	2227828	2280283	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2474980	2515849	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2572367	2632300	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2831966	2875472	-	-		
Cluster 13	T1pks-Nrps	3149082	3243763	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000362_c1		
Cluster 14	Terpene	3795812	3816720	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4210537	4296157	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium bovis* BCG Mexico**			
Cluster 1	Nrps	88231	137614	-	-		
Cluster 2	T1pks	468248	511088	Nigericin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000114_c1		
Cluster 3	Bacteriocin	887173	897970	-	-		
Cluster 4	T1pks-Nrps	1295288	1357230	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1520261	1561442	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1684703	1731029	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1829706	1887830	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1933408	1975006	-	-		
Cluster 9	T1pks	2237548	2290003	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2484700	2525569	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2582087	2642020	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2841683	2885189	-	-		
Cluster 13	T1pks-Nrps	3158799	3253480	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		

Cluster 14	Terpene	3769719	3790627	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4187713	4272679	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium bovis* BCG Toyko 172**			
Cluster 1	Nrps	88231	137614	-	-		
Cluster 2	T1pks	468247	511087	Nigericin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000114_c1		
Cluster 3	Bacteriocin	888611	899408	-	-		
Cluster 4	T1pks-Nrps	1296347	1359837	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
Cluster 5	T3pks	1522869	1564050	BE-7585A_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000203_c1		
Cluster 6	T1pks	1687317	1733643	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 7	T3pks-T1pks	1832329	1890453	Streptomycin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000717_c1	1	CYP139A1
Cluster 8	Nrps	1936031	1977629	-	-		
Cluster 9	T1pks	2250961	2303416	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 10	Other	2498107	2538976	-	-	3	CYP124A1; CYP128A1; CYP121A1
Cluster 11	Nrps	2595494	2655427	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1		
Cluster 12	Other	2855091	2898597	-	-		
Cluster 13	T1pks-Nrps	3172261	3266942	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 14	Terpene	3788267	3809175	Hopene_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000663_c1		
Cluster 15	T1pks-Nrps	4205541	4291158	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium abscessus* ATCC 19977**			
Cluster 1	T1pks	158481	203829	-	-		
Cluster 2	Other	487819	531847	-	-		
Cluster 3	Other	645339	689499	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 4	Bacteriocin	696411	707208	-	-		
Cluster 5	T1pks-Nrps	907298	966146	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1	1	CYP1110B1
Cluster 6	T2pks	2010675	2051931	-	-	1	CYP153A
Cluster 7	Nrps	2101960	2154998	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 8	Ectoine-T1pks-Nrps	2210723	2332581	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	Ectoine	2625531	2635881	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 10	Other	2997425	3044572	-	-		
Cluster 11	Bacteriocin	3071596	3082492	-	-		
Cluster 12	T1pks	3168420	3214662	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1		

Cluster 13	Nrps	3335855	3383528	-	-	1	CYP1128A
Cluster 14	Other	3398186	3441677	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 15	T1pks	3598780	3641758	RK-682_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000140_c1		
Cluster 16	Nrps	4122854	4180960	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 17	Bacteriocin	4711818	4722678	-	-		
Cluster 18	Nrps	4729126	4847667	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1	1	CYP135B
				Mycobacterium abscessus **subsp.** ***bolletti*** **50594**			
Cluster 1	T1pks	161195	206585	-	-		
Cluster 2	Other	504696	548724	-	-		
Cluster 3	Other	661435	705595	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 4	Bacteriocin	712494	723291	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 5	T1pks-Nrps	922521	981375	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 6	T2pks-Nrps	2020698	2103922	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 7	Ectoine-T1pks-Nrps	2166118	2265937	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Ectoine	2588452	2598802	-	-		
Cluster 9	Other	2932894	2980050	-	-		
Cluster 10	Bacteriocin	3006899	3017795	-	-		
Cluster 11	T1pks	3103495	3149776	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 12	Nrps	3266186	3313859	Lomaiviticin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000240_c1	1	CYP1128A
Cluster 13	Other	3329761	3373252	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 14	Bacteriocin	4676174	4687034	-	-		
Cluster 15	Nrps	4693688	4812188	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1	1	CYP135B
				Mycobacterium abscessus **47J26**			
Cluster 1	T1pks	158293	203647	-	-		
Cluster 2	Other	477159	521187	-	-		
Cluster 3	Other	634852	679012	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 4	Bacteriocin	686966	697763	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 5	T1pks-Nrps	824318	883172	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 6	T2pks-Nrps	2006372	2089393	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 7	Ectoine-T1pks-Nrps	2150144	2250498	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 8	Ectoine	2569896	2580150	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 9	Other	2963708	3010807	-	-		
Cluster 10	Bacteriocin	3039563	3050459	-	-		

Cluster 11	T1pks	3133453	3179734	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 12	Nrps	3295071	3342744	Lomaiviticin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000240_c1	1	CYP1128A
Cluster 13	Other	3356857	3400348	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 14	Nrps	4139758	4197864	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 15	Bacteriocin	4688809	4699606	-	-		
Cluster 16	Nrps	4706323	4826135	Glycopeptidolipid_biosynthetic_gene_cluster (47% of genes show similarity)	BGC0000364_c1	1	CYP135B
				***Mycobacterium abscessus* 103**			
Cluster 1	T1pks	158484	203832	-	-		
Cluster 2	Other	472620	516648	-	-		
Cluster 3	Other	630140	674300	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 4	Bacteriocin	681212	692009	-	-		
Cluster 5	T1pks-Nrps	891844	950692	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1	1	CYP1110B1
Cluster 6	T2pks	1995058	2036314	-	-	1	CYP153A
Cluster 7	Nrps	2086343	2139381	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 8	Ectoine-T1pks-Nrps	2195106	2316966	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	Ectoine	2609951	2620205	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 10	Other	2981734	3028881	-	-		
Cluster 11	Bacteriocin	3055905	3066801	-	-		
Cluster 12	T1pks	3152718	3198999	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1		
Cluster 13	Nrps	3320153	3367826	-	-	1	CYP1128A
Cluster 14	Other	3382484	3425975	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 15	T1pks	3583078	3626056	RK-682_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000140_c1		
Cluster 16	Nrps	4107149	4163992	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 17	Bacteriocin	4696087	4706884	-	-		
Cluster 18	Nrps	4713384	4831926	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1	1	CYP135B
				***Mycobacterium abscessus* subsp. *bolletti* MA 1948**			
Cluster 1	T1pks	158459	203807	-	-		
Cluster 2	Other	487797	531825	-	-		
Cluster 3	Other	645317	689477	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 4	Bacteriocin	696389	707186	-	-		
Cluster 5	T1pks-Nrps	907074	965922	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1	1	CYP1110B1
Cluster 6	T2pks	2010031	2051287	-	-	1	CYP153A
Cluster 7	Nrps	2101316	2154354	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		

Cluster 8	Ectoine-T1pks-Nrps	2210079	2331923	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	Ectoine	2624826	2635080	Clavulanic_acid_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000845_c1		
Cluster 10	Other	2996595	3043742	-	-		
Cluster 11	Bacteriocin	3070767	3081663	-	-		
Cluster 12	T1pks	3167591	3213872	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1		
Cluster 13	Nrps	3335032	3382705	-	-	1	CYP1128A
Cluster 14	Other	3397363	3440854	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 15	T1pks	3597915	3640893	RK-682_biosynthetic_gene_cluster (36% of genes show similarity)	BGC0000140_c1		
Cluster 16	Nrps	4127741	4176842	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 17	Bacteriocin	4708919	4719716	-	-		
Cluster 18	Nrps	4726200	4844741	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1	1	CYP135B
				Mycobacterium abscessus **VO6705**			
Cluster 1	Nrps	144035	244947	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1	1	CYP135B
Cluster 2	Bacteriocin	269250	280047	-	-		
Cluster 3	Nrps	770368	827211	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 4	Other	1483184	1526675	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 5	Nrps	1548800	1596473	-	-	1	CYP1128A
Cluster 6	T1pks	1726616	1772897	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 7	Bacteriocin	1858614	1869510	-	-		
Cluster 8	Other	1898270	1941794	-	-		
Cluster 9	Ectoine	2315260	2325514	-	-		
Cluster 10	T1pks-Ectoine-Nrps	2623115	2722933	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 11	T2pks-Nrps	2783626	2866813	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 12	T1pks-Nrps	3801727	3860575	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 13	Bacteriocin	3997591	4008388	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 14	Other	4172247	4216275	-	-		
Cluster 15	T1pks	4478252	4523642	-	-		
				Mycobacterium avium **104**			
Cluster 1	T1pks	190988	236363	-	-		
Cluster 2	Bacteriocin	707909	718706	-	-		
Cluster 3	T3pks-T1pks	1207060	1293496	Kanamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000703_c1		
Cluster 4	T1pks-Nrps	1718145	1777594	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 5	Nrps	1966429	2033194	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1	1	CYP187A

Cluster 6	T1pks	2363595	2409891	-	-	1	CYP150A
Cluster 7	T1pks	2454065	2506580	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1	1	CYP105NSF1
Cluster 8	Nrps	3073635	3144900	-	-		
Cluster 9	T3pks-T1pks	3153360	3211590	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1	1	CYP139A
Cluster 10	Nrps	3299015	3402918	Glycopeptidolipid_biosynthetic_gene_cluster (69% of genes show similarity)	BGC0000362_c1		
Cluster 11	Other	3599656	3643177	-	-		
Cluster 12	Terpene	4007133	4028083	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 13	Other	4224404	4267655	Glycopeptidolipid_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000362_c1		
Cluster 14	Nrps	4995861	5046139	-	-		
				***Mycobacterium avium* subsp. *paratuberculosis* K10**			
Cluster 1	T1pks	208518	253842	-	-		
Cluster 2	Bacteriocin	648470	659267	-	-		
Cluster 3	Other	1064778	1108299	-	-		
Cluster 4	Nrps	1289241	1341324	Glycopeptidolipid_biosynthetic_gene_cluster (35% of genes show similarity)	BGC0000362_c1		
Cluster 5	T3pks-T1pks	1452154	1504179	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1	1	CYP139A
Cluster 6	Nrps	1512373	1571527	Telomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001406_c1		
Cluster 7	Nrps	1834059	1888514	-	-		
Cluster 8	T1pks	1939801	1992313	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1	1	CYP105NSF1
Cluster 9	T1pks-Nrps	2024496	2083965	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1	1	CYP150A
Cluster 10	Nrps	2382034	2451169	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1	1	CYP1034A
Cluster 11	T1pks-Nrps	2459656	2519101	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 12	T1pks	2913453	2955744	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 13	T3pks	2955877	2996926	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP187A
Cluster 14	Terpene	3407499	3428230	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 15	Other	3624143	3667490	-	-		
Cluster 16	T1pks-Nrps	4111530	4228843	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium avium* subsp. *paratuberculosis* MAP4**			
Cluster 1	Nrps	1	99437	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 2	Other	543572	586823	-	-		
Cluster 3	Terpene	782734	803684	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 4	T3pks	1213604	1254653	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP187A
Cluster 5	T1pks	1254780	1297071	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1691452	1750897	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		

Cluster 7	Nrps	1757972	1827107	Mycobactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001021_c1	1	CYP1034A
Cluster 8	T1pks-Nrps	2125298	2180594	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000363_c1	1	CYP150A
Cluster 9	T1pks	2216949	2269461	Herbimycin_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000074_c1	1	CYP105NSF1
Cluster 10	Nrps	2320747	2375201	-	-		
Cluster 11	Nrps	2637717	2696871	Telomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001406_c1		
Cluster 12	T3pks-T1pks	2705065	2757090	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1	1	CYP139A
Cluster 13	Nrps	2846485	2919999	Glycopeptidolipid_biosynthetic_gene_cluster (35% of genes show similarity)	BGC0000362_c1		
Cluster 14	Other	3100942	3144463	-	-		
Cluster 15	Bacteriocin	3549953	3560750	-	-		
Cluster 16	T1pks	3955383	4000758	-	-		
Cluster 17	T1pks	4182204	4228500	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1	1	CYP144A
				***Mycobacterium intracellulare* ATCC 13950**			
Cluster 1	T1pks	205651	250972	-	-		
Cluster 2	Bacteriocin	635320	646117	-	-		
Cluster 3	Nrps	1107358	1150645	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 4	T3pks	1164439	1205461	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP187A
Cluster 5	T1pks	1205576	1251938	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1873947	1932779	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	Nrps	2038653	2111736	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	T1pks-Nrps	2437934	2503761	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1	1	CYP150A
Cluster 9	T1pks	2539388	2591924	FD-891_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000058_c1	2	CYP279A; CYP105U
Cluster 10	Nrps	2996715	3067965	-	-		
Cluster 11	T3pks-T1pks	3082075	3140357	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 12	Nrps	3231290	3336183	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000362_c1		
Cluster 13	Nrps	3347222	3397502	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 14	Other	3535808	3579332	-	-		
Cluster 15	Terpene	3940114	3961067	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 16	Other	4161097	4204345	-	-	1	CYP1122A1
Cluster 17	Other	4702833	4746399	Heme_D1_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000905_c1		
Cluster 18	Nrps	4997133	5047399	-	-		
Cluster 19	Other	5234552	5278040	-	-		
				***Mycobacterium intracellulare* MOTT-02**			
Cluster 1	T1pks	202276	247597	-	-		

Cluster 2	Bacteriocin	631683	642480	-	-		
Cluster 3	Nrps	1104554	1147841	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 4	T3pks	1165970	1207088	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	2	CYP187A; CYP150A
Cluster 5	T1pks	1207102	1253464	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1839531	1898363	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	Nrps	2015556	2088616	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	T1pks-Nrps	2442610	2508437	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1	1	CYP150A
Cluster 9	T1pks	2544113	2596649	FD-891_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000058_c1	2	CYP279A; CYP105U
Cluster 10	Nrps	3004717	3075967	-	-		
Cluster 11	T3pks-T1pks	3086027	3144309	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 12	Nrps	3235279	3340169	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000362_c1		
Cluster 13	Nrps	3351211	3401491	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 14	Other	3539706	3583230	-	-		
Cluster 15	Terpene	3933994	3954947	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 16	Other	4160267	4203515	-	-		
Cluster 17	Other	4727192	4770758	Heme_D1_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000905_c1	1	CYP1128A
Cluster 18	Nrps	5004974	5055243	-	-		
Cluster 19	Other	5242614	5286102	-	-		
				***Mycobacterium intracellulare* MOTT-64**			
Cluster 1	T1pks	204915	250227	-	-		
Cluster 2	Bacteriocin	632658	643455	-	-		
Cluster 3	T3pks-T1pks	1130404	1217633	Kanamycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000703_c1	1	CYP187A
Cluster 4	T1pks-Nrps	1775427	1834259	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 5	Nrps	1931020	2004097	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 6	T1pks	2329063	2375413	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1	1	CYP150A
Cluster 7	T1pks	2411044	2463577	Geldanamycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000066_c1	2	CYP279A; CYP105U
Cluster 8	Nrps	2868444	2939694	-	-		
Cluster 9	T3pks-T1pks	2948713	3006995	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 10	Nrps	3144860	3202786	Glycopeptidolipid_biosynthetic_gene_cluster (46% of genes show similarity)	BGC0000362_c1		
Cluster 11	Other	3371314	3414838	-	-		
Cluster 12	Terpene	3763092	3784045	Isorenieratene_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000664_c1		
Cluster 13	Other	3975840	4019088	-	-		
Cluster 14	Other	4511862	4555428	Heme_D1_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000905_c1		

Cluster 15	Nrps	4780724	4830977	-	-		
Cluster 16	Other	5017137	5060703	-	-		
				***Mycobacterium intracellulare* MOTT-36Y**			
Cluster 1	T1pks	199992	245304	-	-		
Cluster 2	Bacteriocin	629625	640422	-	-		
Cluster 3	Nrps	1105073	1148354	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 4	T3pks	1164196	1205314	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP187A
Cluster 5	T1pks	1205322	1251708	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1612829	1671661	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	Nrps	1969691	2040739	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	T1pks-Nrps	2450171	2516232	Griseoviridin_/_viridogrisein_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000459_c1	1	CYP150A
Cluster 9	T1pks	2554583	2607128	FD-891_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000058_c1	2	CYP279A; CYP105U
Cluster 10	Nrps	3026559	3097719	-	-		
Cluster 11	Nrps	3120372	3169978	Nocobactin_NA_biosynthetic_gene_cluster (62% of genes show similarity)	BGC0001027_c1		
Cluster 12	T3pks-T1pks	3194941	3253223	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 13	Nrps	3341126	3445965	Glycopeptidolipid_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000362_c1		
Cluster 14	Nrps	3454194	3504474	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 15	Other	3686359	3729883	-	-		
Cluster 16	Terpene	4095204	4116157	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 17	Other	4317879	4361127	-	-		
Cluster 18	Other	4928567	4972133	Heme_D1_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000905_c1		
Cluster 19	Nrps	5199528	5249784	-	-		
Cluster 20	Other	5437412	5480900	-	-		
				***Mycobacterium indicus pranii* MTCC 9506**			
Cluster 1	T1pks	381606	426918	-	-		
Cluster 2	Bacteriocin	810927	821724	-	-		
Cluster 3	Nrps	1267209	1310496	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 4	T3pks	1328632	1369750	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP1123A1
Cluster 5	T1pks	1371370	1417732	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1838180	1897014	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	Nrps	2013424	2086499	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	T1pks-Nrps	2378278	2444351	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 9	T1pks	2479850	2532386	FD-891_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000058_c1		

Cluster 10	Nrps	2964807	3036045	-	-	1	CYP126NSF1
Cluster 11	Nrps	3096521	3146118	Nocobactin_NA_biosynthetic_gene_cluster (62% of genes show similarity)	BGC0001027_c1		
Cluster 12	T3pks-T1pks	3177808	3236093	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 13	Nrps	3330916	3435746	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000362_c1		
Cluster 14	Nrps	3445034	3495314	Glycopeptidolipid_biosynthetic_gene_cluster (25% of genes show similarity)	BGC0000362_c1		
Cluster 15	Other	3673617	3717141	-	-		
Cluster 16	Terpene	4089867	4110820	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 17	Other	4316039	4359287	-	-		
Cluster 18	Other	4913374	4956940	Heme_D1_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000905_c1		
Cluster 19	Nrps	5182202	5232471	-	-		
Cluster 20	Other	5423381	5466869	-	-		
				***Mycobacterium leprae* Br4923**			
Cluster 1	T1pks	106545	151899	-	-		
Cluster 2	T1pks	160054	220598	Meridamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001011_c1		
Cluster 3	Other	564390	607956	-	-		
Cluster 4	T1pks-Nrps	1434324	1489339	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T1pks	2774826	2841607	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium leprae* TN**			
Cluster 1	T1pks	106518	151872	-	-		
Cluster 2	T1pks	160027	220571	Meridamycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001011_c1		
Cluster 3	Other	564381	607947	-	-		
Cluster 4	T1pks-Nrps	1434299	1489314	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 5	T1pks	2774928	2841709	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
				***Mycobacterium* sp. JDM601**			
Cluster 1	T1pks-Nrps	321014	379784	Glycopeptidolipid_biosynthetic_gene_cluster (30% of genes show similarity)	BGC0000365_c1		
Cluster 2	Nrps	744617	787744	-	-		
Cluster 3	T3pks	846764	887831	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 4	T1pks-Nrps	963349	1054885	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1		
Cluster 5	Bacteriocin	1154086	1164883	-	-		
Cluster 6	Bacteriocin	1202427	1213302	-	-		
Cluster 7	Other	2438176	2480758	-	-		
Cluster 8	Other	2752165	2799298	-	-		
Cluster 9	T1pks-Nrps	2955531	3005017	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1	1	CYP135B
Cluster 10	Nrps	3091566	3160817	Glycopeptidolipid_biosynthetic_gene_cluster (52% of genes show similarity)	BGC0000363_c1		

Cluster 11	Ectoine	3681298	3691690	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 12	T1pks-Nrps	3989573	4057345	Mycobactin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0001021_c1		
Cluster 13	Other	4192488	4236717	-	-		
Cluster 14	Other	5626427	5670359	-	-		
Cluster 15	Otherks	5736804	5777820	-	-		
Cluster 16	T1pks	5971186	6016612	-	-		
				Mycobacterium liflandi **128FXT**			
Cluster 1	Nrps	53996	113069	-	-		
Cluster 2	Lantipeptide	1028670	1051960	Prodigiosin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000257_c1		
Cluster 3	T1pks-Nrps	2025342	2118939	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 4	Other	2191790	2234579	Herboxidiene_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0001065_c1		
Cluster 5	Nrps	2519702	2575129	-	-	1	CYP143A3
Cluster 6	Nrps	2698186	2742700	-	-	2	CYP140A5; CYP125A6
Cluster 7	T1pks	2975658	3028221	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 8	Other	3088621	3132163	-	-	1	CYP147G
Cluster 9	T3pks	3174471	3215652	BE-7585A_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000203_c1		
Cluster 10	Other	3237240	3280764	-	-		
Cluster 11	Nrps	3293349	3348506	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000315_c1		
Cluster 12	T3pks-T1pks	3362786	3421021	Streptomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000717_c1	1	CYP139A3
Cluster 13	T1pks-Nrps	3513352	3591569	-	-		
Cluster 14	Terpene	3732104	3753120	Merochlorin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001083_c1		
Cluster 15	Nrps	4247597	4310181	Nocobactin_NA_biosynthetic_gene_cluster (87% of genes show similarity)	BGC0001027_c1		
Cluster 16	T3pks	4894395	4935558	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 17	Terpene	5448989	5469948	Carotenoid_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000633_c1		
Cluster 18	Bacteriocin	5544946	5555752	-	-		
Cluster 19	Other	5971253	6015179	-	-		
Cluster 20	T1pks	6046854	6092211	-	-		
				Mycobacterium ulcerans **Agy99**			
Cluster 1	Terpene	376470	397429	Carotenoid_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000636_c1		
Cluster 2	Bacteriocin	413436	424242	-	-		
Cluster 3	Nrps	1633725	1675233	-	-		
Cluster 4	T3pks-T1pks	1797861	1842169	Streptomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000717_c1		
Cluster 5	Other	1878764	1922288	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000363_c1		
Cluster 6	T3pks	1942027	1983208	BE-7585A_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000203_c1		

Cluster 7	T1pks-Nrps	2194258	2286509	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1		
Cluster 8	T1pks	2501288	2553863	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 9	Nrps	2920775	2970209	Sch47554_/_Sch47555_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000268_c1		
Cluster 10	Nrps	4009686	4072249	Nocobactin_NA_biosynthetic_gene_cluster (87% of genes show similarity)	BGC0001027_c1		
Cluster 11	Other	4813556	4857482	-	-		
Cluster 12	T1pks	5505568	5550919	-	-		
				Mycobacterium marinum			
Cluster 1	T1pks-Nrps	61110	142230	Borrelidin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000031_c1		
Cluster 2	Amglyccycl	622806	644011	Acarbose_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000691_c1		
Cluster 3	T1pks	770757	818013	Divergolide_biosynthetic_gene_cluster (17% of genes show similarity)	BGC0001119_c1		
Cluster 4	Nrps	937309	1003509	Yatakemycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000466_c1	1	CYP185A4
Cluster 5	Lantipeptide	1048397	1077803	Prodigiosin_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000257_c1		
Cluster 6	T1pks-Nrps	1315964	1396552	Meridamycin_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0001011_c1		
Cluster 7	Nrps	1447040	1496513	Sch47554_/_Sch47555_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000268_c1		
Cluster 8	T1pks-Nrps	1976632	2069138	Maklamicin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0001288_c1		
Cluster 9	Other	2145225	2188281	Herboxidiene_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0001065_c1		
Cluster 10	Other	2414473	2457997	-	-		
Cluster 11	T3pks	2479648	2520829	BE-7585A_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000203_c1		
Cluster 12	T1pks-Nrps	2653622	2725353	Glycopeptidolipid_biosynthetic_gene_cluster (16% of genes show similarity)	BGC0000365_c1		
Cluster 13	T3pks-T1pks	2834948	2893181	Streptomycin_biosynthetic_gene_cluster (8% of genes show similarity)	BGC0000717_c1	1	CYP139A3
Cluster 14	Nrps	2909898	2958315	Calcium-dependent_antibiotic_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000315_c1		
Cluster 15	Nrps	3039481	3094347	-	-	1	CYP143A3
Cluster 16	Nrps	3212598	3257064	-	-	2	CYP140A5; CYP125A6
Cluster 17	Other	3386607	3430149	-	-	1	CYP147G1
Cluster 18	T1pks	3490898	3543461	Reveromycin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000135_c1		
Cluster 19	T1pks-Nrps	3586300	3656515	FD-891_biosynthetic_gene_cluster (62% of genes show similarity)	BGC0000058_c1		
Cluster 20	Nrps	3674228	3734879	Glycopeptidolipid_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000364_c1		
Cluster 21	Terpene	3750419	3771435	Merochlorin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0001083_c1		
Cluster 22	Nrps	3799489	3888779	Glycopeptidolipid_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000362_c1		
Cluster 23	Nrps	4272219	4321743	Salinomycin_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000144_c1		
Cluster 24	Nrps	4343500	4406063	Nocobactin_NA_biosynthetic_gene_cluster (87% of genes show similarity)	BGC0001027_c1		
Cluster 25	T3pks	4991265	5032314	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	2	CYP187A; CYP187A
Cluster 26	Terpene	5563644	5584603	Carotenoid_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0000633_c1		
Cluster 27	Bacteriocin	5637840	5648646	-	-		

Cluster 28	Other	6060204	6104130	-	-	1	CYP164A3
Cluster 29	T1pks	6166568	6211916	-	-		
				Mycobacterium massiliense			
Cluster 1	T1pks	186478	231814	-	-		
Cluster 2	Bacteriocin	618241	629038	-	-		
Cluster 3	Nrps	1076477	1119758	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000362_c1		
Cluster 4	T3pks	1131990	1173072	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP187A
Cluster 5	T1pks	1174122	1220460	Marinacarboline_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0001137_c1		
Cluster 6	T1pks-Nrps	1595844	1654671	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 7	Nrps	1774929	1849514	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	T1pks-Nrps	2235796	2301900	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000365_c1	1	CYP150A
Cluster 9	T1pks	2339988	2392539	FD-891_biosynthetic_gene_cluster (50% of genes show similarity)	BGC0000058_c1	3	CYP279A; CYP279A; CYP105U
Cluster 10	Other	2686540	2730067	-	-	2	CYP105Q; CYP189A
Cluster 11	Nrps	2779613	2850947	-	-		
Cluster 12	T3pks-T1pks	2875790	2934084	Streptomycin_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0000717_c1		
Cluster 13	Nrps	3044916	3128206	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000362_c1		
Cluster 14	Other	3358669	3402181	-	-		
Cluster 15	Terpene	3792921	3813874	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 16	Nrps	4014408	4076495	Borrelidin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0000031_c1		
Cluster 17	Nrps	4131350	4182830	Galbonolides_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000065_c1		
Cluster 18	Nrps	4839148	4892609	-	-		
Cluster 19	Other	5083791	5127279	Glycopeptidolipid_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000364_c1		
				***Mycobacterium kansassi* ATCC 12478**			
Cluster 1	Other	144113	187649	Glycopeptidolipid_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0000362_c1		
Cluster 2	Nrps	200094	245025	-	-		
Cluster 3	Bacteriocin	269265	280125	-	-		
Cluster 4	Nrps	769230	827336	Glycopeptidolipid_biosynthetic_gene_cluster (94% of genes show similarity)	BGC0000364_c1		
Cluster 5	Other	1483355	1526846	Thiolactomycin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001353_c2		
Cluster 6	Nrps	1548971	1596644	-	-	1	CYP1128A
Cluster 7	T1pks	1726826	1773068	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 8	Bacteriocin	1858783	1869679	-	-		
Cluster 9	Other	1898439	1941963	-	-		
Cluster 10	Ectoine	2315434	2325784	-	-		

Cluster 11	T1pks-Ectoine-Nrps	2623296	2723115	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 12	T2pks-Nrps	2783808	2866995	Nocobactin_NA_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0001027_c1		
Cluster 13	T1pks-Nrps	3802034	3860882	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 14	Bacteriocin	3998170	4008967	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 15	Other	4172826	4216854	-	-		
Cluster 16	T1pks	4478946	4524336	-	-		
				***Mycobacterium* sp. JLS**			
Cluster 1	T1pks-Nrps	236908	294426	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 2	T3pks	1143068	1184120	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 3	Other	2046311	2088803	-	-		
Cluster 4	Other	2387869	2431393	-	-		
Cluster 5	T3pks	2459971	2501071	Alkylresorcinol_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000282_c1		
Cluster 6	T1pks-Nrps	2952303	3010907	Maklamicin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001288_c1		
Cluster 7	T1pks-Nrps	3247657	3304169	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 8	T1pks-Nrps	3628609	3696583	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 9	Ectoine	4648250	4658648	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 10	Nrps	5097915	5151556	Arsenopolyketides_biosynthetic_gene_cluster (12% of genes show similarity)	BGC0001283_c1		
Cluster 11	Other	5394805	5438740	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 12	T1pks	5627176	5672701	-	-		
Cluster 13	Terpene	5708418	5729368	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
				***Mycobacterium* sp. KMS**			
Cluster 1	T1pks-Nrps	259328	316819	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 2	T3pks	1139543	1180595	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 3	Other	2125389	2167881	-	-		
Cluster 4	Other	2404377	2447901	-	-		
Cluster 5	T3pks	2476640	2517560	Alkylresorcinol_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000282_c1		
Cluster 6	T1pks-Nrps	2980304	3039499	Maklamicin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001288_c1		
Cluster 7	T1pks-Nrps	3292694	3358542	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 8	T1pks-Nrps	3683064	3748128	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 9	Ectoine	4479778	4490167	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 10	Other	5080400	5124335	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 11	T1pks	5321914	5367466	-	-		
Cluster 12	Terpene	5403154	5424104	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
				***Mycobacterium* sp. MCS**			

Cluster 1	T1pks-Nrps	251988	309479	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 2	T3pks	1135234	1176286	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 3	Other	2106405	2148897	-	-		
Cluster 4	Other	2385393	2428917	-	-		
Cluster 5	T3pks	2457656	2498576	Alkylresorcinol_biosynthetic_gene_cluster (66% of genes show similarity)	BGC0000282_c1		
Cluster 6	T1pks-Nrps	2962416	3021458	Maklamicin_biosynthetic_gene_cluster (4% of genes show similarity)	BGC0001288_c1		
Cluster 7	T1pks-Nrps	3264412	3330260	Glycopeptidolipid_biosynthetic_gene_cluster (20% of genes show similarity)	BGC0000365_c1		
Cluster 8	T1pks-Nrps	3654782	3719846	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 9	Ectoine	4451114	4461503	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 10	Other	5042742	5086677	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 11	T1pks	5284292	5329844	-	-		
Cluster 12	Terpene	5365532	5386482	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity	BGC0000664_c1		
				***Mycobacterium vanbaalenii* PYR-1**			
Cluster 1	T1pks-Nrps	273453	330979	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 2	T1pks-Nrps	1007476	1069625	Galbonolides_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000065_c1		
Cluster 3	T3pks	1255771	1296844	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 4	Terpene	1662600	1683547	Isorenieratene_biosynthetic_gene_cluster (57% of genes show similarity)	BGC0000664_c1		
Cluster 5	Other	2325146	2367734	-	-		
Cluster 6	Other	2696581	2740069	-	-		
Cluster 7	Other	2808426	2852319	BE-7585A_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000203_c1		
Cluster 8	Linaridin	2937292	2957792	-	-		
Cluster 9	T1pks-Nrps	3277119	3344407	Microsclerodermins_biosynthetic_gene_cluster (18% of genes show similarity)	BGC0001019_c1	1	CYP138C1
Cluster 10	T1pks-Nrps	4074903	4141538	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 11	Bacteriocin	5481316	5492113	-	-		
Cluster 12	Ectoine	5641882	5652274	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 13	Other	5742762	5786718	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 14	T1pks	6002514	6048036	-	-		
Cluster 15	Terpene	6292612	6313811	-	-		
				***Mycobacterium smegmatis* MC2 155**			
Cluster 1	Nrps	1	61623	Albachelin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0000714_c1		
Cluster 2	T1pks-Nrps	427899	509098	Glycopeptidolipid_biosynthetic_gene_cluster (96% of genes show similarity)	BGC0001211_c1		
Cluster 3	T3pks	873684	914772	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000365_c1	1	CYP185A1
Cluster 4	Bacteriocin	2227832	2238686	-	BGC0000282_c1		
Cluster 5	Terpene	2416068	2437015	Isorenieratene_biosynthetic_gene_cluster (57% of genes show similarity)	-		

Cluster 6	Other	2531374	2573953	-	BGC0000664_c1		
Cluster 7	Other	2995829	3039335	-	-		
Cluster 8	Nrps	3739540	3805988	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	-		
Cluster 9	Ectoine	3966007	3976399	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000365_c1		
Cluster 10	Nrps	4565368	4625560	Mycobactin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000853_c1		
Cluster 11	T1pks-Nrps	4799250	4851664	Glycopeptidolipid_biosynthetic_gene_cluster (19% of genes show similarity)	BGC0001021_c1		
Cluster 12	Nrps	5027070	5080900	Arginomycin_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000769_c1		
Cluster 13	Other	5801365	5844886	-	BGC0000883_c1		
Cluster 14	Bacteriocin	5892680	5903477	-	-		
Cluster 15	Other	5982575	6025196	-	-		
Cluster 16	Other	6180052	6223987	Glycopeptidolipid_biosynthetic_gene_cluster (6% of genes show similarity)	-		
Cluster 17	T1pks	6436780	6482305	-	BGC0000365_c1		
Cluster 18	T1pks	6791076	6836550	Sisomicin_biosynthetic_gene_cluster (5% of genes show similarity)	-		
				***Mycobacterium chubuense* NBB4**			
Cluster 1	T1pks-Nrps	213443	270925	Glycopeptidolipid_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000365_c1		
Cluster 2	T3pks	840785	881870	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 3	Terpene	1177480	1198424	Carotenoid_biosynthetic_gene_cluster (21% of genes show similarity)	BGC0000636_c1		
Cluster 4	Arylpolyene	2017291	2058448	-	-	3	CYP187A; CYP150A; CYP189A
Cluster 5	Other	2344446	2387940	-	-		
Cluster 6	Ectoine	2388530	2398922	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 7	T1pks-Nrps	2837828	2905289	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000026_c1	1	CYP138C
Cluster 8	Other	3386862	3429642	U-68204_biosynthetic_gene_cluster (14% of genes show similarity)	BGC0001354_c1		
Cluster 9	Nrps	3659238	3730463	Glycopeptidolipid_biosynthetic_gene_cluster (13% of genes show similarity)	BGC0000365_c1		
Cluster 10	T1pks	4550517	4596045	-	-	1	CYP292A
Cluster 11	Bacteriocin	4717275	4728072	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 12	Other	4958728	5002657	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 13	T1pks	5216614	5262085	-	-		
				***Mycobacterium gilvum* PYR-GCK**			
Cluster 1	T1pks-Nrps	380671	438247	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 2	Terpene	983162	1004367	-	-		
Cluster 3	T1pks	1194968	1240304	-	-		
Cluster 4	Other	1443556	1487530	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 5	Bacteriocin	1691217	1702014	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 6	Terpene	1906811	1927755	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1	1	CYP188A

Cluster 7	T1pks-Nrps	2796226	2861142	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 8	Other	2995862	3038351	-	-		
Cluster 9	T1pks-Nrps	3562186	3629559	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000026_c1	1	CYP138C2
Cluster 10	T3pks	4225912	4266985	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1		
Cluster 11	Other	4374244	4416826	-	-	3	CYP189A; CYP150A; CYP187A
Cluster 12	Ectoine	5143127	5153519	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 13	Other	5282888	5323730	-	-		
Cluster 14	T3pks	5449695	5490777	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
				***Mycobacterium gilvum* Spyr1**			
Cluster 1	T1pks-Nrps	339200	396776	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 2	Bacteriocin	1026345	1037142	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1		
Cluster 3	Terpene	1258378	1279322	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1	1	CYP188A
Cluster 4	T1pks-Nrps	2157546	2222588	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 5	T1pks-Nrps	2775797	2843206	Avilamycin_A_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000026_c1	1	CYP138C2
Cluster 6	T3pks	3435596	3476669	Herboxidiene_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0001065_c1		
Cluster 7	Other	3582553	3625135	-	-	3	CYP189A; CYP150A; CYP187A
Cluster 8	Ectoine	4395958	4406350	Ectoine_biosynthetic_gene_cluster (75% of genes show similarity)	BGC0000853_c1		
Cluster 9	Other	4540020	4580862	-	-		
Cluster 10	T3pks	4706085	4747167	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1		
Cluster 11	Other	4928470	4972444	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 12	T1pks	5182179	5227515	-	-		
Cluster 13	Terpene	5411716	5432921	-	-		
				***Mycobacterium smegmatis* JS623**			
Cluster 1	T1pks-Nrps	195961	253457	Glycopeptidolipid_biosynthetic_gene_cluster (26% of genes show similarity)	BGC0000365_c1		
Cluster 2	Nrps	346982	404899	Glycopeptidolipid_biosynthetic_gene_cluster (78% of genes show similarity)	BGC0000364_c1		
Cluster 3	Other	627984	671520	-	-		
Cluster 4	T3pks	724354	765415	Alkylresorcinol_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000282_c1	1	CYP135B
Cluster 5	T3pks	1146215	1187333	-	-		
Cluster 6	Other	2284486	2326996	-	-	2	CYP187A; CYP150A
Cluster 7	Other	2640333	2683839	-	-		
Cluster 8	Nrps	3391916	3433310	Glycopeptidolipid_biosynthetic_gene_cluster (7% of genes show similarity)	BGC0000362_c1		
Cluster 9	T1pks	4162220	4206377	Meilingmycin_biosynthetic_gene_cluster (2% of genes show similarity)	BGC0000093_c1		
Cluster 10	T3pks	4294384	4335520	Griseoviridin_/_viridogrisein_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000459_c1		

Cluster 11	Terpene	4848846	4869796	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 12	T1pks-Nrps	5451816	5505010	-	-	1	CYP136NSF2
Cluster 13	Bacteriocin	5598281	5609078	-	-		
Cluster 14	T1pks-Nrps	5785277	5864758	Chartreusin_biosynthetic_gene_cluster (15% of genes show similarity)	BGC0000206_c2		
Cluster 15	Other	5892270	5936181	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 16	T1pks	6130226	6175661	-	-		
				Mycobacterium rhodesiae			
Cluster 1	T1pks	48296	93830	Galbonolides_biosynthetic_gene_cluster (6% of genes show similarity)	BGC0000065_c1	2	CYP189A; CYP102NSF1
Cluster 2	T1pks-Nrps	249686	327946	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000362_c1	1	CYP1121A1
Cluster 3	Arylpolyene	486822	528012	-	-		
Cluster 4	Nrps	1009235	1052347	-	-		
Cluster 5	Lantipeptide	1503784	1532987	-	-		
Cluster 6	Terpene	1776658	1797842	-	-		
Cluster 7	T1pks	1951592	1997159	-	-		
Cluster 8	Other	2181020	2224934	Phosphonoglycans_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000806_c1		
Cluster 9	Nrps	2272026	2324007	-	-	1	CYP125A
Cluster 10	Bacteriocin	2535310	2546107	-	-		
Cluster 11	Terpene	3638976	3659923	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 12	T1pks-Nrps	4300696	4361762	Mycobactin_biosynthetic_gene_cluster (60% of genes show similarity)	BGC0001021_c1		
Cluster 13	Nrps	4719612	4799700	Glycopeptidolipid_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000365_c1	1	CYP189A
Cluster 14	Arylpolyene	4940071	4981234	Glycopeptidolipid_biosynthetic_gene_cluster (5% of genes show similarity)	BGC0000362_c1	1	CYP124A
Cluster 15	Nrps	5038727	5113037	Pentalenolactone_biosynthetic_gene_cluster (23% of genes show similarity)	BGC0000678_c1		
Cluster 16	Other	5543496	5586996	-	-		
Cluster 17	Other	5848025	5890520	-	-		
Cluster 18	Arylpolyene	6144777	6185937	-	-	1	CYP144A
				***Mycobacterium neoaurum* VKM Ac-18150**			
Cluster 1	T1pks	62335	107761	-	-		
Cluster 2	Other	154612	198061	Herboxidiene_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0001065_c1		
Cluster 3	Terpene	561323	582507	-	-		
Cluster 4	T1pks-Nrps	632798	691946	Glycopeptidolipid_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000365_c1		
Cluster 5	Other	2319764	2362295	-	-		
Cluster 6	Other	2706443	2750177	BE-7585A_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000203_c1		
Cluster 7	T1pks-Nrps	2819680	2872045	Griseobactin_biosynthetic_gene_cluster (11% of genes show similarity)	BGC0000368_c1		

Cluster 8	Ectoine	3002251	3012649	Ectoine_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000853_c1		
Cluster 9	T1pks	3678348	3723822	Laspartomycin_biosynthetic_gene_cluster (9% of genes show similarity)	BGC0000379_c1		
Cluster 10	T1pks-Nrps	3912925	3978393	Mycobactin_biosynthetic_gene_cluster (80% of genes show similarity)	BGC0001021_c1		
Cluster 11	Terpene	4742141	4810153	Isorenieratene_biosynthetic_gene_cluster (71% of genes show similarity)	BGC0000664_c1		
Cluster 12	Bacteriocin	4977471	4988268	-	-		
Cluster 13	Other	5022054	5065536	Rifamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000136_c1	1	CYP161NSF1
Cluster 14	T1pks	5094761	5139101	-	-		
Cluster 15	Other	5274956	5318840	Galbonolides_biosynthetic_gene_cluster (10% of genes show similarity)	BGC0000065_c1		

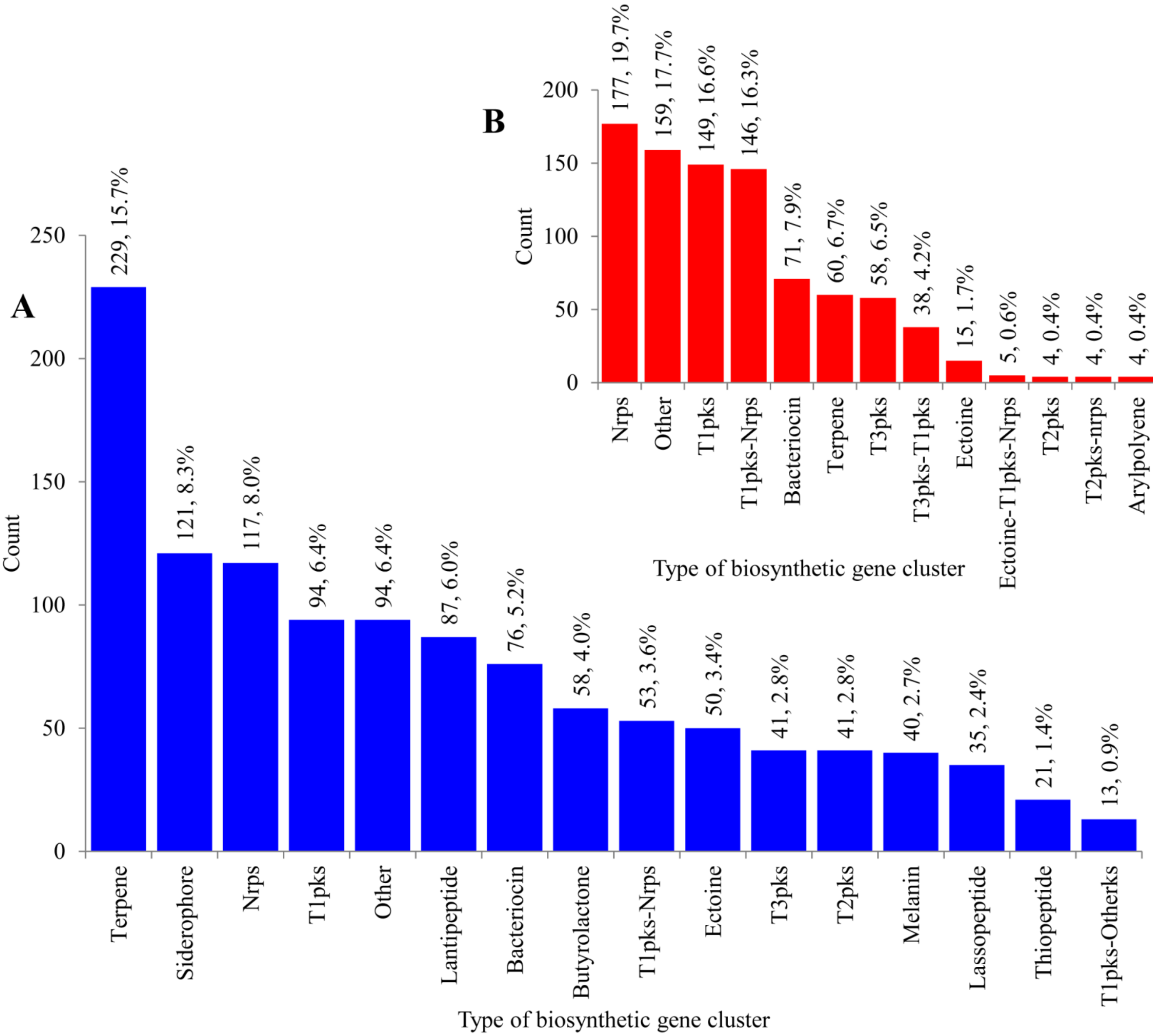


Figure 4. 3 Comparative analysis of types of BGCs between *Streptomyces* species (A) and mycobacterial species (B). The numbers next to bars represent the number of secondary metabolite BGCs and their percentage in the total number of BGCs found in 48 *Streptomyces* species (A) or 60 mycobacterial species (B). Comparative analysis of types of secondary metabolite BGCs in *Streptomyces* species and mycobacterial species was presented in Table 4.1. Furthermore,

comprehensive comparative analysis of different types of secondary metabolite BGCs between *Streptomyces* and *Mycobacterium* is presented in Table 4.2.

As mentioned earlier, quite a big difference was observed with respect to the types of secondary metabolite BGCs between *Streptomyces* and mycobacterial species (Figure 4.3 and Table 4.2). Among 159 types of secondary metabolite BGCs found in *Streptomyces* species, only 13 types of BGCs contributed 80% to the total percentage of BGCs (Figure 4.3A), suggesting that the secondary metabolites produced by these BGCs were highly important in *Streptomyces* species' physiology. The secondary metabolite BGC terpene was dominant, followed by siderophore, Nrps and T1pks in *Streptomyces* species (Figure 4.3A and Table 4.2). Among 18 types of secondary metabolite BGCs identified in mycobacterial species, Nrps was the dominant secondary metabolite BGC, followed by Other, T1pks and T1pks-Nrps (Figure 4.3B and Table 4.2). Despite the presence of 15 common types of secondary metabolite BGCs between the genera *Streptomyces* and *Mycobacterium*, large differences were observed in terms of the number of BGCs (Figure 4.4), indicating that the selective enrichment of particular secondary metabolite BGCs in both genera is possibly due to the different lifestyle, as discussed in the subsequent section.

Table 4. 2 Comparative analysis of secondary metabolite BGCs between the genera *Streptomyces* and *Mycobacterium*.

Secondary metabolite BGC	**Number of clusters**	
	Streptomyces	***Mycobacterium***
Nrps	117	177
Other	94	159
T1pks	94	149
T1pks-Nrps	53	146
Bacteriocin	76	71
Terpene	229	60
T3pks	41	58
T3pks-T1pks	0	38
Ectoine	50	15
Ectoine-T1pks-Nrps	0	5
T2pks	41	4
T2pks-nrps	2	4
Arylpolyene	3	4
Lantipeptide	87	3
Amglyccycl	7	2
T1pks-Ectoine-Nrps	0	1
otherKs	8	1
linaridin	3	1
Siderophore	121	Not identified
Butyrolactone	58	Not identified
Melanin	40	Not identified
Lassopeptide	35	Not identified
Thiopeptide	21	Not identified
T1pks-Otherks	13	Not identified
Indole	9	Not identified
Bacteriocin-Lantipeptide	8	Not identified
Transatpks-T1pks-Nrps	8	Not identified
Bacteriocin-Nrps	8	Not identified
T3pks-Nrps	7	Not identified
Terpene-Nrps	7	Not identified
Lantipeptide-Nrps	5	Not identified
Melanin-Nrps	5	Not identified
T2pks-Terpene	5	Not identified
Ladderane	5	Not identified

Terpene-T1pks	5	Not identified
Transatpks-Nrps	5	Not identified
Nrps-T1pks-Otherks	4	Not identified
Lantipeptide-T1pks-Nrps	4	Not identified
T1pks-Butyrolactone-Nrps	4	Not identified
T2pks-Otherks	4	Not identified
Lantipeptide-Terpene	4	Not identified
T2pks-Butryolactone	4	Not identified
Melanin-Terpene	4	Not identified
T3pks-Terpene-Nrps	3	Not identified
T2pks-T1pks-Otherks	3	Not identified
Ladderane-Arylpolyene-Nrps	3	Not identified
Arylpolyene-Ladderane	3	Not identified
Bacteriocin-T1pks-Nrps	3	Not identified
T1pks-Siderophore	3	Not identified
Blactam	3	Not identified
Otherks-Nrps	3	Not identified
Lantipeptide-Terpene-Nrps	3	Not identified
T3pks-T1pks-Nrps	3	Not identified
Nucleoside	3	Not identified
T1pks-Butyrolactone-otherks	2	Not identified
Butyrolactone-Otherks	2	Not identified
T1pks-Linaridin	2	Not identified
Hserlactone	2	Not identified
T1pks-Lassopeptide	2	Not identified
T3pks-Terpene	2	Not identified
Nrps-Otherks	2	Not identified
Blactam-T1pks-Nrps	2	Not identified
Phenazine-Nrps	2	Not identified
T2pks-Ladderane-Nrps	2	Not identified
T2pks-T1pks	2	Not identified
Bacteriocin-Terpene	2	Not identified
Lassopeptide-Nrps	2	Not identified
Lantipeptide-Lassopeptide	2	Not identified
T2pks-Oligosaccharide-Nucleoside-Nrps	2	Not identified
Butyrolactone-T1pks-Nrps	2	Not identified
Terpene-T3pks-T1pks-Nrps	2	Not identified
T2pks-Oligosaccharide-Nrps-Otherks	2	Not identified
Terpene-T1pks-Nrps	2	Not identified
Bacteriocin-T1pks	2	Not identified
Phosphoglycolipid	2	Not identified

Thiopeptide-Bacteriocin	2	Not identified
T1pks-Butyrolactone	1	Not identified
T1pks-Terpene	1	Not identified
Transatpks-T1pks-Otherks-Nrps	1	Not identified
Bacteriocin-Bottromycin	1	Not identified
Butyrolactone-T1pks-Otherks	1	Not identified
Indole-T1pks	1	Not identified
T2pks-Butyrolactone-Nrps	1	Not identified
Bacteriocin-Lantipeptide-T1pks-Otherks-Nrps	1	Not identified
Ectoine-Terpene	1	Not identified
Transatpks-Otherks-Nrps	1	Not identified
Bacteriocin-Lantipeptide-T1pks	1	Not identified
Nrps-Furan-T1pks-Otherks	1	Not identified
Siderophore-Nrps	1	Not identified
T2pks-Oligosaccharide-Otherks	1	Not identified
Transatpks-Terpene-Nrps	1	Not identified
Ladderane-Nrps	1	Not identified
Butyrolactone-Terpene	1	Not identified
Bacteriocin-Oligosaccharide	1	Not identified
Terpene-T3pks-Cyanobactin-Nrps	1	Not identified
Phosphonate	1	Not identified
Arylpolyene-Nrps	1	Not identified
Melanin-Arylpolyene-Ladderane	1	Not identified
T1pks-Phenazine	1	Not identified
Terpene-Ectoine	1	Not identified
Bacteriocin-Otherks	1	Not identified
Nrps-Transatpks-T1pks-Otherks	1	Not identified
Thiopeptide-T2pks-Otherks-Nrps	1	Not identified
Nrps-Ladderane	1	Not identified
Lantipeptide-Lassopeptide-Nrps	1	Not identified
T1pks-Arylpolyene-Ladderane	1	Not identified
Bacteriocin-Nrps-Lantipeptide-T1pks-Otherks	1	Not identified
Nrps-Arylpolyene-Ladderane	1	Not identified
T3pks-Otherks-Butyrolactone-Nrps	1	Not identified
Otherks-Butyrolactone-Nrps	1	Not identified
Butyrolactone-T1pks	1	Not identified
T2pks-Lantipeptide-Terpene	1	Not identified
T1pks-Arylpolyene	1	Not identified
Bacteriocin-Butyrolactone	1	Not identified
Thiopeptide-T1pks	1	Not identified
T3pks-Fused-Nrps	1	Not identified

Transatpks	1	Not identified
Cyanobactin-T1pks-Nrps	1	Not identified
T2pks-Oligosaccharide	1	Not identified
Lantipeptide-T1pks	1	Not identified
Lantipeptide-Linaridin	1	Not identified
Linaridin-T1pks-Lassopeptide-Nrps	1	Not identified
Terpene-Otherks	1	Not identified
T2pks-T3pks	1	Not identified
T1pks-Transatpks-Terpene	1	Not identified
Fused	1	Not identified
T3pks-Terpene-Otherks	1	Not identified
Phenazine	1	Not identified
T1pks-Terpene-Nrps	1	Not identified
Oligosaccharide-T1pks-Nrps	1	Not identified
Oligosaccharide-Ectoine-T2pks-Nrps-T1pks-Otherks	1	Not identified
Thiopeptide-Nrps	1	Not identified
Thiopeptide-T2pks	1	Not identified
Ectoine-Nrps	1	Not identified
T2pks-Ectoine-Otherks	1	Not identified
Thiopeptide-T1pks-Nrps	1	Not identified
Ectoine-Butyrolactone	1	Not identified
Transatpks-T1pks-Otherks-Nrps	1	Not identified
Bacteriocin-Lassopeptide-Nrps	1	Not identified
T2pks-T3pks-Otherks	1	Not identified
Ectoine-T1pks-Otherks	1	Not identified
Butyrolactone-Amglyccycl-T1pks-Nrps	1	Not identified
Nrps-T2pks-Otherks-T1pks-Phenazine	1	Not identified
Nrps-Transatpks-Terpene-Otherks	1	Not identified
Butyrolactone-Amglyccycl	1	Not identified
T3pks-Butyrolactone	1	Not identified
Nucleoside-Lassopeptide-Nrps	1	Not identified
Phosphonate-Nrps	1	Not identified
Thiopeptide-Terpene	1	Not identified
Bacteriocin-Terpene-Nrps	1	Not identified
Indole-Terpene-Nrps	1	Not identified
Blactam-Nrps	1	Not identified
Phosphonate-Bacteriocin	1	Not identified
Siderophore-T1pks-Nrps	1	Not identified
Phosphonate-Terpene	1	Not identified
Lantipeptide-T1pks-Otherks	1	Not identified
Phosphonate-T3pks-Nrps-Ladderane	1	Not identified

Indole-T3pks	1	Not identified
Amglyccycl-Butyrolactone	1	Not identified
Bacteriocin-T2pks	1	Not identified
Terpene-Butyrolactone	1	Not identified
Nrps-Siderophore	1	Not identified

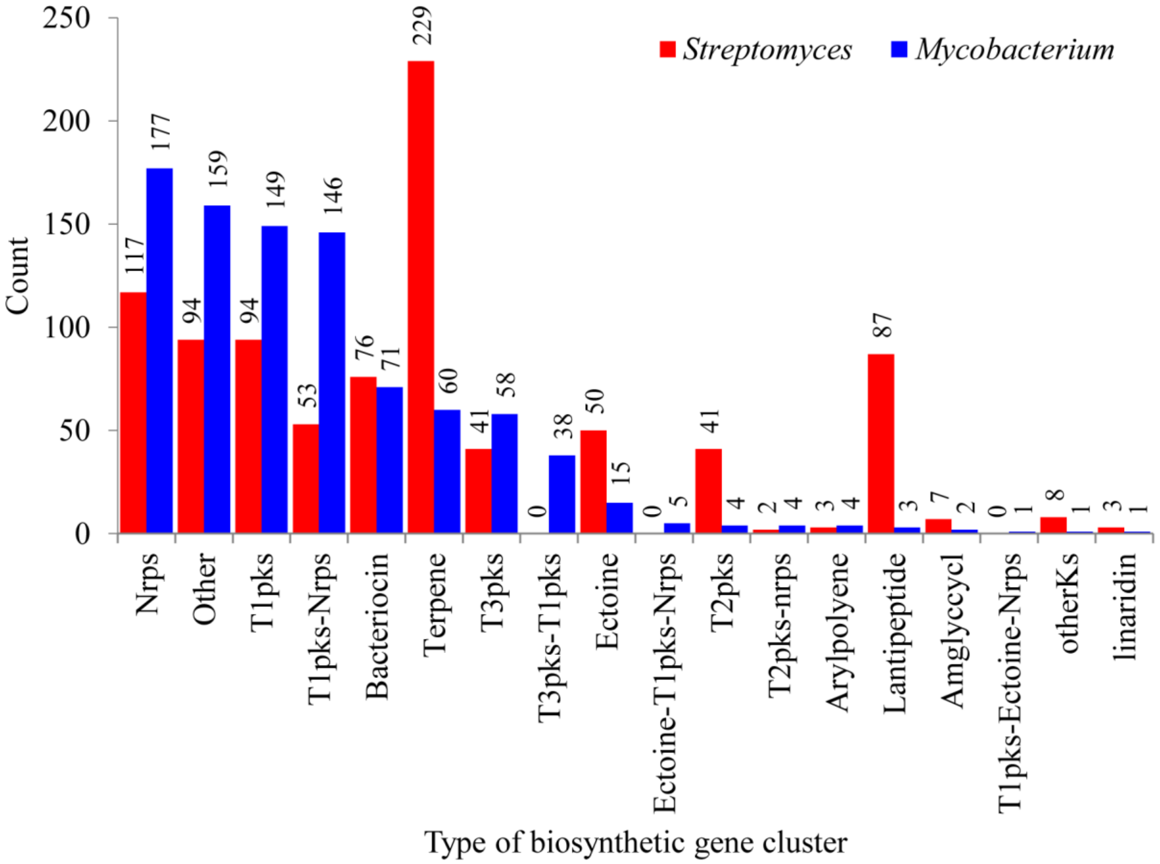


Figure 4. 4 Comparative analysis of secondary metabolite BGCs commonly found in both *Streptomyces* and mycobacterial species. The number on top of each bar represents the number of types of BGCs present in 48 Streptomyces and 60 mycobacterial species.

4.2. *Streptomyces* species have a large and diverse number of P450s in secondary metabolite BGCs

Comparative analysis of P450s that are part of secondary metabolite BGCs revealed the presence of a large number of diverse P450s as part of these secondary metabolite BGCs in *Streptomyces*, compared to *Mycobacterium* (Figures 4.1 and 4.5; Tables 4.3 and 4.4). Not all secondary metabolite BGCs found in *Streptomyces* and *Mycobacterium* have P450s. Among 1 461 in *Streptomyces* species, only 554 secondary metabolite BGCs were found to have P450s, whereas in mycobacterial species, among 898 only 204 secondary metabolite BGCs have P450s (Figure 4.1). Moreover, not all types of secondary metabolite BGCs have P450s: 64% and 50% of types of secondary metabolite BGCs of respectively *Streptomyces* and *Mycobacterium* were found to have P450s (Figures 4.1 and 4.5; Tables 4.3 and 4.4). Furthermore, a large difference was observed in the number of different P450 families that are part of secondary metabolite BGCs between the genera *Streptomyces* and *Mycobacterium;* the former genus has 88 P450 families and the latter only 31 P450 families, strongly indicating the possibility that diverse P450s are involved in the generation of diverse secondary metabolites in *Streptomyces* compared to *Mycobacterium*. Overall, 554 and 204 P450s were found to be part of secondary metabolite BGCs in *Streptomyces* and mycobacterial species (Figures 4.1 and 4.5; Tables 4.3 and 4.4).

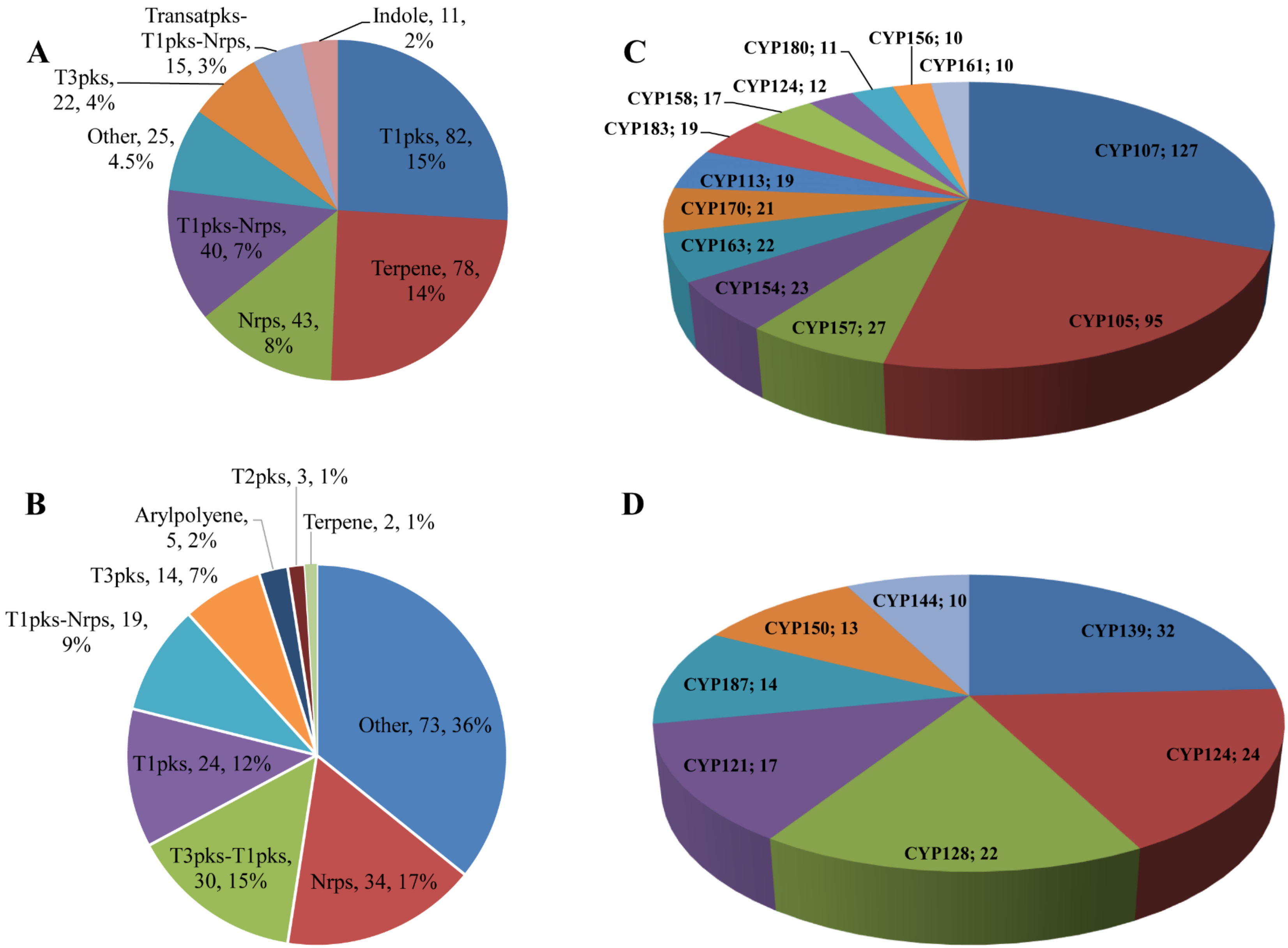

A
Transatpks-T1pks-Nrps, 15, 3%
Indole, 11, 2%
T3pks, 22, 4%
Other, 25, 4.5%
T1pks, 82, 15%
T1pks-Nrps, 40, 7%
Terpene, 78, 14%
Nrps, 43, 8%
C
CYP180; 11
CYP156; 10
CYP161; 10
CYP124; 12
CYP158; 17
CYP183; 19
CYP107; 127
CYP113; 19
CYP170; 21
CYP163; 22
CYP154; 23
CYP157; 27
CYP105; 95
B
T2pks, 3, 1%
Arylpolyene, 5, 2%
Terpene, 2, 1%
T3pks, 14, 7%
T1pks-Nrps, 19, 9%
Other, 73, 36%
T1pks, 24, 12%
T3pks-T1pks, 30, 15%
Nrps, 34, 17%
D
CYP144; 10
CYP150; 13
CYP139; 32
CYP187; 14
CYP121; 17
CYP124; 24
CYP128; 22

Figure 4. 5 Comparative analysis of P450s associated with secondary metabolism. Comparative analysis of BGCs containing P450s in 48 *Streptomyces* species (A) and 60 mycobacterial species (B). Numbers next to BGCs indicate the number of BGCs and their percentage in the total number of BGCs containing P450s (for details see Tables 4.3 and 4.4). Comparative analysis of P450 families that are part of secondary metabolite BGCs in *Streptomyces* species (C) and mycobacterial species (D). The P450 families that are dominantly present in different BGCs are presented in the figure. The number after the P450 name indicates the number of member P450s. Detailed information on P450s that are part of BGCs is presented in Table 4.5.

Table 4. 3 Comparative analysis of secondary metabolite biosynthetic gene clusters and P450s that are part of these clusters in *Streptomyces* species.

Species code	**Cluster name**	**Number of P450s**	**P450 name**
sco	T3pks	1	CYP158A2
	Terpene	1	CYP170A1
	T3pks-Terpene-Nrps	1	CYP105N1
sma	T1pks	2	CYP105D6; CYP105P1
	Nrps	1	CYP147B1
	Nrps-T1pks-Otherks	2	CYP178A1; CYP178A3P
	T1pks	1	CYP171A1
	Terpene	1	CYP180A1
	T2pks-T1pks-Otherks	2	CYP107Y1; CYP181A1
	T1pks	2	CYP107W1; CYP105B23
	Terpene	1	CYP183A1
	Terpene	1	CYP170A2
	Butyrolactone-Otherks	2	CYP107V1; CYP107U2
	T3pks	1	CYP158A3
	T1pks	1	CYP105R1
sgr	T1pks-Nrps	1	CYP105D1
	Melanin	1	CYP124G2
	T1pks-Nrps	3	CYP162C1; CYP208A1; CYP154M2

	T1pks-Nrps	1	CYP107BX5
	Nrps	1	CYP107BY1
	Ladderane-Arylpolyene-Nrps	2	CYP163B5; CYP107BZ1
	T3pks	1	CYP107F4
	Transatpks-T1pks-Otherks-Nrps	1	CYP107CA2
sgb	T3pks	1	CYP107F4
	Arylpolyene-Ladderane	1	CYP1373A2
	Bacteriocin-T1pks-Nrps	1	CYP107BX10
	Melanin	1	CYP124G14
	T1pks-Nrps	1	CYP105D30
scb	Terpene	1	CYP154A4
	Lantipeptide-Nrps	4	CYP246A1; CYP1048A1; CYP156D1; CYP154L1
	T1pks-Nrps	1	CYP107AM1
	Bacteriocin-Bottromycin	1	CYP283A1
	Butyrolactone-T1pks-Otherks	1	CYP107AL1
	Terpene	1	CYP157C5
	Indole-T1pks	1	CYP156B2
	T1pks	1	CYP107AK1
ssx	Melanin	1	CYP124G3
	Nrps	1	CYP105N1
	T2pks-T1pks-Otherks	2	CYP181A1; CYP107Y1
	T1pks	2	CYP105AZ1; CYP105AZ2
	T1pks-Nrps	1	CYP107BX4
	T2pks-Butyrolactone-Nrps	1	CYP105A4
svl	Terpene	2	CYP107BW1; CYP1013A2
	Nrps	2	CYP162A3; CYP107CK1
	T1pks	1	CYP124B3
	T1pks	2	CYP107BW1; CYP105AX1
	Otherks	2	CYP183F2; CYP105AV1
	Bacteriocin-Lantipeptide-T1pks-Otherks-Nrps	4	CYP105AQ2; CYP155A5; CYP107E9; CYP105AN3
	T1pks	1	CYP107AD1
	Lantipeptide-T1pks-Nrps	1	CYP105AY1
	T1pks	1	CYP105U1
	Terpene	2	CYP156C9; CYP125A20
	Indole	2	CYP107U9; CYP156B6
	Ladderane-Arylpolyene-Nrps	3	CYP163B4; CYP107CF1; CYP107CE1

	Terpene	1	CYP147F5
sct	T1pks	2	CYP107AS; CYP107CR1
	Lantipeptide	1	CYP107AE6
	T1pks-Nrps	1	CYP184A4
	Transatpks-T1pks-Nrps	2	CYP107CS1; CYP107W2
	T3pks-Terpene	1	CYP158A13
	Lantipeptide	1	CYP105AA10
	T1pks-Butyrolactone-Nrps	2	CYP107CT1; CYP105B25
scy	T1pks	3	CYP107AS; CYP1274A1; CYP107CR1
	Lantipeptide	1	CYP107AE6
	T1pks-Nrps	1	CYP184A4
	Transatpks-T1pks-Nrps	2	CYP107CS1; CYP107W2
	T3pks-Terpene	1	CYP158A13
	Lantipeptide	1	CYP105AA10
	T1pks-Butyrolactone-Nrps	2	CYP107CT1; CYP105B25
sfa	Blactam-T1pks-Nrps	2	CYP247A3; CYP107BX5
	T1pks	2	CYP105AZ2; CYP105AZ1
	T1pks-Nrps	3	CYP1029A2; CYP1423A2; CYP285A2
	Terpene	1	CYP157K1
	Melanin	1	CYP124G4
	Nrps	2	CYP1035A4; CYP156B9
sbh	Bacteriocin-T1pks-Nrps	2	CYP183C1; CYP183D1
	Terpene	1	CYP183E1
	Bacteriocin-Lantipeptide-T1pks	1	CYP1039A1
	Transatpks-T1pks-Nrps	3	CYP105H6; CYP107BK1; CYP171A2
	Nrps	2	CYP107BM3; CYP157B13
	T1pks-Nrps	1	CYP113G1
	Other	1	CYP154P1
	T1pks-Nrps	1	CYP1037A1
	Otherks	1	CYP268A4
	T1pks	1	CYP124B2
	Otherks-Nrps	1	CYP163C1
	Transatpks-Terpene-Nrps	2	CYP161C1; CYP183A2
shy	T1pks	1	CYP105B22
	Terpene	1	CYP107X1
	Nrps	1	CYP163B6
	Nrps	1	CYP285B1

	T1pks	2	CYP105AZ2; CYP105AZ1
	T3pks	1	CYP158A14
	Terpene	1	CYP170A10
	Terpene	1	CYP180A6
	Bacteriocin-Nrps	1	CYP113K3
sho	T1pks	1	CYP105B22
	Terpene	1	CYP107X1
	Nrps	1	CYP163B6
	Nrps	1	CYP285B1
	T1pks	2	CYP105AZ2; CYP105AZ1
	T3pks	1	CYP158A14
	Terpene	1	CYP170A10
	Terpene	1	CYP180A6
	Bacteriocin-Nrps	1	CYP113K3
sve	Lantipeptide-Terpene	1	CYP157C14
	Indole	1	CYP245A3
	Other	1	CYP121A2
	T3pks	1	CYP158A5
	Other	2	CYP105AC2; CYP180A5
	Ladderane-Nrps	4	CYP1056A1; CYP107CL1; CYP162A4; CYP163B5
sdv	T1pks-Nrps	1	CYP105BA1
	Other	1	CYP1005B2
	Bacteriocin-Lantipeptide	1	CYP179B1
	Terpene	1	CYP183K1
	Lantipeptide-T1pks-Nrps	1	CYP179A3
	Butyrolactone-Terpene	1	CYP180A6
	Bacteriocin-Oligosaccharide	2	CYP107CN1; CYP107CP1
	Terpene-Nrps	1	CYP170A9
	T1pks-Nrps	3	CYP113J1; CYP113J2; CYP162A5
	Otherks-Nrps	2	CYP125A22; CYP163C2
	T3pks	1	CYP158A7
	Terpene-T3pks-Cyanobactin-Nrps	2	CYP1041A2; CYP1058A1
salb	T1pks-Nrps	1	CYP107BX2
	Otherks	1	CYP1420A1
	Nrps	1	CYP146A3
	Terpene	1	CYP170B5
	Lantipeptide	1	CYP154A1
	T3pks	1	CYP107F4

	Lantipeptide-T1pks-Nrps	1	CYP105H3
sals	Nrps	1	CYP105BK3
	T1pks-Butyrolactone-Nrps	1	CYP107EJ1
	T1pks-Otherks	2	CYP113Y1; CYP105DB1
	T1pks	1	CYP107DU1
	Terpene	1	CYP170B5
	Arylpolyene-Nrps	1	CYP107T3
	Arylpolyene	1	CYP107KW1
	T2pks-Otherks	1	CYP1193A1
	T1pks-Nrps	1	CYP1194A1
strp	Nrps	2	CYP156B9; CYP1035A4
	Melanin	1	CYP124G4
	Terpene	1	CYP157K1
	T1pks-Nrps	3	CYP285A2, CYP1423A2, CYP1029A2
	T1pks	2	CYP105AZ1; CYP105AZ2
	Bacteriocin-Otherks	1	CYP1057A1
	Blactam-T1pks-Nrps	2	CYP107BX5; CYP247A3
sfi	T3pks	1	CYP107F4
	T1pks-Nrps	1	CYP107BX3
	Melanin	1	CYP124G2
sci	Transatpks-T1pks-Nrps	2	CYP107CQ1; CYP105AJ2
	Bacteriocin	2	CYP1059A1; CYP105B21
	T3pks	1	CYP158A2
	Terpene	1	CYP170A10
	T1pks	2	CYP105BC1; CYP105AH2
	Terpene	1	CYP180A6
	Terpene	1	CYP183A4
	Bacteriocin-Nrps	1	CYP113K3
	Transatpks-T1pks-Nrps	2	CYP105AJ2; CYP107CQ1
src	T1pks	1	CYP105AX1
	T1pks	1	CYP124B3
	T1pks-Nrps	3	CYP161D1; CYP105AT1; CYP107L12
	Terpene	1	CYP1013A2
	T1pks-Nrps	1	CYP105AU1
	Terpene	1	CYP147F5
	Nrps-Arylpolyene-Ladderane	3	CYP107CE1; CYP107CF1; CYP163B4
	Indole	2	CYP156B6; CYP107U9
	Terpene	2	CYP125A20; CYP156C8

	T1pks	3	CYP194B3; CYP194B4; CYP107BS2
	T1pks-Nrps	3	CYP105AW1; CYP122A4; CYP107G2
	Otherks	1	CYP183F1
	T1pks-Arylpolyene-Ladderane	1	CYP107B3
	T1pks-Nrps	1	CYP105AY1
	T1pks	1	CYP107AD1
	Bacteriocin-Nrps-Lantipeptide-T1pks-Otherks	3	CYP105AN3; CYP107E9; CYP155A5
	Terpene	1	CYP105AV1
	T1pks	1	CYP107CD1
salu	Butyrolactone	1	CYP107L43
	Other	1	CYP1190A1
	Other	1	CYP1192A1
	T1pks-Nrps	1	CYP1191A1
	Nrps	1	CYP107EB1
	Transatpks-T1pks-Nrps	2	CYP163B9; CYP105AA13
	T1pks	2	CYP105H9; CYP161A7
	Transatpks-Nrps	3	CYP107B6; CYP1189A1; CYP1189A2
	T3pks-Otherks-Butyrolactone-Nrps	2	CYP107F9; CYP163C3
	T2pks-Oligosaccharide-Nucleoside-Nrps	2	CYP113D6; CYP157C28
	Butyrolactone	1	CYP107AE9
	Lantipeptide	1	CYP251G1
	Terpene-T1pks	2	CYP161A6; CYP105H1
sall	Nrps	3	CYP107EL1; CYP163B8; CYP107EA2
	Butyrolactone	1	CYP107L43
	Other	1	CYP1190A1
	Other	3	CYP147F21; CYP1060A2; CYP1192A1
	T1pks	1	CYP1191A1
	Transatpks-T1pks-Nrps	2	CYP163B9; CYP105AA13
	T1pks	1	CYP105H9
	Transatpks-Nrps	2	CYP1189A1; CYP1189A2
	T3pks	1	CYP107F9
	Otherks-Butyrolactone-Nrps	1	CYP163C3
	T2pks-Oligosaccharide-Nucleoside-Nrps	2	CYP113D6; CYP157C28
	Butyrolactone	1	CYP107AE9

	Lantipeptide	1	CYP251G1
	T1pks	2	CYP161A6; CYP105H1
	Nrps	3	CYP107EA2; CYP163B8; CYP107EL1
slv	T3pks-Terpene-Nrps	1	CYP105N1
	Terpene	1	CYP170A1
	T3pks	1	CYP158A2
sgu	Other	1	CYP178B1
	Nrps	1	CYP163B10
	Terpene	1	CYP170A22
	Terpene	1	CYP180A9
	T2pks	1	CYP107AH4
	Terpene	1	CYP157K3
	Nrps	1	CYP113K5
svt	Other	1	CYP121A2
	T2pks-Nrps	3	CYP1029A3; CYP1423A1; CYP285A5
	Lantipeptide	1	CYP107LD1
	T2pks-Lantipeptide-Terpene	2	CYP154C11; CYP157A19
stre	Butyrolactone-T1pks-Nrps	1	CYP105BA3
	T1pks-Arylpolyene	3	CYP107EM1; CYP1198A1; CYP105BV1
	Terpene	1	CYP157C31
	T1pks	2	CYP105H1; CYP161A6
	Butyrolactone	1	CYP107AE10
	T3pks	1	CYP107F9
	T1pks	3	CYP105DE1; CYP105BS1; CYP1197A1
	Thiopeptide-T1pks	1	CYP184A8
	Nrps	1	CYP1196A1
	Transatpks-Nrps	2	CYP107CA2; CYP154D14
	Lantipeptide	1	CYP107L42
	Lantipeptide-Nrps	2	CYP163B; CYP1278B1
	Terpene-T1pks	1	CYP105H8
	T1pks-Butyrolactone-Nrps	1	CYP105BA3
scw	T1pks	2	CYP107L35; CYP105BT1
	Terpene	1	CYP170A17
	T1pks	1	CYP107W3
	Siderophore	1	CYP105AC8
	Terpene	2	CYP161C4; CYP183A4

	Terpene	1	CYP157K4
	T3pks-Fused-Nrps	1	CYP105AC17
sld	T2pks	1	CYP105BW1
	Transatpks	2	CYP147K2; CYP1038A7
	Terpene	1	CYP147F28P
	Butyrolactone	1	CYP107AE8
	Other	1	CYP1469A2
	Terpene	1	CYP157C29
	T3pks-Nrps	2	CYP107F8; CYP105D25
	Terpene	1	CYP157C42
	T2pks-Oligosaccharide	1	CYP113D5
	Lassopeptide-Nrps	2	CYP1278B2; CYP163B11
	Other	1	CYP121A3
	T1pks	2	CYP161A5; CYP105H3
	T1pks	1	CYP186D1
sxi	Terpene	1	CYP157C32
	T1pks-Nrps	2	CYP1029A4; CYP285A6
	Lantipeptide-Linaridin	1	CYP1223B1
	Linaridin-T1pks-Lassopeptide-Nrps	1	CYP107LF1
	Terpene	1	CYP183W1
	T3pks-Terpene-Nrps	1	CYP107F11
strm	Terpene-Nrps	1	CYP154Q2
	Lantipeptide-Terpene	2	CYP157C26; CYP134A3
	Other	1	CYP105DF1
	Thiopeptide	2	CYP2238A1; CYP1048A3
	Terpene-Otherks	2	CYP154D15; CYP157C27
	T1pks	2	CYP105L3; CYP1995C1
	Terpene	1	CYP251F1
strc	T1pks-Transatpks-Terpene	1	CYP105AC15
	Nrps	2	CYP107LC1; CYP105BK2
	T2pks	1	CYP1064A5
	Fused	1	CYP1341E2
	T3pks	2	CYP157A20; CYP154C13
	T3pks-Terpene-Otherks	1	CYP123D1
	T1pks-Nrps	1	CYP105BA2
	T3pks-Nrps	2	CYP165E2; CYP165B8
	Terpene	1	CYP157C32
samb	T2pks-Butyrolactone	1	CYP154K2
	Indole	1	CYP156B15

	Terpene	1	CYP170A1
	Oligosaccharide-T1pks-Nrps	2	CYP107EP1; CYP113B4
	Terpene	1	CYP157K5
	T1pks	2	CYP107EF1, CYP107EP1
	T2pks-Butyrolactone	1	CYP154K2
spri	Oligosaccharide-Ectoine-T2pks-Nrps-T1pks-Otherks	3	CYP154A22; CYP107EH1; CYP113C2
	Melanin	1	CYP124G6
	T2pks-Oligosaccharide-Nrps-Otherks	3	CYP154B6; CYP113C2, CYP107EH1
	T1pks-Ectoine-Otherks	1	CYP154A22
scz	Melanin	1	CYP124G2
	Bacteriocin-T1pks-Nrps	1	CYP107BX7
	Nrps	1	CYP154A18
	T3pks	1	CYP107F4
	Arylpolyene	1	CYP105D20
scx	Indole	1	CYP145C3
	Terpene	1	CYP180A29
	Terpene	1	CYP170A19
	Terpene	2	CYP157C39; CYP183B5
srw	T1pks	1	CYP166A3
	Bacteriocin-Nrps	1	CYP113K6
	Other	1	CYP162B2
	Other	2	CYP121A5; CYP154U7
	T2pks-T3pks-Otherks	1	CYP158A14
	Nrps	2	CYP107LB1; CYP105BK2
	Butyrolactone-Amglyccycl-T1pks-Nrps	1	CYP1037A2
	Terpene	1	CYP170A23
	Nrps	1	CYP2045A1
	Terpene	1	CYP180A28
strf	Nrps-T2pks-Otherks-T1pks-Phenazine	1	CYP105DD1
	Terpene	1	CYP170A16
	T2pks-Otherks	1	CYP105DD1
sle	T3pks-T1pks-Nrps	3	CYP107L35; CYP105BT1; CYP154B4
	Terpene	1	CYP157K4
	Lassopeptide	1	CYP102B20
	Nrps	1	CYP113K3
	Nrps-Transatpks-Terpene-Otherks	2	CYP107EG1; CYP105BR1

	Terpene-T1pks	3	CYP107Q3; CYP105D28; CYP166A2
	T1pks	3	CYP154Z1; CYP1416A1; CYP2266A2
	Terpene	2	CYP183A4; CYP161C4
	T1pks-Siderophore	2	CYP107L33; CYP105AC8
	T3pks	1	CYP107F10
	Terpene	1	CYP170A17
	T1pks	1	CYP1418A1
	T1pks	1	CYP1031A3
	Other	1	CYP107AM11
srn	Terpene	3	CYP251A3; CYP157C21; CYP158A20
	Indole	2	CYP245A6; CYP244A3
	Nrps	2	CYP159A23; CYP157B32
	Thiopeptide	2	CYP183H3; CYP183G3
	Terpene	1	CYP251F2
	Lantipeptide-Nrps	1	CYP1207A10
	T3pks-Butyrolactone	1	CYP158A19
	Nrps	2	CYP107E12; CYP285D1
spav	Indole	2	CYP156B15; CYP183J3
	Terpene	1	CYP170A1
	Terpene	2	CYP157K6; CYP105D33
slc	T1pks	1	CYP147F26
	Terpene-T1pks-Nrps	2	CYP107FH2; CYP107B26
	T1pks-Nrps	1	CYP163G1
	Thiopeptide	1	CYP147F27
	Butyrolactone	1	CYP107AE12
	Melanin-Nrps	1	CYP107FV4
	Other	1	CYP1005B7
	Nucleoside-Lassopeptide-Nrps	1	CYP157C36
	T3pks-Nrps	1	CYP107F15
strt	Phosphonate-Nrps	1	CYP1618A1
	Thiopeptide-Terpene	1	CYP180B6
	Butyrolactone	1	CYP105B73
	Terpene	1	CYP183X4
	T3pks	1	CYP158A25
	Other	1	CYP107P31
	Terpene	1	CYP170A18
	Bacteriocin-T1pks	1	CYP158A24
	Phosphoglycolipid	1	CYP107E32
	Bacteriocin-Terpene-Nrps	2	CYP1722A3; CYP1618A2

sclf	Terpene-T1pks-Nrps	3	CYP105BG1; CYP163B7; CYP251E1
	T3pks	1	CYP107F7
	Indole-Terpene-Nrps	2	CYP107NSF1; CYP107BY2
	T1pks-Nrps	1	CYP136E1
	Blactam-Nrps	1	CYP105M1
	Melanin	1	CYP124G5
	T1pks-Butyrolactone-Otherks	1	CYP107AL2
	T1pks	1	CYP154A14
sgs	Thiopeptide-Bacteriocin	1	CYP113V2
	Terpene	1	CYP170A10
	T1pks-Nrps	1	CYP247A3_ortholog
	T1pks	1	CYP105BC2
	Terpene	1	CYP180A26
	Lantipeptide-T1pks-Nrps	2	CYP208A9; CYP107BK3
	Nrps	1	CYP107KX1
	Other	2	CYP121A4; CYP154U6
	Terpene	1	CYP183X2
	Phosphonate-T3pks-Nrps-Ladderane	1	CYP158A21
stsi	Butyrolactone	1	CYP154K3
	Terpene	1	CYP170A15
	Nrps	2	CYP163B15; CYP113Z1
sls	Ladderane	1	CYP105B41
	Nrps	1	CYP163A5
	Nrps	1	CYP1424A1
	T3pks	1	CYP158A15
	Terpene	2	CYP183Y1; CYP157C22
	Terpene	1	CYP170A20
	Nrps-Siderophore	1	CYP107L32
	T2pks	1	CYP105B41
snr	T1pks	5	CYP105BV1; CYP1198A1; CYP107EM1; CYP1060A2; CYP147F29
	Terpene	1	CYP157C31
	T1pks	2	CYP105H1; CYP161A1
	Butyrolactone	1	CYP107AE10
	Other	1	CYP1248A3
	T1pks	1	CYP107EQ1
	T1pks	3	CYP107KZ1; CYP1420A1; CYP107A3

	T3pks	1	CYP107F9
	Thiopeptide-Bacteriocin	1	CYP113D4
	T1pks	1	CYP105AB15
	Transatpks-Nrps	3	CYP107CA2; CYP154D14; CYP105AC16
	Terpene	1	CYP105A7
	Lantipeptide-Nrps	2	CYP163B; CYP1278B1
	Terpene-T1pks	1	CYP105H8

Table 4. 4 Comparative analysis of secondary metabolite biosynthetic gene clusters and P450s that are part of these clusters in mycobacterial species.

Species code	**Cluster name**	**Number of P450s**	**P450 name**
maf	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mto	T3pks-T1pks	1	CYP139A1
	Nrps	1	CYP144A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mtf	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mra	T3pks-T1pks	1	CYP139A1
	T1pks	1	CYP139A1
	Other	2	CYP124A1; CYP128A1
mtu	T3pks-T1pks	1	CYP139A1
	Nrps	1	CYP144A1
	Other	2	CYP124A1; CYP128A1
mtul	T3pks-T1pks	1	CYP139A1
mtb	Other	3	CYP121A1; CYP128A1; CYP124A1
	Nrps	1	CYP144A1
	T3pks-T1pks	1	CYP139A1
mtz	Other	3	CYP121A1; CYP128A1; CYP124A1
	Nrps	1	CYP144A1
	T3pks-T1pks	1	CYP139A1
mtk	Other	3	CYP121A1; CYP128A1; CYP124A1
	Nrps	1	CYP144A1
	T3pks-T1pks	1	CYP139A1
mtg	Other	2	CYP124A1; CYP102B25
mtc	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mte	T3pks-T1pks	1	CYP139A1
	T1pks	3	CYP124A1; CYP128A1; CYP121A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mtub	T3pks-T1pks	1	CYP139A1
mtj	T3pks-T1pks	1	CYP139A1
	Nrps	1	CYP144A1
	Other	3	CYP124A1; CYP128A1; CYP121A1

mtuc	T3pks	1	CYP139A1
	Other	2	CYP124A1; CYP128A1
mtx	T3pks-T1pks	1	CYP139A1
	Nrps	1	CYP144A1
mtuh	T3pks	1	CYP139A1
mtn	T3pks-T1pks	1	CYP139A1
mtd	T3pks-T1pks	1	CYP139A1
	Other	2	CYP124A1; CYP128A1
mce	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mcq	T3pks-T1pks	1	CYP139A1
	Other	2	CYP124A1; CYP128A1
mcx	T3pks-T1pks	1	CYP139A1
	Nrps	1	CYP144A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mbo	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mbb	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mbk	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mbm	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mbt	T3pks-T1pks	1	CYP139A1
	Other	3	CYP124A1; CYP128A1; CYP121A1
mab	T1pks-Nrps	1	CYP1110B1
	T2pks	1	CYP153A
	Nrps	1	CYP1128A
	Nrps	1	CYP135B
mabb	Nrps	1	CYP1128A
	Nrps	1	CYP135B
mabl	Nrps	1	CYP1128A
	Nrps	1	CYP135B
maz	T1pks-Nrps	1	CYP1110B1
	T2pks	1	CYP153A
	Nrps	1	CYP1128A
	Nrps	1	CYP135B
may	T1pks-Nrps	1	CYP1110B1
	T2pks	1	CYP153A

	Nrps	1	CYP1128A
	Nrps	1	CYP135B
mys	Nrps	1	CYP135B
	Nrps	1	CYP1128A
mav	Nrps	1	CYP187A
	T1pks	1	CYP150A
	T1pks	1	CYP105NSF1
	T3pks-T1pks	1	CYP139A
mpa	T3pks-T1pks	1	CYP139A
	T1pks	1	CYP105NSF1
	T1pks-Nrps	1	CYP150A
	Nrps	1	CYP1034A
	T3pks	1	CYP187A
mao	T3pks	1	CYP187A
	Nrps	1	CYP1034A
	T1pks-Nrps	1	CYP150A
	T1pks	1	CYP105NSF1
	T3pks-T1pks	1	CYP139A
	T1pks	1	CYP144A
mia	T3pks	1	CYP187A
	T1pks-Nrps	1	CYP150A
	T1pks	2	CYP279A; CYP105U
	Other	1	CYP1122A1
mit	T3pks	2	CYP187A; CYP150A
	T1pks-Nrps	1	CYP150A
	T1pks	2	CYP279A; CYP105U
	Other	1	CYP1128A
mie	T3pks-T1pks	1	CYP187A
	T1pks	1	CYP150A
	T1pks	2	CYP279A; CYP105U
mmm	T3pks	1	CYP187A
	T1pks-Nrps	1	CYP150A
	T1pks	2	CYP279A; CYP105U
mid	T3pks	1	CYP1123A1
	Nrps	1	CYP126NSF1
myv	T1pks-Nrps	1	CYP135B
mli	Nrps	1	CYP143A3
	Nrps	2	CYP140A5; CYP125A6
	Other	1	CYP147G

	T3pks-T1pks	1	CYP139A3
mmae	Nrps	1	CYP185A4
	T3pks-T1pks	1	CYP139A3
	Nrps	1	CYP143A3
	Nrps	2	CYP140A5; CYP125A6
	Other	1	CYP147G1
	T3pks	2	CYP187A; CYP187A
	Other	1	CYP164A3
mmal	T3pks	1	CYP187A
	T1pks-Nrps	1	CYP150A
	T1pks	3	CYP279A; CYP279A; CYP105U
	Other	2	CYP105Q; CYP189A
mmv	Nrps	1	CYP1128A
mva	T1pks-Nrps	1	CYP138C1
msb	T3pks	1	CYP185A1
mcb	Arylpolyene	3	CYP187A; CYP150A; CYP189A
	T1pks-Nrps	1	CYP138C
	T1pks	1	CYP292A
mgi	Terpene	1	CYP188A
	T1pks-Nrps	1	CYP138C2
	T1pks-Nrps	3	CYP189A; CYP150A; CYP187A
msp	Terpene	1	CYP188A
	T1pks-Nrps	1	CYP138C2
	Other	3	CYP189A; CYP150A; CYP187A
msa	T3pks	1	CYP135B
	Other	2	CYP187A; CYP150A
	T1pks-Nrps	1	CYP136NSF2
mrh	T1pks	2	CYP189A; CYP102NSF1
	T1pks-Nrps	1	CYP1121A1
	Nrps	1	CYP125A
	Nrps	1	CYP189A
	Arylpolyene	1	CYP124A
	Arylpolyene	1	CYP144A
mne	Other	1	CYP161NSF1

An interesting pattern was observed when comparing the number of P450s that are part of different types of secondary metabolite BGCs, revealing that dominant secondary metabolite BGCs are not necessarily dominant in terms of having P450s (Figure 4.5). In *Streptomyces* species, the secondary metabolite BGC, T1pks, the fourth dominant BGC (Figure 4.3A), has the highest number of P450s (82 P450s) (Figure 4.5A). Terpene, despite the dominant BGC in *Streptomyces* (Figure 4.3A), has the second highest number of P450s (Figure 4.5A). The same pattern was observed in mycobacterial species (Figure 4.5B) where 'others', the second dominant BGC (Figure 4.3B), have the highest number of P450s compared to Nrps, the dominant BGC (Figure 4.3B), which has the second highest number of P450s (Figure 4.5B).

Among 88 P450 families that are part of different secondary metabolite BGCs, some P450 families are highly dominant in *Streptomyces* species (Figure 4.5C and Table 4.3), indicating their key role in the synthesis of different secondary metabolites. These P450 families (Figure 4.5C) were found to be the same that are highly populated in *Streptomyces* species, with some exceptions. This strongly indicates that these P450 families provide an advantage to *Streptomyces* species by generating diverse secondary metabolites, thus letting these species thrive in nature. Despite P450s families such as CYP102, CYP159, CYP125, CYP1035, CYP1038 and CYP155 being highly populated in *Streptomyces* species, their percentage contribution as part of secondary metabolite BGCs is quite negligible (Table 4.5), indicating further selectivity in terms of which P450s should be part of secondary metabolite BGCs. Mycobacterial species' secondary metabolite BGC P450 profiles (Figure 4.5D) are contrasted with *Streptomyces* species, where the dominant P450 families are not necessarily dominant as part of secondary metabolite BGCs. Ten P450 families, namely CYP51, CYP123, CYP125, CYP130, CYP135, CYP136, CYP138, CYP140, CYP144 and CYP1128, are conserved and highly populated across 60 mycobacterial species (Parvez *et al*., 2016). However, none of these P450 families is dominant as part of different secondary metabolite BGCs (Figure 4.5D and Table 4.5). In fact, P450 families such as CYP123, CYP130 and CYP1128 are not found to be part of any secondary metabolite BGCs and P450 families such as CYP136, CYP125, CYP138 and CYP140 are rarely present as part of different secondary metabolite BGCs (Table 4.4). Their percentage contribution as part of secondary metabolite BGCs is thus very low (Figure 4.5D and Table 4.5). The CYP139 P450 family was found to be the dominant family as part of secondary metabolite BGCs (Figure 4.5D). Although eight P450 families, namely CYP124, CYP121, CYP105, CYP125, CYP102, CYP147, CYP136 and CYP161, which are part of secondary metabolite BGCs, were commonly found between the genera *Streptomyces* and *Mycobacterium*, the number of P450s in these families was found to be different (Table 4.5).

Table 4. 5 Comparative analysis of P450s that are part of secondary metabolite biosynthetic gene clusters between the genera *Streptomyces* and *Mycobacterium*. The P450 families commonly found in both genera are highlighted in bold font.

Streptomyces		***Mycobacterium***	
P450 family	No. of P450s	P450 family	No. of P450s
CYP107	127	CYP139	32
CYP105	**95**	**CYP124**	**24**
CYP157	27	CYP128	22
CYP154	23	**CYP121**	**17**
CYP163	22	CYP187	14
CYP170	21	CYP150	13
CYP113	19	CYP144	10
CYP183	19	**CYP105**	**9**
CYP158	17	CYP1128	8
CYP124	**12**	CYP135	8
CYP180	11	CYP189	6
CYP156	10	CYP279	6
CYP161	**10**	CYP138	4
CYP147	**9**	CYP1110	3
CYP285	7	**CYP125**	**3**
CYP251	6	CYP153	3
CYP121	**5**	**CYP102**	**2**
CYP162	5	CYP1034	2
CYP1029	4	CYP140	2
CYP1189	4	CYP143	2
CYP125	**3**	**CYP147**	**2**
CYP1278	3	CYP185	2
CYP1423	3	CYP188	2
CYP178	3	CYP1121	1
CYP184	3	CYP1122	1
CYP247	3	CYP126	1
CYP1005	2	**CYP136**	**1**
CYP1013	2	**CYP161**	**1**
CYP1035	2	CYP164	1
CYP1037	2	CYP292	1
CYP1048	2	CYP1123	1
CYP1060	2		
CYP1190	2		
CYP1191	2		
CYP1192	2		
CYP1198	2		

CYP1420	2		
CYP155	2		
CYP1618	2		
CYP165	2		
CYP166	2		
CYP171	2		
CYP179	2		
CYP181	2		
CYP194	2		
CYP208	2		
CYP245	2		
CYP102	**1**		
CYP1031	1		
CYP1038	1		
CYP1039	1		
CYP1041	1		
CYP1056	1		
CYP1057	1		
CYP1058	1		
CYP1059	1		
CYP1064	1		
CYP1193	1		
CYP1194	1		
CYP1196	1		
CYP1197	1		
CYP1207	1		
CYP1223	1		
CYP122	1		
CYP123	1		
CYP1248	1		
CYP1274	1		
CYP1341	1		
CYP134	1		
CYP136	**1**		
CYP1373	1		
CYP1416	1		
CYP1418	1		
CYP1424	1		
CYP145	1		
CYP1469	1		
CYP146	1		
CYP159	1		
CYP1722	1		
CYP186	1		
CYP1995	1		

CYP2045	1		
CYP2238	1		
CYP2266	1		
CYP244	1		
CYP246	1		
CYP268	1		
CYP283	1		

4.3. Functional relevance of secondary metabolite biosynthetic gene clusters and associated P450s in *Streptomyces* and *Mycobacterium*

Among the P450 families involved in secondary metabolite production, 88 P450 families are uniquely present in *Streptomyces* species compared to mycobacterial species (Figure 4.1 and Table 4.5). P450 families, namely CYP105, CYP107, CYP161, and CYP183, which are highly populated in *Streptomyces* species compared to mycobacterial species, were found to be involved in secondary metabolite production (Figure 4.5C). This strongly suggests that these P450 families have been populated in *Streptomyces* species owing to their importance and necessity in secondary metabolite production. Therefore, the diversity among these P450 families, judged by the large number of P450 subfamilies, presumably serves to increase the resultant chemical diversity further across different *Streptomyces* species. It is well established that P450s are one of the key enzymes contributing to the diversity of secondary metabolites in organisms (Greule *et al*., 2018). In contrast to the P450 families highly populated in *Streptomyces* species, P450 families that are highly populated in mycobacterial species such as CYP125, CYP124, CYP108, CYP140 and CYP268 are involved in steroid (cholesterol) and hydrocarbon (lipids, alkenes, long chain acetate and ketone) hydroxylation (Hasemann *et al*., 1994, Mve-Obiang *et al*., 2005, Johnston *et al*., 2009, McLean *et al*., 2009, Ouellet *et al*., 2010, Child *et al*., 2018), suggesting that these P450 families possibly help mycobacterial species to assimilate the host compounds. It is noteworthy that results from this study revealed that some of these P450 families are rarely (CYP125 and CYP140) or not at all (CYP268) part of secondary metabolite BGCs in mycobacterial species (Table 4.5).

References

CHILD, S. A., NAUMANN, E. F., BRUNING, J. B. & BELL, S. G. 2018. Structural and functional characterisation of the cytochrome P450 enzyme CYP268A2 from *Mycobacterium marinum*. *Biochem J,* 475**,** 705-722.

GREULE, A., STOK, J. E., DE VOSS, J. J. & CRYLE, M. J. 2018. Unrivalled diversity: the many roles and reactions of bacterial cytochromes P450 in secondary metabolism. *Nat Prod Rep,* 35**,** 757-791.

HASEMANN, C. A., RAVICHANDRAN, K. G., PETERSON, J. A. & DEISENHOFER, J. 1994. Crystal structure and refinement of cytochrome P450terp at 2.3 A resolution. *J Mol Biol,* 236**,** 1169-85.

HWANG, K.-S., KIM, H. U., CHARUSANTI, P., PALSSON, B. Ø. & LEE, S. Y. 2014. Systems biology and biotechnology of *Streptomyces* species for the production of secondary metabolites. *Biotechnology Advances,* 32**,** 255-268.

JOHNSTON, J. B., KELLS, P. M., PODUST, L. M. & ORTIZ DE MONTELLANO, P. R. 2009. Biochemical and structural characterization of CYP124: a methyl-branched lipid omega-hydroxylase from *Mycobacterium tuberculosis*. *Proc Natl Acad Sci U S A,* 106**,** 20687-92.

MCLEAN, K. J., LAFITE, P., LEVY, C., CHEESMAN, M. R., MAST, N., PIKULEVA, I. A., LEYS, D. & MUNRO, A. W. 2009. The structure of *Mycobacterium tuberculosis* CYP125: molecular basis for cholesterol binding in a P450 needed for host infection. *J Biol Chem,* 284**,** 35524-33.

MVE-OBIANG, A., LEE, R. E., UMSTOT, E. S., TROTT, K. A., GRAMMER, T. C., PARKER, J. M., RANGER, B. S., GRAINGER, R., MAHROUS, E. A. & SMALL, P. L. 2005. A newly discovered mycobacterial pathogen isolated from laboratory colonies of *Xenopus* species with lethal infections produces a novel form of mycolactone, the *Mycobacterium ulcerans* macrolide toxin. *Infect Immun,* 73**,** 3307-12.

OUELLET, H., JOHNSTON, J. B. & ORTIZ DE MONTELLANO, P. R. 2010. The *Mycobacterium tuberculosis* cytochrome P450 system. *Arch Biochem Biophys,* 493**,** 82-95.

PARVEZ, M., QHANYA, L. B., MTHAKATHI, N. T., KGOSIEMANG, I. K., BAMAL, H. D., PAGADALA, N. S., XIE, T., YANG, H., CHEN, H., THERON, C. W., MONYAKI, R., RASELEMANE, S. C., SALEWE, V., MONGALE, B. L., MATOWANE, R. G., ABDALLA, S. M., BOOI, W. I., VAN WYK, M., OLIVIER, D., BOUCHER, C. E., NELSON, D. R., TUSZYNSKI, J. A., BLACKBURN, J. M., YU, J. H., MASHELE, S. S., CHEN, W. & SYED, K. 2016. Molecular evolutionary dynamics of cytochrome P450 monooxygenases across kingdoms: special focus on *Mycobacterial* P450s. *Sci Rep,* 6**,** 33099.

WEBER, T., BLIN, K., DUDDELA, S., KRUG, D., KIM, H. U., BRUCCOLERI, R., LEE, S. Y., FISCHBACH, M. A., MULLER, R., WOHLLEBEN, W., BREITLING, R., TAKANO, E. & MEDEMA, M. H. 2015. antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res,* 43**,** W237-43.

CHAPTER 5: CONCLUSION AND FUTURE PERSPECTIVES

Streptomyces species are generally saprophytes living in soil or decaying vegetation, where the rule of survival of the fittest applies. Some studies reported symbiosis in *Streptomyces,* including parasitism. In response to this type of ecological niche, *Streptomyces* adapted to produce different secondary metabolites, which are harmful to other bacteria and thus *Streptomyces* species, can survive and utilise the readily available carbon sources in their environment. In contrast to *Streptomyces* species, mycobacterial species are well-known pathogens of humans and other animals, despite some saprophytes being present in this genus. The pathogenic nature of mycobacterial species forced them to adapt to lifestyles such as living in a host where evading the host's immune system and utilising host carbon sources for survival are the prime tasks. It is clear that different lifestyles influenced the P450 profiles in *Streptomyces* and *Mycobacterium,* hence the differences observed between the two genera in terms of number and type of secondary metabolite BGCs and P450s that are associated with secondary metabolite BGCs. The presence of quite a large number of polyketide synthase BGCs (identified in this study) that are involved in the production of unique lipids and glycolipid conjugates further strengthens the argument that *Mycobacterium* P450s are involved in lipid metabolism. The saprophytic and symbiotic lifestyle of *Streptomyces* resulted in the highest diversity of secondary metabolite BGCs and P450s, thus helping these organisms to generate chemically diverse secondary metabolites to adapt to different ecological niches. For this reason, *Streptomyces* species have been found to have large and diverse secondary metabolite BGCs and P450s compared to mycobacterial species. Future work involves culturing of *Streptomyces* species and mycobacterial species that are identified to produce the highest number of different types of secondary metabolites and assessing the properties of secondary metabolites produced by these species.