

Discovery, Biosynthesis and Bioengineering of Novel Antibiotics from Bacteria

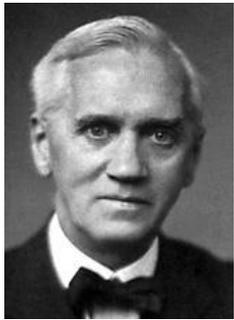
Dr. Matthew Jenner

RSC Toxicology Group: Tackling Antimicrobial Resistance
September 17th 2018



Traditional Approach for Bioactive Natural Product Discovery

'Grind and Find' Methodology



Alexander Fleming



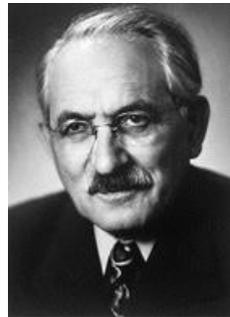
Howard Florey



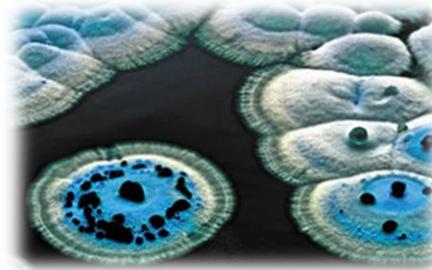
Dorothy Hodgkin



Ernst Chain



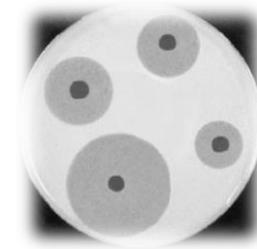
Selman Waksman



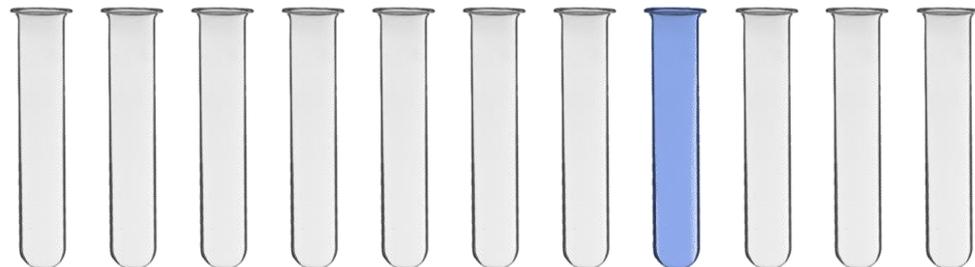
Extraction



Extract Bioactivity?



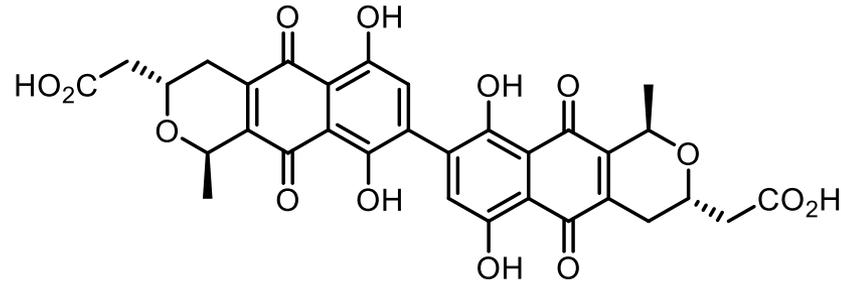
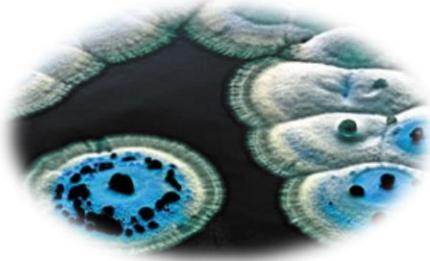
Metabolite Separation & Purification



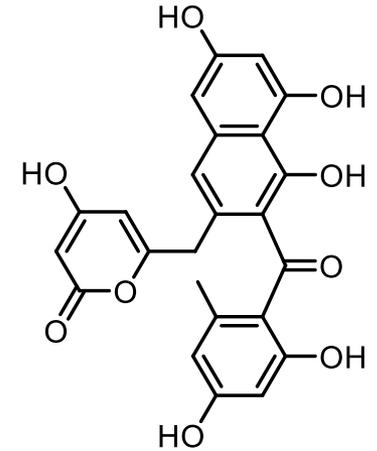
Identify Bioactive Fraction → ANTIBIOTIC!

Streptomyces coelicolor – A Prolific Producer of Specialised Metabolites

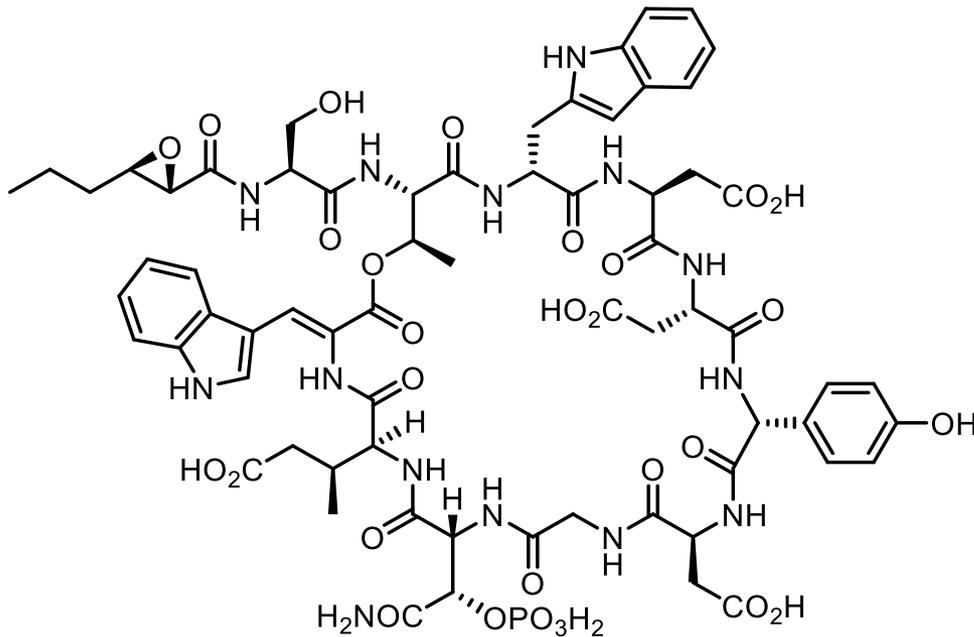
'Grind and Find' Methodology



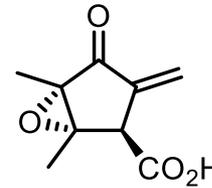
actinorhodins (*act*)



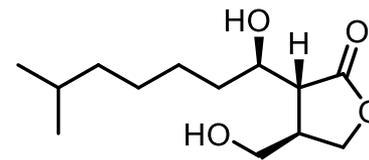
grey spore pigment (*whiE*)



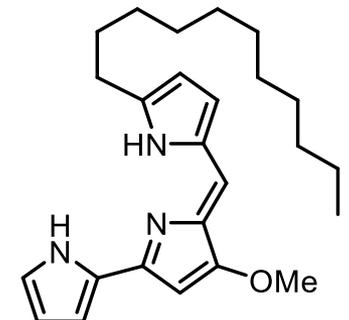
calcium-dependent antibiotics (*cda*)



methylenomycins (*mmy*)



***S. coelicolor* butyrolactones (*scb*)**



undecylprodigiosin (*red*)

Streptomyces coelicolor – A Prolific Producer of Specialised Metabolites

'Grind and Find' Methodology

articles

Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2)

S. D. Bentley*, K. F. Chater†, A.-M. Cerdeño-Tárraga*, G. L. Challis†‡, N. R. Thomson*, K. D. James*, D. E. Harris*, M. A. Quail*, H. Kieser†, D. Harper*, A. Bateman*, S. Brown*, G. Chandra†, C. W. Chen§, M. Collins*, A. Cronin*, A. Fraser*, A. Goble*, J. Hidalgo*, T. Hornsby*, S. Howarth*, C.-H. Huang§, T. Kieser†, L. Larke*, L. Murphy*, K. Oliver*, S. O'Neill*, E. Rabinowitsch*, M.-A. Rajandream*, K. Rutherford*, S. Rutter*, K. Seeger*, D. Saunders*, S. Sharp*, R. Squares*, S. Squares*, K. Taylor*, T. Warren*, A. Wietzorrek†, J. Woodward*, B. G. Barrell*, J. Parkhill* & D. A. Hopwood†

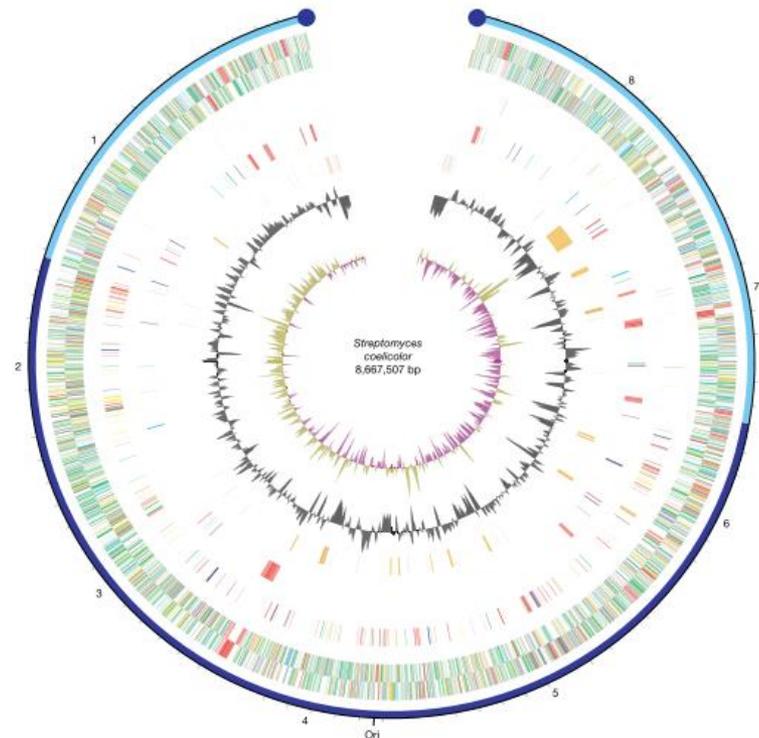
* The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

† John Innes Centre, Norwich Research Park, Colney, Norwich NR4 7UH, UK

‡ Department of Chemistry, University of Warwick, Coventry CV4 7AL, UK

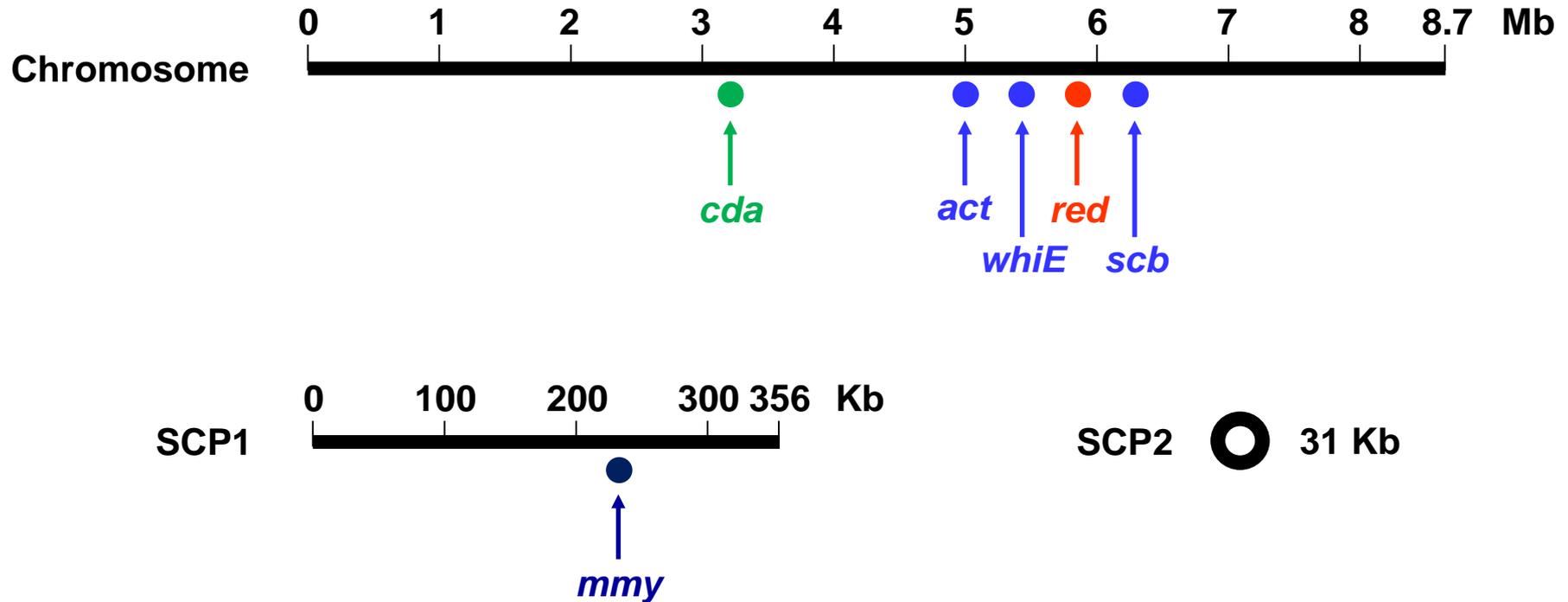
§ Institute of Genetics, National Yang-Ming University, Shih-Pai, Taipei 112, Taiwan

Streptomyces coelicolor is a representative of the group of soil-dwelling, filamentous bacteria responsible for producing most natural antibiotics used in human and veterinary medicine. Here we report the 8,667,507 base pair linear chromosome of this organism, containing the largest number of genes so far discovered in a bacterium. The 7,825 predicted genes include more than 20 clusters coding for known or predicted secondary metabolites. The genome contains an unprecedented proportion of regulatory genes, predominantly those likely to be involved in responses to external stimuli and stresses, and many duplicated gene sets that may represent 'tissue-specific' isoforms operating in different phases of colonial development, a unique situation for a bacterium. An ancient synteny was revealed between the central 'core' of the chromosome and the whole chromosome of pathogens *Mycobacterium tuberculosis* and *Corynebacterium diphtheriae*. The genome sequence will greatly increase our understanding of microbial life in the soil as well as aiding the generation of new drug candidates by genetic engineering.



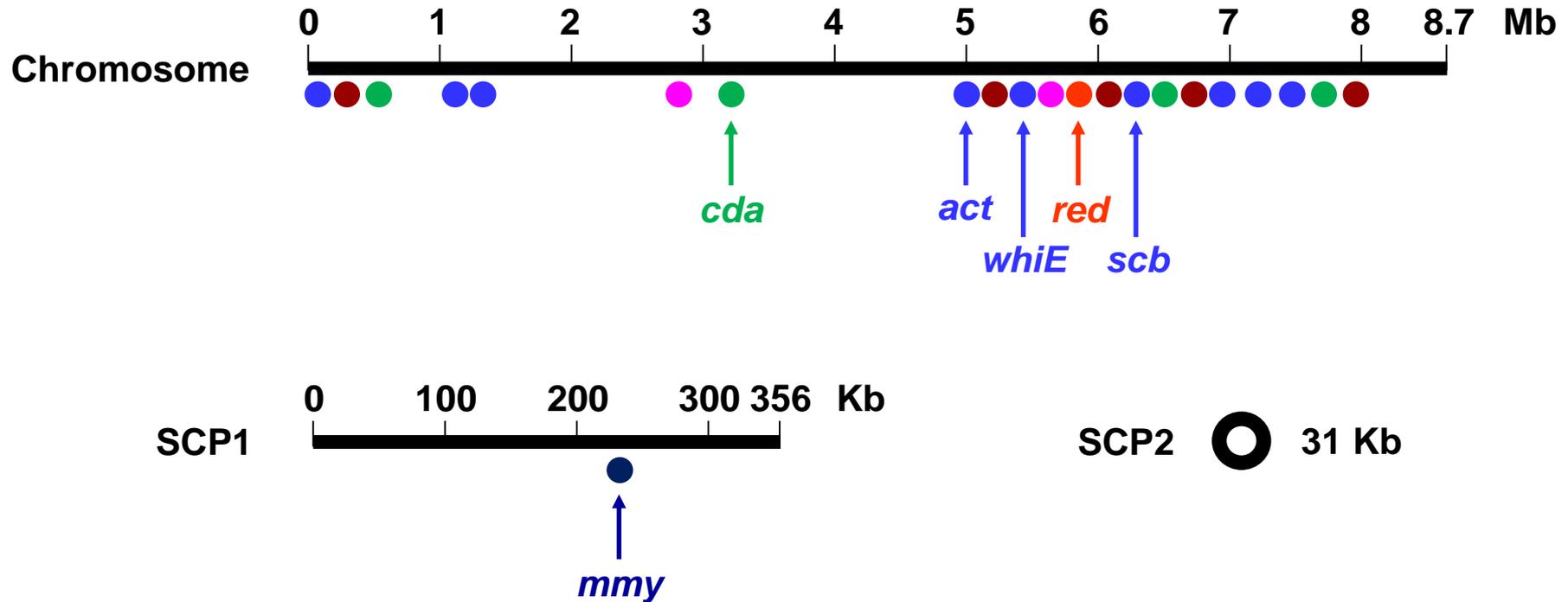
Streptomyces coelicolor – A Prolific Producer of Specialised Metabolites

'Grind and Find' Methodology



Streptomyces coelicolor – A Prolific Producer of Specialised Metabolites

'Grind and Find' Methodology

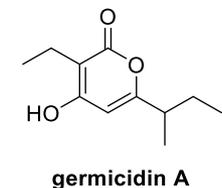
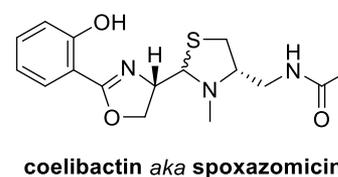
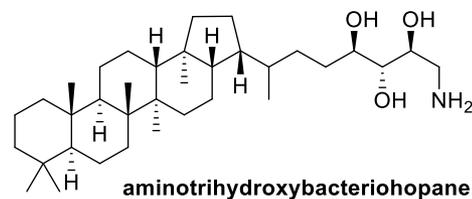
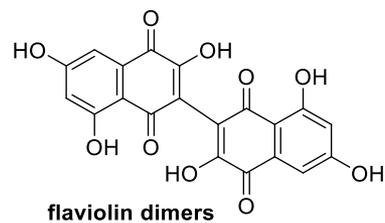
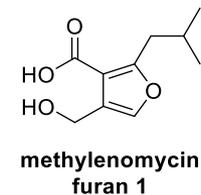
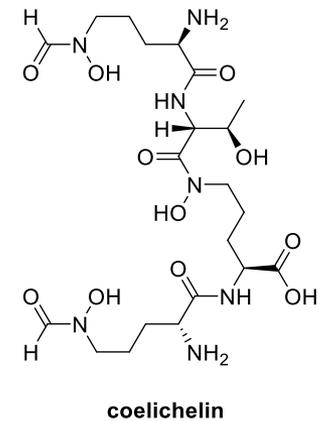
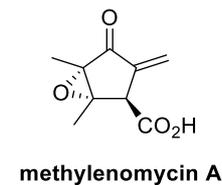
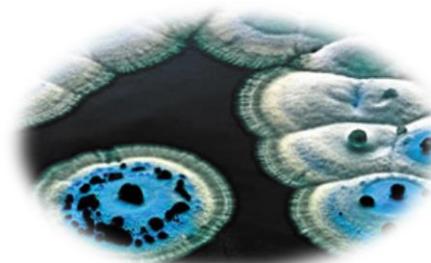
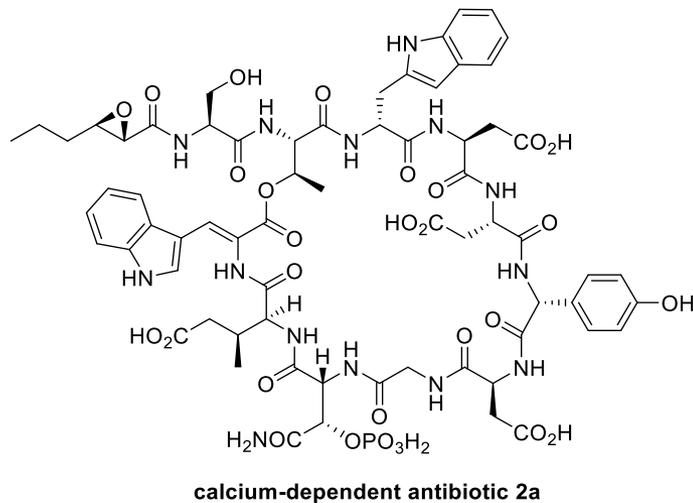
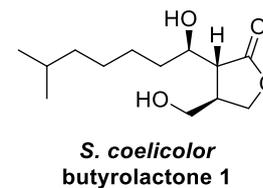
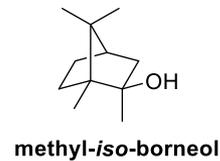
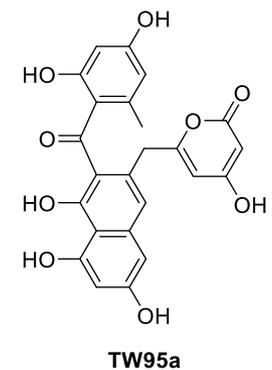
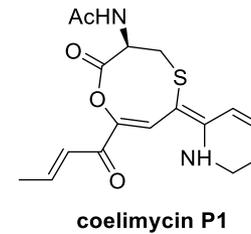
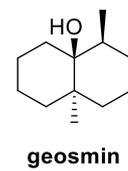
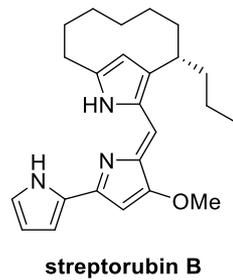
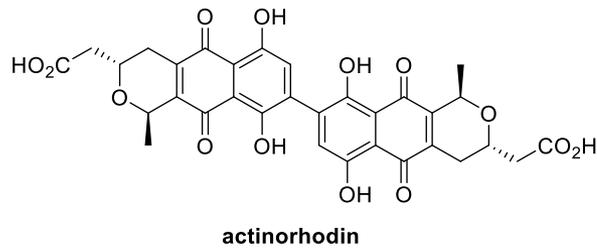


- terpene synthase
- nonribosomal peptide synthetase (NRPS)
- NRPS-independent siderophore synthetase

- polyketide synthase (PKS)
- hybrid NRPS / PKS / α -oxamine synthase
- hybrid PKS / butenolide synthase

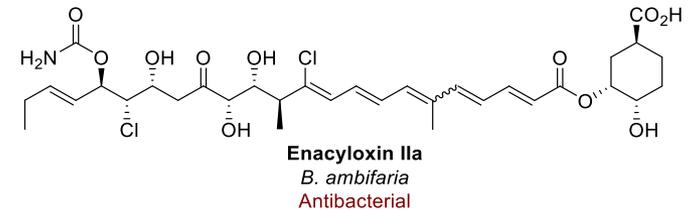
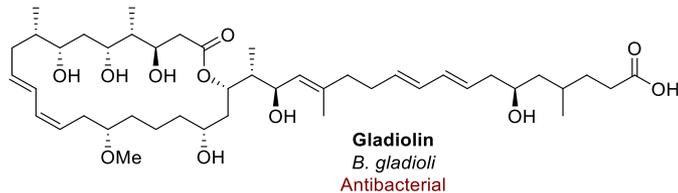
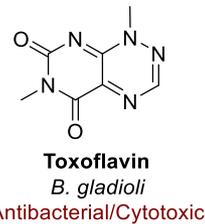
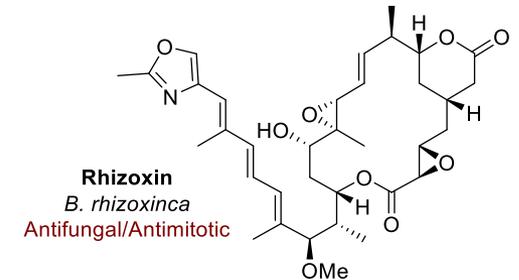
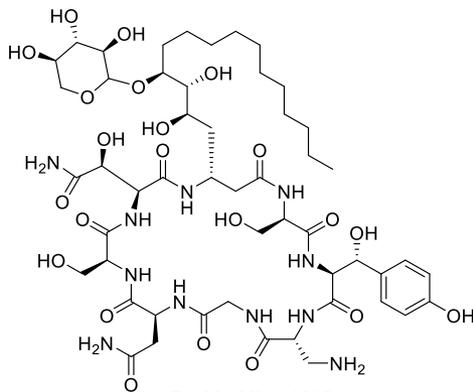
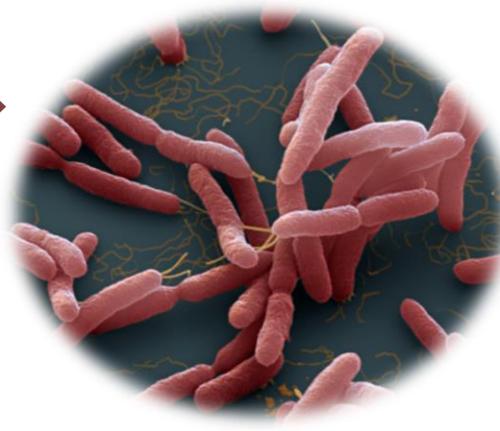
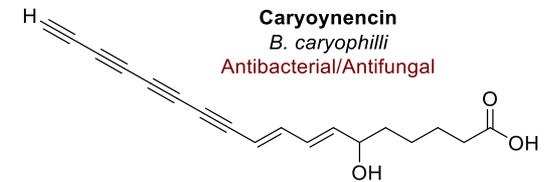
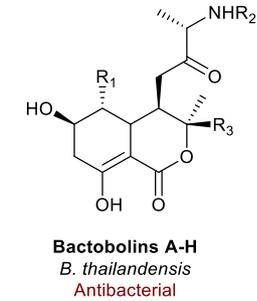
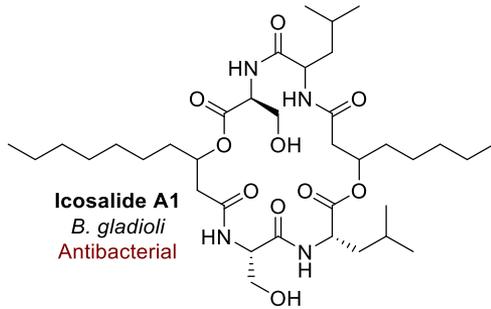
Streptomyces coelicolor – A Full Metabolic Profile

Application of Genomics-Based Discovery



Natural Products from *Burkholderia*

Diverse Metabolic Arsenal

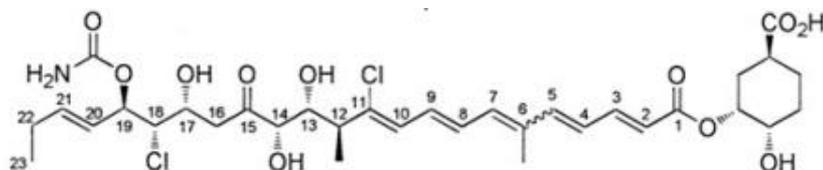
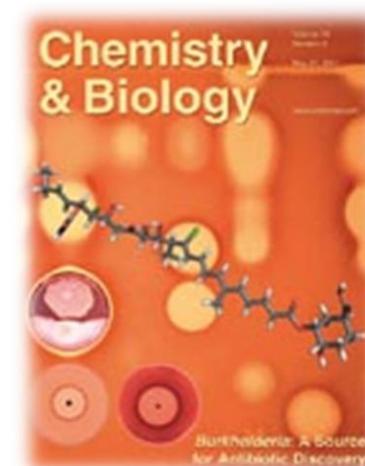
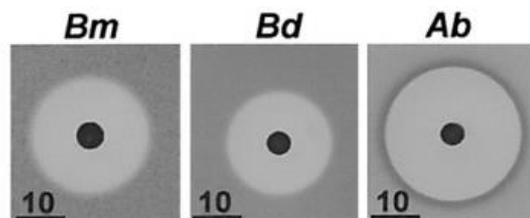


Exploiting *Burkholderia* for Novel Antimicrobial Compounds

'An untapped source of novel bioactive metabolites'

Enacyloxins Are Products of an Unusual Hybrid Modular Polyketide Synthase Encoded by a Cryptic *Burkholderia ambifaria* Genomic Island

Eshwar Mahenthiralingam,^{1,*} Lijiang Song,² Andrea Sass,¹ Judith White,¹ Ceri Wilmot,¹ Angela Marchbank,¹ Othman Boaisha,¹ James Paine,³ David Knight,³ and Gregory L. Challis^{2,*}



enacyloxin IIa (Δ -4,5 = *E*)
iso-enacyloxin IIa (Δ -4,5 = *Z*)

Acinetobacter baumannii (MIC 2 μ g/mL)

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CARDIFF
UNIVERSITY

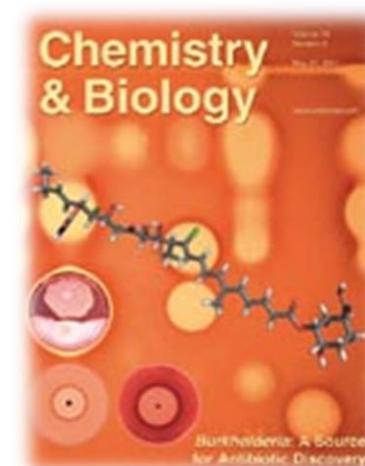
wellcome trust
sanger
institute

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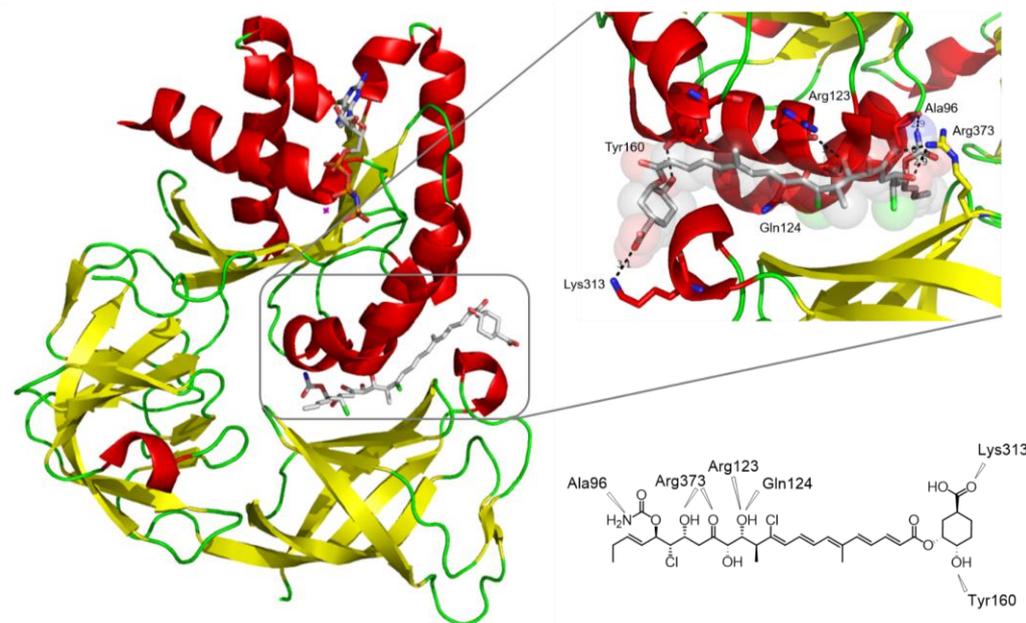
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CARDIFF
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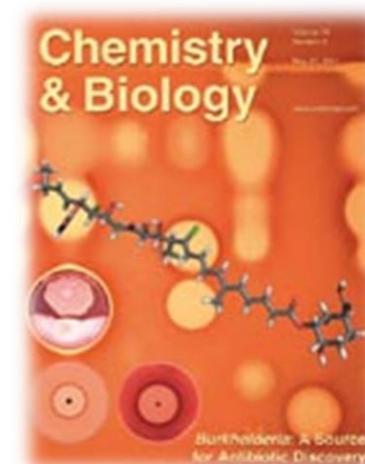


Exploiting *Burkholderia* for Novel Antimicrobial Compounds

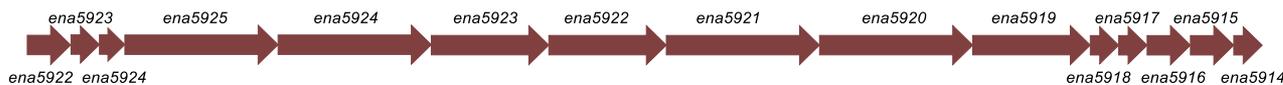
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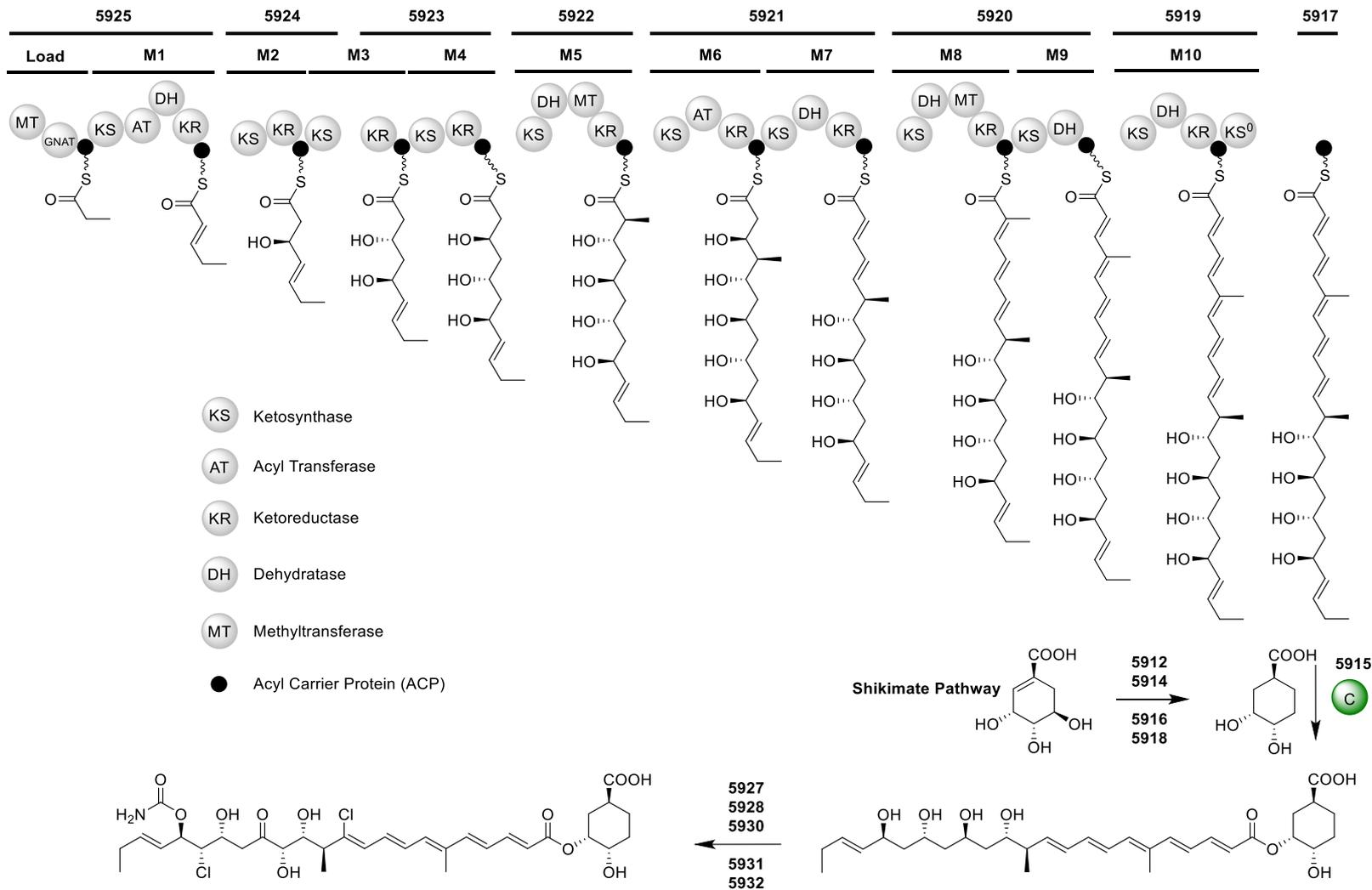


Enacyloxin Biosynthetic Gene Cluster



Biosynthesis of Enacyloxin IIa

Hybrid *cis/trans*-AT Modular Polyketide Synthase



Screening Metabolites from *Burkholderia gladioli* BCC0238

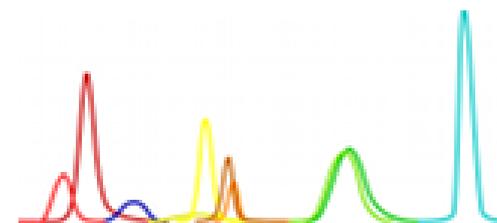
A Highly Bioactive Strain



Cystic fibrosis patient
Minneapolis, USA.
1996

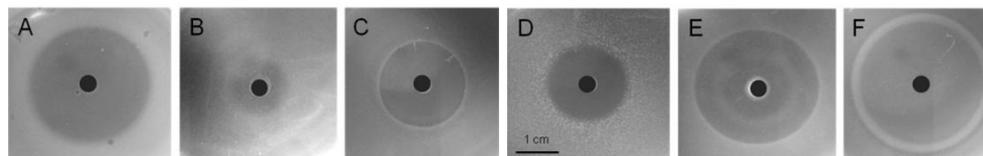


Burkholderia gladioli
BCC0238



Metabolite Screening

B. gladioli BCC0238 overlays



MRSA

B. multivorans

B. subtilis

R. mannitolilytica

E. faecium

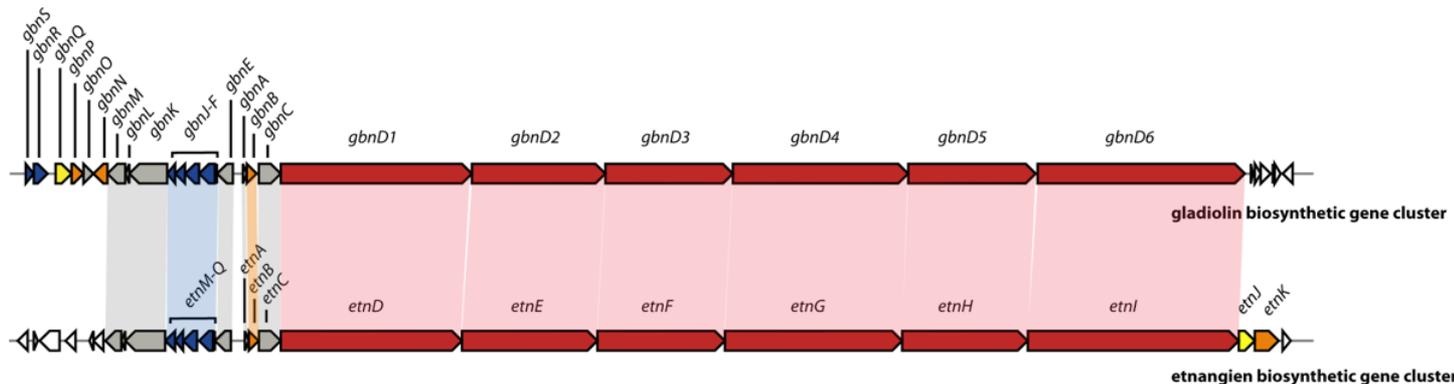
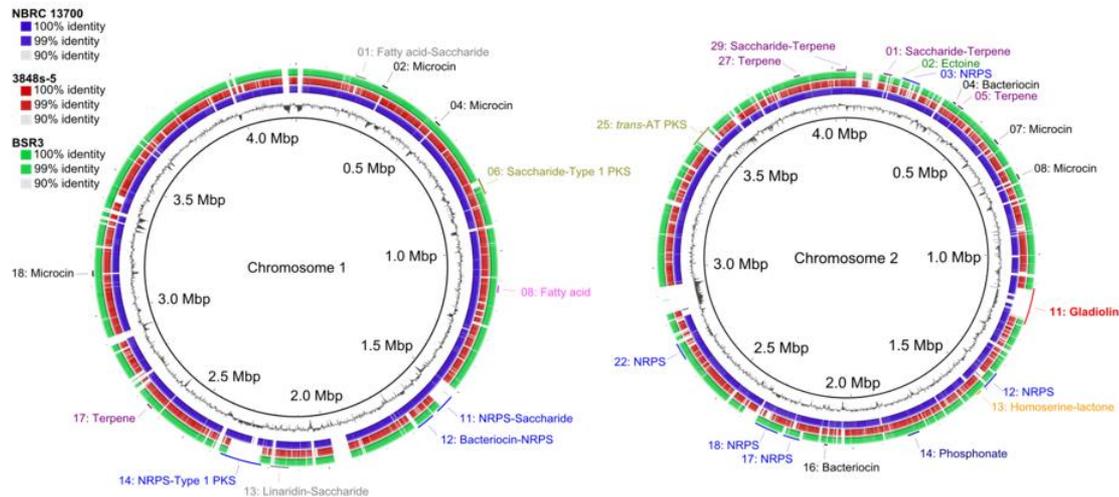
C. albicans

Genome Sequencing of *Burkholderia gladioli* BCC0238

Biosynthetic Gene Cluster Analysis

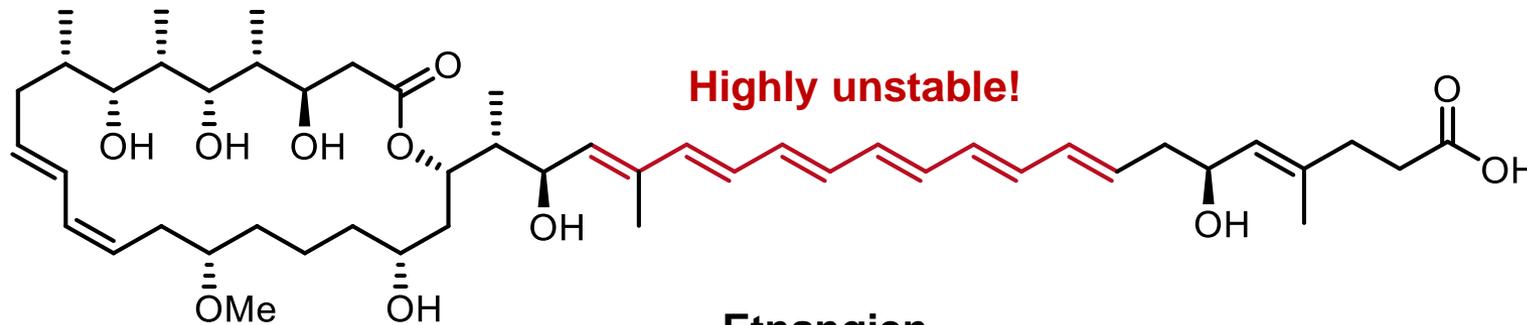
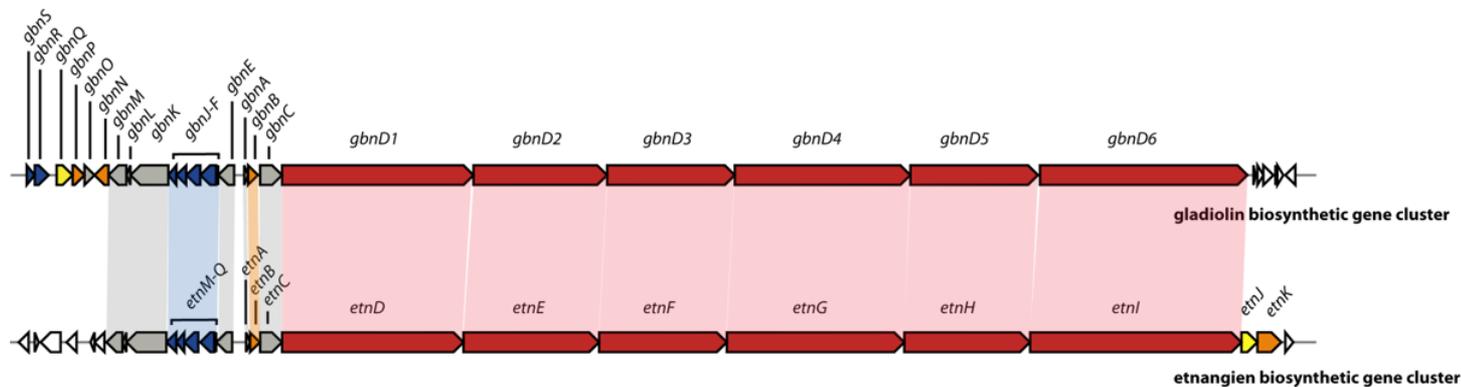


Burkholderia gladioli
BCC0238



Discovery of Gladiolin: A Novel Macrolide Antibiotic

Structure Elucidation and Comparison to Etnangien



Highly unstable!

Etnangien

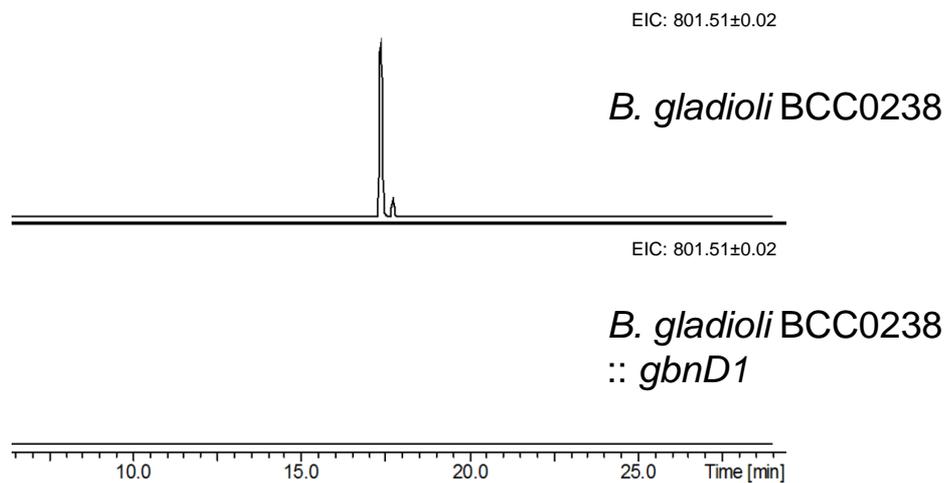
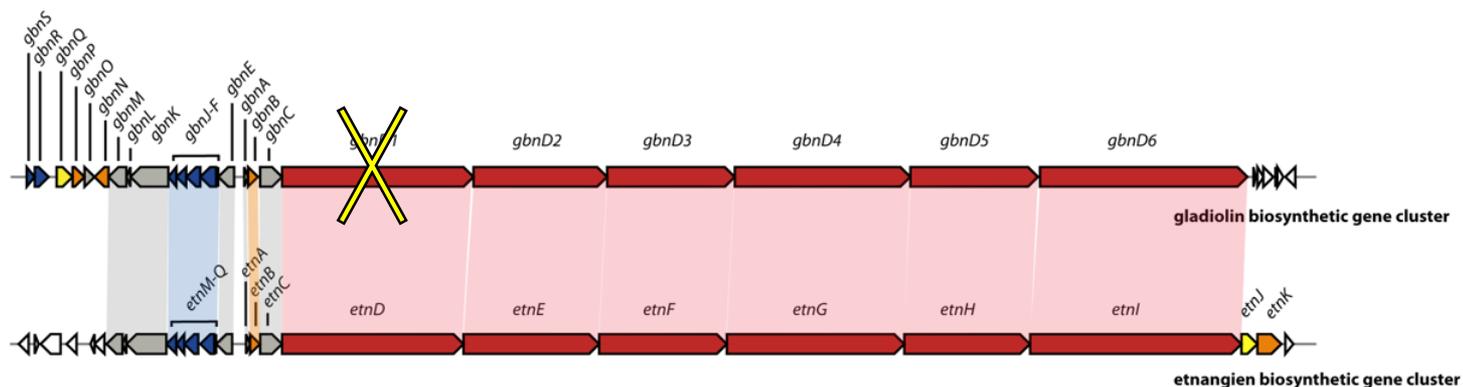
Sorangium cellulosum

Mycobacterium smegmatis (MIC 1 $\mu\text{g/mL}$)

Inhibits *E. coli* RNA Polymerase

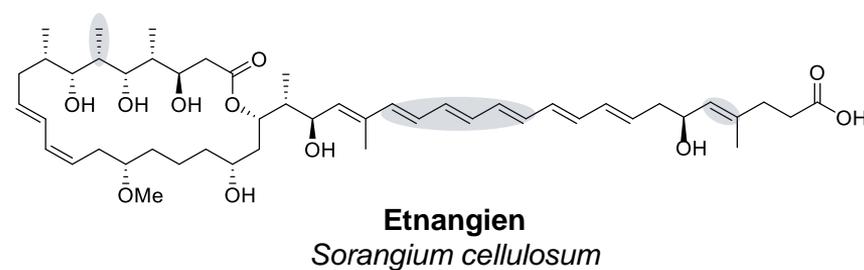
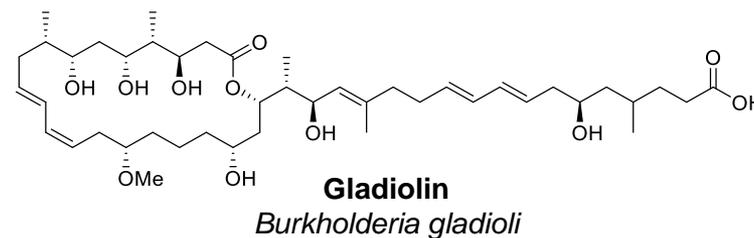
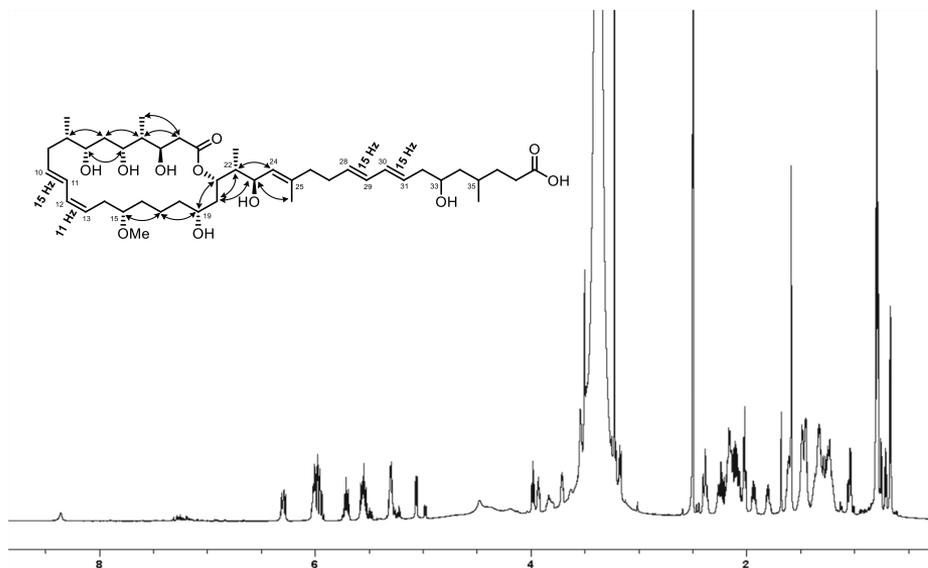
Genome Sequencing of *Burkholderia gladioli* BCC0238

Insertional Mutation Abolishes Gladiolin Production



Discovery of Gladiolin: A Novel Macrolide Antibiotic

Structure Elucidation and Comparison to Etnangien

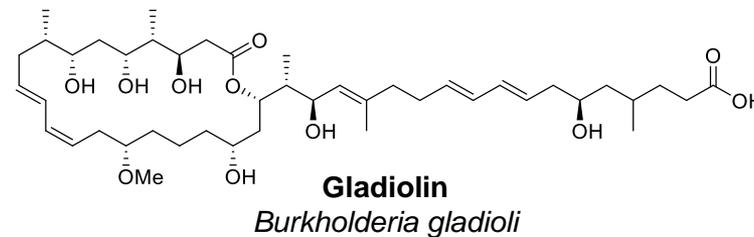
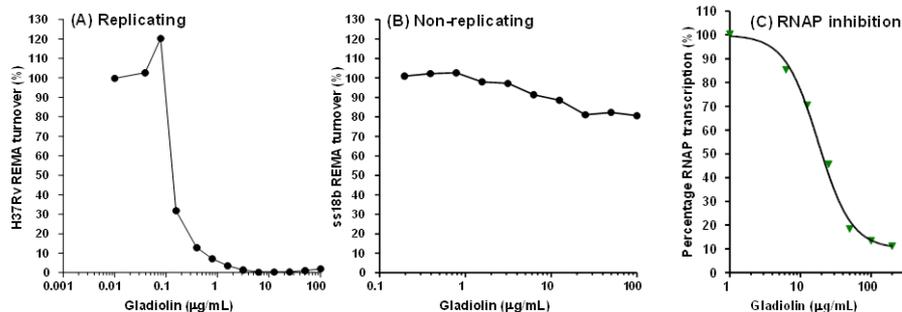


Mycobacterium smegmatis (MIC 1 µg/mL)

Inhibits *E. coli* RNA Polymerase

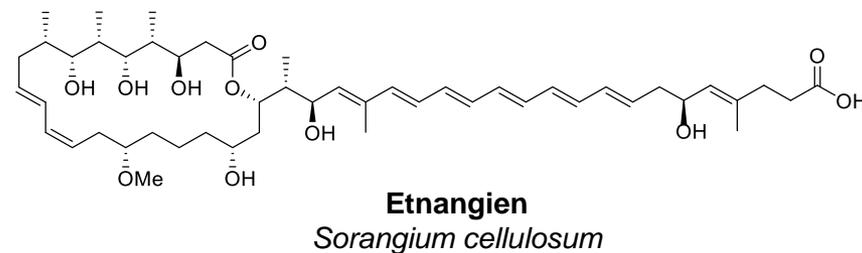
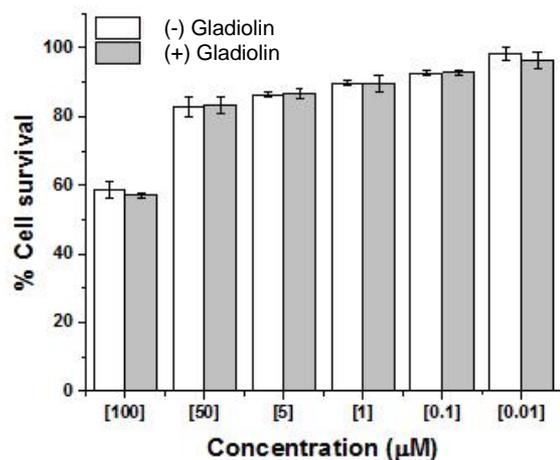
Discovery of Gladiolin: A Novel Macrolide Antibiotic

Gladiolin Inhibition of RNA Polymerase and Cytotoxicity



Mycobacterium tuberculosis (MIC 0.3 μg/mL)

Inhibits *Mycobacterium smegmatis* RNA Polymerase (23 μM)



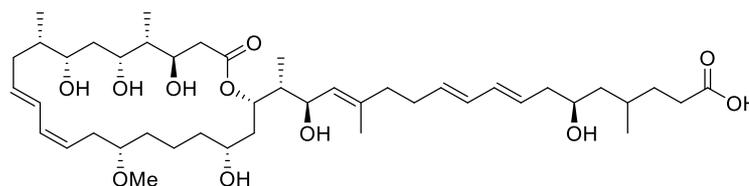
Mycobacterium smegmatis (MIC 1 μg/mL)

Inhibits *E. coli* RNA Polymerase

Discovery of Gladiolin: A Novel Macrolide Antibiotic

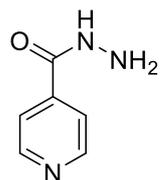
Cross-Resistance with Rifampicin and Isoniazid

Strain	Mutation	Resistance	MIC ($\mu\text{g/mL}$)		
			Gladiolin	Isoniazid	Rifampicin
H37Rv	None	None	0.3	0.04	0.001
HUG.MB.6726	<i>inhA</i>	Isoniazid	0.3	2.2	0.001
CHUV80037024	<i>inhA/katG/rpoB</i>	Isoniazid/Rifampicin	1.7	>10	>10



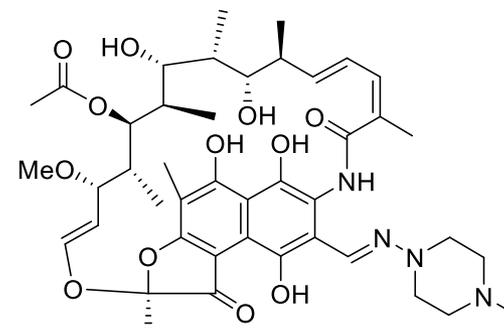
Gladiolin

Target: *M. tuberculosis* RNA Polymerase



Isoniazid

Target: *M. tuberculosis* Enoyl-ACP Reductase (InhA)
&
M. tuberculosis Catalase peroxidase (KatG)



Rifampicin

Target: *M. tuberculosis* RNA Polymerase β -subunit (RpoB)

Discovery of Gladiolin: A Novel Macrolide Antibiotic

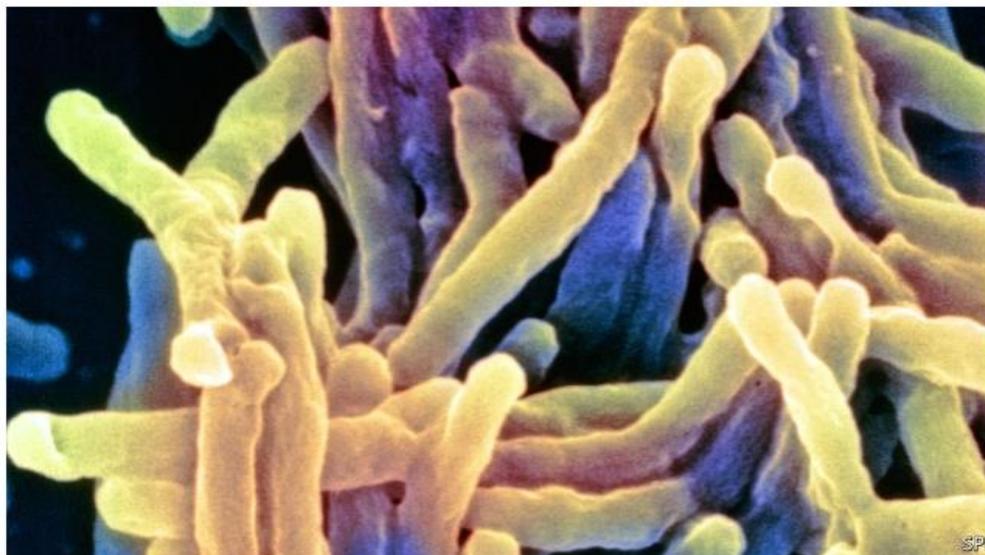
A Bit of Press Attention...

The
Economist

The enemy of my enemy

A new antibiotic for drug-resistant tuberculosis

A bug that infects people with cystic fibrosis may yield a treatment for TB



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