

Michael G Thomas

List of Publications by Year in descending order

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21
papers

731
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777949

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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Mining and Metabolomics Unveil Pseudonochelin: A Siderophore Containing 5-Aminosalicylate from a Marine-Derived <i>Pseudonocardia</i> sp. Bacterium. <i>Organic Letters</i> , 2022, 24, 3998-4002.	2.4	7
2	Utilization of lignocellulosic biofuel conversion residue by diverse microorganisms. , 2022, 15, .		2
3	Bacillibactins E and F from a Marine Sponge-Associated <i>Bacillus</i> sp.. <i>Journal of Natural Products</i> , 2021, 84, 136-141.	1.5	13
4	Stepwise genetic engineering of <i>Pseudomonas putida</i> enables robust heterologous production of prodigiosin and glidobactin A. <i>Metabolic Engineering</i> , 2021, 67, 112-124.	3.6	16
5	Structural and Biosynthetic Analysis of the Fabrubactins, Unusual Siderophores from <i>Agrobacterium fabrum</i> Strain C58. <i>ACS Chemical Biology</i> , 2021, 16, 125-135.	1.6	4
6	MS-Derived Isotopic Fine Structure Reveals Forazoline A as a Thioketone-Containing Marine-Derived Natural Product. <i>Organic Letters</i> , 2020, 22, 1275-1279.	2.4	12
7	Directed Evolution Reveals the Functional Sequence Space of an Adenylation Domain Specificity Code. <i>ACS Chemical Biology</i> , 2019, 14, 2044-2054.	1.6	16
8	An Orphan MbtH-Like Protein Interacts with Multiple Nonribosomal Peptide Synthetases in <i>Myxococcus xanthus</i> DK1622. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	18
9	Alanine Scanning of YbdZ, an MbtH-like Protein, Reveals Essential Residues for Functional Interactions with Its Nonribosomal Peptide Synthetase Partner EntF. <i>Biochemistry</i> , 2018, 57, 4125-4134.	1.2	14
10	Directed Evolution of an Adenylation Domain Specificity Code. <i>FASEB Journal</i> , 2018, 32, 530.6.	0.2	0
11	Characterization of the Functional Variance in MbtH-like Protein Interactions with a Nonribosomal Peptide Synthetase. <i>Biochemistry</i> , 2017, 56, 5380-5390.	1.2	30
12	Genomic and Secondary Metabolite Analyses of <i>Streptomyces</i> sp. 2AW Provide Insight into the Evolution of the Cycloheximide Pathway. <i>Frontiers in Microbiology</i> , 2016, 7, 573.	1.5	17
13	Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016, 4, .	0.8	19
14	A Polyketide Synthase Acyltransferase Domain Structure Suggests a Recognition Mechanism for Its Hydroxymalonyl-Acyl Carrier Protein Substrate. <i>PLoS ONE</i> , 2014, 9, e110965.	1.1	23
15	Analyses of MbtB, MbtE, and MbtF Suggest Revisions to the Mycobactin Biosynthesis Pathway in <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2809-2818.	1.0	108
16	Harnessing Unusual Precursors in Polyketide Biosynthesis. <i>FASEB Journal</i> , 2012, 26, 347.1.	0.2	0
17	MbtH-Like Proteins as Integral Components of Bacterial Nonribosomal Peptide Synthetases. <i>Biochemistry</i> , 2010, 49, 8815-8817.	1.2	141
18	Chapter 7 Formation and Characterization of Acyl Carrier Protein-Linked Polyketide Synthase Extender Units. <i>Methods in Enzymology</i> , 2009, 459, 143-163.	0.4	10

#	ARTICLE	IF	CITATIONS
19	Identification of the Biosynthetic Gene Cluster and an Additional Gene for Resistance to the Antituberculosis Drug Capreomycin. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4162-4170.	1.4	90
20	Identification and analysis of a siderophore biosynthetic gene cluster from <i>Agrobacterium tumefaciens</i> C58. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3857-3866.	0.7	64
21	Deciphering Tuberactinomycin Biosynthesis: Isolation, Sequencing, and Annotation of the Viomycin Biosynthetic Gene Cluster. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 2823-2830.	1.4	125