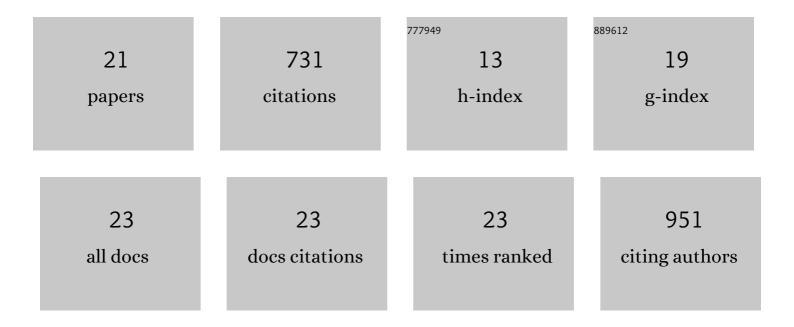
Michael G Thomas

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome Mining and Metabolomics Unveil Pseudonochelin: A Siderophore Containing 5-Aminosalicylate from a Marine-Derived <i>Pseudonocardia</i> sp. Bacterium. Organic Letters, 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 Bacillus sp Journal of Natural Products, 2021, 84, 136-141.	1.5	13
4	Stepwise genetic engineering of Pseudomonas putida enables robust heterologous production of prodigiosin and glidobactin A. Metabolic Engineering, 2021, 67, 112-124.	3.6	16
5	Structural and Biosynthetic Analysis of the Fabrubactins, Unusual Siderophores from <i>Agrobacterium fabrum</i> Strain C58. ACS Chemical Biology, 2021, 16, 125-135.	1.6	4
6	MS-Derived Isotopic Fine Structure Reveals Forazoline A as a Thioketone-Containing Marine-Derived Natural Product. Organic Letters, 2020, 22, 1275-1279.	2.4	12
7	Directed Evolution Reveals the Functional Sequence Space of an Adenylation Domain Specificity Code. ACS Chemical Biology, 2019, 14, 2044-2054.	1.6	16
8	An Orphan MbtH-Like Protein Interacts with Multiple Nonribosomal Peptide Synthetases in Myxococcus xanthus DK1622. Journal of Bacteriology, 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. Biochemistry, 2018, 57, 4125-4134.	1.2	14
10	Directed Evolution of an Adenylation Domain Specificity Code. FASEB Journal, 2018, 32, 530.6.	0.2	0
11	Characterization of the Functional Variance in MbtH-like Protein Interactions with a Nonribosomal Peptide Synthetase. Biochemistry, 2017, 56, 5380-5390.	1.2	30
12	Genomic and Secondary Metabolite Analyses of Streptomyces sp. 2AW Provide Insight into the Evolution of the Cycloheximide Pathway. Frontiers in Microbiology, 2016, 7, 573.	1.5	17
13	Draft Genome Sequence of Biocontrol Agent Bacillus cereus UW85. Genome Announcements, 2016, 4, .	0.8	19
14	A Polyketide Synthase Acyltransferase Domain Structure Suggests a Recognition Mechanism for Its Hydroxymalonyl-Acyl Carrier Protein Substrate. PLoS ONE, 2014, 9, e110965.	1.1	23
15	Analyses of MbtB, MbtE, and MbtF Suggest Revisions to the Mycobactin Biosynthesis Pathway in Mycobacterium tuberculosis. Journal of Bacteriology, 2012, 194, 2809-2818.	1.0	108
16	Harnessing Unusual Precursors in Polyketide Biosynthesis. FASEB Journal, 2012, 26, 347.1.	0.2	0
17	MbtH-Like Proteins as Integral Components of Bacterial Nonribosomal Peptide Synthetases. Biochemistry, 2010, 49, 8815-8817.	1.2	141
18	Chapter 7 Formation and Characterization of Acyl Carrier Protein–Linked Polyketide Synthase Extender Units. Methods in Enzymology, 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. Applied and Environmental Microbiology, 2007, 73, 4162-4170.	1.4	90
20	ldentification and analysis of a siderophore biosynthetic gene cluster from Agrobacterium tumefaciens C58. Microbiology (United Kingdom), 2004, 150, 3857-3866.	0.7	64
21	Deciphering Tuberactinomycin Biosynthesis: Isolation, Sequencing, and Annotation of the Viomycin Biosynthetic Gene Cluster. Antimicrobial Agents and Chemotherapy, 2003, 47, 2823-2830.	1.4	125