

# Tilmann Weber

## List of Publications by Year in descending order

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109  
papers

17,341  
citations

61857

43  
h-index

28224

105  
g-index

121  
all docs

121  
docs citations

121  
times ranked

13713  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of gargantulides B and C, new 52-membered macrolactones from <i>Amycolatopsis</i> sp. Complete absolute stereochemistry of the gargantulide family. <i>Organic Chemistry Frontiers</i> , 2022, 9, 462-470.	2.3	4
2	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 900-910.	1.8	9
3	BiG-FAM: the biosynthetic gene cluster families database. <i>Nucleic Acids Research</i> , 2021, 49, D490-D497.	6.5	122
4	The antiSMASH database version 3: increased taxonomic coverage and new query features for modular enzymes. <i>Nucleic Acids Research</i> , 2021, 49, D639-D643.	6.5	100
5	Genomic and Chemical Diversity of <i>Bacillus subtilis</i> Secondary Metabolites against Plant Pathogenic Fungi. <i>MSystems</i> , 2021, 6, .	1.7	55
6	Distribution of $\mu$ -Poly- <i>l</i> -Lysine Synthetases in Coryneform Bacteria Isolated from Cheese and Human Skin. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	9
7	Phylogenetic Distribution of Secondary Metabolites in the <i>Bacillus subtilis</i> Species Complex. <i>MSystems</i> , 2021, 6, .	1.7	39
8	antiSMASH 6.0: improving cluster detection and comparison capabilities. <i>Nucleic Acids Research</i> , 2021, 49, W29-W35.	6.5	1,520
9	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain CA-256286. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029021.	0.3	1
10	Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from <i>Kutzneria</i> sp. CA-103260. <i>ACS Chemical Biology</i> , 2021, 16, 1456-1468.	1.6	8
11	Complete Genome Sequence of the Rare Actinobacterium <i>Kutzneria</i> sp. Strain CA-103260. <i>Microbiology Resource Announcements</i> , 2021, 10, e0049921.	0.3	1
12	A Regulator Based "Semi-Targeted" Approach to Activate Silent Biosynthetic Gene Clusters. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7567.	1.8	10
13	The Design-Build-Test-Learn cycle for metabolic engineering of Streptomycetes. <i>Essays in Biochemistry</i> , 2021, 65, 261-275.	2.1	17
14	Towards the sustainable discovery and development of new antibiotics. <i>Nature Reviews Chemistry</i> , 2021, 5, 726-749.	13.8	439
15	Complete Genome Sequence of <i>Amycolatopsis</i> sp. CA-230715, Encoding a 35-Module Type I Polyketide Synthase. <i>Microbiology Resource Announcements</i> , 2021, 10, e0080521.	0.3	1
16	Characterization and engineering of <i>Streptomyces griseofuscus</i> DSM 40191 as a potential host for heterologous expression of biosynthetic gene clusters. <i>Scientific Reports</i> , 2021, 11, 18301.	1.6	11
17	Computational Applications in Secondary Metabolite Discovery (CAiSMD): an online workshop. <i>Journal of Cheminformatics</i> , 2021, 13, 64.	2.8	3
18	The Structure of Cyclodecatriene Collinolactone, its Biosynthesis, and Semisynthetic Analogues: Effects of Monoastal Phenotype and Protection from Intracellular Oxidative Stress. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 23212-23216.	7.2	5

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19	Die Struktur des Cyclodecatriens Collinolacton, seine Biosynthese und semisynthetische Derivate: monopolare Spindeln und Schutz vor intrazellulÄrem oxidativem Stress. <i>Angewandte Chemie</i> , 2021, 133, 23399.	1.6	0
20	A versatile genetic engineering toolkit for E. coli based on CRISPR-prime editing. <i>Nature Communications</i> , 2021, 12, 5206.	5.8	49
21	Activation and Identification of a Griseusin Cluster in <i>Streptomyces</i> sp. CA-256286 by Employing Transcriptional Regulators and Multi-Omics Methods. <i>Molecules</i> , 2021, 26, 6580.	1.7	9
22	MIBiG 2.0: a repository for biosynthetic gene clusters of known function. <i>Nucleic Acids Research</i> , 2020, 48, D454-D458.	6.5	351
23	Genome Mining Approaches to Bacterial Natural Product Discovery. , 2020, , 19-33.		5
24	Automating Cloning by Natural Transformation. <i>ACS Synthetic Biology</i> , 2020, 9, 3228-3235.	1.9	11
25	Recent Advances in Re-engineering Modular PKS and NRPS Assembly Lines. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 886-894.	1.4	28
26	ARTS 2.0: feature updates and expansion of the Antibiotic Resistant Target Seeker for comparative genome mining. <i>Nucleic Acids Research</i> , 2020, 48, W546-W552.	6.5	116
27	Designing sgRNAs for CRISPR-BEST base editing applications with CRISPy-web 2.0. <i>Synthetic and Systems Biotechnology</i> , 2020, 5, 99-102.	1.8	20
28	CRISPRâ€Cas9, CRISPRi and CRISPR-BEST-mediated genetic manipulation in streptomycetes. <i>Nature Protocols</i> , 2020, 15, 2470-2502.	5.5	50
29	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. <i>Synthetic and Systems Biotechnology</i> , 2020, 5, 11-18.	1.8	13
30	Complete Genome Sequences of 13 <i>Bacillus subtilis</i> Soil Isolates for Studying Secondary Metabolite Diversity. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	13
31	High-Quality Sequencing, Assembly, and Annotation of the <i>Streptomyces griseofuscus</i> DSM 40191 Genome. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
32	Genomeâ€scale Metabolic Reconstruction of Actinomycetes for Antibiotics Production. <i>Biotechnology Journal</i> , 2019, 14, e1800377.	1.8	22
33	Highly efficient DSB-free base editing for streptomycetes with CRISPR-BEST. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20366-20375.	3.3	119
34	Engineering of cell factories for the production of natural products. <i>Natural Product Reports</i> , 2019, 36, 1231-1232.	5.2	4
35	Depiction of secondary metabolites and antifungal activity of <i>Bacillus velezensis</i> DTU001. <i>Synthetic and Systems Biotechnology</i> , 2019, 4, 142-149.	1.8	46
36	antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. <i>Nucleic Acids Research</i> , 2019, 47, W81-W87.	6.5	2,410

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37	Synthetic biology and metabolic engineering of actinomycetes for natural product discovery. <i>Biotechnology Advances</i> , 2019, 37, 107366.	6.0	109
38	Antitumor astins originate from the fungal endophyte <i>Cyanoderma asteris</i> living within the medicinal plant <i>Aster tataricus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26909-26917.	3.3	39
39	CRISPR/Cas-based genome engineering in natural product discovery. <i>Natural Product Reports</i> , 2019, 36, 1262-1280.	5.2	88
40	The antiSMASH database version 2: a comprehensive resource on secondary metabolite biosynthetic gene clusters. <i>Nucleic Acids Research</i> , 2019, 47, D625-D630.	6.5	150
41	Sequence-based classification of type II polyketide synthase biosynthetic gene clusters for antiSMASH. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 469-475.	1.4	22
42	Recent development of antiSMASH and other computational approaches to mine secondary metabolite biosynthetic gene clusters. <i>Briefings in Bioinformatics</i> , 2019, 20, 1103-1113.	3.2	118
43	The Draft Whole-Genome Sequence of the Antibiotic Producer <i>Empedobacter haloabium</i> ATCC 31962 Provides Indications for Its Taxonomic Reclassification. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
44	Filling the Gaps in the Kirromycin Biosynthesis: Deciphering the Role of Genes Involved in Ethylmalonyl-CoA Supply and Tailoring Reactions. <i>Scientific Reports</i> , 2018, 8, 3230.	1.6	17
45	Omics and multi-omics approaches to study the biosynthesis of secondary metabolites in microorganisms. <i>Current Opinion in Microbiology</i> , 2018, 45, 109-116.	2.3	101
46	Patscanui: an intuitive web interface for searching patterns in DNA and protein data. <i>Nucleic Acids Research</i> , 2018, 46, W205-W208.	6.5	6
47	Toward Systems Metabolic Engineering of Streptomycetes for Secondary Metabolites Production. <i>Biotechnology Journal</i> , 2018, 13, 1700465.	1.8	32
48	CRISPR-Cas9 Toolkit for Actinomycete Genome Editing. <i>Methods in Molecular Biology</i> , 2018, 1671, 163-184.	0.4	24
49	Lysoquinone-TH1, a New Polyphenolic Tridecaketide Produced by Expressing the Lysolipin Minimal PKS II in <i>Streptomyces albus</i> . <i>Antibiotics</i> , 2018, 7, 53.	1.5	7
50	Polyketide Bioderivatization Using the Promiscuous Acyltransferase KirCII. <i>ACS Synthetic Biology</i> , 2017, 6, 421-427.	1.9	42
51	antiSMASH 4.0's improvements in chemistry prediction and gene cluster boundary identification. <i>Nucleic Acids Research</i> , 2017, 45, W36-W41.	6.5	1,196
52	The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery. <i>Nucleic Acids Research</i> , 2017, 45, W42-W48.	6.5	142
53	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. <i>Nature Communications</i> , 2017, 8, 15784.	5.8	287
54	Recent development of computational resources for new antibiotics discovery. <i>Current Opinion in Microbiology</i> , 2017, 39, 113-120.	2.3	34

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55	Linking secondary metabolites to biosynthesis genes in the fungal endophyte <i>Cyanoderrella asteris</i> : The anti-cancer bisanthraquinone skyrin. <i>Journal of Biotechnology</i> , 2017, 257, 233-239.	1.9	33
56	The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. <i>Nucleic Acids Research</i> , 2017, 45, D555-D559.	6.5	207
57	<i>Cyanoderrella asteris</i> sp. nov. ( <i>Ostropales</i> ) from the inflorescence axis of <i>Aster tataricus</i> . <i>Mycotaxon</i> , 2017, 132, 107-123.	0.1	16
58	The cyclochlorotine mycotoxin is produced by the nonribosomal peptide synthetase CctN in <i>Talaromyces islandicus</i> (â€œ <i>Penicillium islandicum</i> â€™). <i>Environmental Microbiology</i> , 2016, 18, 3728-3741.	1.8	15
59	CRISPy-web: An online resource to design sgRNAs for CRISPR applications. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 118-121.	1.8	117
60	Metabolic engineering with systems biology tools to optimize production of prokaryotic secondary metabolites. <i>Natural Product Reports</i> , 2016, 33, 933-941.	5.2	52
61	Introduction to the Special Issue â€œBioinformatic tools and approaches for Synthetic Biology of natural productsâ€™. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 67-68.	1.8	2
62	The evolution of genome mining in microbes â€œ a review. <i>Natural Product Reports</i> , 2016, 33, 988-1005.	5.2	538
63	Elucidating the molecular physiology of lantibiotic NAI-107 production in <i>Microbispora</i> ATCC-PTA-5024. <i>BMC Genomics</i> , 2016, 17, 42.	1.2	10
64	The secondary metabolite bioinformatics portal: Computational tools to facilitate synthetic biology of secondary metabolite production. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 69-79.	1.8	153
65	Identification and activation of novel biosynthetic gene clusters by genome mining in the kirromycin producer <i>Streptomyces collinus</i> TÅ¼ 365. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 277-291.	1.4	37
66	Bioinformatics Tools for the Discovery of New Nonribosomal Peptides. <i>Methods in Molecular Biology</i> , 2016, 1401, 209-232.	0.4	8
67	Streptocollin, a Typeâ€œ...IV Lanthipeptide Produced by <i>Streptomyces collinus</i> TÅ¼ 365. <i>ChemBioChem</i> , 2015, 16, 2615-2623.	1.3	43
68	antiSMASH 3.0â€™ a comprehensive resource for the genome mining of biosynthetic gene clusters. <i>Nucleic Acids Research</i> , 2015, 43, W237-W243.	6.5	1,764
69	CRISPR-Cas9 Based Engineering of Actinomycetal Genomes. <i>ACS Synthetic Biology</i> , 2015, 4, 1020-1029.	1.9	365
70	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	3.9	715
71	Draft genome sequence of <i>Talaromyces islandicus</i> (â€œ <i>Penicillium islandicum</i> â€™) WF-38-12, a neglected mold with significant biotechnological potential. <i>Journal of Biotechnology</i> , 2015, 211, 101-102.	1.9	17
72	Metabolic engineering of antibiotic factories: new tools for antibiotic production in actinomycetes. <i>Trends in Biotechnology</i> , 2015, 33, 15-26.	4.9	159

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73	CLUSEAN, Overview. , 2015, , 93-95.		0
74	Improved Lanthipeptide Detection and Prediction for antiSMASH. PLoS ONE, 2014, 9, e89420.	1.1	45
75	Novel <i>Amycolatopsis balhimycina</i> biochemical abilities unveiled by proteomics. FEMS Microbiology Letters, 2014, 351, 209-215.	0.7	4
76	Draft Genome Sequence of the <i>Microbispora</i> sp. Strain ATCC-PTA-5024, Producing the Lantibiotic NAI-107. Genome Announcements, 2014, 2, .	0.8	12
77	Reprogramming Acyl Carrier Protein Interactions of an Acyl-CoA Promiscuous trans-Acyltransferase. Chemistry and Biology, 2014, 21, 636-646.	6.2	43
78	In silico tools for the analysis of antibiotic biosynthetic pathways. International Journal of Medical Microbiology, 2014, 304, 230-235.	1.5	84
79	Complete genome sequence of the actinobacterium <i>Amycolatopsis japonica</i> MG417-CF17T (=DSM 44213T) producing (S,S)-N,N <sup>2</sup> -ethylenediaminedisuccinic acid. Journal of Biotechnology, 2014, 189, 46-47.	1.9	16
80	Biosynthesis of Phenylannolone A, a Multidrug Resistance Reversal Agent from the Halotolerant Myxobacterium <i>Nannocystis pusilla</i> B150. ChemBioChem, 2014, 15, 757-765.	1.3	19
81	The AT <sub>2</sub> Domain of KirCI Loads Malonyl Extender Units to the ACPs of the Kirromycin PKS. ChemBioChem, 2013, 14, 1343-1352.	1.3	26
82	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> TÅ¼ 365 consisting of a linear chromosome and two linear plasmids. Journal of Biotechnology, 2013, 168, 739-740.	1.9	23
83	antiSMASH 2.0 – a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Research, 2013, 41, W204-W212.	6.5	753
84	Detection and quantification of a mycorrhization helper bacterium and a mycorrhizal fungus in plant-soil microcosms at different levels of complexity. BMC Microbiology, 2013, 13, 205.	1.3	39
85	Poly Specific <i>trans</i> -Acyltransferase Machinery Revealed <i>via</i> Engineered Acyl-CoA Synthetases. ACS Chemical Biology, 2013, 8, 200-208.	1.6	60
86	Discrete acyltransferases involved in polyketide biosynthesis. MedChemComm, 2012, 3, 871.	3.5	34
87	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . Biotechnology and Bioengineering, 2012, 109, 1798-1807.	1.7	19
88	Synthetic Biology of secondary metabolite biosynthesis in actinomycetes: Engineering precursor supply as a way to optimize antibiotic production. FEBS Letters, 2012, 586, 2171-2176.	1.3	53
89	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. Nucleic Acids Research, 2011, 39, W339-W346.	6.5	1,622
90	The phosphopantetheinyl transferase KirP activates the ACP and PCP domains of the kirromycin NRPS/PKS of <i>Streptomyces collinus</i> TÅ¼ 365. FEMS Microbiology Letters, 2011, 319, 26-33.	0.7	20

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91	Characterization of the "pristinamycin supercluster"™ of <i>Streptomyces pristinaespiralis</i> . <i>Microbial Biotechnology</i> , 2011, 4, 192-206.	2.0	119
92	Supramolecular Templating in Kirromycin Biosynthesis: The Acyltransferase KirCII Loads Ethylmalonyl-CoA Extender onto a Specific ACP of the trans-AT PKS. <i>Chemistry and Biology</i> , 2011, 18, 438-444.	6.2	50
93	NRSPredictor2" a web server for predicting NRPS adenylation domain specificity. <i>Nucleic Acids Research</i> , 2011, 39, W362-W367.	6.5	559
94	Increased glycopeptide production after overexpression of shikimate pathway genes being part of the balhimycin biosynthetic gene cluster. <i>Metabolic Engineering</i> , 2010, 12, 455-461.	3.6	49
95	Making <i>E. coli</i> an Erythromycin Production Plant. <i>Chemistry and Biology</i> , 2010, 17, 1168-1169.	6.2	2
96	Differential proteomic analysis reveals novel links between primary metabolism and antibiotic production in <i>Amycolatopsis balhimycina</i> . <i>Proteomics</i> , 2010, 10, 1336-1358.	1.3	28
97	Genome mining in <i>Amycolatopsis balhimycina</i> for ferredoxins capable of supporting cytochrome P450 enzymes involved in glycopeptide antibiotic biosynthesis. <i>FEMS Microbiology Letters</i> , 2010, 306, 45-53.	0.7	4
98	Isolation of the lysolipin gene cluster of <i>Streptomyces tendae</i> 4042. <i>Gene</i> , 2010, 461, 5-14.	1.0	42
99	The kirromycin gene cluster of <i>Streptomyces collinus</i> 365 codes for an aspartate- $\beta$ -decarboxylase, KirD, which is involved in the biosynthesis of the precursor $\beta$ -alanine. <i>Journal of Antibiotics</i> , 2009, 62, 465-468.	1.0	15
100	CLUSEAN: A computer-based framework for the automated analysis of bacterial secondary metabolite biosynthetic gene clusters. <i>Journal of Biotechnology</i> , 2009, 140, 13-17.	1.9	160
101	Module Extension of a Non-Ribosomal Peptide Synthetase of the Glycopeptide Antibiotic Balhimycin Produced by <i>Amycolatopsis balhimycina</i> . <i>ChemBioChem</i> , 2008, 9, 1195-1200.	1.3	49
102	Molecular Analysis of the Kirromycin Biosynthetic Gene Cluster Revealed $\beta$ -Alanine as Precursor of the Pyridone Moiety. <i>Chemistry and Biology</i> , 2008, 15, 175-188.	6.2	101
103	Phylogenetic analysis of condensation domains in NRPS sheds light on their functional evolution. <i>BMC Evolutionary Biology</i> , 2007, 7, 78.	3.2	301
104	Comparative analysis and insights into the evolution of gene clusters for glycopeptide antibiotic biosynthesis. <i>Molecular Genetics and Genomics</i> , 2005, 274, 40-50.	1.0	74
105	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). <i>Nucleic Acids Research</i> , 2005, 33, 5799-5808.	6.5	388
106	Exploiting the genetic potential of polyketide producing streptomycetes. <i>Journal of Biotechnology</i> , 2003, 106, 221-232.	1.9	127
107	Evidence that an Additional Mutation Is Required To Tolerate Insertional Inactivation of the <i>Streptomyces lividans</i> recA Gene. <i>Journal of Bacteriology</i> , 2001, 183, 4374-4381.	1.0	19
108	Transcriptional and Mutational Analyses of the <i>Streptomyces lividans</i> recX Gene and Its Interference with RecA Activity. <i>Journal of Bacteriology</i> , 2000, 182, 4005-4011.	1.0	59

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109	CRISPR/Cas-based genome engineering in natural product discovery. , 0, .		1