Tilmann Weber

List of Publications by Year
in descending order

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	antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. Nucleic Acids Research, 2019, 47, W81-W87.	6.5	2,410
2	antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Research, 2015, 43, W237-W243.	6.5	1,764
3	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
4	antiSMASH 6.0: improving cluster detection and comparison capabilities. Nucleic Acids Research, 2021, 49, W29-W35.	6.5	1,520
5	antiSMASH 4.0—improvements in chemistry prediction and gene cluster boundary identification. Nucleic Acids Research, 2017, 45, W36-W41.	6.5	1,196
6	antiSMASH 2.0—a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Research, 2013, 41, W204-W212.	6.5	753
7	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	3.9	715
8	NRPSpredictor2—a web server for predicting NRPS adenylation domain specificity. Nucleic Acids Research, 2011, 39, W362-W367.	6.5	559
9	The evolution of genome mining in microbes – a review. Natural Product Reports, 2016, 33, 988-1005.	5.2	538
10	Towards the sustainable discovery and development of new antibiotics. Nature Reviews Chemistry, 2021, 5, 726-749.	13.8	439
11	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). Nucleic Acids Research, 2005, 33, 5799-5808.	6.5	388
12	CRISPR-Cas9 Based Engineering of Actinomycetal Genomes. ACS Synthetic Biology, 2015, 4, 1020-1029.	1.9	365
13	MIBiG 2.0: a repository for biosynthetic gene clusters of known function. Nucleic Acids Research, 2020, 48, D454-D458.	6.5	351
14	Phylogenetic analysis of condensation domains in NRPS sheds light on their functional evolution. BMC Evolutionary Biology, 2007, 7, 78.	3.2	301
15	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. Nature Communications, 2017, 8, 15784.	5.8	287
16	The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2017, 45, D555-D559.	6.5	207
17	CLUSEAN: A computer-based framework for the automated analysis of bacterial secondary metabolite biosynthetic gene clusters. Journal of Biotechnology, 2009, 140, 13-17.	1.9	160
18	Metabolic engineering of antibiotic factories: new tools for antibiotic production in actinomycetes. Trends in Biotechnology, 2015, 33, 15-26.	4.9	159

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19	The secondary metabolite bioinformatics portal: Computational tools to facilitate synthetic biology of secondary metabolite production. Synthetic and Systems Biotechnology, 2016, 1, 69-79.	1.8	153
20	The antiSMASH database version 2: a comprehensive resource on secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2019, 47, D625-D630.	6.5	150
21	The Antibiotic Resistant Target Seeker (ARTS), an exploration engine for antibiotic cluster prioritization and novel drug target discovery. Nucleic Acids Research, 2017, 45, W42-W48.	6.5	142
22	Exploiting the genetic potential of polyketide producing streptomycetes. Journal of Biotechnology, 2003, 106, 221-232.	1.9	127
23	BiG-FAM: the biosynthetic gene cluster families database. Nucleic Acids Research, 2021, 49, D490-D497.	6.5	122
24	Characterization of the 'pristinamycin supercluster' of *Streptomyces pristinaespiralis*. Microbial Biotechnology, 2011, 4, 192-206.	2.0	119
25	Highly efficient DSB-free base editing for streptomycetes with CRISPR-BEST. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20366-20375.	3.3	119
26	Recent development of antiSMASH and other computational approaches to mine secondary metabolite biosynthetic gene clusters. Briefings in Bioinformatics, 2019, 20, 1103-1113.	3.2	118
27	CRISPy-web: An online resource to design sgRNAs for CRISPR applications. Synthetic and Systems Biotechnology, 2016, 1, 118-121.	1.8	117
28	ARTS 2.0: feature updates and expansion of the Antibiotic Resistant Target Seeker for comparative genome mining. Nucleic Acids Research, 2020, 48, W546-W552.	6.5	116
29	Synthetic biology and metabolic engineering of actinomycetes for natural product discovery. Biotechnology Advances, 2019, 37, 107366.	6.0	109
30	Molecular Analysis of the Kirromycin Biosynthetic Gene Cluster Revealed β-Alanine as Precursor of the Pyridone Moiety. Chemistry and Biology, 2008, 15, 175-188.	6.2	101
31	Omics and multi-omics approaches to study the biosynthesis of secondary metabolites in microorganisms. Current Opinion in Microbiology, 2018, 45, 109-116.	2.3	101
32	The antiSMASH database version 3: increased taxonomic coverage and new query features for modular enzymes. Nucleic Acids Research, 2021, 49, D639-D643.	6.5	100
33	CRISPR/Cas-based genome engineering in natural product discovery. Natural Product Reports, 2019, 36, 1262-1280.	5.2	88
34	In silico tools for the analysis of antibiotic biosynthetic pathways. International Journal of Medical Microbiology, 2014, 304, 230-235.	1.5	84
35	Comparative analysis and insights into the evolution of gene clusters for glycopeptide antibiotic biosynthesis. Molecular Genetics and Genomics, 2005, 274, 40-50.	1.0	74
36	Poly Specific *trans*-Acyltransferase Machinery Revealed *via* Engineered Acyl-CoA Synthetases. ACS Chemical Biology, 2013, 8, 200-208.	1.6	60

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37	Transcriptional and Mutational Analyses of theStreptomyces lividans recX Gene and Its Interference with RecA Activity. Journal of Bacteriology, 2000, 182, 4005-4011.	1.0	59
38	Genomic and Chemical Diversity of Bacillus subtilis Secondary Metabolites against Plant Pathogenic Fungi. MSystems, 2021, 6, .	1.7	55
39	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
40	Metabolic engineering with systems biology tools to optimize production of prokaryotic secondary metabolites. Natural Product Reports, 2016, 33, 933-941.	5.2	52
41	Supramolecular Templating in Kirromycin Biosynthesis: The Acyltransferase KirCII Loads Ethylmalonyl-CoA Extender onto a Specific ACP of the trans-AT PKS. Chemistry and Biology, 2011, 18, 438-444.	6.2	50
42	CRISPRâ€"Cas9, CRISPRi and CRISPR-BEST-mediated genetic manipulation in streptomycetes. Nature Protocols, 2020, 15, 2470-2502.	5.5	50
43	Module Extension of a Nonâ€Ribosomal Peptide Synthetase of the Glycopeptide Antibiotic Balhimycin Produced by <i>Amycolatopsis balhimycina</i>. ChemBioChem, 2008, 9, 1195-1200.	1.3	49
44	Increased glycopeptide production after overexpression of shikimate pathway genes being part of the balhimycin biosynthetic gene cluster. Metabolic Engineering, 2010, 12, 455-461.	3.6	49
45	A versatile genetic engineering toolkit for E. coli based on CRISPR-prime editing. Nature Communications, 2021, 12, 5206.	5.8	49
46	Depiction of secondary metabolites and antifungal activity of Bacillus velezensis DTU001. Synthetic and Systems Biotechnology, 2019, 4, 142-149.	1.8	46
47	Improved Lanthipeptide Detection and Prediction for antiSMASH. PLoS ONE, 2014, 9, e89420.	1.1	45
48	Reprogramming Acyl Carrier Protein Interactions of an Acyl-CoA Promiscuous trans-Acyltransferase. Chemistry and Biology, 2014, 21, 636-646.	6.2	43
49	Streptocollin, a Typeâ€¦IV Lanthipeptide Produced by <i>Streptomyces collinus</i> TÃ¼ 365. ChemBioChem, 2015, 16, 2615-2623.	1.3	43
50	Isolation of the lysolipin gene cluster of Streptomyces tendae TÃ¼ 4042. Gene, 2010, 461, 5-14.	1.0	42
51	Polyketide Bioderivatization Using the Promiscuous Acyltransferase KirCII. ACS Synthetic Biology, 2017, 6, 421-427.	1.9	42
52	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
53	Antitumor astins originate from the fungal endophyte <i>Cyanodermella asteris</i> living within the medicinal plant <i>Aster tataricus</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26909-26917.	3.3	39
54	Phylogenetic Distribution of Secondary Metabolites in the Bacillus subtilis Species Complex. MSystems, 2021, 6, .	1.7	39

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55	Identification and activation of novel biosynthetic gene clusters by genome mining in the kirromycin producer <i>Streptomyces collinus</i> TÃ¼ 365. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 277-291.	1.4	37
56	Discrete acyltransferases involved in polyketide biosynthesis. MedChemComm, 2012, 3, 871.	3.5	34
57	Recent development of computational resources for new antibiotics discovery. Current Opinion in Microbiology, 2017, 39, 113-120.	2.3	34
58	Linking secondary metabolites to biosynthesis genes in the fungal endophyte Cyanodermella asteris: The anti-cancer bisanthraquinone skyrin. Journal of Biotechnology, 2017, 257, 233-239.	1.9	33
59	Toward Systems Metabolic Engineering of Streptomycetes for Secondary Metabolites Production. Biotechnology Journal, 2018, 13, 1700465.	1.8	32
60	Differential proteomic analysis reveals novel links between primary metabolism and antibiotic production in <i>Amycolatopsis balhimycina</i>. Proteomics, 2010, 10, 1336-1358.	1.3	28
61	Recent Advances in Re-engineering Modular PKS and NRPS Assembly Lines. Biotechnology and Bioprocess Engineering, 2020, 25, 886-894.	1.4	28
62	The AT$_2$ Domain of KirCI Loads Malonyl Extender Units to the ACPs of the Kirromycin PKS. ChemBioChem, 2013, 14, 1343-1352.	1.3	26
63	CRISPR-Cas9 Toolkit for Actinomycete Genome Editing. Methods in Molecular Biology, 2018, 1671, 163-184.	0.4	24
64	Complete genome sequence of the kirromycin producer Streptomyces collinus TÃ¼ 365 consisting of a linear chromosome and two linear plasmids. Journal of Biotechnology, 2013, 168, 739-740.	1.9	23
65	Genomeâ€Scale Metabolic Reconstruction of Actinomycetes for Antibiotics Production. Biotechnology Journal, 2019, 14, e1800377.	1.8	22
66	Sequence-based classification of type II polyketide synthase biosynthetic gene clusters for antiSMASH. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 469-475.	1.4	22
67	The phosphopantetheinyl transferase KirP activates the ACP and PCP domains of the kirromycin NRPS/PKS of Streptomyces collinus TÃ¼ 365. FEMS Microbiology Letters, 2011, 319, 26-33.	0.7	20
68	Designing sgRNAs for CRISPR-BEST base editing applications with CRISPy-web 2.0. Synthetic and Systems Biotechnology, 2020, 5, 99-102.	1.8	20
69	Evidence that an Additional Mutation Is Required To Tolerate Insertional Inactivation of the Streptomyces lividans recA Gene. Journal of Bacteriology, 2001, 183, 4374-4381.	1.0	19
70	Genomeâ€scale metabolic representation of <i>Amycolatopsis balhimycina</i>. Biotechnology and Bioengineering, 2012, 109, 1798-1807.	1.7	19
71	Biosynthesis of Phenylnannolone A, a Multidrug Resistance Reversal Agent from the Halotolerant Myxobacterium <i>Nannocystis pusilla</i> B150. ChemBioChem, 2014, 15, 757-765.	1.3	19
72	Draft genome sequence of Talaromyces islandicus (â€œPenicillium islandicumâ€) WF-38-12, a neglected mold with significant biotechnological potential. Journal of Biotechnology, 2015, 211, 101-102.	1.9	17

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73	Filling the Gaps in the Kirromycin Biosynthesis: Deciphering the Role of Genes Involved in Ethylmalonyl-CoA Supply and Tailoring Reactions. Scientific Reports, 2018, 8, 3230.	1.6	17
74	The Design-Build-Test-Learn cycle for metabolic engineering of Streptomycetes. Essays in Biochemistry, 2021, 65, 261-275.	2.1	17
75	Complete genome sequence of the actinobacterium Amycolatopsis japonica MG417-CF17T (=DSM 44213T) producing (S,S)-N,Nâ€²-ethylenediaminedisuccinic acid. Journal of Biotechnology, 2014, 189, 46-47.	1.9	16
76	<i>Cyanodermella asteris</i> sp. nov. (<i>Ostropales</i>) from the inflorescence axis of <i> Aster tataricus</i>. Mycotaxon, 2017, 132, 107-123.	0.1	16
77	The kirromycin gene cluster of Streptomyces collinus TÃ¼ 365 codes for an aspartate-Î±-decarboxylase, KirD, which is involved in the biosynthesis of the precursor Î²-alanine. Journal of Antibiotics, 2009, 62, 465-468.	1.0	15
78	The cyclochlorotine mycotoxin is produced by the nonribosomal peptide synthetase CctN in <i>Talaromyces islandicus</i> (â€˜<i>Penicillium islandicum</i>â€™). Environmental Microbiology, 2016, 18, 3728-3741.	1.8	15
79	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. Synthetic and Systems Biotechnology, 2020, 5, 11-18.	1.8	13
80	Complete Genome Sequences of 13 Bacillus subtilis Soil Isolates for Studying Secondary Metabolite Diversity. Microbiology Resource Announcements, 2020, 9, .	0.3	13
81	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
82	Automating Cloning by Natural Transformation. ACS Synthetic Biology, 2020, 9, 3228-3235.	1.9	11
83	Characterization and engineering of Streptomyces griseofuscus DSM 40191 as a potential host for heterologous expression of biosynthetic gene clusters. Scientific Reports, 2021, 11, 18301.	1.6	11
84	Elucidating the molecular physiology of lantibiotic NAI-107 production in Microbispora ATCC-PTA-5024. BMC Genomics, 2016, 17, 42.	1.2	10
85	A Regulator Based â€œSemi-Targetedâ€•Approach to Activate Silent Biosynthetic Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 7567.	1.8	10
86	Distribution of Îµ-Poly- <scp>l</scp> -Lysine Synthetases in Coryneform Bacteria Isolated from Cheese and Human Skin. Applied and Environmental Microbiology, 2021, 87, .	1.4	9
87	High-Quality Sequencing, Assembly, and Annotation of the Streptomyces griseofuscus DSM 40191 Genome. Microbiology Resource Announcements, 2020, 9, .	0.3	9
88	Activation and Identification of a Griseusin Cluster in Streptomyces sp. CA-256286 by Employing Transcriptional Regulators and Multi-Omics Methods. Molecules, 2021, 26, 6580.	1.7	9
89	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. Synthetic and Systems Biotechnology, 2022, 7, 900-910.	1.8	9
90	Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from <i>Kutzneria</i> sp. CA-103260. ACS Chemical Biology, 2021, 16, 1456-1468.	1.6	8

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91	Bioinformatics Tools for the Discovery of New Nonribosomal Peptides. Methods in Molecular Biology, 2016, 1401, 209-232.	0.4	8
92	Lysoquinone-TH1, a New Polyphenolic Tridecaketide Produced by Expressing the Lysolipin Minimal PKS II in Streptomyces albus. Antibiotics, 2018, 7, 53.	1.5	7
93	Patscanui: an intuitive web interface for searching patterns in DNA and protein data. Nucleic Acids Research, 2018, 46, W205-W208.	6.5	6
94	Genome Mining Approaches to Bacterial Natural Product Discovery. , 2020, , 19-33.		5
95	The Structure of Cyclodecatriene Collinolactone, its Biosynthesis, and Semisynthetic Analogues: Effects of Monoastral Phenotype and Protection from Intracellular Oxidative Stress. Angewandte Chemie - International Edition, 2021, 60, 23212-23216.	7.2	5
96	Genome mining in*Amycolatopsis balhimycina*for ferredoxins capable of supporting cytochrome P450 enzymes involved in glycopeptide antibiotic biosynthesis. FEMS Microbiology Letters, 2010, 306, 45-53.	0.7	4
97	Novel*Amycolatopsis balhimycina*biochemical abilities unveiled by proteomics. FEMS Microbiology Letters, 2014, 351, 209-215.	0.7	4
98	Engineering of cell factories for the production of natural products. Natural Product Reports, 2019, 36, 1231-1232.	5.2	4
99	The Draft Whole-Genome Sequence of the Antibiotic Producer Empedobacter haloabium ATCC 31962 Provides Indications for Its Taxonomic Reclassification. Microbiology Resource Announcements, 2019, 8, .	0.3	4
100	Discovery of gargantulides B and C, new 52-membered macrolactones from *Amycolatopsis* sp. Complete absolute stereochemistry of the gargantulide family. Organic Chemistry Frontiers, 2022, 9, 462-470.	2.3	4
101	Computational Applications in Secondary Metabolite Discovery (CAiSMD): an online workshop. Journal of Cheminformatics, 2021, 13, 64.	2.8	3
102	Making E. coli an Erythromycin Production Plant. Chemistry and Biology, 2010, 17, 1168-1169.	6.2	2
103	Introduction to the Special Issue â€œBioinformatic tools and approaches for Synthetic Biology of natural productsâ€• Synthetic and Systems Biotechnology, 2016, 1, 67-68.	1.8	2
104	Complete Genome Sequence of Streptomyces sp. Strain CA-256286. Microbiology Resource Announcements, 2021, 10, e0029021.	0.3	1
105	Complete Genome Sequence of the Rare Actinobacterium Kutzneria sp. Strain CA-103260. Microbiology Resource Announcements, 2021, 10, e0049921.	0.3	1
106	Complete Genome Sequence of *Amycolatopsis* sp. CA-230715, Encoding a 35-Module Type I Polyketide Synthase. Microbiology Resource Announcements, 2021, 10, e0080521.	0.3	1
107	CRISPR/Cas-based genome engineering in natural product discovery. , 0, .		1
108	Die Struktur des Cyclodecatriens Collinolacton, seine Biosynthese und semisynthetische Derivate: monopolare Spindeln und Schutz vor intrazellulÃ¤rem oxidativem Stress. Angewandte Chemie, 2021, 133, 23399.	1.6	0

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109	CLUSEAN, Overview. , 2015, , 93-95.		0