Kai Blin

List of Publications by Year
in descending order

41 papers	**13,167** citations	218381 **26** h-index	301761 **39** g-index
49 all docs	**49** docs citations	**49** times ranked	**12661** citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	BiG-FAM: the biosynthetic gene cluster families database. Nucleic Acids Research, 2021, 49, D490-D497.	6.5	122
3	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
4	antiSMASH 6.0: improving cluster detection and comparison capabilities. Nucleic Acids Research, 2021, 49, W29-W35.	6.5	1,520
5	Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from *Kutzneria* sp. CA-103260. ACS Chemical Biology, 2021, 16, 1456-1468.	1.6	8
6	A Regulator Based "Semi-Targeted" Approach to Activate Silent Biosynthetic Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 7567.	1.8	10
7	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
8	ARTS-DB: a database for antibiotic resistant targets. Nucleic Acids Research, 2021, , .	6.5	11
9	MIBiG 2.0: a repository for biosynthetic gene clusters of known function. Nucleic Acids Research, 2020, 48, D454-D458.	6.5	351
10	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
11	Designing sgRNAs for CRISPR-BEST base editing applications with CRISPy-web 2.0. Synthetic and Systems Biotechnology, 2020, 5, 99-102.	1.8	20
12	CRISPR–Cas9, CRISPRi and CRISPR-BEST-mediated genetic manipulation in streptomycetes. Nature Protocols, 2020, 15, 2470-2502.	5.5	50
13	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. Synthetic and Systems Biotechnology, 2020, 5, 11-18.	1.8	13
14	Disclosing the Potential of the SARP-Type Regulator PapR2 for the Activation of Antibiotic Gene Clusters in Streptomycetes. Frontiers in Microbiology, 2020, 11, 225.	1.5	38
15	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
16	antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. Nucleic Acids Research, 2019, 47, W81-W87.	6.5	2,410
17	The antiSMASH database version 2: a comprehensive resource on secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2019, 47, D625-D630.	6.5	150
18	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

#	Article	IF	Citations
19	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
20	Patscanui: an intuitive web interface for searching patterns in DNA and protein data. Nucleic Acids Research, 2018, 46, W205-W208.	6.5	6
21	CRISPR-Cas9 Toolkit for Actinomycete Genome Editing. Methods in Molecular Biology, 2018, 1671, 163-184.	0.4	24
22	antiSMASH 4.0â€"improvements in chemistry prediction and gene cluster boundary identification. Nucleic Acids Research, 2017, 45, W36-W41.	6.5	1,196
23	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
24	plantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters. Nucleic Acids Research, 2017, 45, W55-W63.	6.5	193
25	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. Nature Communications, 2017, 8, 15784.	5.8	287
26	Recent development of computational resources for new antibiotics discovery. Current Opinion in Microbiology, 2017, 39, 113-120.	2.3	34
27	The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2017, 45, D555-D559.	6.5	207
28	CRISPy-web: An online resource to design sgRNAs for CRISPR applications. Synthetic and Systems Biotechnology, 2016, 1, 118-121.	1.8	117
29	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	1.5	96
30	Engineering of actinomycetes using CRISPR/Cas9 technologies. Planta Medica, 2016, 81, S1-S381.	0.7	0
31	DoRiNA 2.0â€"upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. Nucleic Acids Research, 2015, 43, D160-D167.	6.5	136
32	antiSMASH 3.0â€"a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Research, 2015, 43, W237-W243.	6.5	1,764
33	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	3.9	715
34	CLUSEAN, Overview. , 2015, , 93-95.		0
35	Proteomic Approach to Reveal the Regulatory Function of Aconitase AcnA in Oxidative Stress Response in the Antibiotic Producer Streptomyces viridochromogenes TÃ¼494. PLoS ONE, 2014, 9, e87905.	1.1	14
36	Improved Lanthipeptide Detection and Prediction for antiSMASH. PLoS ONE, 2014, 9, e89420.	1.1	45

#	Article	IF	Citations
37	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
38	antiSMASH 2.0â€"a versatile platform for genome mining of secondary metabolite producers. Nucleic Acids Research, 2013, 41, W204-W212.	6.5	753
39	The bifunctional role of aconitase in <i><scp>S</scp>treptomyces viridochromogenes</i><scp>T</scp>Ã¼494. Environmental Microbiology, 2012, 14, 3203-3219.	1.8	13
40	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
41	NRPSpredictor2â€"a web server for predicting NRPS adenylation domain specificity. Nucleic Acids Research, 2011, 39, W362-W367.	6.5	559