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	antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. Nucleic Acids Research, 2019, 47, W81-W87.	6.5	2,410
2	antiSMASH 3.0â€"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 4.0â€"improvements in chemistry prediction and gene cluster boundary identification. Nucleic Acids Research, 2017, 45, W36-W41.	6.5	1,196
6	antiSMASH 2.0â€"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	NRPSpredictor2â€"a web server for predicting NRPS adenylation domain specificity. Nucleic Acids Research, 2011, 39, W362-W367.	6.5	559
9	MIBiG 2.0: a repository for biosynthetic gene clusters of known function. Nucleic Acids Research, 2020, 48, D454-D458.	6.5	351
10	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. Nature Communications, 2017, 8, 15784.	5.8	287
11	The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2017, 45, D555-D559.	6.5	207
12	plantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters. Nucleic Acids Research, 2017, 45, W55-W63.	6.5	193
13	The antiSMASH database version 2: a comprehensive resource on secondary metabolite biosynthetic gene clusters. Nucleic Acids Research, 2019, 47, D625-D630.	6.5	150
14	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
15	DoRiNA 2.0â€"upgrading the doRiNA database of RNA interactions in post-transcriptional regulation. Nucleic Acids Research, 2015, 43, D160-D167.	6.5	136
16	BiG-FAM: the biosynthetic gene cluster families database. Nucleic Acids Research, 2021, 49, D490-D497.	6.5	122
17	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
18	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

#	Article	IF	Citations
19	CRISPy-web: An online resource to design sgRNAs for CRISPR applications. Synthetic and Systems Biotechnology, 2016, 1, 118-121.	1.8	117
20	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
21	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
22	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	1.5	96
23	CRISPRâ€"Cas9, CRISPRi and CRISPR-BEST-mediated genetic manipulation in streptomycetes. Nature Protocols, 2020, 15, 2470-2502.	5.5	50
24	Improved Lanthipeptide Detection and Prediction for antiSMASH. PLoS ONE, 2014, 9, e89420.	1.1	45
25	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
26	Recent development of computational resources for new antibiotics discovery. Current Opinion in Microbiology, 2017, 39, 113-120.	2.3	34
27	CRISPR-Cas9 Toolkit for Actinomycete Genome Editing. Methods in Molecular Biology, 2018, 1671, 163-184.	0.4	24
28	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
29	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
30	Designing sgRNAs for CRISPR-BEST base editing applications with CRISPy-web 2.0. Synthetic and Systems Biotechnology, 2020, 5, 99-102.	1.8	20
31	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
32	The bifunctional role of aconitase in *S*treptomyces viridochromogenes*TÃ¼494. Environmental Microbiology, 2012, 14, 3203-3219.	1.8	13
33	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. Synthetic and Systems Biotechnology, 2020, 5, 11-18.	1.8	13
34	ARTS-DB: a database for antibiotic resistant targets. Nucleic Acids Research, 2021, , .	6.5	11
35	A Regulator Based â€œSemi-Targetedâ€•Approach to Activate Silent Biosynthetic Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 7567.	1.8	10
36	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

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37	Patscanui: an intuitive web interface for searching patterns in DNA and protein data. Nucleic Acids Research, 2018, 46, W205-W208.	6.5	6
38	Discovery of gargantulides B and C, new 52-membered macrolactones from <i>Amycolatopsis</i> sp. Complete absolute stereochemistry of the gargantulide family. Organic Chemistry Frontiers, 2022, 9, 462-470.	2.3	4
39	Complete Genome Sequence of <i>Amycolatopsis</i> sp. CA-230715, Encoding a 35-Module Type I Polyketide Synthase. Microbiology Resource Announcements, 2021, 10, e0080521.	0.3	1
40	CLUSEAN, Overview. , 2015, , 93-95.		0
41	Engineering of actinomycetes using CRISPR/Cas9 technologies. Planta Medica, 2016, 81, S1-S381.	0.7	0