

Dominik G Grimm

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

3,821
citations

331670

21
h-index

414414

32
g-index

41
all docs

41
docs citations

41
times ranked

6447
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated synthesis of steady-state continuous processes using reinforcement learning. <i>Frontiers of Chemical Science and Engineering</i> , 2022, 16, 288-302.	4.4	10
2	Machine Learning Outperforms Classical Forecasting on Horticultural Sales Predictions. <i>Machine Learning With Applications</i> , 2022, 7, 100239.	4.4	14
3	Genetic Characterization of Rat Hepatic Stellate Cell Line HSC-T6 for In Vitro Cell Line Authentication. <i>Cells</i> , 2022, 11, 1783.	4.1	11
4	Network-guided search for genetic heterogeneity between gene pairs. <i>Bioinformatics</i> , 2021, 37, 57-65.	4.1	9
5	Current challenges and best-practice protocols for microbiome analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 178-193.	6.5	268
6	Design and Analysis of RNA Sequencing Data. <i>Learning Materials in Biosciences</i> , 2021, , 143-175.	0.4	0
7	Automated Process Synthesis Using Reinforcement Learning. <i>Computer Aided Chemical Engineering</i> , 2021, 50, 209-214.	0.5	1
8	Automated Flowsheet Synthesis Using Hierarchical Reinforcement Learning: Proof of Concept. <i>Chemie-Ingenieur-Technik</i> , 2021, 93, 2010-2018.	0.8	12
9	The AIME registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , 2021, 18, 1128-1131.	19.0	38
10	AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2020, 48, D1063-D1068.	14.5	44
11	Accurate machine learning-based germination detection, prediction and quality assessment of three grain crops. <i>Plant Methods</i> , 2020, 16, 157.	4.3	41
12	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
13	Exosome-based detection of activating and resistance <i>EGFR</i> mutations from plasma of non-small cell lung cancer patients. <i>Oncotarget</i> , 2019, 10, 2911-2920.	1.8	35
14	Improved EGFR mutation detection using combined exosomal RNA and circulating tumor DNA in NSCLC patient plasma. <i>Annals of Oncology</i> , 2018, 29, 700-706.	1.2	187
15	The AraGWAS Catalog: a curated and standardized <i>Arabidopsis thaliana</i> GWAS catalog. <i>Nucleic Acids Research</i> , 2018, 46, D1150-D1156.	14.5	83
16	Exosome-Based Detection of <i>EGFR</i> T790M in Plasma from Non-Small Cell Lung Cancer Patients. <i>Clinical Cancer Research</i> , 2018, 24, 2944-2950.	7.0	157
17	Methods and Tools in Genome-wide Association Studies. <i>Methods in Molecular Biology</i> , 2018, 1819, 93-136.	0.9	11
18	Linking Genomic and Metabolomic Natural Variation Uncovers Nematode Pheromone Biosynthesis. <i>Cell Chemical Biology</i> , 2018, 25, 787-796.e12.	5.2	31

#	ARTICLE	IF	CITATIONS
19	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018, 14, e1007155.	3.5	116
20	Abstract LB-B03: Exosome-based Detection of EGFR T790M in Plasma from Non-Small Cell Lung Cancer Patients. , 2018, , .		0
21	AraPheno: a public database for <i>Arabidopsis thaliana</i> phenotypes. <i>Nucleic Acids Research</i> , 2017, 45, D1054-D1059.	14.5	91
22	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. <i>Plant Cell</i> , 2017, 29, 5-19.	6.6	98
23	Abstract 5686: Long RNA sequencing of human plasma exosomes reveals full coverage of diverse protein coding and long non coding RNA. , 2017, , .		0
24	Plasma EGFR T790M mutation detection in NSCLC patients using a combined exosomal RNA and circulating tumor DNA qPCR assay. <i>European Journal of Cancer</i> , 2016, 69, S3.	2.8	0
25	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	28.9	594
26	Genetic architecture of nonadditive inheritance in <i>Arabidopsis thaliana</i> hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7317-E7326.	7.1	58
27	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	28.9	1,107
28	Genomic Profiles of Diversification and Genotype-Phenotype Association in Island Nematode Lineages. <i>Molecular Biology and Evolution</i> , 2016, 33, 2257-2272.	8.9	31
29	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
30	The Evaluation of Tools Used to Predict the Impact of Missense Variants Is Hindered by Two Types of Circularity. <i>Human Mutation</i> , 2015, 36, 513-523.	2.5	283
31	Genome-wide detection of intervals of genetic heterogeneity associated with complex traits. <i>Bioinformatics</i> , 2015, 31, i240-i249.	4.1	23
32	Genome-wide analysis of local chromatin packing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2015, 25, 246-256.	5.5	254
33	Multi-Task Feature Selection on Multiple Networks via Maximum Flows. , 2014, , .		7
34	Accurate indel prediction using paired-end short reads. <i>BMC Genomics</i> , 2013, 14, 132.	2.8	30
35	Efficient network-guided multi-locus association mapping with graph cuts. <i>Bioinformatics</i> , 2013, 29, i171-i179.	4.1	52
36	Geometric Tree Kernels: Classification of COPD from Airway Tree Geometry. <i>Lecture Notes in Computer Science</i> , 2013, 23, 171-183.	1.3	8

#	ARTICLE	IF	CITATIONS
37	Computational inference of difficult word boundaries in DNA languages. , 2011, , .		1