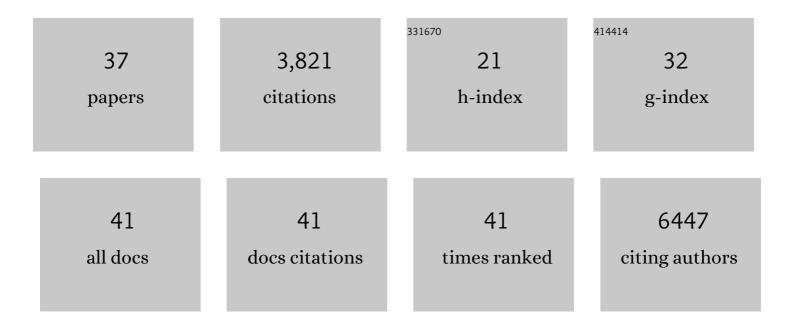
Dominik G Grimm

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8179378/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. Cell, 2016, 166, 481-491.	28.9	1,107
2	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	28.9	594
3	The Evaluation of Tools Used to Predict the Impact of Missense Variants Is Hindered by Two Types of Circularity. Human Mutation, 2015, 36, 513-523.	2.5	283
4	Current challenges and best-practice protocols for microbiome analysis. Briefings in Bioinformatics, 2021, 22, 178-193.	6.5	268
5	Genome-wide analysis of local chromatin packing in <i>Arabidopsis thaliana</i> . Genome Research, 2015, 25, 246-256.	5.5	254
6	Improved EGFR mutation detection using combined exosomal RNA and circulating tumor DNA in NSCLC patient plasma. Annals of Oncology, 2018, 29, 700-706.	1.2	187
7	Exosome-Based Detection of <i>EGFR</i> T790M in Plasma from Non–Small Cell Lung Cancer Patients. Clinical Cancer Research, 2018, 24, 2944-2950.	7.0	157
8	The rate and potential relevance of new mutations in a colonizing plant lineage. PLoS Genetics, 2018, 14, e1007155.	3.5	116
9	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. Plant Cell, 2017, 29, 5-19.	6.6	98
10	AraPheno: a public database for <i>Arabidopsis thaliana</i> phenotypes. Nucleic Acids Research, 2017, 45, D1054-D1059.	14.5	91
11	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
12	The AraGWAS Catalog: a curated and standardized Arabidopsis thaliana GWAS catalog. Nucleic Acids Research, 2018, 46, D1150-D1156.	14.5	83
13	Genetic architecture of nonadditive inheritance in <i>Arabidopsis thaliana</i> hybrids. Proceedings of the United States of America, 2016, 113, E7317-E7326.	7.1	58
14	Efficient network-guided multi-locus association mapping with graph cuts. Bioinformatics, 2013, 29, i171-i179.	4.1	52
15	AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for Arabidopsis thaliana. Nucleic Acids Research, 2020, 48, D1063-D1068.	14.5	44
16	Accurate machine learning-based germination detection, prediction and quality assessment of three grain crops. Plant Methods, 2020, 16, 157.	4.3	41
17	The AIMe registry for artificial intelligence in biomedical research. Nature Methods, 2021, 18, 1128-1131.	19.0	38
18	Exosome-based detection of activating and resistance <i>EGFR</i> mutations from plasma of non-small cell lung cancer patients. Oncotarget, 2019, 10, 2911-2920.	1.8	35

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#	Article	IF	CITATIONS
19	Genomic Profiles of Diversification and Genotype–Phenotype Association in Island Nematode Lineages. Molecular Biology and Evolution, 2016, 33, 2257-2272.	8.9	31
20	Linking Genomic and Metabolomic Natural Variation Uncovers Nematode Pheromone Biosynthesis. Cell Chemical Biology, 2018, 25, 787-796.e12.	5.2	31
21	Accurate indel prediction using paired-end short reads. BMC Genomics, 2013, 14, 132.	2.8	30
22	Genome-wide detection of intervals of genetic heterogeneity associated with complex traits. Bioinformatics, 2015, 31, i240-i249.	4.1	23
23	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
24	Machine Learning Outperforms Classical Forecasting on Horticultural Sales Predictions. Machine Learning With Applications, 2022, 7, 100239.	4.4	14
25	Automated Flowsheet Synthesis Using Hierarchical Reinforcement Learning: Proof of Concept. Chemie-Ingenieur-Technik, 2021, 93, 2010-2018.	0.8	12
26	Methods and Tools in Genome-wide Association Studies. Methods in Molecular Biology, 2018, 1819, 93-136.	0.9	11
27	Genetic Characterization of Rat Hepatic Stellate Cell Line HSC-T6 for In Vitro Cell Line Authentication. Cells, 2022, 11, 1783.	4.1	11
28	Automated synthesis of steady-state continuous processes using reinforcement learning. Frontiers of Chemical Science and Engineering, 2022, 16, 288-302.	4.4	10
29	Network-guided search for genetic heterogeneity between gene pairs. Bioinformatics, 2021, 37, 57-65.	4.1	9
30	Geometric Tree Kernels: Classification of COPD from Airway Tree Geometry. Lecture Notes in Computer Science, 2013, 23, 171-183.	1.3	8
31	Multi-Task Feature Selection on Multiple Networks via Maximum Flows. , 2014, , .		7
32	Computational inference of difficult word boundaries in DNA languages. , 2011, , .		1
33	Automated Process Synthesis Using Reinforcement Learning. Computer Aided Chemical Engineering, 2021, 50, 209-214.	0.5	1
34	Plasma EGFR T790M mutation detection in NSCLC patients using a combined exosomal RNA and circulating tumor DNA qPCR assay. European Journal of Cancer, 2016, 69, S3.	2.8	0
35	Design and Analysis of RNA Sequencing Data. Learning Materials in Biosciences, 2021, , 143-175.	0.4	0
36	Abstract 5686: Long RNA sequencing of human plasma exosomes reveals full coverage of diverse protein coding and long non coding RNA. , 2017, , .		0

#	Article	IF	CITATIONS
37	Abstract LB-B03: Exosome-based Detection ofEGFRT790M in Plasma from Non-Small Cell Lung Cancer Patients. , 2018, , .		0