Bo Peng

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1545080/publications.pdf

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50	2,296	304368	276539
papers	citations	22	41
		h-index	g-index

65	65	65	5449
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ElemCor: accurate data analysis and enrichment calculation for high-resolution LC-MS stable isotope labeling experiments. BMC Bioinformatics, 2019, 20, 89.	1.2	402
2	simuPOP: a forward-time population genetics simulation environment. Bioinformatics, 2005, 21, 3686-3687.	1.8	287
3	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2017, 72, 641-649.	0.9	170
4	Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools. Bioinformatics, 2012, 28, 421-422.	1.8	121
5	Genomeâ€Wide Association Study of Dermatomyositis Reveals Genetic Overlap With Other Autoimmune Disorders. Arthritis and Rheumatism, 2013, 65, 3239-3247.	6.7	113
6	Pharmacoproteomic analysis of prechemotherapy and postchemotherapy plasma samples from patients receiving neoadjuvant or adjuvant chemotherapy for breast carcinoma. Cancer, 2004, 100, 1814-1822.	2.0	110
7	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	1.5	96
8	Variant Association Tools for Quality Control and Analysis of Large-Scale Sequence and Genotyping Array Data. American Journal of Human Genetics, 2014, 94, 770-783.	2.6	71
9	Sarcomatoid Renal Cell Carcinoma Has a Distinct Molecular Pathogenesis, Driver Mutation Profile, and Transcriptional Landscape. Clinical Cancer Research, 2017, 23, 6686-6696.	3.2	66
10	Forward-time simulations of non-random mating populations using simuPOP. Bioinformatics, 2008, 24, 1408-1409.	1.8	64
11	Normalizing a large number of quantitative traits using empirical normal quantile transformation. BMC Proceedings, 2007, 1, S156.	1.8	55
12	Nasal administration of mesenchymal stem cells restores cisplatin-induced cognitive impairment and brain damage in mice. Oncotarget, 2018, 9, 35581-35597.	0.8	55
13	Screen for Footprints of Selection during Domestication/Captive Breeding of Atlantic Salmon. Comparative and Functional Genomics, 2012, 2012, 1-14.	2.0	50
14	Simulations Provide Support for the Common Diseaseâ€“Common Variant Hypothesis. Genetics, 2007, 175, 763-776.	1.2	47
15	Forward-Time Simulations of Human Populations with Complex Diseases. PLoS Genetics, 2007, 3, e47.	1.5	46
16	Stapled peptide inhibitors of RAB25 target context-specific phenotypes in cancer. Nature Communications, 2017, 8, 660.	5.8	44
17	Distinct Biological Types of Ocular Adnexal Sebaceous Carcinoma: HPV-Driven and Virus-Negative Tumors Arise through Nonoverlapping Molecular-Genetic Alterations. Clinical Cancer Research, 2019, 25, 1280-1290.	3.2	39
18	The fibroblast-derived protein PI16 controls neuropathic pain. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5463-5471.	3.3	39

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19	Cell-specific role of histone deacetylase 6 in chemotherapy-induced mechanical allodynia and loss of intraepidermal nerve fibers. Pain, 2019, 160, 2877-2890.	2.0	37
20	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. Modern Pathology, 2019, 32, 1698-1707.	2.9	35
21	Forward-time simulation of realistic samples for genome-wide association studies. BMC Bioinformatics, 2010, 11, 442.	1.2	30
22	Genetic Simulation Resources: a website for the registration and discovery of genetic data simulators. Bioinformatics, 2013, 29, 1101-1102.	1.8	29
23	Mutations of HNRNPA0 and WIF1 predispose members of a large family to multiple cancers. Familial Cancer, 2015, 14, 297-306.	0.9	28
24	Genetic Data Simulators and their Applications: An Overview. Genetic Epidemiology, 2015, 39, 2-10.	0.6	26
25	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	0.6	22
26	Power analysis for caseâ€“control association studies of samples with known family histories. Human Genetics, 2010, 127, 699-704.	1.8	18
27	Power analysis and sample size estimation for sequence-based association studies. Bioinformatics, 2014, 30, 2377-2378.	1.8	18
28	SNP characteristics predict replication success in association studies. Human Genetics, 2014, 133, 1477-1486.	1.8	17
29	Simulating Sequences of the Human Genome with Rare Variants. Human Heredity, 2010, 70, 287-291.	0.4	15
30	Script of Scripts: A pragmatic workflow system for daily computational research. PLoS Computational Biology, 2019, 15, e1006843.	1.5	11
31	Inhibition of dual leucine zipper kinase prevents chemotherapy-induced peripheral neuropathy and cognitive impairments. Pain, 2021, 162, 2599-2612.	2.0	10
32	Genome-wide algorithm for detecting CNV associations with diseases. BMC Bioinformatics, 2011, 12, 331.	1.2	9
33	Molecular determinants of post-mastectomy breast cancer recurrence. Npj Breast Cancer, 2018, 4, 34.	2.3	9
34	DERIVED SNP ALLELES ARE USED MORE FREQUENTLY THAN ANCESTRAL ALLELES AS RISK-ASSOCIATED VARIANTS IN COMMON HUMAN DISEASES. Journal of Bioinformatics and Computational Biology, 2012, 10, 1241008.	0.3	8
35	Reducing COVID-19 quarantine with SARS-CoV-2 testing: a simulation study. BMJ Open, 2021, 11, e050473.	0.8	8
36	Estimating the growth rates of primary lung tumours from samples with missing measurements. Statistics in Medicine, 2005, 24, 1117-1134.	0.8	7

#	Article	IF	Citations
37	Detection of disease-associated deletions in caseâ€“control studies using SNP genotypes with application to rheumatoid arthritis. Human Genetics, 2009, 126, 303-315.	1.8	7
38	SoS Notebook: an interactive multi-language data analysis environment. Bioinformatics, 2018, 34, 3768-3770.	1.8	7
39	A modified forward multiple regression in highâ€density genomeâ€wide association studies for complex traits. Genetic Epidemiology, 2009, 33, 518-525.	0.6	6
40	Genetic Simulation Resources and the GSR Certification Program. Bioinformatics, 2019, 35, 709-710.	1.8	6
41	Population simulations of COVID-19 outbreaks provide tools for risk assessment and continuity planning. JAMIA Open, 2021, 4, ooaa074.	1.0	6
42	Empirical estimation of sequencing error rates using smoothing splines. BMC Bioinformatics, 2016, 17, 177.	1.2	5
43	Simulating gene-environment interactions in complex human diseases. Genome Medicine, 2010, 2, 21.	3.6	4
44	Reproducible Simulations of Realistic Samples for Nextâ€Generation Sequencing Studies Using Variant Simulation Tools. Genetic Epidemiology, 2015, 39, 45-52.	0.6	4
45	On the application, reporting, and sharing of in silico simulations for genetic studies. Genetic Epidemiology, 2021, 45, 131-141.	0.6	4
46	Response envelope analysis for quantitative evaluation of drug combinations. Bioinformatics, 2019, 35, 3761-3770.	1.8	3
47	Genome Sequencing in the Cloud. , 2016, , 67-87.		1
48	Forward-time Simulations of Human Populations with Complex Diseases. PLoS Genetics, 2005, preprint, e47.	1.5	0
49	Linkage Analysis of Quantitative Traits. , 2009, , 119-145.		0
50	Genome Sequencing in the Cloud. Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series, 2015, , 318-339.	0.5	0