Bo Peng

List of Publications by Year
in descending order

50	2,296	304743 22	276875 41
papers	citations	h-index	g-index

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

#	Article	IF	Citations
1	On the application, reporting, and sharing of in silico simulations for genetic studies. Genetic Epidemiology, 2021, 45, 131-141.	1.3	4
2	Inhibition of dual leucine zipper kinase prevents chemotherapy-induced peripheral neuropathy and cognitive impairments. Pain, 2021, 162, 2599-2612.	4.2	10
3	Reducing COVID-19 quarantine with SARS-CoV-2 testing: a simulation study. BMJ Open, 2021, 11, e050473.	1.9	8
4	Population simulations of COVID-19 outbreaks provide tools for risk assessment and continuity planning. JAMIA Open, 2021, 4, ooaa074.	2.0	6
5	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.	7.1	39
6	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. Modern Pathology, 2019, 32, 1698-1707.	5.5	35
7	Script of Scripts: A pragmatic workflow system for daily computational research. PLoS Computational Biology, 2019, 15, e1006843.	3.2	11
8	Response envelope analysis for quantitative evaluation of drug combinations. Bioinformatics, 2019, 35, 3761-3770.	4.1	3
9	ElemCor: accurate data analysis and enrichment calculation for high-resolution LC-MS stable isotope labeling experiments. BMC Bioinformatics, 2019, 20, 89.	2.6	402
10	Cell-specific role of histone deacetylase 6 in chemotherapy-induced mechanical allodynia and loss of intraepidermal nerve fibers. Pain, 2019, 160, 2877-2890.	4.2	37
11	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.	7.0	39
12	Genetic Simulation Resources and the GSR Certification Program. Bioinformatics, 2019, 35, 709-710.	4.1	6
13	Nasal administration of mesenchymal stem cells restores cisplatin-induced cognitive impairment and brain damage in mice. Oncotarget, 2018, 9, 35581-35597.	1.8	55
14	Molecular determinants of post-mastectomy breast cancer recurrence. Npj Breast Cancer, 2018, 4, 34.	5.2	9
15	SoS Notebook: an interactive multi-language data analysis environment. Bioinformatics, 2018, 34, 3768-3770.	4.1	7
16	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2017, 72, 641-649.	1.9	170
17	Stapled peptide inhibitors of RAB25 target context-specific phenotypes in cancer. Nature Communications, 2017, 8, 660.	12.8	44
18	Sarcomatoid Renal Cell Carcinoma Has a Distinct Molecular Pathogenesis, Driver Mutation Profile, and Transcriptional Landscape. Clinical Cancer Research, 2017, 23, 6686-6696.	7.0	66

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19	Empirical estimation of sequencing error rates using smoothing splines. BMC Bioinformatics, 2016, 17, 177.	2.6	5
20	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	3.2	96
21	Genome Sequencing in the Cloud. , 2016, , 67-87.		1
22	Reproducible Simulations of Realistic Samples for Nextâ€Generation Sequencing Studies Using Variant Simulation Tools. Genetic Epidemiology, 2015, 39, 45-52.	1.3	4
23	Genetic Data Simulators and their Applications: An Overview. Genetic Epidemiology, 2015, 39, 2-10.	1.3	26
24	Mutations of HNRNPA0 and WIF1 predispose members of a large family to multiple cancers. Familial Cancer, 2015, 14, 297-306.	1.9	28
25	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
26	Genome Sequencing in the Cloud. Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series, 2015, , 318-339.	0.5	0
27	SNP characteristics predict replication success in association studies. Human Genetics, 2014, 133, 1477-1486.	3.8	17
28	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.	6.2	71
29	Power analysis and sample size estimation for sequence-based association studies. Bioinformatics, 2014, 30, 2377-2378.	4.1	18
30	Genomeâ€Wide Association Study of Dermatomyositis Reveals Genetic Overlap With Other Autoimmune Disorders. Arthritis and Rheumatism, 2013, 65, 3239-3247.	6.7	113
31	Genetic Simulation Resources: a website for the registration and discovery of genetic data simulators. Bioinformatics, 2013, 29, 1101-1102.	4.1	29
32	Screen for Footprints of Selection during Domestication/Captive Breeding of Atlantic Salmon. Comparative and Functional Genomics, 2012, 2012, 1-14.	2.0	50
33	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.	0.8	8
34	Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools. Bioinformatics, 2012, 28, 421-422.	4.1	121
35	Genome-wide algorithm for detecting CNV associations with diseases. BMC Bioinformatics, 2011, 12, 331.	2.6	9
36	Power analysis for caseâ€“control association studies of samples with known family histories. Human Genetics, 2010, 127, 699-704.	3.8	18

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37	Forward-time simulation of realistic samples for genome-wide association studies. BMC Bioinformatics, 2010, 11, 442.	2.6	30
38	Simulating Sequences of the Human Genome with Rare Variants. Human Heredity, 2010, 70, 287-291.	0.8	15
39	Simulating gene-environment interactions in complex human diseases. Genome Medicine, 2010, 2, 21.	8.2	4
40	A modified forward multiple regression in highâ€density genomeâ€wide association studies for complex traits. Genetic Epidemiology, 2009, 33, 518-525.	1.3	6
41	Detection of disease-associated deletions in caseâ€“control studies using SNP genotypes with application to rheumatoid arthritis. Human Genetics, 2009, 126, 303-315.	3.8	7
42	Linkage Analysis of Quantitative Traits. , 2009, , 119-145.		0
43	Forward-time simulations of non-random mating populations using simuPOP. Bioinformatics, 2008, 24, 1408-1409.	4.1	64
44	Forward-Time Simulations of Human Populations with Complex Diseases. PLoS Genetics, 2007, 3, e47.	3.5	46
45	Simulations Provide Support for the Common Diseaseâ€“Common Variant Hypothesis. Genetics, 2007, 175, 763-776.	2.9	47
46	Normalizing a large number of quantitative traits using empirical normal quantile transformation. BMC Proceedings, 2007, 1, S156.	1.6	55
47	Estimating the growth rates of primary lung tumours from samples with missing measurements. Statistics in Medicine, 2005, 24, 1117-1134.	1.6	7
48	simuPOP: a forward-time population genetics simulation environment. Bioinformatics, 2005, 21, 3686-3687.	4.1	287
49	Forward-time Simulations of Human Populations with Complex Diseases. PLoS Genetics, 2005, preprint, e47.	3.5	0
50	Pharmacoproteomic analysis of prechemotherapy and postchemotherapy plasma samples from patients receiving neoadjuvant or adjuvant chemotherapy for breast carcinoma. Cancer, 2004, 100, 1814-1822.	4.1	110