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List of Publications by Year
in descending order

Version: 2024-02-01

61 papers	3,934 citations	279798 23 h-index	144013 57 g-index
76 all docs	76 docs citations	76 times ranked	7563 citing authors

#	Article	IF	Citations
1	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
2	From squiggle to basepair: computational approaches for improving nanopore sequencing read accuracy. Genome Biology, 2018, 19, 90.	8.8	485
3	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	12.8	315
4	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	27.8	297
5	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. Cell, 2013, 154, 914-927.	28.9	283
6	Enhancer hubs and loop collisions identified from single-allele topologies. Nature Genetics, 2018, 50, 1151-1160.	21.4	189
7	Insertional mutagenesis identifies multiple networks of cooperating genes driving intestinal tumorigenesis. Nature Genetics, 2011, 43, 1202-1209.	21.4	172
8	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. Cell, 2008, 133, 727-741.	28.9	167
9	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. Nature Communications, 2020, 11, 728.	12.8	140
10	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2006, 2, e166.	3.2	111
11	Chromatin Landscapes of Retroviral and Transposon Integration Profiles. PLoS Genetics, 2014, 10, e1004250.	3.5	80
12	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	1.4	72
13	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	6.5	65
14	Genome Wide DNA Methylation Profiles Provide Clues to the Origin and Pathogenesis of Germ Cell Tumors. PLoS ONE, 2015, 10, e0122146.	2.5	63
15	Identification of cancer genes using a statistical framework for multiexperiment analysis of nondiscretized array CGH data. Nucleic Acids Research, 2008, 36, e13-e13.	14.5	62
16	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. PLoS Computational Biology, 2015, 11, e1004221.	3.2	45
17	Novel Candidate Cancer Genes Identified by a Large-Scale Cross-Species Comparative Oncogenomics Approach. Cancer Research, 2010, 70, 883-895.	0.9	40
18	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. Genome Biology, 2013, 14, R113.	9.6	40

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19	FERAL: network-based classifier with application to breast cancer outcome prediction. Bioinformatics, 2015, 31, i311-i319.	4.1	36
20	Molecular heterogeneity and early metastatic clone selection in testicular germ cell cancer development. British Journal of Cancer, 2019, 120, 444-452.	6.4	35
21	3D hotspots of recurrent retroviral insertions reveal long-range interactions with cancer genes. Nature Communications, 2015, 6, 6381.	12.8	34
22	Insertional Mutagenesis in Mice Deficient for p15Ink4b, p16Ink4a, p21Cip1, and p27Kip1 Reveals Cancer Gene Interactions and Correlations with Tumor Phenotypes. Cancer Research, 2010, 70, 520-531.	0.9	31
23	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. BMC Bioinformatics, 2013, 14, 29.	2.6	31
24	Multi-contact 4C: long-molecule sequencing of complex proximity ligation products to uncover local cooperative and competitive chromatin topologies. Nature Protocols, 2020, 15, 364-397.	12.0	25
25	Computational identification of insertional mutagenesis targets for cancer gene discovery. Nucleic Acids Research, 2011, 39, e105-e105.	14.5	24
26	Integration of gene expression and DNA-methylation profiles improves molecular subtype classification in acute myeloid leukemia. BMC Bioinformatics, 2015, 16, S5.	2.6	24
27	Predicting treatment benefit in multiple myeloma through simulation of alternative treatment effects. Nature Communications, 2018, 9, 2943.	12.8	23
28	Co-occurrence analysis of insertional mutagenesis data reveals cooperating oncogenes. Bioinformatics, 2007, 23, i133-i141.	4.1	20
29	RAINFOREST: a random forest approach to predict treatment benefit in data from (failed) clinical drug trials. Bioinformatics, 2020, 36, i601-i609.	4.1	20
30	Insertional Mutagenesis and Deep Profiling Reveals Gene Hierarchies and a Myc/p53-Dependent Bottleneck in Lymphomagenesis. PLoS Genetics, 2014, 10, e1004167.	3.5	17
31	sv-callers: a highly portable parallel workflow for structural variant detection in whole-genome sequence data. PeerJ, 2020, 8, e8214.	2.0	17
32	Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities. PLoS Computational Biology, 2014, 10, e1003708.	3.2	15
33	MetaboShiny: interactive analysis and metabolite annotation of mass spectrometry-based metabolomics data. Metabolomics, 2020, 16, 99.	3.0	15
34	Cancer Type Classification in Liquid Biopsies Based on Sparse Mutational Profiles Enabled through Data Augmentation and Integration. Life, 2022, 12, 1.	2.4	15
35	Accurate detection of circulating tumor DNA using nanopore consensus sequencing. Npj Genomic Medicine, 2021, 6, 106.	3.8	14
36	A data-driven interactome of synergistic genes improves network-based cancer outcome prediction. PLoS Computational Biology, 2019, 15, e1006657.	3.2	13

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37	Allele-specific expression of GATA2 due to epigenetic dysregulation in CEBPA double-mutant AML. Blood, 2021, 138, 160-177.	1.4	13
38	Integration of multiple lineage measurements from the same cell reconstructs parallel tumor evolution. Cell Genomics, 2022, 2, 100096.	6.5	13
39	Scale-space measures for graph topology link protein network architecture to function. Bioinformatics, 2014, 30, i237-i245.	4.1	12
40	Alternate approach to stroke phenotyping identifies a genetic risk locus for small vessel stroke. European Journal of Human Genetics, 2020, 28, 963-972.	2.8	12
41	Highlights from the 5th International Society for Computational Biology Student Council Symposium at the 17th Annual International Conference on Intelligent Systems for Molecular Biology and the 8th European Conference on Computational Biology. BMC Bioinformatics, 2009, 10, I1.	2.6	10
42	An Electronic Throttle Simulation Model with Automatic Parameter Tuning. , 0, , .		9
43	Three-dimensional analysis of single molecule FISH in human colon organoids. Biology Open, 2019, 8, .	1.2	9
44	Gamma-Retrovirus Integration Marks Cell Type-Specific Cancer Genes: A Novel Profiling Tool in Cancer Genomics. PLoS ONE, 2016, 11, e0154070.	2.5	8
45	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5747-5752.	7.1	7
46	TargetClone: A multi-sample approach for reconstructing subclonal evolution of tumors. PLoS ONE, 2018, 13, e0208002.	2.5	7
47	A Single Complex Agpat2 Allele in a Patient With Partial Lipodystrophy. Frontiers in Physiology, 2018, 9, 1363.	2.8	7
48	HAT: Hypergeometric Analysis of Tiling-arrays with application to promoter-GeneChip data. BMC Bioinformatics, 2010, 11, 275.	2.6	6
49	Applications of DNA integrating elements: Facing the bias bully. Mobile Genetic Elements, 2014, 4, 1-6.	1.8	5
50	Gene Networks Constructed Through Simulated Treatment Learning can Predict Proteasome Inhibitor Benefit in Multiple Myeloma. Clinical Cancer Research, 2020, 26, 5952-5961.	7.0	5
51	Integrating Protein Family Sequence Similarities with Gene Expression to Find Signature Gene Networks in Breast Cancer Metastasis. Lecture Notes in Computer Science, 2011, , 247-259.	1.3	4
52	svMIL: predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants throughÂmultiple instance learning. Bioinformatics, 2020, 36, i692-i699.	4.1	4
53	PolarMorphism enables discovery of shared genetic variants across multiple traits from GWAS summary statistics. Bioinformatics, 2022, 38, i212-i219.	4.1	4
54	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. PLoS Computational Biology, 2013, 9, e1002834.	3.2	3

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55	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	3.2	2
56	ECCB 2016: The 15th European Conference on Computational Biology. Bioinformatics, 2016, 32, i389-i392.	4.1	2
57	A portable and scalable workflow for detecting structural variants in whole-genome sequencing data. , 2018, , .		1
58	Predicting pathogenic non-coding SVs disrupting the 3D genome in 1646 whole cancer genomes using multiple instance learning. Scientific Reports, 2021, 11, 14411.	3.3	1
59	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2005, preprint, e166.	3.2	1
60	Adavosertib in combination with carboplatin in advanced TP53-mutated platinum-resistant ovarian cancer.. Journal of Clinical Oncology, 2022, 40, 5516-5516.	1.6	1
61	Mutational Genomics for Cancer Pathway Discovery. Lecture Notes in Computer Science, 2013, , 35-46.	1.3	0