Benjamin J Raphael

List of Publications by Year
in descending order

84 papers	17,852 citations	66343 42 h-index	66911 78 g-index
108 all docs	108 docs citations	108 times ranked	27998 citing authors

#	Article	IF	Citations
1	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
2	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
3	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
4	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
5	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	21.4	830
6	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
7	Network propagation: a universal amplifier of genetic associations. Nature Reviews Genetics, 2017, 18, 551-562.	16.3	514
8	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
9	Algorithms for Detecting Significantly Mutated Pathways in Cancer. Journal of Computational Biology, 2011, 18, 507-522.	1.6	434
10	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
11	De novo discovery of mutated driver pathways in cancer. Genome Research, 2012, 22, 375-385.	5.5	391
12	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	19.0	297
13	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
14	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
15	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
16	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
17	Simultaneous Identification of Multiple Driver Pathways in Cancer. PLoS Computational Biology, 2013, 9, e1003054.	3.2	231
18	THetA: inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. Genome Biology, 2013, 14, R80.	9.6	209

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19	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70.	4.1	194
20	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. Genome Medicine, 2014, 6, 5.	8.2	186
21	CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. Genome Biology, 2015, 16, 160.	8.8	182
22	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
23	Expanding the computational toolbox for mining cancer genomes. Nature Reviews Genetics, 2014, 15, 556-570.	16.3	166
24	Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. Genome Research, 2017, 27, 1885-1894.	5.5	156
25	Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53.	6.2	140
26	A geometric approach for classification and comparison of structural variants. Bioinformatics, 2009, 25, i222-i230.	4.1	138
27	Identification of hierarchical chromatin domains. Bioinformatics, 2016, 32, 1601-1609.	4.1	134
28	An integrative probabilistic model for identification of structural variation in sequencing data. Genome Biology, 2012, 13, R22.	9.6	123
29	Quantifying tumor heterogeneity in whole-genome and whole-exome sequencing data. Bioinformatics, 2014, 30, 3532-3540.	4.1	115
30	Visible Machine Learning for Biomedicine. Cell, 2018, 173, 1562-1565.	28.9	115
31	Hierarchical HotNet: identifying hierarchies of altered subnetworks. Bioinformatics, 2018, 34, i972-i980.	4.1	102
32	A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data. Bioinformatics, 2014, 30, i78-i86.	4.1	100
33	Characterizing allele- and haplotype-specific copy numbers in single cells with CHISEL. Nature Biotechnology, 2021, 39, 207-214.	17.5	97
34	Network analysis of GWAS data. Current Opinion in Genetics and Development, 2013, 23, 602-610.	3.3	95
35	Inferring parsimonious migration histories for metastatic cancers. Nature Genetics, 2018, 50, 718-726.	21.4	93
36	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	12.8	73

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37	Alignment and integration of spatial transcriptomics data. Nature Methods, 2022, 19, 567-575.	19.0	73
38	Expression Profiling of Primary and Metastatic Ovarian Tumors Reveals Differences Indicative of Aggressive Disease. PLoS ONE, 2014, 9, e94476.	2.5	66
39	Accurate quantification of copy-number aberrations and whole-genome duplications in multi-sample tumor sequencing data. Nature Communications, 2020, 11, 4301.	12.8	62
40	netNMF-sc: leveraging geneâ€“gene interactions for imputation and dimensionality reduction in single-cell expression analysis. Genome Research, 2020, 30, 195-204.	5.5	61
41	SCARLET: Single-Cell Tumor Phylogeny Inference with Copy-Number Constrained Mutation Losses. Cell Systems, 2020, 10, 323-332.e8.	6.2	61
42	Identifying structural variants using linked-read sequencing data. Bioinformatics, 2018, 34, 353-360.	4.1	60
43	DISCOVERY OF MUTATED SUBNETWORKS ASSOCIATED WITH CLINICAL DATA IN CANCER. , 2011, , .		59
44	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. Nature Communications, 2021, 12, 5086.	12.8	58
45	Characterization of structural variants with single molecule and hybrid sequencing approaches. Bioinformatics, 2014, 30, 3458-3466.	4.1	56
46	Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases. Genetics, 2016, 204, 783-798.	2.9	56
47	A weighted exact test for mutually exclusive mutations in cancer. Bioinformatics, 2016, 32, i736-i745.	4.1	46
48	Tumor phylogeny inference using tree-constrained importance sampling. Bioinformatics, 2017, 33, i152-i160.	4.1	46
49	CALDER: Inferring Phylogenetic Trees from Longitudinal Tumor Samples. Cell Systems, 2019, 8, 514-522.e5.	6.2	46
50	Detecting non-allelic homologous recombination from high-throughput sequencing data. Genome Biology, 2015, 16, 72.	8.8	40
51	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
52	Reconstructing cancer genomes from paired-end sequencing data. BMC Bioinformatics, 2012, 13, S10.	2.6	36
53	STARCH: copy number and clone inference from spatial transcriptomics data. Physical Biology, 2021, 18, 035001.	1.8	35
54	Structural variation analysis with strobe reads. Bioinformatics, 2010, 26, 1291-1298.	4.1	33

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55	A sequence-based survey of the complex structural organization of tumor genomes. Genome Biology, 2008, 9, R59.	9.6	31
56	Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. Journal of Computational Biology, 2015, 22, 510-527.	1.6	28
57	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708.	1.6	28
58	Complexity and algorithms for copy-number evolution problems. Algorithms for Molecular Biology, 2017, 12, 13.	1.2	27
59	Chapter 6: Structural Variation and Medical Genomics. PLoS Computational Biology, 2012, 8, e1002821.	3.2	26
60	MAGI: visualization and collaborative annotation of genomic aberrations. Nature Methods, 2015, 12, 483-484.	19.0	25
61	Accurate Computation of Survival Statistics in Genome-Wide Studies. PLoS Computational Biology, 2015, 11, e1004071.	3.2	24
62	Reconstructing tumor amplisomes. Bioinformatics, 2004, 20, i265-i273.	4.1	22
63	Detecting independent and recurrent copy number aberrations using interval graphs. Bioinformatics, 2014, 30, i195-i203.	4.1	22
64	Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149.	1.3	17
65	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	5.5	15
66	Identifying tumor clones in sparse single-cell mutation data. Bioinformatics, 2020, 36, i186-i193.	4.1	15
67	Haplotype phasing in single-cell DNA-sequencing data. Bioinformatics, 2018, 34, i211-i217.	4.1	13
68	Reconstruction of clone- and haplotype-specific cancer genome karyotypes from bulk tumor samples. Genome Research, 2020, 30, 1274-1290.	5.5	12
69	DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. Cell Systems, 2021, 12, 1004-1018.e10.	6.2	12
70	Copy number evolution with weighted aberrations in cancer. Bioinformatics, 2020, 36, i344-i352.	4.1	11
71	NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. Journal of Computational Biology, 2021, 28, 469-484.	1.6	8
72	Novel Gene and Network Associations Found for Acute Lymphoblastic Leukemia Using Caseâ€“Control and Family-Based Studies in Multiethnic Populations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1531-1539.	2.5	7

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73	On the Sample Complexity of Cancer Pathways Identification. Journal of Computational Biology, 2016, 23, 30-41.	1.6	6
74	Open adjacencies and k-breaks: detecting simultaneous rearrangements in cancer genomes. BMC Genomics, 2014, 15, S4.	2.8	5
75	Identifying simultaneous rearrangements in cancer genomes. Bioinformatics, 2018, 34, 346-352.	4.1	4
76	Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. Nature Genetics, 2016, 48, 106-108.	21.4	2
77	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099.	6.5	2
78	A PARSIMONY APPROACH TO ANALYSIS OF HUMAN SEGMENTAL DUPLICATIONS. , 2008, , .		1
79	MODELING CELL HETEROGENEITY: FROM SINGLE-CELL VARIATIONS TO MIXED CELLS. , 2012, , .		1
80	Workshop: Algorithms for discovery of mutated pathways in cancer. , 2012, , .		0
81	POST-NGS: INTERPRETATION AND ANALYSIS OF NEXT GENERATION SEQUENCING DATA FOR BASIC AND TRANSLATIONAL SCIENCE. , 2012, , .		0
82	Identifying significant mutations in large cohorts of cancer genomes. , 2013, , .		0
83	Workshop: Reconstructing the organization of cancer genomes. , 2013, , .		0
84	Using controls to limit false discovery in the era of big data. BMC Bioinformatics, 2018, 19, 323.	2.6	0