Benjamin J Raphael

List of Publications by Year
in descending order

84 papers	17,852 citations	66234 42 h-index	66788 78 g-index
108 all docs	108 docs citations	108 times ranked	27998 citing authors

#	Article	IF	Citations
1	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099.	3.0	2
2	Alignment and integration of spatial transcriptomics data. Nature Methods, 2022, 19, 567-575.	9.0	73
3	Characterizing allele- and haplotype-specific copy numbers in single cells with CHISEL. Nature Biotechnology, 2021, 39, 207-214.	9.4	97
4	STARCH: copy number and clone inference from spatial transcriptomics data. Physical Biology, 2021, 18, 035001.	0.8	35
5	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
6	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. Nature Communications, 2021, 12, 5086.	5.8	58
7	DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. Cell Systems, 2021, 12, 1004-1018.e10.	2.9	12
8	NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. Journal of Computational Biology, 2021, 28, 469-484.	0.8	8
9	Reconstruction of clone- and haplotype-specific cancer genome karyotypes from bulk tumor samples. Genome Research, 2020, 30, 1274-1290.	2.4	12
10	Identifying tumor clones in sparse single-cell mutation data. Bioinformatics, 2020, 36, i186-i193.	1.8	15
11	Copy number evolution with weighted aberrations in cancer. Bioinformatics, 2020, 36, i344-i352.	1.8	11
12	Accurate quantification of copy-number aberrations and whole-genome duplications in multi-sample tumor sequencing data. Nature Communications, 2020, 11, 4301.	5.8	62
13	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
14	netNMF-sc: leveraging geneâ€“gene interactions for imputation and dimensionality reduction in single-cell expression analysis. Genome Research, 2020, 30, 195-204.	2.4	61
15	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
16	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
17	SCARLET: Single-Cell Tumor Phylogeny Inference with Copy-Number Constrained Mutation Losses. Cell Systems, 2020, 10, 323-332.e8.	2.9	61
18	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	0.6	171

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19	CALDER: Inferring Phylogenetic Trees from Longitudinal Tumor Samples. Cell Systems, 2019, 8, 514-522.e5.	2.9	46
20	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	1.5	40
21	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708.	0.8	28
22	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
23	Identifying structural variants using linked-read sequencing data. Bioinformatics, 2018, 34, 353-360.	1.8	60
24	Identifying simultaneous rearrangements in cancer genomes. Bioinformatics, 2018, 34, 346-352.	1.8	4
25	Inferring parsimonious migration histories for metastatic cancers. Nature Genetics, 2018, 50, 718-726.	9.4	93
26	Using controls to limit false discovery in the era of big data. BMC Bioinformatics, 2018, 19, 323.	1.2	0
27	Hierarchical HotNet: identifying hierarchies of altered subnetworks. Bioinformatics, 2018, 34, i972-i980.	1.8	102
28	Haplotype phasing in single-cell DNA-sequencing data. Bioinformatics, 2018, 34, i211-i217.	1.8	13
29	Visible Machine Learning for Biomedicine. Cell, 2018, 173, 1562-1565.	13.5	115
30	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	2.4	15
31	Network propagation: a universal amplifier of genetic associations. Nature Reviews Genetics, 2017, 18, 551-562.	7.7	514
32	Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. Genome Research, 2017, 27, 1885-1894.	2.4	156
33	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.	1.1	7
34	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
35	Complexity and algorithms for copy-number evolution problems. Algorithms for Molecular Biology, 2017, 12, 13.	0.3	27
36	Tumor phylogeny inference using tree-constrained importance sampling. Bioinformatics, 2017, 33, i152-i160.	1.8	46

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37	A weighted exact test for mutually exclusive mutations in cancer. Bioinformatics, 2016, 32, i736-i745.	1.8	46
38	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
39	Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149.	1.0	17
40	Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. Cell Systems, 2016, 3, 43-53.	2.9	140
41	Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases. Genetics, 2016, 204, 783-798.	1.2	56
42	Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. Nature Genetics, 2016, 48, 106-108.	9.4	2
43	On the Sample Complexity of Cancer Pathways Identification. Journal of Computational Biology, 2016, 23, 30-41.	0.8	6
44	Identification of hierarchical chromatin domains. Bioinformatics, 2016, 32, 1601-1609.	1.8	134
45	Detecting non-allelic homologous recombination from high-throughput sequencing data. Genome Biology, 2015, 16, 72.	3.8	40
46	CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. Genome Biology, 2015, 16, 160.	3.8	182
47	Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. Journal of Computational Biology, 2015, 22, 510-527.	0.8	28
48	MAGI: visualization and collaborative annotation of genomic aberrations. Nature Methods, 2015, 12, 483-484.	9.0	25
49	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	5.8	243
50	Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. Bioinformatics, 2015, 31, i62-i70.	1.8	194
51	Accurate Computation of Survival Statistics in Genome-Wide Studies. PLoS Computational Biology, 2015, 11, e1004071.	1.5	24
52	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	9.0	297
53	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
54	Expression Profiling of Primary and Metastatic Ovarian Tumors Reveals Differences Indicative of Aggressive Disease. PLoS ONE, 2014, 9, e94476.	1.1	66

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55	A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data. Bioinformatics, 2014, 30, i78-i86.	1.8	100
56	Detecting independent and recurrent copy number aberrations using interval graphs. Bioinformatics, 2014, 30, i195-i203.	1.8	22
57	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
58	Characterization of structural variants with single molecule and hybrid sequencing approaches. Bioinformatics, 2014, 30, 3458-3466.	1.8	56
59	Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. Genome Medicine, 2014, 6, 5.	3.6	186
60	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
61	Expanding the computational toolbox for mining cancer genomes. Nature Reviews Genetics, 2014, 15, 556-570.	7.7	166
62	Quantifying tumor heterogeneity in whole-genome and whole-exome sequencing data. Bioinformatics, 2014, 30, 3532-3540.	1.8	115
63	Open adjacencies and k-breaks: detecting simultaneous rearrangements in cancer genomes. BMC Genomics, 2014, 15, S4.	1.2	5
64	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	13.7	3,695
65	Network analysis of GWAS data. Current Opinion in Genetics and Development, 2013, 23, 602-610.	1.5	95
66	THetA: inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. Genome Biology, 2013, 14, R80.	13.9	209
67	Simultaneous Identification of Multiple Driver Pathways in Cancer. PLoS Computational Biology, 2013, 9, e1003054.	1.5	231
68	Identifying significant mutations in large cohorts of cancer genomes. , 2013, , .		0
69	Workshop: Reconstructing the organization of cancer genomes. , 2013, , .		0
70	Chapter 6: Structural Variation and Medical Genomics. PLoS Computational Biology, 2012, 8, e1002821.	1.5	26
71	Workshop: Algorithms for discovery of mutated pathways in cancer. , 2012, , .		0
72	MODELING CELL HETEROGENEITY: FROM SINGLE-CELL VARIATIONS TO MIXED CELLS. , 2012, , .		1

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73	POST-NGS: INTERPRETATION AND ANALYSIS OF NEXT GENERATION SEQUENCING DATA FOR BASIC AND TRANSLATIONAL SCIENCE. , 2012, , .		0
74	An integrative probabilistic model for identification of structural variation in sequencing data. Genome Biology, 2012, 13, R22.	13.9	123
75	De novo discovery of mutated driver pathways in cancer. Genome Research, 2012, 22, 375-385.	2.4	391
76	Reconstructing cancer genomes from paired-end sequencing data. BMC Bioinformatics, 2012, 13, S10.	1.2	36
77	DISCOVERY OF MUTATED SUBNETWORKS ASSOCIATED WITH CLINICAL DATA IN CANCER. , 2011, , .		59
78	Algorithms for Detecting Significantly Mutated Pathways in Cancer. Journal of Computational Biology, 2011, 18, 507-522.	0.8	434
79	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
80	Structural variation analysis with strobe reads. Bioinformatics, 2010, 26, 1291-1298.	1.8	33
81	A geometric approach for classification and comparison of structural variants. Bioinformatics, 2009, 25, i222-i230.	1.8	138
82	A sequence-based survey of the complex structural organization of tumor genomes. Genome Biology, 2008, 9, R59.	13.9	31
83	A PARSIMONY APPROACH TO ANALYSIS OF HUMAN SEGMENTAL DUPLICATIONS. , 2008, , .		1
84	Reconstructing tumor amplisomes. Bioinformatics, 2004, 20, i265-i273.	1.8	22