

Nathan C Sheffield

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

58 papers	17,728 citations	24 h-index	77 g-index
77 ext. papers	22,051 ext. citations	13 avg, IF	8.18 L-index

#	Paper	IF	Citations
58	Detecting molecular subtypes from multi-omics datasets using SUMO.. <i>Cell Reports Methods</i> , 2022 , 2, 100152-100152		1
57	GenomicDistributions: fast analysis of genomic intervals with Bioconductor.. <i>BMC Genomics</i> , 2022 , 23, 299	4.5	0
56	PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab101	3.7	3
55	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
54	Identity and compatibility of reference genome resources. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab036	3.7	4
53	Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines. <i>GigaScience</i> , 2021 , 10,	7.6	2
52	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. <i>Nature Communications</i> , 2021 , 12, 3230	17.4	17
51	PEPPRO: quality control and processing of nascent RNA profiling data. <i>Genome Biology</i> , 2021 , 22, 155	18.3	7
50	Embeddings of genomic region sets capture rich biological associations in lower dimensions. <i>Bioinformatics</i> , 2021 ,	7.2	1
49	Refget: standardised access to reference sequences. <i>Bioinformatics</i> , 2021 ,	7.2	4
48	Bedshift: perturbation of genomic interval sets. <i>Genome Biology</i> , 2021 , 22, 238	18.3	4
47	Linking big biomedical datasets to modular analysis with Portable Encapsulated Projects. <i>GigaScience</i> , 2021 , 10,	7.6	3
46	Refgenie: a reference genome resource manager. <i>GigaScience</i> , 2020 , 9,	7.6	15
45	Analytical Approaches for ATAC-seq Data Analysis. <i>Current Protocols in Human Genetics</i> , 2020 , 106, e1013.2		4
44	Seqpare: a self-consistent metric of similarity between genomic interval sets. <i>F1000Research</i> , 2020 , 9, 581	3.6	4
43	IGD: high-performance search for large-scale genomic interval datasets. <i>Bioinformatics</i> , 2020 ,	7.2	2
42	COCOA: coordinate covariation analysis of epigenetic heterogeneity. <i>Genome Biology</i> , 2020 , 21, 240	18.3	8

41	: a self-consistent metric of similarity between genomic interval sets. <i>F1000Research</i> , 2020 , 9, 581	3.6	1
40	Augmented Interval List: a novel data structure for efficient genomic interval search. <i>Bioinformatics</i> , 2019 , 35, 4907-4911	7.2	9
39	MIRA: an R package for DNA methylation-based inference of regulatory activity. <i>Bioinformatics</i> , 2018 , 34, 2649-2650	7.2	11
38	BART: a transcription factor prediction tool with query gene sets or epigenomic profiles. <i>Bioinformatics</i> , 2018 , 34, 2867-2869	7.2	46
37	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. <i>Nature Medicine</i> , 2018 , 24, 1611-1624	50.5	124
36	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucleic Acids Research</i> , 2018 , 46, W186-W193	20.1	13
35	simpleCache: R caching for reproducible, distributed, large-scale projects. <i>Journal of Open Source Software</i> , 2018 , 3, 463	5.2	1
34	LOLAweb: a containerized web server for interactive genomic locus overlap enrichment analysis. <i>Nucleic Acids Research</i> , 2018 , 46, W194-W199	20.1	14
33	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
32	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. <i>Nature Medicine</i> , 2017 , 23, 386-395	50.5	128
31	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , 2017 , 18, 15	18.3	61
30	LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. <i>Bioinformatics</i> , 2016 , 32, 587-9	7.2	194
29	The second European interdisciplinary Ewing sarcoma research summit--A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , 2016 , 7, 8613-24	3.3	38
28	Multi-Omics of Single Cells: Strategies and Applications. <i>Trends in Biotechnology</i> , 2016 , 34, 605-608	15.1	99
27	Single-cell DNA methylome sequencing and bioinformatic inference of epigenomic cell-state dynamics. <i>Cell Reports</i> , 2015 , 10, 1386-97	10.6	290
26	Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. <i>Cell Reports</i> , 2015 , 10, 1082-95	10.6	129
25	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. <i>Nature Methods</i> , 2015 , 12, 963-965	21.6	267
24	Differential DNA Methylation Analysis without a Reference Genome. <i>Cell Reports</i> , 2015 , 13, 2621-2633	10.6	21

23	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. <i>Genome Research</i> , 2013 , 23, 777-88	9.7	153
22	The Interaction between Base Compositional Heterogeneity and Among-Site Rate Variation in Models of Molecular Evolution 2013 , 2013, 1-8		3
21	Chromatin accessibility reveals insights into androgen receptor activation and transcriptional specificity. <i>Genome Biology</i> , 2012 , 13, R88	18.3	53
20	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
19	Predicting cell-type-specific gene expression from regions of open chromatin. <i>Genome Research</i> , 2012 , 22, 1711-22	9.7	175
18	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012 , 489, 75-82	50.4	1900
17	Identifying and characterizing regulatory sequences in the human genome with chromatin accessibility assays. <i>Genes</i> , 2012 , 3, 651-70	4.2	24
16	Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection. <i>PLoS Genetics</i> , 2012 , 8, e1002789	6	85
15	Abstract A12: Chromatin accessibility reveals insight into androgen receptor activation and transcriptional specificity. <i>Cancer Research</i> , 2012 , 72, A12-A12	10.1	
14	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
13	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , 2011 , 21, 1757-67	9.7	391
12	Mitochondrial genomics in Orthoptera using MOSAS. <i>Mitochondrial DNA</i> , 2010 , 21, 87-104		55
11	When phylogenetic assumptions are violated: base compositional heterogeneity and among-site rate variation in beetle mitochondrial phylogenomics. <i>Systematic Entomology</i> , 2010 , 35, 429-448	3.4	102
10	Nonstationary evolution and compositional heterogeneity in beetle mitochondrial phylogenomics. <i>Systematic Biology</i> , 2009 , 58, 381-94	8.4	134
9	A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2499-509	8.3	183
8	Calculating expected DNA remnants from ancient founding events in human population genetics. <i>BMC Genetics</i> , 2008 , 9, 66	2.6	
7	Bulker: a multi-container environment manager		7
6	Augmented Interval List: a novel data structure for efficient genomic interval search		1

5	IGD: high-performance search for large-scale genomic interval datasets	1
4	Linking big biomedical datasets to modular analysis with Portable Encapsulated Projects	3
3	PEPATAC: An optimized pipeline for ATAC-seq data analysis with serial alignments	4
2	Bedshift: perturbation of genomic interval sets	1
1	Refgenie: a reference genome resource manager	4