

# Nathan C Sheffield

## List of Publications by Citations

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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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
57	The accessible chromatin landscape of the human genome. <i>Nature</i> , <b>2012</b> , 489, 75-82	50.4	1900
56	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
55	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , <b>2018</b> , 362,	33.3	392
54	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , <b>2011</b> , 21, 1757-67	9.7	391
53	Single-cell DNA methylome sequencing and bioinformatic inference of epigenomic cell-state dynamics. <i>Cell Reports</i> , <b>2015</b> , 10, 1386-97	10.6	290
52	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. <i>Nature Methods</i> , <b>2015</b> , 12, 963-965	21.6	267
51	LOLA: enrichment analysis for genomic region sets and regulatory elements in R and Bioconductor. <i>Bioinformatics</i> , <b>2016</b> , 32, 587-9	7.2	194
50	A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 2499-509	8.3	183
49	Predicting cell-type-specific gene expression from regions of open chromatin. <i>Genome Research</i> , <b>2012</b> , 22, 1711-22	9.7	175
48	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. <i>Genome Research</i> , <b>2013</b> , 23, 777-88	9.7	153
47	Nonstationary evolution and compositional heterogeneity in beetle mitochondrial phylogenomics. <i>Systematic Biology</i> , <b>2009</b> , 58, 381-94	8.4	134
46	Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1. <i>Cell Reports</i> , <b>2015</b> , 10, 1082-95	10.6	129
45	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. <i>Nature Medicine</i> , <b>2017</b> , 23, 386-395	50.5	128
44	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. <i>Nature Medicine</i> , <b>2018</b> , 24, 1611-1624	50.5	124
43	When phylogenetic assumptions are violated: base compositional heterogeneity and among-site rate variation in beetle mitochondrial phylogenomics. <i>Systematic Entomology</i> , <b>2010</b> , 35, 429-448	3.4	102
42	Multi-Omics of Single Cells: Strategies and Applications. <i>Trends in Biotechnology</i> , <b>2016</b> , 34, 605-608	15.1	99

41	Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002789	6	85
40	Single-cell epigenomic variability reveals functional cancer heterogeneity. <i>Genome Biology</i> , <b>2017</b> , 18, 15	18.3	61
39	Mitochondrial genomics in Orthoptera using MOSAS. <i>Mitochondrial DNA</i> , <b>2010</b> , 21, 87-104		55
38	Chromatin accessibility reveals insights into androgen receptor activation and transcriptional specificity. <i>Genome Biology</i> , <b>2012</b> , 13, R88	18.3	53
37	BART: a transcription factor prediction tool with query gene sets or epigenomic profiles. <i>Bioinformatics</i> , <b>2018</b> , 34, 2867-2869	7.2	46
36	The second European interdisciplinary Ewing sarcoma research summit--A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , <b>2016</b> , 7, 8613-24	3.3	38
35	Identifying and characterizing regulatory sequences in the human genome with chromatin accessibility assays. <i>Genes</i> , <b>2012</b> , 3, 651-70	4.2	24
34	Differential DNA Methylation Analysis without a Reference Genome. <i>Cell Reports</i> , <b>2015</b> , 13, 2621-2633	10.6	21
33	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , <b>2021</b> , 1, 100029-100029		20
32	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. <i>Nature Communications</i> , <b>2021</b> , 12, 3230	17.4	17
31	Refgenie: a reference genome resource manager. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	15
30	LOLAweb: a containerized web server for interactive genomic locus overlap enrichment analysis. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W194-W199	20.1	14
29	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W186-W193	20.1	13
28	MIRA: an R package for DNA methylation-based inference of regulatory activity. <i>Bioinformatics</i> , <b>2018</b> , 34, 2649-2650	7.2	11
27	Augmented Interval List: a novel data structure for efficient genomic interval search. <i>Bioinformatics</i> , <b>2019</b> , 35, 4907-4911	7.2	9
26	COCOA: coordinate covariation analysis of epigenetic heterogeneity. <i>Genome Biology</i> , <b>2020</b> , 21, 240	18.3	8
25	Bulker: a multi-container environment manager		7
24	PEPPRO: quality control and processing of nascent RNA profiling data. <i>Genome Biology</i> , <b>2021</b> , 22, 155	18.3	7

23	Analytical Approaches for ATAC-seq Data Analysis. <i>Current Protocols in Human Genetics</i> , <b>2020</b> , 106, e1013.2	4
22	Sequare: a self-consistent metric of similarity between genomic interval sets. <i>F1000Research</i> , <b>2020</b> , 9, 581	3.6 4
21	PEPATAC: An optimized pipeline for ATAC-seq data analysis with serial alignments	4
20	Refgenie: a reference genome resource manager	4
19	Identity and compatibility of reference genome resources. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab036	3.7 4
18	Refget: standardised access to reference sequences. <i>Bioinformatics</i> , <b>2021</b> ,	7.2 4
17	Bedshift: perturbation of genomic interval sets. <i>Genome Biology</i> , <b>2021</b> , 22, 238	18.3 4
16	PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab101	3.7 3
15	The Interaction between Base Compositional Heterogeneity and Among-Site Rate Variation in Models of Molecular Evolution <b>2013</b> , 2013, 1-8	3
14	Linking big biomedical datasets to modular analysis with Portable Encapsulated Projects	3
13	Linking big biomedical datasets to modular analysis with Portable Encapsulated Projects. <i>GigaScience</i> , <b>2021</b> , 10,	7.6 3
12	IGD: high-performance search for large-scale genomic interval datasets. <i>Bioinformatics</i> , <b>2020</b> ,	7.2 2
11	Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines. <i>GigaScience</i> , <b>2021</b> , 10,	7.6 2
10	Detecting molecular subtypes from multi-omics datasets using SUMO.. <i>Cell Reports Methods</i> , <b>2022</b> , 2, 100152-100152	1
9	simpleCache: R caching for reproducible, distributed, large-scale projects. <i>Journal of Open Source Software</i> , <b>2018</b> , 3, 463	5.2 1
8	Augmented Interval List: a novel data structure for efficient genomic interval search	1
7	IGD: high-performance search for large-scale genomic interval datasets	1
6	Bedshift: perturbation of genomic interval sets	1

5	Embeddings of genomic region sets capture rich biological associations in lower dimensions. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
4	: a self-consistent metric of similarity between genomic interval sets. <i>F1000Research</i> , <b>2020</b> , 9, 581	3.6	1
3	GenomicDistributions: fast analysis of genomic intervals with Bioconductor.. <i>BMC Genomics</i> , <b>2022</b> , 23, 299	4.5	0
2	Calculating expected DNA remnants from ancient founding events in human population genetics. <i>BMC Genetics</i> , <b>2008</b> , 9, 66	2.6	
1	Abstract A12: Chromatin accessibility reveals insight into androgen receptor activation and transcriptional specificity. <i>Cancer Research</i> , <b>2012</b> , 72, A12-A12	10.1	