Nicholas E Navin

List of Publications by Year
in descending order

72	14,121	76326	88630
papers	citations	40 h-index	70 g-index

83	83	83	18717
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Tumour evolution inferred by single-cell sequencing. Nature, 2011, 472, 90-94.	27.8	2,313
2	Large-Scale Copy Number Polymorphism in the Human Genome. Science, 2004, 305, 525-528.	12.6	2,293
3	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	27.8	911
4	Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. Cell, 2018, 173, 879-893.e13.	28.9	777
5	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
6	Advances and Applications of Single-Cell Sequencing Technologies. Molecular Cell, 2015, 58, 598-609.	9.7	485
7	Inferring tumor progression from genomic heterogeneity. Genome Research, 2010, 20, 68-80.	5.5	440
8	WW Domain-containing Protein YAP Associates with ErbB-4 and Acts as a Co-transcriptional Activator for the Carboxyl-terminal Fragment of ErbB-4 That Translocates to the Nucleus. Journal of Biological Chemistry, 2003, 278, 33334-33341.	3.4	404
9	Punctuated copy number evolution and clonal stasis in triple-negative breast cancer. Nature Genetics, 2016, 48, 1119-1130.	21.4	396
10	Genome-wide copy number analysis of single cells. Nature Protocols, 2012, 7, 1024-1041.	12.0	332
11	The first five years of single-cell cancer genomics and beyond. Genome Research, 2015, 25, 1499-1507.	5.5	324
12	Multiclonal Invasion in Breast Tumors Identified by Topographic Single Cell Sequencing. Cell, 2018, 172, 205-217.e12.	28.9	324
13	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	17.5	306
14	Novel patterns of genome rearrangement and their association with survival in breast cancer. Genome Research, 2006, 16, 1465-1479.	5.5	291
15	Cancer genomics: one cell at a time. Genome Biology, 2014, 15, 452.	8.8	264
16	Tumor evolution: Linear, branching, neutral or punctuated?. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 151-161.	7.4	239
17	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. Nature Communications, 2020, 11, 5327.	12.8	208
18	Insight into the heterogeneity of breast cancer through next-generation sequencing. Journal of Clinical Investigation, 2011, 121, 3810-3818.	8.2	207

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19	Single-cell DNA sequencing reveals a late-dissemination model in metastatic colorectal cancer. Genome Research, 2017, 27, 1287-1299.	5.5	189
20	Advancing Cancer Research and Medicine with Single-Cell Genomics. Cancer Cell, 2020, 37, 456-470.	16.8	187
21	Future medical applications of single-cell sequencing in cancer. Genome Medicine, 2011, 3, 31.	8.2	180
22	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. Genome Biology, 2017, 18, 178.	8.8	152
23	Monovar: single-nucleotide variant detection in single cells. Nature Methods, 2016, 13, 505-507.	19.0	150
24	Breast tumours maintain a reservoir of subclonal diversity during expansion. Nature, 2021, 592, 302-308.	27.8	145
25	Accumulation of long-chain fatty acids in the tumor microenvironment drives dysfunction in intrapancreatic CD8+ T cells. Journal of Experimental Medicine, 2020, 217, .	8.5	142
26	Tracing the tumor lineage. Molecular Oncology, 2010, 4, 267-283.	4.6	122
27	Cabazitaxel plus carboplatin for the treatment of men with metastatic castration-resistant prostate cancers: a randomised, open-label, phase 1â€“2 trial. Lancet Oncology, The, 2019, 20, 1432-1443.	10.7	115
28	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. Nature Genetics, 2021, 53, 1456-1468.	21.4	111
29	Nanogrid single-nucleus RNA sequencing reveals phenotypic diversity in breast cancer. Nature Communications, 2017, 8, 228.	12.8	105
30	SiCloneFit: Bayesian inference of population structure, genotype, and phylogeny of tumor clones from single-cell genome sequencing data. Genome Research, 2019, 29, 1847-1859.	5.5	97
31	Novel genomic alterations and clonal evolution in chronic lymphocytic leukemia revealed by representational oligonucleotide microarray analysis (ROMA). Blood, 2009, 113, 1294-1303.	1.4	94
32	SNES: single nucleus exome sequencing. Genome Biology, 2015, 16, 55.	9.6	83
33	Methods for copy number aberration detection from single-cell DNA-sequencing data. Genome Biology, 2020, 21, 208.	8.8	72
34	Spatial charting of single-cell transcriptomes in tissues. Nature Biotechnology, 2022, 40, 1190-1199.	17.5	72
35	Genome evolution in ductal carcinoma in situ: invasion of the clones. Journal of Pathology, 2017, 241, 208-218.	4.5	70
36	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	17.5	64

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37	Identification of alterations in DNA copy number in host stromal cells during tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19848-19853.	7.1	55
38	Single-Cell Circulating Tumor Cell Analysis Reveals Genomic Instability as a Distinctive Feature of Aggressive Prostate Cancer. Clinical Cancer Research, 2020, 26, 4143-4153.	7.0	50
39	Tumor Evolution in Response to Chemotherapy: Phenotype versus Genotype. Cell Reports, 2014, 6, 417-419.	6.4	49
40	Highly multiplexed targeted DNA sequencing from single nuclei. Nature Protocols, 2016, 11, 214-235.	12.0	49
41	Somatic Trp53 mutations differentially drive breast cancer and evolution of metastases. Nature Communications, 2018, 9, 3953.	12.8	45
42	SCOPIT: sample size calculations for single-cell sequencing experiments. BMC Bioinformatics, 2019, 20, 566.	2.6	41
43	Analyzing tumor heterogeneity and driver genes in single myeloid leukemia cells with SBCapSeq. Nature Biotechnology, 2016, 34, 962-972.	17.5	40
44	Computing tumor trees from single cells. Genome Biology, 2016, 17, 113.	8.8	40
45	Computational approaches for inferring tumor evolution from single-cell genomic data. Current Opinion in Systems Biology, 2018, 7, 16-25.	2.6	36
46	Delineating cancer evolution with single-cell sequencing. Science Translational Medicine, 2015, 7, 296fs29.	12.4	35
47	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	21.4	34
48	Assessing the performance of methods for copy number aberration detection from single-cell DNA sequencing data. PLoS Computational Biology, 2020, 16, e1008012.	3.2	33
49	PROBER: oligonucleotide FISH probe design software. Bioinformatics, 2006, 22, 2437-2438.	4.1	32
50	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	3.2	30
51	Transient commensal clonal interactions can drive tumor metastasis. Nature Communications, 2020, 11, 5799.	12.8	30
52	Mutational Heterogeneity in APC and KRAS Arises at the Crypt Level and Leads to Polyclonality in Early Colorectal Tumorigenesis. Clinical Cancer Research, 2017, 23, 5936-5947.	7.0	25
53	Mesenchymal and stem-like prostate cancer linked to therapy-induced lineage plasticity and metastasis. Cell Reports, 2022, 39, 110595.	6.4	25
54	Distribution of short paired duplications in mammalian genomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10349-10354.	7.1	23

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55	Simple oligonucleotide-based multiplexing of single-cell chromatin accessibility. Molecular Cell, 2021, 81, 4319-4332.e10.	9.7	22
56	Single-Cell Sequencing Reveals Trajectory of Tumor-Infiltrating Lymphocyte States in Pancreatic Cancer. Cancer Discovery, 2022, 12, 2330-2349.	9.4	22
57	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19
58	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. Nature Communications, 2020, 11, 1839.	12.8	15
59	Decoding the evolutionary response to prostate cancer therapy by plasma genome sequencing. Genome Biology, 2020, 21, 162.	8.8	14
60	Genotyping tumor clones from single-cell data. Nature Methods, 2016, 13, 555-556.	19.0	13
61	Toward an Integrated Knowledge Environment to Support Modern Oncology. Cancer Journal (Sudbury, Mass), 2011, 17, 257-263.	2.0	8
62	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
63	New frontiers in single-cell genomics. Genome Research, 2021, 31, ix-x.	5.5	3
64	Targeting Polo-like Kinase 4 Triggers Polyploidy and Apoptotic Cell Death in TP53-Mutant Acute Myeloid Leukemia. Blood, 2021, 138, 1167-1167.	1.4	3
65	Corrigendum to â€œTracing the tumor lineageâ€•[Mol. Oncol. 4 (2010) 267â€“283]. Molecular Oncology, 2011, 5, 302-302.	4.6	1
66	Resident Breast T Cells: The Troops Are Already There. Trends in Molecular Medicine, 2018, 24, 821-822.	6.7	1
67	Comments on the model parameters in â€œSiFit: inferring tumor trees from single-cell sequencing data under finite-sites modelsâ€• Genome Biology, 2019, 20, 95.	8.8	1
68	Identification of Gene Expression Signatures in Leukemia Stem Cells and Minimal Residual Disease Following Treatment of Adverse Risk Acute Myeloid Leukemia. Blood, 2019, 134, 2717-2717.	1.4	1
69	OTME-23. Single-cell transcriptomic and epigenomic immune landscape of isocitrate dehydrogenase stratified human gliomas. Neuro-Oncology Advances, 2021, 3, ii18-ii18.	0.7	0
70	High-Resolution Array-Based Comparative Genome Hybridization (CGH) Identifies Novel and Recurrent Regions in CLL.. Blood, 2008, 112, 2058-2058.	1.4	0
71	BET Bromodomain Inhibition Reduces Leukemic Burden and Prolongs Survival In The EÎ¼-TCL1 Transgenic Mouse Model Of Chronic Lymphocytic Leukemia (CLL) Independent Of TP53 Mutation Status. Blood, 2013, 122, 876-876.	1.4	0
72	Distinct Gene Expression Patterns of Minimal Residual Disease (MRD) Cells in High-Risk AML Patients Identified By RNA-Sequencing. Blood, 2018, 132, 2757-2757.	1.4	0