Nicholas E Navin

List of Publications by Year
in descending order

72 **papers**	14,121 **citations**	76326 40 **h-index**	88630 70 **g-index**
83 **all docs**	83 **docs citations**	83 **times ranked**	18717 **citing authors**

#	Article	IF	Citations
1	Spatial charting of single-cell transcriptomes in tissues. Nature Biotechnology, 2022, 40, 1190-1199.	17.5	72
2	Mesenchymal and stem-like prostate cancer linked to therapy-induced lineage plasticity and metastasis. Cell Reports, 2022, 39, 110595.	6.4	25
3	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	21.4	34
4	Single-Cell Sequencing Reveals Trajectory of Tumor-Infiltrating Lymphocyte States in Pancreatic Cancer. Cancer Discovery, 2022, 12, 2330-2349.	9.4	22
5	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19
6	Breast tumours maintain a reservoir of subclonal diversity during expansion. Nature, 2021, 592, 302-308.	27.8	145
7	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
8	Single-cell multimodal glioma analyses identify epigenetic regulators of cellular plasticity and environmental stress response. Nature Genetics, 2021, 53, 1456-1468.	21.4	111
9	New frontiers in single-cell genomics. Genome Research, 2021, 31, ix-x.	5.5	3
10	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	17.5	306
11	Simple oligonucleotide-based multiplexing of single-cell chromatin accessibility. Molecular Cell, 2021, 81, 4319-4332.e10.	9.7	22
12	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
13	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. Nature Communications, 2020, 11, 5327.	12.8	208
14	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
15	Transient commensal clonal interactions can drive tumor metastasis. Nature Communications, 2020, 11, 5799.	12.8	30
16	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
17	Methods for copy number aberration detection from single-cell DNA-sequencing data. Genome Biology, 2020, 21, 208.	8.8	72
18	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

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19	Decoding the evolutionary response to prostate cancer therapy by plasma genome sequencing. Genome Biology, 2020, 21, 162.	8.8	14
20	Advancing Cancer Research and Medicine with Single-Cell Genomics. Cancer Cell, 2020, 37, 456-470.	16.8	187
21	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. Nature Communications, 2020, 11, 1839.	12.8	15
22	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
23	SCOPIT: sample size calculations for single-cell sequencing experiments. BMC Bioinformatics, 2019, 20, 566.	2.6	41
24	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	3.2	30
25	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
26	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
27	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
28	Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. Cell, 2018, 173, 879-893.e13.	28.9	777
29	Multiclonal Invasion in Breast Tumors Identified by Topographic Single Cell Sequencing. Cell, 2018, 172, 205-217.e12.	28.9	324
30	Computational approaches for inferring tumor evolution from single-cell genomic data. Current Opinion in Systems Biology, 2018, 7, 16-25.	2.6	36
31	Somatic Trp53 mutations differentially drive breast cancer and evolution of metastases. Nature Communications, 2018, 9, 3953.	12.8	45
32	Resident Breast T Cells: The Troops Are Already There. Trends in Molecular Medicine, 2018, 24, 821-822.	6.7	1
33	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
34	Tumor evolution: Linear, branching, neutral or punctuated?. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 151-161.	7.4	239
35	Single-cell DNA sequencing reveals a late-dissemination model in metastatic colorectal cancer. Genome Research, 2017, 27, 1287-1299.	5.5	189
36	Nanogrid single-nucleus RNA sequencing reveals phenotypic diversity in breast cancer. Nature Communications, 2017, 8, 228.	12.8	105

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37	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
38	Genome evolution in ductal carcinoma *in situ*: invasion of the clones. Journal of Pathology, 2017, 241, 208-218.	4.5	70
39	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. Genome Biology, 2017, 18, 178.	8.8	152
40	Monovar: single-nucleotide variant detection in single cells. Nature Methods, 2016, 13, 505-507.	19.0	150
41	Analyzing tumor heterogeneity and driver genes in single myeloid leukemia cells with SBCapSeq. Nature Biotechnology, 2016, 34, 962-972.	17.5	40
42	Punctuated copy number evolution and clonal stasis in triple-negative breast cancer. Nature Genetics, 2016, 48, 1119-1130.	21.4	396
43	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	17.5	64
44	Computing tumor trees from single cells. Genome Biology, 2016, 17, 113.	8.8	40
45	Genotyping tumor clones from single-cell data. Nature Methods, 2016, 13, 555-556.	19.0	13
46	Highly multiplexed targeted DNA sequencing from single nuclei. Nature Protocols, 2016, 11, 214-235.	12.0	49
47	Advances and Applications of Single-Cell Sequencing Technologies. Molecular Cell, 2015, 58, 598-609.	9.7	485
48	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
49	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
50	Delineating cancer evolution with single-cell sequencing. Science Translational Medicine, 2015, 7, 296fs29.	12.4	35
51	SNES: single nucleus exome sequencing. Genome Biology, 2015, 16, 55.	9.6	83
52	The first five years of single-cell cancer genomics and beyond. Genome Research, 2015, 25, 1499-1507.	5.5	324
53	Tumor Evolution in Response to Chemotherapy: Phenotype versus Genotype. Cell Reports, 2014, 6, 417-419.	6.4	49
54	Cancer genomics: one cell at a time. Genome Biology, 2014, 15, 452.	8.8	264

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55	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	27.8	911
56	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
57	Genome-wide copy number analysis of single cells. Nature Protocols, 2012, 7, 1024-1041.	12.0	332
58	Future medical applications of single-cell sequencing in cancer. Genome Medicine, 2011, 3, 31.	8.2	180
59	Corrigendum to â€œTracing the tumor lineageâ€•[Mol. Oncol. 4 (2010) 267â€"283]. Molecular Oncology, 2011, 5, 302-302.	4.6	1
60	Toward an Integrated Knowledge Environment to Support Modern Oncology. Cancer Journal (Sudbury, Mass), 2011, 17, 257-263.	2.0	8
61	Tumour evolution inferred by single-cell sequencing. Nature, 2011, 472, 90-94.	27.8	2,313
62	Insight into the heterogeneity of breast cancer through next-generation sequencing. Journal of Clinical Investigation, 2011, 121, 3810-3818.	8.2	207
63	Inferring tumor progression from genomic heterogeneity. Genome Research, 2010, 20, 68-80.	5.5	440
64	Tracing the tumor lineage. Molecular Oncology, 2010, 4, 267-283.	4.6	122
65	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
66	High-Resolution Array-Based Comparative Genome Hybridization (CGH) Identifies Novel and Recurrent Regions in CLL.. Blood, 2008, 112, 2058-2058.	1.4	0
67	PROBER: oligonucleotide FISH probe design software. Bioinformatics, 2006, 22, 2437-2438.	4.1	32
68	Novel patterns of genome rearrangement and their association with survival in breast cancer. Genome Research, 2006, 16, 1465-1479.	5.5	291
69	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
70	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
71	Large-Scale Copy Number Polymorphism in the Human Genome. Science, 2004, 305, 525-528.	12.6	2,293
72	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