Michael Wigler

List of Publications by Year
in descending order

105 papers	44,601 citations	10956 71 h-index	29081 104 g-index
112 all docs	112 docs citations	112 times ranked	40068 citing authors

#	Article	IF	Citations
1	PTEN, a Putative Protein Tyrosine Phosphatase Gene Mutated in Human Brain, Breast, and Prostate Cancer. Science, 1997, 275, 1943-1947.	6.0	4,506
2	Strong Association of De Novo Copy Number Mutations with Autism. Science, 2007, 316, 445-449.	6.0	2,497
3	Tumour evolution inferred by single-cell sequencing. Nature, 2011, 472, 90-94.	13.7	2,313
4	Large-Scale Copy Number Polymorphism in the Human Genome. Science, 2004, 305, 525-528.	6.0	2,293
5	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	13.7	2,188
6	Circular binary segmentation for the analysis of array-based DNA copy number data. Biostatistics, 2004, 5, 557-572.	0.9	1,903
7	Transformation of mammalian cells with genes from procaryotes and eucaryotes. Cell, 1979, 16, 777-785.	13.5	1,613
8	Transfer of purified herpes virus thymidine kinase gene to cultured mouse cells. Cell, 1977, 11, 223-232.	13.5	1,548
9	Biochemical transfer of single-copy eucaryotic genes using total cellular DNA as donor. Cell, 1978, 14, 725-731.	13.5	1,402
10	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	3.8	1,311
11	In yeast, RAS proteins are controlling elements of adenylate cyclase. Cell, 1985, 40, 27-36.	13.5	1,209
12	The lipid phosphatase activity of PTEN is critical for its tumor supressor function. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 13513-13518.	3.3	1,101
13	Identification and Validation of Oncogenes in Liver Cancer Using an Integrative Oncogenomic Approach. Cell, 2006, 125, 1253-1267.	13.5	989
14	The NF1 locus encodes a protein functionally related to mammalian GAP and yeast IRA proteins. Cell, 1990, 63, 851-859.	13.5	808
15	P-TEN, the tumor suppressor from human chromosome 10q23, is a dual-specificity phosphatase. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 9052-9057.	3.3	765
16	Linkage, Association, and Gene-Expression Analyses Identify CNTNAP2 as an Autism-Susceptibility Gene. American Journal of Human Genetics, 2008, 82, 150-159.	2.6	738
17	Activation of the T24 bladder carcinoma transforming gene is linked to a single amino acid change. Nature, 1982, 300, 762-765.	13.7	716
18	Three different genes in S. cerevisiae encode the catalytic subunits of the cAMP-dependent protein kinase. Cell, 1987, 50, 277-287.	13.5	705

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19	Rare De Novo Variants Associated with Autism Implicate a Large Functional Network of Genes Involved in Formation and Function of Synapses. Neuron, 2011, 70, 898-907.	3.8	641
20	Rare De Novo and Transmitted Copy-Number Variation in Autistic Spectrum Disorders. Neuron, 2011, 70, 886-897.	3.8	639
21	Structure and activation of the human N-ras gene. Cell, 1983, 34, 581-586.	13.5	529
22	The S. cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase pathway. Cell, 1987, 48, 789-799.	13.5	523
23	Genetic and physical linkage of exogenous sequences in transformed cells. Cell, 1980, 22, 309-317.	13.5	511
24	Isolation and preliminary characterization of a human transforming gene from T24 bladder carcinoma cells. Nature, 1982, 296, 404-409.	13.7	489
25	Complex synthetic chemical libraries indexed with molecular tags. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 10922-10926.	3.3	478
26	DNA sequence and characterization of the S. cerevisiae gene encoding adenylate cyclase. Cell, 1985, 43, 493-505.	13.5	468
27	Human-tumor-derived cell lines contain common and different transforming genes. Cell, 1981, 27, 467-476.	13.5	455
28	Isolation and characterization of a new cellular oncogene encoding a protein with multiple potential transmembrane domains. Cell, 1986, 45, 711-719.	13.5	449
29	Inferring tumor progression from genomic heterogeneity. Genome Research, 2010, 20, 68-80.	2.4	440
30	Structure of the Ki-ras gene of the human lung carcinoma cell line Calu-1. Nature, 1983, 304, 497-500.	13.7	406
31	An Oncogenomics-Based In Vivo RNAi Screen Identifies Tumor Suppressors in Liver Cancer. Cell, 2008, 135, 852-864.	13.5	404
32	Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated Myc regulation. Genes and Development, 2013, 27, 2648-2662.	2.7	394
33	Differential activation of yeast adenylate cyclase by wild type and mutant RAS proteins. Cell, 1985, 41, 763-769.	13.5	392
34	Representational Oligonucleotide Microarray Analysis: A High-Resolution Method to Detect Genome Copy Number Variation. Genome Research, 2003, 13, 2291-2305.	2.4	376
35	RAS proteins can induce meiosis in xenopus oocytes. Cell, 1985, 43, 615-621.	13.5	360
36	Functional homology of mammalian and yeast RAS genes. Cell, 1985, 40, 19-26.	13.5	350

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37	The role of de novo mutations in the genetics of autism spectrum disorders. Nature Reviews Genetics, 2014, 15, 133-141.	7.7	339
38	Tumour promotor induces plasminogen activator. Nature, 1976, 259, 232-233.	13.7	335
39	Genome-wide copy number analysis of single cells. Nature Protocols, 2012, 7, 1024-1041.	5.5	332
40	Cooperative interaction of S. pombe proteins required for mating and morphogenesis. Cell, 1994, 79, 131-141.	13.5	300
41	cAMP-independent control of sporulation, glycogen metabolism, and heat shock resistance in S. cerevisiae. Cell, 1988, 53, 555-566.	13.5	291
42	Novel patterns of genome rearrangement and their association with survival in breast cancer. Genome Research, 2006, 16, 1465-1479.	2.4	291
43	Dosage-dependent phenotypes in models of 16p11.2 lesions found in autism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17076-17081.	3.3	289
44	A unified genetic theory for sporadic and inherited autism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12831-12836.	3.3	284
45	RAM, a gene of yeast required for a functional modification of RAS proteins and for production of mating pheromone a-factor. Cell, 1986, 47, 413-422.	13.5	275
46	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. Cancer Cell, 2003, 3, 297-302.	7.7	229
47	PTEN controls tumor-induced angiogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 4622-4627.	3.3	221
48	Interactive analysis and assessment of single-cell copy-number variations. Nature Methods, 2015, 12, 1058-1060.	9.0	220
49	A Role for the Ral Guanine Nucleotide Dissociation Stimulator in Mediating Ras-induced Transformation. Journal of Biological Chemistry, 1996, 271, 16439-16442.	1.6	219
50	Isolation of the chicken thymidine kinase gene by plasmid rescue. Nature, 1980, 285, 207-210.	13.7	216
51	Evidence for a functional link between profilin and CAP in the yeast S. cerevisiae. Cell, 1991, 66, 497-505.	13.5	206
52	DBC2, a candidate for a tumor suppressor gene involved in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13647-13652.	3.3	202
53	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. Genome Research, 2009, 19, 1593-1605.	2.4	198
54	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. Nature Methods, 2014, 11, 1033-1036.	9.0	194

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55	Signaling pathways in Ras-mediated tumorigenicity and metastasis. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 8773-8778.	3.3	178
56	DLC1 is a chromosome 8p tumor suppressor whose loss promotes hepatocellular carcinoma. Genes and Development, 2008, 22, 1439-1444.	2.7	167
57	Characteristics of an SV40-plasmid recombinant and its movement into and out of the genome of a murine cell. Cell, 1980, 21, 127-139.	13.5	164
58	Transformation of mammalian cells with an amplifiable dominant-acting gene.. Proceedings of the National Academy of Sciences of the United States of America, 1980, 77, 3567-3570.	3.3	156
59	Functional Identification of Tumor-Suppressor Genes through an In Vivo RNA Interference Screen in a Mouse Lymphoma Model. Cancer Cell, 2009, 16, 324-335.	7.7	155
60	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. Science Translational Medicine, 2010, 2, 38ra47.	5.8	138
61	A cluster of cooperating tumor-suppressor gene candidates in chromosomal deletions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8212-8217.	3.3	138
62	Recurrent DNA copy number variation in the laboratory mouse. Nature Genetics, 2007, 39, 1384-1389.	9.4	129
63	Low load for disruptive mutations in autism genes and their biased transmission. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5600-7.	3.3	129
64	Rapid Phenotypic and Genomic Change in Response to Therapeutic Pressure in Prostate Cancer Inferred by High Content Analysis of Single Circulating Tumor Cells. PLoS ONE, 2014, 9, e101777.	1.1	127
65	Comparative genomic analysis of tumors: detection of DNA losses and amplification.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 151-155.	3.3	123
66	DNA methylation patterns in luminal breast cancers differ from nonâ€luminal subtypes and can identify relapse risk independent of other clinical variables. Molecular Oncology, 2011, 5, 77-92.	2.1	116
67	Optimizing sparse sequencing of single cells for highly multiplex copy number profiling. Genome Research, 2015, 25, 714-724.	2.4	115
68	The contribution of de novo and rare inherited copy number changes to congenital heart disease in an unselected sample of children with conotruncal defects or hypoplastic left heart disease. Human Genetics, 2014, 133, 11-27.	1.8	112
69	Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548.	5.5	99
70	Novel genomic alterations and clonal evolution in chronic lymphocytic leukemia revealed by representational oligonucleotide microarray analysis (ROMA). Blood, 2009, 113, 1294-1303.	0.6	94
71	Intraductal Transplantation Models of Human Pancreatic Ductal Adenocarcinoma Reveal Progressive Transition of Molecular Subtypes. Cancer Discovery, 2020, 10, 1566-1589.	7.7	90
72	Single-Chromosomal Gains Can Function as Metastasis Suppressors and Promoters in Colon Cancer. Developmental Cell, 2020, 52, 413-428.e6.	3.1	65

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73	[19] Representational difference analysis in detection of genetic lesions in cancer. Methods in Enzymology, 1995, 254, 291-304.	0.4	64
74	Annotating Large Genomes With Exact Word Matches. Genome Research, 2003, 13, 2306-2315.	2.4	62
75	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.	3.3	55
76	A versatile statistical analysis algorithm to detect genome copy number variation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16292-16297.	3.3	53
77	Damaging de novo mutations diminish motor skills in children on the autism spectrum. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1859-E1866.	3.3	49
78	Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing. ELife, 2020, 9, .	2.8	47
79	Cell culture studies provide new information on tumour promoters. Nature, 1977, 270, 659-660.	13.7	40
80	Copy-number variants in patients with a strong family history of pancreatic cancer. Cancer Biology and Therapy, 2007, 6, 1592-1599.	1.5	36
81	Application of ROMA (representational oligonucleotide microarray analysis) to patients with cytogenetic rearrangements. Genetics in Medicine, 2005, 7, 111-118.	1.1	32
82	PROBER: oligonucleotide FISH probe design software. Bioinformatics, 2006, 22, 2437-2438.	1.8	32
83	SMASH, a fragmentation and sequencing method for genomic copy number analysis. Genome Research, 2016, 26, 844-851.	2.4	31
84	Utility of Single-Cell Genomics in Diagnostic Evaluation of Prostate Cancer. Cancer Research, 2018, 78, 348-358.	0.4	24
85	Rates of contributory de novo mutation in high and low-risk autism families. Communications Biology, 2021, 4, 1026.	2.0	24
86	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.	3.3	23
87	Mouse genomic representational oligonucleotide microarray analysis: Detection of copy number variations in normal and tumor specimens. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11234-11239.	3.3	22
88	Rare De Novo Germline Copy-Number Variation in Testicular Cancer. American Journal of Human Genetics, 2012, 91, 379-383.	2.6	21
89	Broad applications of single-cell nucleic acid analysis in biomedical research. Genome Medicine, 2012, 4, 79.	3.6	11
90	The cancer stem cell: Cell type or cell state?. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2013, 83A, 5-7.	1.1	11

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91	Target inference from collections of genomic intervals. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2271-E2278.	3.3	11
92	Quantitative multigene FISH on breast carcinomas identifies der(1;16)(q10;p10) as an early event in luminal A tumors. Genes Chromosomes and Cancer, 2015, 54, 235-248.	1.5	11
93	Early Detection of Cancer in Blood Using Single-Cell Analysis: A Proposal. Trends in Molecular Medicine, 2017, 23, 594-603.	3.5	9
94	Measuring shared variants in cohorts of discordant siblings with applications to autism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7073-7076.	3.3	9
95	Copolymerization of single-cell nucleic acids into balls of acrylamide gel. Genome Research, 2020, 30, 49-61.	2.4	9
96	The adenylyl cyclase-encoding gene from Saccharomyces kluyveri. Gene, 1991, 102, 129-132.	1.0	8
97	Reducing system noise in copy number data using principal components of self-self hybridizations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E103-E110.	3.3	8
98	Facilitated sequence counting and assembly by template mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4632-7.	3.3	7
99	GENETICS: Wild by Nature. Science, 2002, 296, 1407-1408.	6.0	6
100	Partial bisulfite conversion for unique template sequencing. Nucleic Acids Research, 2018, 46, e10-e10.	6.5	6
101	A Sense of Life: Computational and Experimental Investigations with Models of Biochemical and Evolutionary Processes. OMICS A Journal of Integrative Biology, 2003, 7, 253-268.	1.0	4
102	Validation of S. Pombe Sequence Assembly by Microarray Hybridization. Journal of Computational Biology, 2006, 13, 1-20.	0.8	2
103	Integrated Computational Pipeline for Single-Cell Genomic Profiling. JCO Clinical Cancer Informatics, 2020, 4, 464-471.	1.0	2
104	Targeted de novo phasing and long-range assembly by template mutagenesis. Nucleic Acids Research, 0, , .	6.5	1
105	The Last Ten Yards. , 2013, , 195-202.		0