

Michael A Black

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

6,651
citations

70961

41
h-index

66788

78
g-index

115
all docs

115
docs citations

115
times ranked

13109
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of transposable elements in heterochromatin and epigenetic control. <i>Nature</i> , 2004, 430, 471-476.	13.7	1,103
2	Clinical risk prediction for pre-eclampsia in nulliparous women: development of model in international prospective cohort. <i>BMJ: British Medical Journal</i> , 2011, 342, d1875-d1875.	2.4	343
3	Mutations in genes encoding the cadherin receptor-ligand pair DCHS1 and FAT4 disrupt cerebral cortical development. <i>Nature Genetics</i> , 2013, 45, 1300-1308.	9.4	247
4	The power and promise of <i>scRNA-seq</i> in ecology and evolution. <i>Molecular Ecology</i> , 2016, 25, 1224-1241.	2.0	219
5	The G Protein-Coupled Receptor GPR30 Inhibits Proliferation of Estrogen Receptor-Positive Breast Cancer Cells. <i>Cancer Research</i> , 2010, 70, 1184-1194.	0.4	204
6	<i>Sleeping Beauty</i> mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5934-5941.	3.3	201
7	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. <i>Oncotimmunology</i> , 2018, 7, e1490854.	2.1	200
8	Early Pregnancy Prediction of Preeclampsia in Nulliparous Women, Combining Clinical Risk and Biomarkers. <i>Hypertension</i> , 2014, 64, 644-652.	1.3	193
9	An Iron Regulatory Gene Signature Predicts Outcome in Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6728-6737.	0.4	181
10	Interactions between immunity, proliferation and molecular subtype in breast cancer prognosis. <i>Genome Biology</i> , 2013, 14, R34.	13.9	168
11	Microsatellite Tandem Repeats Are Abundant in Human Promoters and Are Associated with Regulatory Elements. <i>PLoS ONE</i> , 2013, 8, e54710.	1.1	156
12	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> from Recent Outbreaks of Kiwifruit Bacterial Canker Belong to Different Clones That Originated in China. <i>PLoS ONE</i> , 2013, 8, e57464.	1.1	143
13	Cyclin E2 Overexpression Is Associated with Endocrine Resistance but not Insensitivity to CDK2 Inhibition in Human Breast Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 1488-1499.	1.9	129
14	Multiple Gene Expression Classifiers from Different Array Platforms Predict Poor Prognosis of Colorectal Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 498-507.	3.2	114
15	E-cadherin loss alters cytoskeletal organization and adhesion in non-malignant breast cells but is insufficient to induce an epithelial-mesenchymal transition. <i>BMC Cancer</i> , 2014, 14, 552.	1.1	108
16	YB-1, the E2F Pathway, and Regulation of Tumor Cell Growth. <i>Journal of the National Cancer Institute</i> , 2012, 104, 133-146.	3.0	102
17	Duration of sexual relationship and its effect on preeclampsia and small for gestational age perinatal outcome. <i>Journal of Reproductive Immunology</i> , 2009, 82, 66-73.	0.8	100
18	Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish. <i>Biology of Sex Differences</i> , 2015, 6, 26.	1.8	100

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19	A proteomic approach identifies early pregnancy biomarkers for preeclampsia: Novel linkages between a predisposition to preeclampsia and cardiovascular disease. <i>Proteomics</i> , 2009, 9, 2929-2945.	1.3	99
20	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. <i>Science Advances</i> , 2019, 5, eaaw7006.	4.7	99
21	JMJD6 is a driver of cellular proliferation and motility and a marker of poor prognosis in breast cancer. <i>Breast Cancer Research</i> , 2012, 14, R85.	2.2	90
22	Immunogenic Subtypes of Breast Cancer Delineated by Gene Classifiers of Immune Responsiveness. <i>Cancer Immunology Research</i> , 2016, 4, 600-610.	1.6	86
23	Estimating disease prevalence in the absence of a gold standard. <i>Statistics in Medicine</i> , 2002, 21, 2653-2669.	0.8	83
24	Sugar-sweetened beverage consumption: a risk factor for prevalent gout with <i>SLC2A9</i> genotype-specific effects on serum urate and risk of gout. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2101-2106.	0.5	77
25	Differential Gene Expression in Cultured Osteoblasts and Bone Marrow Stromal Cells From Patients With Paget's Disease of Bone. <i>Journal of Bone and Mineral Research</i> , 2006, 22, 298-309.	3.1	76
26	The Fibroblast Growth Factor-Inducible 14 Receptor Is Highly Expressed in HER2-Positive Breast Tumors and Regulates Breast Cancer Cell Invasive Capacity. <i>Molecular Cancer Research</i> , 2008, 6, 725-734.	1.5	75
27	Calculation of the minimum number of replicate spots required for detection of significant gene expression fold change in microarray experiments. <i>Bioinformatics</i> , 2002, 18, 1609-1616.	1.8	73
28	Fatty acid oxidation is associated with proliferation and prognosis in breast and other cancers. <i>BMC Cancer</i> , 2018, 18, 805.	1.1	65
29	Microarray-based gene set analysis: a comparison of current methods. <i>BMC Bioinformatics</i> , 2008, 9, 502.	1.2	62
30	Predicting Clinical Outcome through Molecular Profiling in Stage III Melanoma. <i>Clinical Cancer Research</i> , 2008, 14, 5173-5180.	3.2	62
31	Transposon mutagenesis identifies genetic drivers of <i>BrafV600E</i> melanoma. <i>Nature Genetics</i> , 2015, 47, 486-495.	9.4	61
32	Transterm: a database to aid the analysis of regulatory sequences in mRNAs. <i>Nucleic Acids Research</i> , 2009, 37, D72-D76.	6.5	59
33	Sensitivity of 70-mer oligonucleotides and cDNAs for microarray analysis of gene expression in <i>Arabidopsis</i> and its related species. <i>Plant Biotechnology Journal</i> , 2004, 2, 45-57.	4.1	55
34	<i>p53</i> isoform promotes tumour invasion and metastasis via interleukin-6 activation of JAK-STAT and RhoA-ROCK signalling. <i>Nature Communications</i> , 2018, 9, 254.	5.8	55
35	Histological and transcriptomic effects of 17 β -methyltestosterone on zebrafish gonad development. <i>BMC Genomics</i> , 2017, 18, 557.	1.2	52
36	A bioinformatics workflow for detecting signatures of selection in genomic data. <i>Frontiers in Genetics</i> , 2014, 5, 293.	1.1	51

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37	Transposon mutagenesis identifies genes that cooperate with mutant Pten in breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7749-E7758.	3.3	48
38	Genomic selection of reference genes for real-time PCR in human myocardium. <i>BMC Medical Genomics</i> , 2008, 1, 64.	0.7	45
39	Paternal Contribution to Small for Gestational Age Babies: A Multicenter Prospective Study. <i>Obesity</i> , 2011, 19, 1035-1039.	1.5	45
40	Combined genomic and phenotype screening reveals secretory factor SPINK1 as an invasion and survival factor associated with patient prognosis in breast cancer. <i>EMBO Molecular Medicine</i> , 2011, 3, 451-464.	3.3	45
41	Dual roles for immune metagenes in breast cancer prognosis and therapy prediction. <i>Genome Medicine</i> , 2014, 6, 80.	3.6	44
42	Slow proliferation as a biological feature of colorectal cancer metastasis. <i>British Journal of Cancer</i> , 2009, 101, 822-828.	2.9	43
43	An altered pattern of circulating apolipoprotein E3 isoforms is implicated in preeclampsia. <i>Journal of Lipid Research</i> , 2009, 50, 71-80.	2.0	43
44	Germline mutations and somatic inactivation of TRIM28 in Wilms tumour. <i>PLoS Genetics</i> , 2018, 14, e1007399.	1.5	41
45	Analyzing tumor heterogeneity and driver genes in single myeloid leukemia cells with SBCapSeq. <i>Nature Biotechnology</i> , 2016, 34, 962-972.	9.4	40
46	Gene expression data: The technology and statistical analysis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2003, 8, 1-28.	0.7	39
47	Incremental cost-effectiveness ratio and incremental net-health benefit: two sides of the same coin. <i>Expert Review of Pharmacoeconomics and Outcomes Research</i> , 2001, 1, 37-46.	0.7	38
48	The Chromosome 9p21.3 Coronary Heart Disease Risk Allele Is Associated with Altered Gene Expression in Normal Heart and Vascular Tissues. <i>PLoS ONE</i> , 2012, 7, e39574.	1.1	37
49	Recurrent loss of heterozygosity correlates with clinical outcome in pancreatic neuroendocrine cancer. <i>Npj Genomic Medicine</i> , 2018, 3, 18.	1.7	37
50	Accounting for Errors in Low Coverage High-Throughput Sequencing Data When Constructing Genetic Maps Using Biparental Outcrossed Populations. <i>Genetics</i> , 2018, 209, 65-76.	1.2	36
51	Lentiviral-Mediated Gene Transfer to the Sheep Brain: Implications for Gene Therapy in Batten Disease. <i>Human Gene Therapy</i> , 2011, 22, 1011-1020.	1.4	35
52	Clinico-pathological factors influencing lymph node yield in colorectal cancer and impact on survival: Analysis of new zealand cancer registry data. <i>Journal of Surgical Oncology</i> , 2015, 111, 451-458.	0.8	34
53	Inflammatory and regulatory T cells contribute to a unique immune microenvironment in tumor tissue of colorectal cancer patients. <i>International Journal of Cancer</i> , 2013, 132, 1842-1850.	2.3	33
54	Genome-wide methylation analysis identifies a core set of hypermethylated genes in CIMP-H colorectal cancer. <i>BMC Cancer</i> , 2017, 17, 228.	1.1	32

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55	Control of the False Discovery Rate Applied to the Detection of Positively Selected Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2006, 23, 919-926.	3.5	28
56	Reduced expression of a gene proliferation signature is associated with enhanced malignancy in colon cancer. <i>British Journal of Cancer</i> , 2008, 99, 966-973.	2.9	27
57	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	1.2	27
58	Transcriptomic analysis of the cardiac left ventricle in a rodent model of diabetic cardiomyopathy: molecular snapshot of a severe myocardial disease. <i>Physiological Genomics</i> , 2007, 28, 284-293.	1.0	26
59	A New Role for ER α : Silencing via DNA Methylation of Basal, Stem Cell, and EMT Genes. <i>Molecular Cancer Research</i> , 2017, 15, 152-164.	1.5	25
60	Real-time Detection of Epileptiform Activity in the EEG: A Blinded Clinical Trial. <i>Clinical EEG (electroencephalography)</i> , 2000, 31, 122-130.	0.9	24
61	E-cadherin-deficient cells have synthetic lethal vulnerabilities in plasma membrane organisation, dynamics and function. <i>Gastric Cancer</i> , 2019, 22, 273-286.	2.7	24
62	The CNVrd2 package: measurement of copy number at complex loci using high-throughput sequencing data. <i>Frontiers in Genetics</i> , 2014, 5, 248.	1.1	22
63	Allosteric AKT Inhibitors Target Synthetic Lethal Vulnerabilities in E-Cadherin-Deficient Cells. <i>Cancers</i> , 2019, 11, 1359.	1.7	22
64	The distribution and impact of common copy-number variation in the genome of the domesticated apple, <i>Malus x domestica</i> Borkh. <i>BMC Genomics</i> , 2015, 16, 848.	1.2	21
65	Identification of sex differences in zebrafish (<i>Danio rerio</i>) brains during early sexual differentiation and masculinization using 17 β -methyltestosterone. <i>Biology of Reproduction</i> , 2018, 99, 446-460.	1.2	21
66	High-Dimensional Mass Cytometric Analysis Reveals an Increase in Effector Regulatory T Cells as a Distinguishing Feature of Colorectal Tumors. <i>Journal of Immunology</i> , 2019, 202, 1871-1884.	0.4	19
67	Comparison of Roche Cell-Free DNA collection Tubes to Streck Cell-Free DNA BCT s for sample stability using healthy volunteers. <i>Practical Laboratory Medicine</i> , 2019, 16, e00125.	0.6	18
68	Prediction of Preeclampsia and Delivery of Small for Gestational Age Babies Based on a Combination of Clinical Risk Factors in High-Risk Women. <i>Hypertension in Pregnancy</i> , 2011, 30, 58-73.	0.5	17
69	Genetic sex assignment in wild populations using genotyping-by-sequencing data: A statistical threshold approach. <i>Molecular Ecology Resources</i> , 2018, 18, 179-190.	2.2	17
70	Association of SLC2A9 genotype with phenotypic variability of serum urate in pre-menopausal women. <i>Frontiers in Genetics</i> , 2015, 6, 313.	1.1	16
71	Functional impairment of infiltrating T cells in human colorectal cancer. <i>Oncolmmunology</i> , 2016, 5, e1234573.	2.1	16
72	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. <i>F1000Research</i> , 2017, 6, 296.	0.8	14

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73	A collection of annotated and harmonized human breast cancer transcriptome datasets, including immunologic classification. <i>F1000Research</i> , 2017, 6, 296.	0.8	14
74	MelanomaDB: A Web Tool for Integrative Analysis of Melanoma Genomic Information to Identify Disease-Associated Molecular Pathways. <i>Frontiers in Oncology</i> , 2013, 3, 184.	1.3	13
75	Altered Transcription of Murine Genes Induced in the Small Bowel by Administration of Probiotic Strain <i>Lactobacillus rhamnosus</i> HN001. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2851-2859.	1.4	13
76	A Statistical Model to Identify Differentially Expressed Proteins in 2D PAGE Gels. <i>PLoS Computational Biology</i> , 2009, 5, e1000509.	1.5	12
77	CNVrd, a Read-Depth Algorithm for Assigning Copy-Number at the FCGR Locus: Population-Specific Tagging of Copy Number Variation at FCGR3B. <i>PLoS ONE</i> , 2013, 8, e63219.	1.1	12
78	Circulating tumor DNA is a sensitive marker for routine monitoring of treatment response in advanced colorectal cancer. <i>Carcinogenesis</i> , 2020, 41, 1507-1517.	1.3	11
79	Oligonucleotide array outperforms SNP array on formalin-fixed paraffin-embedded clinical samples. <i>Cancer Genetics and Cytogenetics</i> , 2010, 198, 1-6.	1.0	10
80	Lack of direct evidence for natural selection at the candidate thrifty gene locus, PPARCC1A. <i>BMC Medical Genetics</i> , 2016, 17, 80.	2.1	10
81	Striatal mRNA expression patterns underlying peak dose L-DOPA-induced dyskinesia in the 6-OHDA hemiparkinsonian rat. <i>Neuroscience</i> , 2016, 324, 238-251.	1.1	10
82	Distinctive Subpopulations of Stromal Cells Are Present in Human Lymph Nodes Infiltrated with Melanoma. <i>Cancer Immunology Research</i> , 2020, 8, 990-1003.	1.6	10
83	Exploring possible DNA structures in real-time polymerase kinetics using Pacific Biosciences sequencer data. <i>BMC Bioinformatics</i> , 2015, 16, 21.	1.2	9
84	SB Driver Analysis: a Sleeping Beauty cancer driver analysis framework for identifying and prioritizing experimentally actionable oncogenes and tumor suppressors. <i>Nucleic Acids Research</i> , 2018, 46, e94-e94.	6.5	9
85	Analysis of the <i>DISC1</i> translocation partner (11q14.3) in genetic risk of schizophrenia. <i>Genes, Brain and Behavior</i> , 2012, 11, 859-863.	1.1	8
86	Evaluating accuracy of diagnostic tests with intermediate results in the absence of a gold standard. <i>Statistics in Medicine</i> , 2013, 32, 2571-2584.	0.8	8
87	Frequency of CYP2C9 polymorphisms in polynesian people and potential relevance to management of gout with benzbromarone. <i>Joint Bone Spine</i> , 2014, 81, 160-163.	0.8	8
88	Copy number variants implicate cardiac function and development pathways in earthquake-induced stress cardiomyopathy. <i>Scientific Reports</i> , 2018, 8, 7548.	1.6	8
89	Prognostic roles for IL-6-producing and CD 69 + T cell subsets in colorectal cancer patients. <i>International Journal of Cancer</i> , 2018, 143, 2008-2016.	2.3	8
90	Sustained software development, not number of citations or journal choice, is indicative of accurate bioinformatic software. <i>Genome Biology</i> , 2022, 23, 56.	3.8	8

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91	Bulk and Single-Cell Profiling of Breast Tumors Identifies TREM-1 as a Dominant Immune Suppressive Marker Associated With Poor Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 734959.	1.3	8
92	E-Cadherin-Deficient Epithelial Cells Are Sensitive to HDAC Inhibitors. <i>Cancers</i> , 2022, 14, 175.	1.7	8
93	SRBreak: A Read-Depth and Split-Read Framework to Identify Breakpoints of Different Events Inside Simple Copy-Number Variable Regions. <i>Frontiers in Genetics</i> , 2016, 7, 160.	1.1	7
94	Noninvasive Assessment of Epidermal Genomic Markers of UV Exposure in Skin. <i>Journal of Investigative Dermatology</i> , 2021, 141, 124-131.e2.	0.3	6
95	Variable expression quantitative trait loci analysis of breast cancer risk variants. <i>Scientific Reports</i> , 2021, 11, 7192.	1.6	6
96	Single-Cell RNA-Seq Reveals Heterogeneous lncRNA Expression in Xenografted Triple-Negative Breast Cancer Cells. <i>Biology</i> , 2021, 10, 987.	1.3	6
97	Heterologous hybridisation to a Pinus microarray: profiling of gene expression in Pinus radiata saplings exposed to ethephon. <i>New Zealand Journal of Forestry Science</i> , 2014, 44, .	0.8	5
98	T cell subpopulations in lymph nodes may not be predictive of patient outcome in colorectal cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2011, 30, 78.	3.5	4
99	graphsim: An R package for simulating gene expression data from graph structures of biological pathways. <i>Journal of Open Source Software</i> , 2020, 5, 2161.	2.0	4
100	Gene expression profiling of breast tumours from New Zealand patients. <i>New Zealand Medical Journal</i> , 2017, 130, 40-56.	0.5	4
101	E-Cadherin-Deficient Cells Are Sensitive to the Multikinase Inhibitor Dasatinib. <i>Cancers</i> , 2022, 14, 1609.	1.7	4
102	Multimodal Assessment of Estrogen Receptor mRNA Profiles to Quantify Estrogen Pathway Activity in Breast Tumors. <i>Clinical Breast Cancer</i> , 2017, 17, 139-153.	1.1	3
103	Increased gene expression variability in BRCA1-associated and basal-like breast tumours. <i>Breast Cancer Research and Treatment</i> , 2021, 189, 363-375.	1.1	3
104	Streptokinase antibodies in patients presenting with acute coronary syndrome in three rural New Zealand populations. <i>Journal of Clinical Pathology</i> , 2011, 64, 426-429.	1.0	2
105	Transposon mutagenesis identifies cooperating genetic drivers during keratinocyte transformation and cutaneous squamous cell carcinoma progression. <i>PLoS Genetics</i> , 2021, 17, e1009094.	1.5	2
106	A Bayesian model for classifying all differentially expressed proteins simultaneously in 2D PAGE gels. <i>BMC Bioinformatics</i> , 2012, 13, 137.	1.2	1
107	Imprinted and ancient gene: a potential mediator of cancer cell survival during tryptophan deprivation. <i>Cell Communication and Signaling</i> , 2018, 16, 88.	2.7	1
108	Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. , 2010, , .		0