

# Patrick O Brown

## List of Publications by Year in descending order

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132  
papers

88,312  
citations

2544

96  
h-index

12597

132  
g-index

139  
all docs

139  
docs citations

139  
times ranked

73038  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular portraits of human breast tumours. <i>Nature</i> , 2000, 406, 747-752.	27.8	13,397
2	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000, 403, 503-511.	27.8	8,977
3	Repeated observation of breast tumor subtypes in independent gene expression data sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8418-8423.	7.1	4,849
4	Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast <i>Saccharomyces cerevisiae</i> by Microarray Hybridization. <i>Molecular Biology of the Cell</i> , 1998, 9, 3273-3297.	2.1	4,372
5	Genomic Expression Programs in the Response of Yeast Cells to Environmental Changes. <i>Molecular Biology of the Cell</i> , 2000, 11, 4241-4257.	2.1	4,281
6	Exploring the Metabolic and Genetic Control of Gene Expression on a Genomic Scale. <i>Science</i> , 1997, 278, 680-686.	12.6	4,204
7	Development of the Human Infant Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e177.	5.6	2,390
8	Exploring the new world of the genome with DNA microarrays. <i>Nature Genetics</i> , 1999, 21, 33-37.	21.4	2,189
9	Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types. <i>PLoS ONE</i> , 2012, 7, e30733.	2.5	2,088
10	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000, 24, 227-235.	21.4	1,946
11	The Transcriptional Program in the Response of Human Fibroblasts to Serum. <i>Science</i> , 1999, 283, 83-87.	12.6	1,895
12	Cell-Type Specific Features of Circular RNA Expression. <i>PLoS Genetics</i> , 2013, 9, e1003777.	3.5	1,544
13	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000, 24, 236-244.	21.4	1,357
14	Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. <i>Molecular Biology of the Cell</i> , 2002, 13, 1977-2000.	2.1	1,352
15	Gene expression profiling identifies clinically relevant subtypes of prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 811-816.	7.1	1,175
16	Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12963-12968.	7.1	1,098
17	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001, 409, 533-538.	27.8	1,030
18	Diversity, topographic differentiation, and positional memory in human fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12877-12882.	7.1	983

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19	Relation of Gene Expression Phenotype to Immunoglobulin Mutation Genotype in B Cell Chronic Lymphocytic Leukemia. <i>Journal of Experimental Medicine</i> , 2001, 194, 1639-1648.	8.5	978
20	Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3738-3743.	7.1	934
21	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	21.4	928
22	[12] DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999, 303, 179-205.	1.0	896
23	Gene Expression Signature of Fibroblast Serum Response Predicts Human Cancer Progression: Similarities between Tumors and Wounds. <i>PLoS Biology</i> , 2004, 2, e7.	5.6	824
24	Gene Expression Patterns in Human Liver Cancers. <i>Molecular Biology of the Cell</i> , 2002, 13, 1929-1939.	2.1	779
25	Individuality and variation in gene expression patterns in human blood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1896-1901.	7.1	723
26	Comparative Gene Expression Profiles Following UV Exposure in Wild-Type and SOS-Deficient <i>Escherichia coli</i> . <i>Genetics</i> , 2001, 158, 41-64.	2.9	721
27	Endothelial cell diversity revealed by global expression profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10623-10628.	7.1	679
28	Precision and functional specificity in mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5860-5865.	7.1	652
29	Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. <i>Nature Genetics</i> , 2001, 28, 327-334.	21.4	642
30	Drug target validation and identification of secondary drug target effects using DNA microarrays. <i>Nature Medicine</i> , 1998, 4, 1293-1301.	30.7	635
31	Genome-wide analysis of mRNA translation profiles in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3889-3894.	7.1	632
32	Gene expression patterns in human embryonic stem cells and human pluripotent germ cell tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13350-13355.	7.1	608
33	Circular RNA Is Expressed across the Eukaryotic Tree of Life. <i>PLoS ONE</i> , 2014, 9, e90859.	2.5	585
34	Diverse RNA-Binding Proteins Interact with Functionally Related Sets of RNAs, Suggesting an Extensive Regulatory System. <i>PLoS Biology</i> , 2008, 6, e255.	5.6	540
35	Molecular characterisation of soft tissue tumours: a gene expression study. <i>Lancet, The</i> , 2002, 359, 1301-1307.	13.7	537
36	Gene Expression Programs in Response to Hypoxia: Cell Type Specificity and Prognostic Significance in Human Cancers. <i>PLoS Medicine</i> , 2006, 3, e47.	8.4	536

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37	Characteristic genome rearrangements in experimental evolution of <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16144-16149.	7.1	514
38	Genomic Expression Responses to DNA-damaging Agents and the Regulatory Role of the Yeast ATR Homolog Mec1p. Molecular Biology of the Cell, 2001, 12, 2987-3003.	2.1	500
39	New Components of a System for Phosphate Accumulation and Polyphosphate Metabolism in <i>Saccharomyces cerevisiae</i> Revealed by Genomic Expression Analysis. Molecular Biology of the Cell, 2000, 11, 4309-4321.	2.1	470
40	Exploration of Global Gene Expression Patterns in Pancreatic Adenocarcinoma Using cDNA Microarrays. American Journal of Pathology, 2003, 162, 1151-1162.	3.8	450
41	Gene expression profiling reveals molecularly and clinically distinct subtypes of glioblastoma multiforme. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5814-5819.	7.1	445
42	The Stanford Microarray Database. Nucleic Acids Research, 2001, 29, 152-155.	14.5	415
43	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. PLoS Genetics, 2006, 2, e119.	3.5	413
44	Systemic and cell type-specific gene expression patterns in scleroderma skin. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12319-12324.	7.1	385
45	Gene expression patterns in human placenta. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5478-5483.	7.1	383
46	Stereotyped and specific gene expression programs in human innate immune responses to bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 972-977.	7.1	371
47	Genome-wide Analysis of Gene Expression Regulated by the Calcineurin/Crz1p Signaling Pathway in <i>Saccharomyces cerevisiae</i> . Journal of Biological Chemistry, 2002, 277, 31079-31088.	3.4	370
48	Regulation of CSF1 Promoter by the SWI/SNF-like BAF Complex. Cell, 2001, 106, 309-318.	28.9	315
49	Transcriptome-Wide Mapping of Pseudouridines: Pseudouridine Synthases Modify Specific mRNAs in <i>S. cerevisiae</i> . PLoS ONE, 2014, 9, e110799.	2.5	305
50	Gene Expression Patterns in Ovarian Carcinomas. Molecular Biology of the Cell, 2003, 14, 4376-4386.	2.1	302
51	Genomic expression programs and the integration of the CD28 costimulatory signal in T cell activation. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11796-11801.	7.1	300
52	Variation in Gene Expression Patterns in Human Gastric Cancers. Molecular Biology of the Cell, 2003, 14, 3208-3215.	2.1	285
53	Genomewide view of gene silencing by small interfering RNAs. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6343-6346.	7.1	283
54	Nonparametric methods for identifying differentially expressed genes in microarray data. Bioinformatics, 2002, 18, 1454-1461.	4.1	276

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55	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. BMC Genomics, 2006, 7, 115.	2.8	275
56	Distinct stages of the translation elongation cycle revealed by sequencing ribosome-protected mRNA fragments. ELife, 2014, 3, e01257.	6.0	272
57	Diverse and Specific Gene Expression Responses to Stresses in Cultured Human Cells. Molecular Biology of the Cell, 2004, 15, 2361-2374.	2.1	268
58	Genomic transcriptional response to loss of chromosomal supercoiling in Escherichia coli. Genome Biology, 2004, 5, R87.	9.6	268
59	Bone morphogenetic protein antagonist gremlin 1 is widely expressed by cancer-associated stromal cells and can promote tumor cell proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14842-14847.	7.1	264
60	Genome microarray analysis of transcriptional activation in multidrug resistance yeast mutants. FEBS Letters, 2000, 470, 156-160.	2.8	243
61	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. Nature Genetics, 2000, 25, 58-62.	21.4	241
62	Combining SSH and cDNA microarrays for rapid identification of differentially expressed genes. Nucleic Acids Research, 1999, 27, 1517-1523.	14.5	240
63	Shotgun DNA microarrays and stage-specific gene expression in Plasmodium falciparum malaria. Molecular Microbiology, 2000, 35, 6-14.	2.5	207
64	The Preclinical Natural History of Serous Ovarian Cancer: Defining the Target for Early Detection. PLoS Medicine, 2009, 6, e1000114.	8.4	205
65	Transformation of follicular lymphoma to diffuse large-cell lymphoma: Alternative patterns with increased or decreased expression of c-myc and its regulated genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8886-8891.	7.1	204
66	A DNA microarray survey of gene expression in normal human tissues. Genome Biology, 2005, 6, R22.	9.6	198
67	Transcriptional Remodeling in Response to Iron Deprivation in Saccharomyces cerevisiae. Molecular Biology of the Cell, 2004, 15, 1233-1243.	2.1	191
68	Modulation of Cellular and Viral Gene Expression by the Latency-Associated Nuclear Antigen of Kaposi's Sarcoma-Associated Herpesvirus. Journal of Virology, 2001, 75, 458-468.	3.4	189
69	Predicting a local recurrence after breast-conserving therapy by gene expression profiling. Breast Cancer Research, 2006, 8, R62.	5.0	184
70	Global and Specific Translational Regulation in the Genomic Response of Saccharomyces cerevisiae to a Rapid Transfer from a Fermentable to a Nonfermentable Carbon Source. Molecular and Cellular Biology, 2001, 21, 916-927.	2.3	183
71	Determination of Stromal Signatures in Breast Carcinoma. PLoS Biology, 2005, 3, e187.	5.6	180
72	Degradation of Proteins from the ER of S. cerevisiae Requires an Intact Unfolded Protein Response Pathway. Molecular Cell, 2000, 5, 729-735.	9.7	171

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73	Identification of the Copper Regulon in <i>Saccharomyces cerevisiae</i> by DNA Microarrays. <i>Journal of Biological Chemistry</i> , 2000, 275, 32310-32316.	3.4	168
74	Desferrioxamine-mediated Iron Uptake in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 10709-10715.	3.4	166
75	Genomic Views of the Immune System. <i>Annual Review of Immunology</i> , 2000, 18, 829-859.	21.8	166
76	Phospholipase A2 group IIA expression in gastric adenocarcinoma is associated with prolonged survival and less frequent metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16203-16208.	7.1	166
77	Characterization of Three Related Glucose Repressors and Genes They Regulate in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998, 150, 1377-1391.	2.9	166
78	Photo-Cross-Linking Studies Suggest a Model for the Architecture of an Active Human Immunodeficiency Virus Type 1 Integrase-DNA Complex. <i>Biochemistry</i> , 1998, 37, 6667-6678.	2.5	164
79	Transcriptional programs activated by exposure of human prostate cancer cells to androgen. <i>Genome Biology</i> , 2002, 3, RESEARCH0032.	9.6	158
80	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	14.5	158
81	miR-142 regulates the tumorigenicity of human breast cancer stem cells through the canonical WNT signaling pathway. <i>ELife</i> , 2014, 3, .	6.0	153
82	RERG Is a Novel ras-related, Estrogen-regulated and Growth-inhibitory Gene in Breast Cancer. <i>Journal of Biological Chemistry</i> , 2001, 276, 42259-42267.	3.4	147
83	Use of cDNA microarrays to analyze dioxin-induced changes in human liver gene expression. <i>Toxicology Letters</i> , 2001, 122, 189-203.	0.8	144
84	Variation in gene expression patterns in follicular lymphoma and the response to rituximab. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1926-1930.	7.1	144
85	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. <i>Genome Research</i> , 2002, 12, 281-291.	5.5	143
86	Gene Expression Patterns and Gene Copy Number Changes in Dermatofibrosarcoma Protuberans. <i>American Journal of Pathology</i> , 2003, 163, 2383-2395.	3.8	142
87	Genomic mismatch scanning: a new approach to genetic linkage mapping. <i>Nature Genetics</i> , 1993, 4, 11-18.	21.4	134
88	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. <i>PLoS ONE</i> , 2010, 5, e9753.	2.5	134
89	Tissue Microarray Validation of Epidermal Growth Factor Receptor and SALL2 in Synovial Sarcoma with Comparison to Tumors of Similar Histology. <i>American Journal of Pathology</i> , 2003, 163, 1449-1456.	3.8	133
90	Genomics and human disease variations on variation. <i>Nature Genetics</i> , 1998, 18, 91-93.	21.4	115

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91	Parallels between Global Transcriptional Programs of Polarizing Caco-2 Intestinal Epithelial Cells In Vitro and Gene Expression Programs in Normal Colon and Colon Cancer. <i>Molecular Biology of the Cell</i> , 2007, 18, 4245-4260.	2.1	114
92	From The Cover: The host response to smallpox: Analysis of the gene expression program in peripheral blood cells in a nonhuman primate model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15190-15195.	7.1	111
93	Functional genomic analysis of a commercial wine strain of <i>Saccharomyces cerevisiae</i> under differing nitrogen conditions. <i>FEMS Yeast Research</i> , 2001, 1, 111-125.	2.3	108
94	Role of thioredoxin reductase in the Yap1p-dependent response to oxidative stress in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2001, 39, 595-605.	2.5	107
95	Discovery and validation of breast cancer subtypes. <i>BMC Genomics</i> , 2006, 7, 231.	2.8	102
96	Gene Expression in the Normal Adult Human Kidney Assessed by Complementary DNA Microarray. <i>Molecular Biology of the Cell</i> , 2004, 15, 649-656.	2.1	97
97	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998, 18, 373-379.	3.8	96
98	Genome-wide analysis of mRNA lengths in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2003, 5, R2.	9.6	92
99	Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007, 8, R261.	9.6	89
100	T Cell Receptor-Independent Basal Signaling via Erk and Abl Kinases Suppresses RAG Gene Expression. <i>PLoS Biology</i> , 2003, 1, e53.	5.6	88
101	Observing the living genome. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 715-722.	3.3	86
102	Gene Expression Patterns in Pancreatic Tumors, Cells and Tissues. <i>PLoS ONE</i> , 2007, 2, e323.	2.5	86
103	Genome-Scale Identification of Membrane-Associated Human mRNAs. <i>PLoS Genetics</i> , 2006, 2, e11.	3.5	84
104	The temporal program of peripheral blood gene expression in the response of nonhuman primates to Ebola hemorrhagic fever. <i>Genome Biology</i> , 2007, 8, R174.	9.6	80
105	DNA Methylation Profiles of Ovarian Epithelial Carcinoma Tumors and Cell Lines. <i>PLoS ONE</i> , 2010, 5, e9359.	2.5	80
106	Characterization of heterotypic interaction effects in vitro to deconvolute global gene expression profiles in cancer. <i>Genome Biology</i> , 2007, 8, R191.	9.6	76
107	Stunned Silence: Gene Expression Programs in Human Cells Infected with Monkeypox or Vaccinia Virus. <i>PLoS ONE</i> , 2011, 6, e15615.	2.5	73
108	Comparative Genome-Scale Analysis of Gene Expression Profiles in T Cell Lymphoma Cells during Malignant Progression Using a Complementary DNA Microarray. <i>American Journal of Pathology</i> , 2001, 158, 1231-1237.	3.8	62

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109	Rapid global phaseout of animal agriculture has the potential to stabilize greenhouse gas levels for 30 years and offset 68 percent of CO2 emissions this century. , 2022, 1, e0000010.		62
110	Transcriptional response of human mast cells stimulated via the Fc(epsilon)RI and identification of mast cells as a source of IL-11. BMC Immunology, 2002, 3, 5.	2.2	56
111	Gene Expression Programs of Human Smooth Muscle Cells: Tissue-Specific Differentiation and Prognostic Significance in Breast Cancers. PLoS Genetics, 2007, 3, e164.	3.5	56
112	Differential gene expression in anatomical compartments of the human eye. Genome Biology, 2005, 6, R74.	9.6	55
113	Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. PLoS Biology, 2015, 13, e1002307.	5.6	54
114	Comparative Analysis of Viral Gene Expression Programs during Poxvirus Infection: A Transcriptional Map of the Vaccinia and Monkeypox Genomes. PLoS ONE, 2008, 3, e2628.	2.5	54
115	ESRRA-C11orf20 Is a Recurrent Gene Fusion in Serous Ovarian Carcinoma. PLoS Biology, 2011, 9, e1001156.	5.6	50
116	Differential gene-expression patterns in genital fibroblasts of normal males and 46,XY females with androgen insensitivity syndrome: evidence for early programming involving the androgen receptor. Genome Biology, 2003, 4, R37.	9.6	45
117	A gene-expression program reflecting the innate immune response of cultured intestinal epithelial cells to infection by Listeria monocytogenes. Genome Biology, 2002, 4, R2.	9.6	43
118	Haa1, a Protein Homologous to the Copper-regulated Transcription Factor Ace1, Is a Novel Transcriptional Activator. Journal of Biological Chemistry, 2001, 276, 38697-38702.	3.4	41
119	Directed Chemical Evolution with an Outsized Genetic Code. PLoS ONE, 2016, 11, e0154765.	2.5	27
120	Cancer characterization and feature set extraction by discriminative margin clustering. BMC Bioinformatics, 2004, 5, 21.	2.6	25
121	Automated Analysis and Classification of Histological Tissue Features by Multi-Dimensional Microscopic Molecular Profiling. PLoS ONE, 2015, 10, e0128975.	2.5	22
122	Minimizing off-target effects by using diced siRNAs for RNA interference. Journal of Rnai and Gene Silencing, 2006, 2, 181-94.	1.2	22
123	Examining the Living Genome in Health and Disease With DNA Microarrays. JAMA - Journal of the American Medical Association, 2000, 283, 2298.	7.4	17
124	Dynamic ASXL1 Exon Skipping and Alternative Circular Splicing in Single Human Cells. PLoS ONE, 2016, 11, e0164085.	2.5	15
125	Virtual Northern Analysis of the Human Genome. PLoS ONE, 2007, 2, e460.	2.5	11
126	Physical mapping of genes in somatic cell radiation hybrids by comparative genomic hybridization to cDNA microarrays. Genome Biology, 2002, 3, research0026.1.	9.6	7



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127	Functional genomic analysis of a commercial wine strain of <i>Saccharomyces cerevisiae</i> under differing nitrogen conditions. <i>FEMS Yeast Research</i> , 2001, 1, 111-125.	2.3	6
128	Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility. , 2005, , 77-100.		2
129	Differential Gene Expression Profiles in CD34+ Myelodysplastic Syndrome Marrow Cells.. <i>Blood</i> , 2005, 106, 3424-3424.	1.4	2
130	Exploring along a Crooked Path**â€œPreviously presented at the annual meeting of The American Society of Human Genetics, in Salt Lake City, on October 29, 2005.. <i>American Journal of Human Genetics</i> , 2006, 79, 429-433.	6.2	1
131	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
132	The Temporal Gene Expression Patterns of Embryonic Hematopoiesis after Hemangioblast Commitment.. <i>Blood</i> , 2005, 106, 4188-4188.	1.4	0