

# Patrick O Brown

## List of Publications by Year in descending order

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docs citations

139  
times ranked

73038  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Directed Chemical Evolution with an Outsized Genetic Code. PLoS ONE, 2016, 11, e0154765.	1.1	27
3	Dynamic ASXL1 Exon Skipping and Alternative Circular Splicing in Single Human Cells. PLoS ONE, 2016, 11, e0164085.	1.1	15
4	Automated Analysis and Classification of Histological Tissue Features by Multi-Dimensional Microscopic Molecular Profiling. PLoS ONE, 2015, 10, e0128975.	1.1	22
5	Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. PLoS Biology, 2015, 13, e1002307.	2.6	54
6	Circular RNA Is Expressed across the Eukaryotic Tree of Life. PLoS ONE, 2014, 9, e90859.	1.1	585
7	Transcriptome-Wide Mapping of Pseudouridines: Pseudouridine Synthases Modify Specific mRNAs in <i>S. cerevisiae</i> . PLoS ONE, 2014, 9, e110799.	1.1	305
8	Distinct stages of the translation elongation cycle revealed by sequencing ribosome-protected mRNA fragments. ELife, 2014, 3, e01257.	2.8	272
9	miR-142 regulates the tumorigenicity of human breast cancer stem cells through the canonical WNT signaling pathway. ELife, 2014, 3, .	2.8	153
10	Cell-Type Specific Features of Circular RNA Expression. PLoS Genetics, 2013, 9, e1003777.	1.5	1,544
11	Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types. PLoS ONE, 2012, 7, e30733.	1.1	2,088
12	ESRRA-C11orf20 Is a Recurrent Gene Fusion in Serous Ovarian Carcinoma. PLoS Biology, 2011, 9, e1001156.	2.6	50
13	Stunned Silence: Gene Expression Programs in Human Cells Infected with Monkeypox or Vaccinia Virus. PLoS ONE, 2011, 6, e15615.	1.1	73
14	DNA Methylation Profiles of Ovarian Epithelial Carcinoma Tumors and Cell Lines. PLoS ONE, 2010, 5, e9359.	1.1	80
15	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. PLoS ONE, 2010, 5, e9753.	1.1	134
16	The Preclinical Natural History of Serous Ovarian Cancer: Defining the Target for Early Detection. PLoS Medicine, 2009, 6, e1000114.	3.9	205
17	Diverse RNA-Binding Proteins Interact with Functionally Related Sets of RNAs, Suggesting an Extensive Regulatory System. PLoS Biology, 2008, 6, e255.	2.6	540
18	Comparative Analysis of Viral Gene Expression Programs during Poxvirus Infection: A Transcriptional Map of the Vaccinia and Monkeypox Genomes. PLoS ONE, 2008, 3, e2628.	1.1	54

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19	Gene Expression Programs of Human Smooth Muscle Cells: Tissue-Specific Differentiation and Prognostic Significance in Breast Cancers. <i>PLoS Genetics</i> , 2007, 3, e164.	1.5	56
20	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.	0.9	114
21	Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007, 8, R261.	13.9	89
22	Characterization of heterotypic interaction effects in vitro to deconvolute global gene expression profiles in cancer. <i>Genome Biology</i> , 2007, 8, R191.	13.9	76
23	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.	13.9	80
24	Development of the Human Infant Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e177.	2.6	2,390
25	Gene Expression Patterns in Pancreatic Tumors, Cells and Tissues. <i>PLoS ONE</i> , 2007, 2, e323.	1.1	86
26	Virtual Northern Analysis of the Human Genome. <i>PLoS ONE</i> , 2007, 2, e460.	1.1	11
27	Predicting a local recurrence after breast-conserving therapy by gene expression profiling. <i>Breast Cancer Research</i> , 2006, 8, R62.	2.2	184
28	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.	2.6	1
29	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006, 34, e5-e5.	6.5	158
30	Gene Expression Programs in Response to Hypoxia: Cell Type Specificity and Prognostic Significance in Human Cancers. <i>PLoS Medicine</i> , 2006, 3, e47.	3.9	536
31	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. <i>BMC Genomics</i> , 2006, 7, 115.	1.2	275
32	Discovery and validation of breast cancer subtypes. <i>BMC Genomics</i> , 2006, 7, 231.	1.2	102
33	Genome-Scale Identification of Membrane-Associated Human mRNAs. <i>PLoS Genetics</i> , 2006, 2, e11.	1.5	84
34	Gene expression patterns in human placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5478-5483.	3.3	383
35	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. <i>PLoS Genetics</i> , 2006, 2, e119.	1.5	413
36	Bone morphogenetic protein antagonist gremlin 1 is widely expressed by cancer-associated stromal cells and can promote tumor cell proliferation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14842-14847.	3.3	264

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37	Minimizing off-target effects by using diced siRNAs for RNA interference. <i>Journal of Rnai and Gene Silencing</i> , 2006, 2, 181-94.	1.2	22
38	Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility. , 2005, , 77-100.		2
39	From The Cover: 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.	3.3	934
40	Gene expression profiling reveals molecularly and clinically distinct subtypes of glioblastoma multiforme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5814-5819.	3.3	445
41	Differential gene expression in anatomical compartments of the human eye. <i>Genome Biology</i> , 2005, 6, R74.	13.9	55
42	A DNA microarray survey of gene expression in normal human tissues. <i>Genome Biology</i> , 2005, 6, R22.	13.9	198
43	Differential Gene Expression Profiles in CD34+ Myelodysplastic Syndrome Marrow Cells.. <i>Blood</i> , 2005, 106, 3424-3424.	0.6	2
44	Determination of Stromal Signatures in Breast Carcinoma. <i>PLoS Biology</i> , 2005, 3, e187.	2.6	180
45	The Temporal Gene Expression Patterns of Embryonic Hematopoiesis after Hemangioblast Commitment.. <i>Blood</i> , 2005, 106, 4188-4188.	0.6	0
46	Diverse and Specific Gene Expression Responses to Stresses in Cultured Human Cells. <i>Molecular Biology of the Cell</i> , 2004, 15, 2361-2374.	0.9	268
47	Gene Expression in the Normal Adult Human Kidney Assessed by Complementary DNA Microarray. <i>Molecular Biology of the Cell</i> , 2004, 15, 649-656.	0.9	97
48	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.	3.3	111
49	Transcriptional Remodeling in Response to Iron Deprivation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2004, 15, 1233-1243.	0.9	191
50	Gene Expression Signature of Fibroblast Serum Response Predicts Human Cancer Progression: Similarities between Tumors and Wounds. <i>PLoS Biology</i> , 2004, 2, e7.	2.6	824
51	Cancer characterization and feature set extraction by discriminative margin clustering. <i>BMC Bioinformatics</i> , 2004, 5, 21.	1.2	25
52	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.	3.3	1,175
53	Genomic transcriptional response to loss of chromosomal supercoiling in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2004, 5, R87.	13.9	268
54	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.	1.9	133

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55	Gene Expression Patterns and Gene Copy Number Changes in Dermatofibrosarcoma Protuberans. American Journal of Pathology, 2003, 163, 2383-2395.	1.9	142
56	Exploration of Global Gene Expression Patterns in Pancreatic Adenocarcinoma Using cDNA Microarrays. American Journal of Pathology, 2003, 162, 1151-1162.	1.9	450
57	Repeated observation of breast tumor subtypes in independent gene expression data sets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8418-8423.	3.3	4,849
58	Genome-wide analysis of mRNA lengths in Saccharomyces cerevisiae. Genome Biology, 2003, 5, R2.	13.9	92
59	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.	13.9	45
60	Individuality and variation in gene expression patterns in human blood. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1896-1901.	3.3	723
61	Variation in Gene Expression Patterns in Human Gastric Cancers. Molecular Biology of the Cell, 2003, 14, 3208-3215.	0.9	285
62	Variation in gene expression patterns in follicular lymphoma and the response to rituximab. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1926-1930.	3.3	144
63	Endothelial cell diversity revealed by global expression profiling. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10623-10628.	3.3	679
64	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.	3.3	385
65	Gene expression patterns in human embryonic stem cells and human pluripotent germ cell tumors. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13350-13355.	3.3	608
66	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.	3.3	283
67	Gene Expression Patterns in Ovarian Carcinomas. Molecular Biology of the Cell, 2003, 14, 4376-4386.	0.9	302
68	Genome-wide analysis of mRNA translation profiles in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3889-3894.	3.3	632
69	T Cell Receptor-Independent Basal Signaling via Erk and Abl Kinases Suppresses RAG Gene Expression. PLoS Biology, 2003, 1, e53.	2.6	88
70	Diversity, topographic differentiation, and positional memory in human fibroblasts. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12877-12882.	3.3	983
71	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.	3.3	371
72	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.	3.3	204

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73	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.	3.3	1,098
74	Genomic expression programs and the integration of the CD28 costimulatory signal in T cell activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11796-11801.	3.3	300
75	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.	3.3	166
76	Genome-wide Analysis of Gene Expression Regulated by the Calcineurin/Crz1p Signaling Pathway in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 31079-31088.	1.6	370
77	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.	0.9	1,352
78	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002, 18, 1454-1461.	1.8	276
79	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. <i>Genome Research</i> , 2002, 12, 281-291.	2.4	143
80	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.	3.3	652
81	Characteristic genome rearrangements in experimental evolution of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16144-16149.	3.3	514
82	A gene-expression program reflecting the innate immune response of cultured intestinal epithelial cells to infection by <i>Listeria monocytogenes</i> . <i>Genome Biology</i> , 2002, 4, R2.	13.9	43
83	Transcriptional programs activated by exposure of human prostate cancer cells to androgen. <i>Genome Biology</i> , 2002, 3, research0032.1.	13.9	158
84	Physical mapping of genes in somatic cell radiation hybrids by comparative genomic hybridization to cDNA microarrays. <i>Genome Biology</i> , 2002, 3, research0026.1.	13.9	7
85	Gene Expression Patterns in Human Liver Cancers. <i>Molecular Biology of the Cell</i> , 2002, 13, 1929-1939.	0.9	779
86	Molecular characterisation of soft tissue tumours: a gene expression study. <i>Lancet, The</i> , 2002, 359, 1301-1307.	6.3	537
87	Transcriptional response of human mast cells stimulated via the Fc(epsilon)RI and identification of mast cells as a source of IL-11. <i>BMC Immunology</i> , 2002, 3, 5.	0.9	56
88	Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. <i>Nature Genetics</i> , 2001, 28, 327-334.	9.4	642
89	Use of cDNA microarrays to analyze dioxin-induced changes in human liver gene expression. <i>Toxicology Letters</i> , 2001, 122, 189-203.	0.4	144
90	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.	1.9	62

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91	Regulation of CSF1 Promoter by the SWI/SNF-like BAF Complex. <i>Cell</i> , 2001, 106, 309-318.	13.5	315
92	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.	1.2	107
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.	1.1	108
94	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001, 409, 533-538.	13.7	1,030
95	Genomic Expression Responses to DNA-damaging Agents and the Regulatory Role of the Yeast ATR Homolog Mec1p. <i>Molecular Biology of the Cell</i> , 2001, 12, 2987-3003.	0.9	500
96	Modulation of Cellular and Viral Gene Expression by the Latency-Associated Nuclear Antigen of Kaposi's Sarcoma-Associated Herpesvirus. <i>Journal of Virology</i> , 2001, 75, 458-468.	1.5	189
97	Haa1, a Protein Homologous to the Copper-regulated Transcription Factor Ace1, Is a Novel Transcriptional Activator. <i>Journal of Biological Chemistry</i> , 2001, 276, 38697-38702.	1.6	41
98	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001, 29, 152-155.	6.5	415
99	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.	4.2	978
100	Global and Specific Translational Regulation in the Genomic Response of <i>Saccharomyces cerevisiae</i> to a Rapid Transfer from a Fermentable to a Nonfermentable Carbon Source. <i>Molecular and Cellular Biology</i> , 2001, 21, 916-927.	1.1	183
101	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.	1.6	147
102	Comparative Gene Expression Profiles Following UV Exposure in Wild-Type and SOS-Deficient <i>Escherichia coli</i> . <i>Genetics</i> , 2001, 158, 41-64.	1.2	721
103	Examining the Living Genome in Health and Disease With DNA Microarrays. <i>JAMA - Journal of the American Medical Association</i> , 2000, 283, 2298.	3.8	17
104	Shotgun DNA microarrays and stage-specific gene expression in <i>Plasmodium falciparum</i> malaria. <i>Molecular Microbiology</i> , 2000, 35, 6-14.	1.2	207
105	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000, 24, 227-235.	9.4	1,946
106	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000, 24, 236-244.	9.4	1,357
107	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000, 25, 58-62.	9.4	241
108	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000, 403, 503-511.	13.7	8,977

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109	Molecular portraits of human breast tumours. <i>Nature</i> , 2000, 406, 747-752.	13.7	13,397
110	New Components of a System for Phosphate Accumulation and Polyphosphate Metabolism in <i>Saccharomyces cerevisiae</i> Revealed by Genomic Expression Analysis. <i>Molecular Biology of the Cell</i> , 2000, 11, 4309-4321.	0.9	470
111	Desferrioxamine-mediated Iron Uptake in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 10709-10715.	1.6	166
112	Genomic Views of the Immune System. <i>Annual Review of Immunology</i> , 2000, 18, 829-859.	9.5	166
113	Identification of the Copper Regulon in <i>Saccharomyces cerevisiae</i> by DNA Microarrays. <i>Journal of Biological Chemistry</i> , 2000, 275, 32310-32316.	1.6	168
114	Degradation of Proteins from the ER of <i>S. cerevisiae</i> Requires an Intact Unfolded Protein Response Pathway. <i>Molecular Cell</i> , 2000, 5, 729-735.	4.5	171
115	Genome microarray analysis of transcriptional activation in multidrug resistance yeast mutants. <i>FEBS Letters</i> , 2000, 470, 156-160.	1.3	243
116	Genomic Expression Programs in the Response of Yeast Cells to Environmental Changes. <i>Molecular Biology of the Cell</i> , 2000, 11, 4241-4257.	0.9	4,281
117	Combining SSH and cDNA microarrays for rapid identification of differentially expressed genes. <i>Nucleic Acids Research</i> , 1999, 27, 1517-1523.	6.5	240
118	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	9.4	928
119	Exploring the new world of the genome with DNA microarrays. <i>Nature Genetics</i> , 1999, 21, 33-37.	9.4	2,189
120	The Transcriptional Program in the Response of Human Fibroblasts to Serum. <i>Science</i> , 1999, 283, 83-87.	6.0	1,895
121	[12] DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999, 303, 179-205.	0.4	896
122	Observing the living genome. <i>Current Opinion in Genetics and Development</i> , 1999, 9, 715-722.	1.5	86
123	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998, 18, 373-379.	2.0	96
124	Drug target validation and identification of secondary drug target effects using DNA microarrays. <i>Nature Medicine</i> , 1998, 4, 1293-1301.	15.2	635
125	Genomics and human disease—variations on variation. <i>Nature Genetics</i> , 1998, 18, 91-93.	9.4	115
126	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.	1.2	164



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127	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.	0.9	4,372
128	Characterization of Three Related Glucose Repressors and Genes They Regulate in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998, 150, 1377-1391.	1.2	166
129	Exploring the Metabolic and Genetic Control of Gene Expression on a Genomic Scale. <i>Science</i> , 1997, 278, 680-686.	6.0	4,204
130	Genomic mismatch scanning: a new approach to genetic linkage mapping. <i>Nature Genetics</i> , 1993, 4, 11-18.	9.4	134
131	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0