

Patrick O Brown

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130
papers

75,480
citations

93
h-index

138
g-index

138
ext. papers

82,493
ext. citations

12.6
avg, IF

7.25
L-index

#	Paper	IF	Citations
130	Molecular portraits of human breast tumours. <i>Nature</i> , 2000 , 406, 747-52	50.4	11221
129	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000 , 403, 503-11	50.4	7592
128	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, 8418-23	11.5	4262
127	Exploring the metabolic and genetic control of gene expression on a genomic scale. <i>Science</i> , 1997 , 278, 680-6	33.3	3744
126	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, 3273-97	3.5	3710
125	Genomic expression programs in the response of yeast cells to environmental changes. <i>Molecular Biology of the Cell</i> , 2000 , 11, 4241-57	3.5	3708
124	Development of the human infant intestinal microbiota. <i>PLoS Biology</i> , 2007 , 5, e177	9.7	1931
123	Exploring the new world of the genome with DNA microarrays. <i>Nature Genetics</i> , 1999 , 21, 33-7	36.3	1922
122	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000 , 24, 227-35	36.3	1739
121	The transcriptional program in the response of human fibroblasts to serum. <i>Science</i> , 1999 , 283, 83-7	33.3	1713
120	Circular RNAs are the predominant transcript isoform from hundreds of human genes in diverse cell types. <i>PLoS ONE</i> , 2012 , 7, e30733	3.7	1531
119	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000 , 24, 236-44	36.3	1173
118	Cell-type specific features of circular RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003777	6	1155
117	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, 811-6	11.5	1047
116	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	3.5	1043
115	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, 12963-8	11.5	980
114	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001 , 409, 533-8	50.4	927

113	Relation of gene expression phenotype to immunoglobulin mutation genotype in B cell chronic lymphocytic leukemia. <i>Journal of Experimental Medicine</i> , 2001 , 194, 1639-47	16.6	882
112	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, 12877-82	11.5	852
111	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, 3738-43	11.5	823
110	DNA arrays for analysis of gene expression. <i>Methods in Enzymology</i> , 1999 , 303, 179-205	1.7	747
109	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999 , 23, 41-6	36.3	712
108	Gene expression signature of fibroblast serum response predicts human cancer progression: similarities between tumors and wounds. <i>PLoS Biology</i> , 2004 , 2, E7	9.7	698
107	Gene expression patterns in human liver cancers. <i>Molecular Biology of the Cell</i> , 2002 , 13, 1929-39	3.5	680
106	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, 1896-901	11.5	640
105	Comparative gene expression profiles following UV exposure in wild-type and SOS-deficient <i>Escherichia coli</i> . <i>Genetics</i> , 2001 , 158, 41-64	4	615
104	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, 10623-8	11.5	597
103	Precision and functional specificity in mRNA decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5860-5	11.5	585
102	Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. <i>Nature Genetics</i> , 2001 , 28, 327-34	36.3	576
101	Drug target validation and identification of secondary drug target effects using DNA microarrays. <i>Nature Medicine</i> , 1998 , 4, 1293-301	50.5	568
100	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, 13350-5	11.5	557
99	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, 3889-94	11.5	543
98	Molecular characterisation of soft tissue tumours: a gene expression study. <i>Lancet, The</i> , 2002 , 359, 1301-7	4.0	484
97	Gene expression programs in response to hypoxia: cell type specificity and prognostic significance in human cancers. <i>PLoS Medicine</i> , 2006 , 3, e47	11.6	476
96	Circular RNA is expressed across the eukaryotic tree of life. <i>PLoS ONE</i> , 2014 , 9, e90859	3.7	457

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	3.5	453
94	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, 16144-9	11.5	449
93	Diverse RNA-binding proteins interact with functionally related sets of RNAs, suggesting an extensive regulatory system. <i>PLoS Biology</i> , 2008 , 6, e255	9.7	442
92	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, 4309-21	3.5	409
91	Exploration of global gene expression patterns in pancreatic adenocarcinoma using cDNA microarrays. <i>American Journal of Pathology</i> , 2003 , 162, 1151-62	5.8	397
90	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, 5814-9	11.5	389
89	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001 , 29, 152-5	20.1	337
88	Stereotyped and specific gene expression programs in human innate immune responses to bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 972-7 ^{11.5}	11.5	337
87	Systemic and cell type-specific gene expression patterns in scleroderma skin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12319-24	11.5	334
86	Anatomic demarcation by positional variation in fibroblast gene expression programs. <i>PLoS Genetics</i> , 2006 , 2, e119	6	329
85	Gene expression patterns in human placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 5478-83	11.5	315
84	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, 31079-88	5.4	315
83	Regulation of CSF1 promoter by the SWI/SNF-like BAF complex. <i>Cell</i> , 2001 , 106, 309-18	56.2	287
82	Gene expression patterns in ovarian carcinomas. <i>Molecular Biology of the Cell</i> , 2003 , 14, 4376-86	3.5	273
81	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, 11796-801	11.5	270
80	Variation in gene expression patterns in human gastric cancers. <i>Molecular Biology of the Cell</i> , 2003 , 14, 3208-15	3.5	253
79	Diverse and specific gene expression responses to stresses in cultured human cells. <i>Molecular Biology of the Cell</i> , 2004 , 15, 2361-74	3.5	250
78	Genomewide view of gene silencing by small interfering RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6343-6	11.5	249

77	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002 , 18, 1454-61	7.2	245
76	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. <i>BMC Genomics</i> , 2006 , 7, 115	4.5	244
75	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, 14842-7	11.5	235
74	Transcriptome-wide mapping of pseudouridines: pseudouridine synthases modify specific mRNAs in <i>S. cerevisiae</i> . <i>PLoS ONE</i> , 2014 , 9, e110799	3.7	227
73	Genomic transcriptional response to loss of chromosomal supercoiling in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2004 , 5, R87	18.3	226
72	Genome microarray analysis of transcriptional activation in multidrug resistance yeast mutants. <i>FEBS Letters</i> , 2000 , 470, 156-60	3.8	218
71	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000 , 25, 58-62	36.3	213
70	Distinct stages of the translation elongation cycle revealed by sequencing ribosome-protected mRNA fragments. <i>ELife</i> , 2014 , 3, e01257	8.9	195
69	Combining SSH and cDNA microarrays for rapid identification of differentially expressed genes. <i>Nucleic Acids Research</i> , 1999 , 27, 1517-23	20.1	193
68	Transformation of follicular lymphoma to diffuse large-cell lymphoma: alternative patterns with increased or decreased expression of c-myc and its regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8886-91	11.5	190
67	Shotgun DNA microarrays and stage-specific gene expression in <i>Plasmodium falciparum</i> malaria. <i>Molecular Microbiology</i> , 2000 , 35, 6-14	4.1	187
66	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, 458-68	6.6	182
65	A DNA microarray survey of gene expression in normal human tissues. <i>Genome Biology</i> , 2005 , 6, R22	18.3	172
64	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, 916-27	4.8	172
63	Transcriptional remodeling in response to iron deprivation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2004 , 15, 1233-43	3.5	170
62	The preclinical natural history of serous ovarian cancer: defining the target for early detection. <i>PLoS Medicine</i> , 2009 , 6, e1000114	11.6	168
61	Degradation of proteins from the ER of <i>S. cerevisiae</i> requires an intact unfolded protein response pathway. <i>Molecular Cell</i> , 2000 , 5, 729-35	17.6	164
60	Predicting a local recurrence after breast-conserving therapy by gene expression profiling. <i>Breast Cancer Research</i> , 2006 , 8, R62	8.3	163

59	Determination of stromal signatures in breast carcinoma. <i>PLoS Biology</i> , 2005 , 3, e187	9.7	161
58	Desferrioxamine-mediated iron uptake in <i>Saccharomyces cerevisiae</i> . Evidence for two pathways of iron uptake. <i>Journal of Biological Chemistry</i> , 2000 , 275, 10709-15	5.4	154
57	Genomic views of the immune system*. <i>Annual Review of Immunology</i> , 2000 , 18, 829-59	34.7	152
56	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, 6667-78	3.2	151
55	Identification of the copper regulon in <i>Saccharomyces cerevisiae</i> by DNA microarrays. <i>Journal of Biological Chemistry</i> , 2000 , 275, 32310-6	5.4	146
54	Rapid quantitative profiling of complex microbial populations. <i>Nucleic Acids Research</i> , 2006 , 34, e5	20.1	145
53	Transcriptional programs activated by exposure of human prostate cancer cells to androgen. <i>Genome Biology</i> , 2002 , 3, RESEARCH0032	18.3	140
52	Characterization of three related glucose repressors and genes they regulate in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998 , 150, 1377-91	4	137
51	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, 16203-8	11.5	134
50	Use of cDNA microarrays to analyze dioxin-induced changes in human liver gene expression. <i>Toxicology Letters</i> , 2001 , 122, 189-203	4.4	130
49	miR-142 regulates the tumorigenicity of human breast cancer stem cells through the canonical WNT signaling pathway. <i>ELife</i> , 2014 , 3,	8.9	128
48	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, 1926-30	11.5	128
47	In vivo regulation of human skeletal muscle gene expression by thyroid hormone. <i>Genome Research</i> , 2002 , 12, 281-91	9.7	124
46	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, 1449-56	5.8	123
45	Dissecting interferon-induced transcriptional programs in human peripheral blood cells. <i>PLoS ONE</i> , 2010 , 5, e9753	3.7	123
44	RERG is a novel ras-related, estrogen-regulated and growth-inhibitory gene in breast cancer. <i>Journal of Biological Chemistry</i> , 2001 , 276, 42259-67	5.4	120
43	Genomic mismatch scanning: a new approach to genetic linkage mapping. <i>Nature Genetics</i> , 1993 , 4, 11-8	36.3	116
42	Gene expression patterns and gene copy number changes in dermatofibrosarcoma protuberans. <i>American Journal of Pathology</i> , 2003 , 163, 2383-95	5.8	115

41	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, 4245-60	3.5	102
40	Functional genomic analysis of a commercial wine strain of <i>Saccharomyces cerevisiae</i> under differing nitrogen conditions. <i>FEMS Yeast Research</i> , 2001 , 1, 111-25	3.1	94
39	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, 15190-5	11.5	93
38	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	4.1	93
37	Gene expression in the normal adult human kidney assessed by complementary DNA microarray. <i>Molecular Biology of the Cell</i> , 2004 , 15, 649-56	3.5	90
36	Discovery and validation of breast cancer subtypes. <i>BMC Genomics</i> , 2006 , 7, 231	4.5	87
35	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998 , 18, 373-9	5.7	82
34	Observing the living genome. <i>Current Opinion in Genetics and Development</i> , 1999 , 9, 715-22	4.9	78
33	Genome-scale identification of membrane-associated human mRNAs. <i>PLoS Genetics</i> , 2006 , 2, e11	6	76
32	Gene-expression patterns reveal underlying biological processes in Kawasaki disease. <i>Genome Biology</i> , 2007 , 8, R261	18.3	76
31	Genome-wide analysis of mRNA lengths in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2003 , 5, R2	18.3	76
30	Gene expression patterns in pancreatic tumors, cells and tissues. <i>PLoS ONE</i> , 2007 , 2, e323	3.7	74
29	T cell receptor-independent basal signaling via Erk and Abl kinases suppresses RAG gene expression. <i>PLoS Biology</i> , 2003 , 1, E53	9.7	74
28	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	18.3	72
27	DNA methylation profiles of ovarian epithelial carcinoma tumors and cell lines. <i>PLoS ONE</i> , 2010 , 5, e9359	3.7	68
26	Characterization of heterotypic interaction effects in vitro to deconvolute global gene expression profiles in cancer. <i>Genome Biology</i> , 2007 , 8, R191	18.3	65
25	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, 1231-7	5.8	59
24	Gene expression programs of human smooth muscle cells: tissue-specific differentiation and prognostic significance in breast cancers. <i>PLoS Genetics</i> , 2007 , 3, 1770-84	6	48

23	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	3.7	45
22	ESRRA-C11orf20 is a recurrent gene fusion in serous ovarian carcinoma. <i>PLoS Biology</i> , 2011 , 9, e1001156	9.7	44
21	Differential gene expression in anatomical compartments of the human eye. <i>Genome Biology</i> , 2005 , 6, R74	18.3	42
20	Haa1, a protein homologous to the copper-regulated transcription factor Ace1, is a novel transcriptional activator. <i>Journal of Biological Chemistry</i> , 2001 , 276, 38697-702	5.4	39
19	Comparative analysis of viral gene expression programs during poxvirus infection: a transcriptional map of the vaccinia and monkeypox genomes. <i>PLoS ONE</i> , 2008 , 3, e2628	3.7	39
18	Stunned silence: gene expression programs in human cells infected with monkeypox or vaccinia virus. <i>PLoS ONE</i> , 2011 , 6, e15615	3.7	36
17	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. <i>Genome Biology</i> , 2003 , 4, R37	18.3	35
16	Evolutionary Conservation and Diversification of Puf RNA Binding Proteins and Their mRNA Targets. <i>PLoS Biology</i> , 2015 , 13, e1002307	9.7	35
15	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> , 2003 , 4, R2	18.3	32
14	Cancer characterization and feature set extraction by discriminative margin clustering. <i>BMC Bioinformatics</i> , 2004 , 5, 21	3.6	23
13	Minimizing off-target effects by using diced siRNAs for RNA interference. <i>Journal of RNAi and Gene Silencing</i> , 2006 , 2, 181-94		22
12	Automated Analysis and Classification of Histological Tissue Features by Multi-Dimensional Microscopic Molecular Profiling. <i>PLoS ONE</i> , 2015 , 10, e0128975	3.7	20
11	Directed Chemical Evolution with an Outsized Genetic Code. <i>PLoS ONE</i> , 2016 , 11, e0154765	3.7	20
10	Dynamic ASXL1 Exon Skipping and Alternative Circular Splicing in Single Human Cells. <i>PLoS ONE</i> , 2016 , 11, e0164085	3.7	12
9	Virtual Northern analysis of the human genome. <i>PLoS ONE</i> , 2007 , 2, e460	3.7	10
8	Examining the Living Genome in Health and Disease With DNA Microarrays. <i>JAMA - Journal of the American Medical Association</i> , 2000 , 283, 2298	27.4	9
7	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		8
6	Physical mapping of genes in somatic cell radiation hybrids by comparative genomic hybridization to cDNA microarrays. <i>Genome Biology</i> , 2002 , 3, RESEARCH0026	18.3	5

5	Differential Gene Expression Profiles in CD34+ Myelodysplastic Syndrome Marrow Cells.. <i>Blood</i> , 2005 , 106, 3424-3424	2.2	2
4	2005 Curt Stern Award address. Exploring along a crooked path. <i>American Journal of Human Genetics</i> , 2006 , 79, 429-33	11	1
3	Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility 2005 , 77-100		1
2	Computational Methods and Bioinformatic Tools769-904		
1	The Temporal Gene Expression Patterns of Embryonic Hematopoiesis after Hemangioblast Commitment.. <i>Blood</i> , 2005 , 106, 4188-4188	2.2	