

David Botstein

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109
papers

88,556
citations

76
h-index

115
g-index

115
ext. papers

99,832
ext. citations

14.3
avg, IF

7.01
L-index

#	Paper	IF	Citations
109	Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. <i>Nature Genetics</i> , 2000 , 25, 25-9	36.3	25593
108	Molecular portraits of human breast tumours. <i>Nature</i> , 2000 , 406, 747-52	50.4	11221
107	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000 , 403, 503-11	50.4	7592
106	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
105	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
104	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
103	Exploring the new world of the genome with DNA microarrays. <i>Nature Genetics</i> , 1999 , 21, 33-7	36.3	1922
102	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000 , 24, 227-35	36.3	1739
101	The transcriptional program in the response of human fibroblasts to serum. <i>Science</i> , 1999 , 283, 83-7	33.3	1713
100	GO::TermFinder--open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. <i>Bioinformatics</i> , 2004 , 20, 3710-5	7.2	1381
99	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003 , 34, 166-76	36.3	1275
98	Discovering genotypes underlying human phenotypes: past successes for mendelian disease, future approaches for complex disease. <i>Nature Genetics</i> , 2003 , 33 Suppl, 228-37	36.3	1182
97	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000 , 24, 236-44	36.3	1173
96	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
95	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
94	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
93	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001 , 409, 533-8	50.4	927

92	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
91	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
90	Prediction of survival in diffuse large-B-cell lymphoma based on the expression of six genes. <i>New England Journal of Medicine</i> , 2004 , 350, 1828-37	59.2	754
89	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999 , 23, 41-6	36.3	712
88	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
87	Gene expression patterns in human liver cancers. <i>Molecular Biology of the Cell</i> , 2002 , 13, 1929-39	3.5	680
86	Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer. <i>Nature</i> , 1998 , 396, 699-703	50.4	658
85	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
84	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
83	Different gene expression patterns in invasive lobular and ductal carcinomas of the breast. <i>Molecular Biology of the Cell</i> , 2004 , 15, 2523-36	3.5	488
82	Molecular characterisation of soft tissue tumours: a gene expression study. <i>Lancet, The</i> , 2002 , 359, 1301-7	47.0	484
81	Expression of cytokeratins 17 and 5 identifies a group of breast carcinomas with poor clinical outcome. <i>American Journal of Pathology</i> , 2002 , 161, 1991-6	5.8	453
80	A Bayesian framework for combining heterogeneous data sources for gene function prediction (in <i>Saccharomyces cerevisiae</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8348-53	11.5	431
79	Coordination of growth rate, cell cycle, stress response, and metabolic activity in yeast. <i>Molecular Biology of the Cell</i> , 2008 , 19, 352-67	3.5	405
78	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
77	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001 , 29, 152-5	20.1	337
76	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	337
75	Yeast: an experimental organism for 21st Century biology. <i>Genetics</i> , 2011 , 189, 695-704	4	335

74	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
73	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003 , 31, 219-23	20.1	325
72	Gene shaving: a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000 , 1, RESEARCH0003	18.3	304
71	Gene expression patterns in ovarian carcinomas. <i>Molecular Biology of the Cell</i> , 2003 , 14, 4376-86	3.5	273
70	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
69	Saccharomyces Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). <i>Nucleic Acids Research</i> , 2002 , 30, 69-72	20.1	265
68	Variation in gene expression patterns in human gastric cancers. <i>Molecular Biology of the Cell</i> , 2003 , 14, 3208-15	3.5	253
67	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
66	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002 , 18, 1454-61	7.2	245
65	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000 , 25, 58-62	36.3	213
64	Requirement of yeast fimbrin for actin organization and morphogenesis in vivo. <i>Nature</i> , 1991 , 354, 404-8	50.4	202
63	Gene Ontology annotations at SGD: new data sources and annotation methods. <i>Nucleic Acids Research</i> , 2008 , 36, D577-81	20.1	196
62	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
61	Defining protein interactions with yeast actin in vivo. <i>Nature Structural Biology</i> , 1995 , 2, 28-35		181
60	A DNA microarray survey of gene expression in normal human tissues. <i>Genome Biology</i> , 2005 , 6, R22	18.3	172
59	Structure of the yeast endoplasmic reticulum: localization of ER proteins using immunofluorescence and immunoelectron microscopy. <i>Yeast</i> , 1991 , 7, 891-911	3.4	163
58	BIM1 encodes a microtubule-binding protein in yeast. <i>Molecular Biology of the Cell</i> , 1997 , 8, 2677-91	3.5	160
57	Systems-level analysis of mechanisms regulating yeast metabolic flux. <i>Science</i> , 2016 , 354,	33.3	157

56	Nutritional homeostasis in batch and steady-state culture of yeast. <i>Molecular Biology of the Cell</i> , 2004 , 15, 4089-104	3.5	139
55	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
54	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
53	Genetic and physical maps of <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 1997 , 387, 67-73	50.4	125
52	Universal Reference RNA as a standard for microarray experiments. <i>BMC Genomics</i> , 2004 , 5, 20	4.5	124
51	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
50	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
49	Precise gene disruption in <i>Saccharomyces cerevisiae</i> by double fusion polymerase chain reaction. <i>Yeast</i> , 1995 , 11, 1275-80	3.4	118
48	Slow growth induces heat-shock resistance in normal and respiratory-deficient yeast. <i>Molecular Biology of the Cell</i> , 2009 , 20, 891-903	3.5	116
47	Gene expression patterns and gene copy number changes in dermatofibrosarcoma protuberans. <i>American Journal of Pathology</i> , 2003 , 163, 2383-95	5.8	115
46	Supervised harvesting of expression trees. <i>Genome Biology</i> , 2001 , 2, RESEARCH0003	18.3	113
45	Extrachromosomal circular DNA is common in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3114-22	11.5	111
44	Gene expression profiles do not consistently predict the clinical treatment response in locally advanced breast cancer. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2914-8	6.1	103
43	Structure-function relationships in yeast tubulins. <i>Molecular Biology of the Cell</i> , 2000 , 11, 1887-903	3.5	103
42	Specificity domains distinguish the Ras-related GTPases Ypt1 and Sec4. <i>Nature</i> , 1993 , 362, 563-5	50.4	99
41	<i>Saccharomyces</i> Genome Database. <i>Methods in Enzymology</i> , 2002 , 350, 329-46	1.7	96
40	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
39	Genome-wide analysis of nucleotide-level variation in commonly used <i>Saccharomyces cerevisiae</i> strains. <i>PLoS ONE</i> , 2007 , 2, e322	3.7	88

38	Inference of combinatorial regulation in yeast transcriptional networks: a case study of sporulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1998-2003	11.5	87
37	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998 , 18, 373-9	5.7	82
36	Genome Snapshot: a new resource at the Saccharomyces Genome Database (SGD) presenting an overview of the Saccharomyces cerevisiae genome. <i>Nucleic Acids Research</i> , 2006 , 34, D442-5	20.1	79
35	Genome-scale identification of membrane-associated human mRNAs. <i>PLoS Genetics</i> , 2006 , 2, e11	6	76
34	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
33	Bmi-1 regulation of INK4A-ARF is a downstream requirement for transformation of hematopoietic progenitors by E2a-Pbx1. <i>Molecular Cell</i> , 2003 , 12, 393-400	17.6	74
32	Saccharomyces genome database: underlying principles and organisation. <i>Briefings in Bioinformatics</i> , 2004 , 5, 9-22	13.4	73
31	Visualization of receptor-mediated endocytosis in yeast. <i>Molecular Biology of the Cell</i> , 1999 , 10, 799-817	3.5	69
30	Disruption of yeast forkhead-associated cell cycle transcription by oxidative stress. <i>Molecular Biology of the Cell</i> , 2004 , 15, 5659-69	3.5	61
29	Probing beta-lactamase structure and function using random replacement mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 29-44	4.2	56
28	Using the Saccharomyces Genome Database (SGD) for analysis of protein similarities and structure. <i>Nucleic Acids Research</i> , 1999 , 27, 74-8	20.1	55
27	Identification of alterations in DNA copy number in host stromal cells during tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 19848-53	11.5	45
26	Saccharomyces Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 216-8	20.1	45
25	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
24	Dominant-lethal alpha-tubulin mutants defective in microtubule depolymerization in yeast. <i>Molecular Biology of the Cell</i> , 2001 , 12, 3973-86	3.5	45
23	Mutational analysis of the role of hydrophobic residues in the 338-348 helix on actin in actomyosin interactions. <i>Biochemistry</i> , 1996 , 35, 3670-6	3.2	39
22	The glycine allele of a glycine/arginine polymorphism in the beta2-adrenergic receptor gene is associated with essential hypertension in a population of Chinese origin. <i>American Journal of Hypertension</i> , 2001 , 14, 1196-200	2.3	36
21	Genetic variation in the human urea transporter-2 is associated with variation in blood pressure. <i>Human Molecular Genetics</i> , 2001 , 10, 2157-64	5.6	34

20	Multiple functions for actin during filamentous growth of <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 1998 , 9, 1873-89	3.5	34
19	Coordinated regulation of sulfur and phospholipid metabolism reflects the importance of methylation in the growth of yeast. <i>Molecular Biology of the Cell</i> , 2011 , 22, 4192-204	3.5	32
18	Changing perspectives in yeast research nearly a decade after the genome sequence. <i>Genome Research</i> , 2005 , 15, 1611-9	9.7	32
17	Combinatorial control of diverse metabolic and physiological functions by transcriptional regulators of the yeast sulfur assimilation pathway. <i>Molecular Biology of the Cell</i> , 2012 , 23, 3008-24	3.5	31
16	Identification of functional connections between calmodulin and the yeast actin cytoskeleton. <i>Genetics</i> , 1998 , 150, 43-58	4	18
15	Genetic Basis of Ammonium Toxicity Resistance in a Sake Strain of Yeast: A Mendelian Case. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 733-740	3.2	13
14	Analysis of Polygenic Mutants Suggests a Role for Mediator in Regulating Transcriptional Activation Distance in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015 , 201, 599-612	4	12
13	Automating the construction of gene ontologies. <i>Nature Biotechnology</i> , 2013 , 31, 34-5	44.5	9
12	It's the data!. <i>Molecular Biology of the Cell</i> , 2010 , 21, 4-6	3.5	9
11	Challenges in developing a molecular characterization of cancer. <i>Seminars in Oncology</i> , 2002 , 29, 280-5	5.5	9
10	Expanding yeast knowledge online. <i>Yeast</i> , 1998 , 14, 1453-69	3.4	8
9	Of genes and genomes. <i>Annals of the New York Academy of Sciences</i> , 1999 , 882, 32-41; discussion 56-65	6.5	7
8	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. <i>MSystems</i> , 2019 , 4,	7.6	6
7	Nucleotide sequence of the SAC2 gene of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1994 , 10, 1211-6	3.4	6
6	Technological innovation leads to fundamental understanding in cell biology. <i>Molecular Biology of the Cell</i> , 2010 , 21, 3791-2	3.5	5
5	Phylogenetic portrait of the <i>Saccharomyces cerevisiae</i> functional genome. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1335-40	3.2	3
4	Missing Value Estimation 2003 , 65-75		1
3	Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility 2005 , 77-100		1

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1 Perspective: Linkage Maps, Communities of Geneticists, and Genome Databases. *Genetics*, 2020, 216, 261-262

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