

# David Botstein

## List of Publications by Year in descending order

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110  
papers

108,249  
citations

8755

77  
h-index

30277

107  
g-index

115  
all docs

115  
docs citations

115  
times ranked

114997  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Ontology: tool for the unification of biology. <i>Nature Genetics</i> , 2000, 25, 25-29.	9.4	34,499
2	Molecular portraits of human breast tumours. <i>Nature</i> , 2000, 406, 747-752.	13.7	13,397
3	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. <i>Nature</i> , 2000, 403, 503-511.	13.7	8,977
4	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.	3.3	4,849
5	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
6	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
7	Exploring the new world of the genome with DNA microarrays. <i>Nature Genetics</i> , 1999, 21, 33-37.	9.4	2,189
8	Systematic variation in gene expression patterns in human cancer cell lines. <i>Nature Genetics</i> , 2000, 24, 227-235.	9.4	1,946
9	The Transcriptional Program in the Response of Human Fibroblasts to Serum. <i>Science</i> , 1999, 283, 83-87.	6.0	1,895
10	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, 3710-3715.	1.8	1,782
11	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	9.4	1,543
12	Discovering genotypes underlying human phenotypes: past successes for mendelian disease, future approaches for complex disease. <i>Nature Genetics</i> , 2003, 33, 228-237.	9.4	1,388
13	A gene expression database for the molecular pharmacology of cancer. <i>Nature Genetics</i> , 2000, 24, 236-244.	9.4	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.	0.9	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.	3.3	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.	3.3	1,098
17	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001, 409, 533-538.	13.7	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.	3.3	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.	4.2	978
20	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	9.4	928
21	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, 1828-1837.	13.9	874
22	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
23	Gene Expression Patterns in Human Liver Cancers. <i>Molecular Biology of the Cell</i> , 2002, 13, 1929-1939.	0.9	779
24	Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer. <i>Nature</i> , 1998, 396, 699-703.	13.7	735
25	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.	3.3	679
26	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
27	Different Gene Expression Patterns in Invasive Lobular and Ductal Carcinomas of the Breast. <i>Molecular Biology of the Cell</i> , 2004, 15, 2523-2536.	0.9	540
28	Molecular characterisation of soft tissue tumours: a gene expression study. <i>Lancet, The</i> , 2002, 359, 1301-1307.	6.3	537
29	Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 352-367.	0.9	524
30	Expression of Cytokeratins 17 and 5 Identifies a Group of Breast Carcinomas with Poor Clinical Outcome. <i>American Journal of Pathology</i> , 2002, 161, 1991-1996.	1.9	494
31	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, 8348-8353.	3.3	491
32	Yeast: An Experimental Organism for 21st Century Biology. <i>Genetics</i> , 2011, 189, 695-704.	1.2	450
33	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
34	The Stanford Microarray Database. <i>Nucleic Acids Research</i> , 2001, 29, 152-155.	6.5	415
35	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000, 1, research0003.1.	13.9	392
36	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, 12319-12324.	3.3	385

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37	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 219-223.	6.5	376
38	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, 972-977.	3.3	371
39	Saccharomyces Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). <i>Nucleic Acids Research</i> , 2002, 30, 69-72.	6.5	322
40	Gene Expression Patterns in Ovarian Carcinomas. <i>Molecular Biology of the Cell</i> , 2003, 14, 4376-4386.	0.9	302
41	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
42	Variation in Gene Expression Patterns in Human Gastric Cancers. <i>Molecular Biology of the Cell</i> , 2003, 14, 3208-3215.	0.9	285
43	Nonparametric methods for identifying differentially expressed genes in microarray data. <i>Bioinformatics</i> , 2002, 18, 1454-1461.	1.8	276
44	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
45	Large-scale identification of secreted and membrane-associated gene products using DNA microarrays. <i>Nature Genetics</i> , 2000, 25, 58-62.	9.4	241
46	Systems-level analysis of mechanisms regulating yeast metabolic flux. <i>Science</i> , 2016, 354, .	6.0	236
47	Requirement of yeast fimbrin for actin organization and morphogenesis in vivo. <i>Nature</i> , 1991, 354, 404-408.	13.7	227
48	Gene Ontology annotations at SGD: new data sources and annotation methods. <i>Nucleic Acids Research</i> , 2007, 36, D577-D581.	6.5	218
49	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.	3.3	205
50	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, 8886-8891.	3.3	204
51	Defining protein interactions with yeast actin in vivo. <i>Nature Structural Biology</i> , 1995, 2, 28-35.	9.7	198
52	A DNA microarray survey of gene expression in normal human tissues. <i>Genome Biology</i> , 2005, 6, R22.	13.9	198
53	Saccharomyces genome database. <i>Methods in Enzymology</i> , 2002, 350, 329-346.	0.4	188
54	Structure of the yeast endoplasmic reticulum: Localization of ER proteins using immunofluorescence and immunoelectron microscopy. <i>Yeast</i> , 1991, 7, 891-911.	0.8	182

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55	<i>BIM1</i> Encodes a Microtubule-binding Protein in Yeast. <i>Molecular Biology of the Cell</i> , 1997, 8, 2677-2691.	0.9	179
56	Nutritional Homeostasis in Batch and Steady-State Culture of Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 4089-4104.	0.9	179
57	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
58	Supervised harvesting of expression trees. <i>Genome Biology</i> , 2001, 2, research0003.1.	13.9	148
59	REG 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
60	Genetic and physical maps of <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 1997, 387, 67-73.	13.7	145
61	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.	3.3	144
62	Gene Expression Patterns and Gene Copy Number Changes in Dermatofibrosarcoma Protuberans. <i>American Journal of Pathology</i> , 2003, 163, 2383-2395.	1.9	142
63	Universal Reference RNA as a standard for microarray experiments. <i>BMC Genomics</i> , 2004, 5, 20.	1.2	140
64	Slow Growth Induces Heat-Shock Resistance in Normal and Respiratory-deficient Yeast. <i>Molecular Biology of the Cell</i> , 2009, 20, 891-903.	0.9	136
65	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
66	Functional analysis reports. Precise gene disruption in <i>Saccharomyces cerevisiae</i> by double fusion polymerase chain reaction. <i>Yeast</i> , 1995, 11, 1275-1280.	0.8	127
67	Gene expression profiles do not consistently predict the clinical treatment response in locally advanced breast cancer. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 2914-2918.	1.9	114
68	Structure-Function Relationships in Yeast Tubulins. <i>Molecular Biology of the Cell</i> , 2000, 11, 1887-1903.	0.9	112
69	Specificity domains distinguish the Ras-related GTPases Ypt1 and Sec4. <i>Nature</i> , 1993, 362, 563-565.	13.7	107
70	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
71	Genome-Wide Analysis of Nucleotide-Level Variation in Commonly Used <i>Saccharomyces cerevisiae</i> Strains. <i>PLoS ONE</i> , 2007, 2, e322.	1.1	100
72	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998, 18, 373-379.	2.0	96

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73	Inference of combinatorial regulation in yeast transcriptional networks: A case study of sporulation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1998-2003.	3.3	95
74	Genome Snapshot: a new resource at the Saccharomyces Genome Database (SGD) presenting an overview of the Saccharomyces cerevisiae genome. Nucleic Acids Research, 2006, 34, D442-D445.	6.5	91
75	T Cell Receptor-Independent Basal Signaling via Erk and Abl Kinases Suppresses RAG Gene Expression. PLoS Biology, 2003, 1, e53.	2.6	88
76	Genome-Scale Identification of Membrane-Associated Human mRNAs. PLoS Genetics, 2006, 2, e11.	1.5	84
77	Saccharomyces genome database: Underlying principles and organisation. Briefings in Bioinformatics, 2004, 5, 9-22.	3.2	83
78	Bmi-1 Regulation of INK4A-ARF Is a Downstream Requirement for Transformation of Hematopoietic Progenitors by E2a-Pbx1. Molecular Cell, 2003, 12, 393-400.	4.5	78
79	Visualization of Receptor-mediated Endocytosis in Yeast. Molecular Biology of the Cell, 1999, 10, 799-817.	0.9	72
80	Disruption of Yeast Forkhead-associated Cell Cycle Transcription by Oxidative Stress. Molecular Biology of the Cell, 2004, 15, 5659-5669.	0.9	71
81	Using the Saccharomyces Genome Database (SGD) for analysis of protein similarities and structure. Nucleic Acids Research, 1999, 27, 74-78.	6.5	66
82	Probing $\beta$ -lactamase structure and function using random replacement mutagenesis. Proteins: Structure, Function and Bioinformatics, 1992, 14, 29-44.	1.5	64
83	Saccharomyces Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. Nucleic Acids Research, 2003, 31, 216-218.	6.5	57
84	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.	0.9	56
85	Dominant-Lethal $\beta$ -Tubulin Mutants Defective in Microtubule Depolymerization in Yeast. Molecular Biology of the Cell, 2001, 12, 3973-3986.	0.9	55
86	Identification of alterations in DNA copy number in host stromal cells during tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19848-19853.	3.3	55
87	The glycine allele of a glycine/arginine polymorphism in the $\beta$ -adrenergic receptor gene is associated with essential hypertension in a population of Chinese origin. American Journal of Hypertension, 2001, 14, 1196-1200.	1.0	43
88	Coordinated regulation of sulfur and phospholipid metabolism reflects the importance of methylation in the growth of yeast. Molecular Biology of the Cell, 2011, 22, 4192-4204.	0.9	43
89	Mutational Analysis of the Role of Hydrophobic Residues in the 338~348 Helix on Actin in Actomyosin Interactions. Biochemistry, 1996, 35, 3670-3676.	1.2	40
90	Changing perspectives in yeast research nearly a decade after the genome sequence. Genome Research, 2005, 15, 1611-1619.	2.4	39

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91	Multiple Functions for Actin during Filamentous Growth of <i>Saccharomyces cerevisiae</i> . Molecular Biology of the Cell, 1998, 9, 1873-1889.	0.9	38
92	Genetic variation in the human urea transporter-2 is associated with variation in blood pressure. Human Molecular Genetics, 2001, 10, 2157-2164.	1.4	38
93	Combinatorial control of diverse metabolic and physiological functions by transcriptional regulators of the yeast sulfur assimilation pathway. Molecular Biology of the Cell, 2012, 23, 3008-3024.	0.9	36
94	It's the Data!. Molecular Biology of the Cell, 2010, 21, 4-6.	0.9	27
95	Identification of Functional Connections Between Calmodulin and the Yeast Actin Cytoskeleton. Genetics, 1998, 150, 43-58.	1.2	21
96	Analysis of Polygenic Mutants Suggests a Role for Mediator in Regulating Transcriptional Activation Distance in <i>Saccharomyces cerevisiae</i> . Genetics, 2015, 201, 599-612.	1.2	16
97	Genetic Basis of Ammonium Toxicity Resistance in a Sake Strain of Yeast: A Mendelian Case. G3: Genes, Genomes, Genetics, 2013, 3, 733-740.	0.8	15
98	Minor Isozymes Tailor Yeast Metabolism to Carbon Availability. MSystems, 2019, 4, .	1.7	14
99	Automating the construction of gene ontologies. Nature Biotechnology, 2013, 31, 34-35.	9.4	12
100	Expanding yeast knowledge online. , 1998, 14, 1453-1469.		11
101	Challenges in developing a molecular characterization of cancer. Seminars in Oncology, 2002, 29, 280-285.	0.8	10
102	Of Genes and Genomes. Annals of the New York Academy of Sciences, 1999, 882, 32-41.	1.8	8
103	IV. Yeast sequencing reports. Nucleotide sequence of the SAC2 gene of <i>Saccharomyces cerevisiae</i> . Yeast, 1994, 10, 1211-1216.	0.8	6
104	Missing Value Estimation. , 2003, , 65-75.		6
105	Technological Innovation Leads to Fundamental Understanding in Cell Biology. Molecular Biology of the Cell, 2010, 21, 3791-3792.	0.9	6
106	Phylogenetic Portrait of the <i>Saccharomyces cerevisiae</i> Functional Genome. G3: Genes, Genomes, Genetics, 2013, 3, 1335-1340.	0.8	4
107	Expression Profiling of Breast Cancer: From Molecular Portraits to Clinical Utility. , 2005, , 77-100.		2
108	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0

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109	P-POD, The Princeton Protein Orthology Database, as a Tool for Identifying Gene Function. Nature Precedings, 2009, , .	0.1	0
110	Perspective: Linkage Maps, Communities of Geneticists, and Genome Databases. Genetics, 2020, 216, 261-262.	1.2	0