

# Brenda Andrews

## List of Publications by Year in descending order

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76  
papers

14,186  
citations

61984

43  
h-index

76900

74  
g-index

78  
all docs

78  
docs citations

78  
times ranked

12147  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phenomics approaches to understand genetic networks and gene function in yeast. <i>Biochemical Society Transactions</i> , 2022, 50, 713-721.	3.4	5
2	Environmental robustness of the global yeast genetic interaction network. <i>Science</i> , 2021, 372, .	12.6	40
3	Global Genetic Networks and the Genotype-to-Phenotype Relationship. <i>Cell</i> , 2019, 177, 85-100.	28.9	170
4	TheCellMap.org: A Web-Accessible Database for Visualizing and Mining the Global Yeast Genetic Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1539-1549.	1.8	114
5	Functional annotation of chemical libraries across diverse biological processes. <i>Nature Chemical Biology</i> , 2017, 13, 982-993.	8.0	76
6	Functional Analysis of Kinases and Transcription Factors in <i>Saccharomyces cerevisiae</i> Using an Integrated Overexpression Library. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 911-921.	1.8	19
7	Synthetic Genetic Array Analysis. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088807.	0.3	27
8	Synthetic Genetic Arrays: Automation of Yeast Genetics. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top086652.	0.3	11
9	Overexpression screens identify conserved dosage chromosome instability genes in yeast and human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9967-9976.	7.1	67
10	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	12.6	979
11	Regulation of histone gene transcription in yeast. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 599-613.	5.4	58
12	Cell cycle-regulated oscillator coordinates core histone gene transcription through histone acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14124-14129.	7.1	32
13	Genetic Networks. , 2013, , 115-135.		1
14	Genetic Interaction Networks: Toward an Understanding of Heritability. <i>Annual Review of Genomics and Human Genetics</i> , 2013, 14, 111-133.	6.2	105
15	Functional genomics in the study of yeast cell polarity: moving in the right direction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130118.	4.0	9
16	Conserved Regulators of Nucleolar Size Revealed by Global Phenotypic Analyses. <i>Science Signaling</i> , 2013, 6, ra70.	3.6	68
17	Global Linkage Map Connects Meiotic Centromere Function to Chromosome Size in Budding Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1741-1751.	1.8	12
18	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	7.2	90

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19	PhenoM: a database of morphological phenotypes caused by mutation of essential genes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, D687-D694.	14.5	13
20	Proteome-Wide Screens in <i>Saccharomyces cerevisiae</i> Using the Yeast GFP Collection. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 169-178.	1.6	14
21	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. <i>Science</i> , 2012, 337, 1353-1356.	12.6	186
22	Exploring the Yeast Acetylome Using Functional Genomics. <i>Cell</i> , 2012, 149, 936-948.	28.9	63
23	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	17.5	352
24	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. <i>Nature Biotechnology</i> , 2011, 29, 505-511.	17.5	90
25	Charting the genetic interaction map of a cell. <i>Current Opinion in Biotechnology</i> , 2011, 22, 66-74.	6.6	103
26	Clathrin light chain directs endocytosis by influencing the binding of the yeast Hip1R homologue, Sla2, to F-actin. <i>Molecular Biology of the Cell</i> , 2011, 22, 3699-3714.	2.1	37
27	Dual functions of Mdt1 in genome maintenance and cell integrity pathways in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2010, 27, 41-52.	1.7	7
28	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010, 7, 1017-1024.	19.0	319
29	Quantitative cell array screening to identify regulators of gene expression. <i>Briefings in Functional Genomics</i> , 2010, 9, 13-23.	2.7	2
30	Functional Dissection of <i>IME1</i> Transcription Using Quantitative Promoter Reporter Screening. <i>Genetics</i> , 2010, 186, 829-841.	2.9	26
31	Ubiquitin Chain Elongation Enzyme Ufd2 Regulates a Subset of Doa10 Substrates. <i>Journal of Biological Chemistry</i> , 2010, 285, 10265-10272.	3.4	20
32	Genetic interactions reveal the evolutionary trajectories of duplicate genes. <i>Molecular Systems Biology</i> , 2010, 6, 429.	7.2	97
33	Illuminating transcription pathways using fluorescent reporter genes and yeast functional genomics. <i>Transcription</i> , 2010, 1, 76-80.	3.1	4
34	Synthetic Genetic Array (SGA) Analysis in <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>Methods in Enzymology</i> , 2010, 470, 145-179.	1.0	175
35	Exploring the conservation of synthetic lethal genetic interaction networks. <i>Communicative and Integrative Biology</i> , 2009, 2, 78-81.	1.4	22
36	Regulation of Cell Polarity through Phosphorylation of Bni4 by Pho85 G1 Cyclin-dependent Kinases in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2009, 20, 3239-3250.	2.1	31

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37	A genome-wide synthetic dosage lethality screen reveals multiple pathways that require the functioning of ubiquitin-binding proteins Rad23 and Dsk2. <i>BMC Biology</i> , 2009, 7, 75.	3.8	30
38	DNA polymerase $\epsilon$ , acetylases and remodellers cooperate to form a specialized chromatin structure at a tRNA insulator. <i>EMBO Journal</i> , 2009, 28, 2583-2600.	7.8	48
39	A molecular barcoded yeast ORF library enables mode-of-action analysis of bioactive compounds. <i>Nature Biotechnology</i> , 2009, 27, 369-377.	17.5	254
40	You too can play with an edge. <i>Nature Methods</i> , 2009, 6, 797-798.	19.0	3
41	Comprehensive genetic analysis of transcription factor pathways using a dual reporter gene system in budding yeast. <i>Methods</i> , 2009, 48, 258-264.	3.8	28
42	Systematic Mapping of Genetic Interaction Networks. <i>Annual Review of Genetics</i> , 2009, 43, 601-625.	7.6	250
43	Systematic genetic array analysis links the <i>Saccharomyces cerevisiae</i> SAGA/SLIK and NuA4 component Tra1 to multiple cellular processes. <i>BMC Genetics</i> , 2008, 9, 46.	2.7	26
44	Structure/Function Analysis of the Phosphatidylinositol-3-Kinase Domain of Yeast Tra1. <i>Genetics</i> , 2007, 177, 151-166.	2.9	32
45	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	27.8	806
46	Pho85, a multifunctional cyclin-dependent protein kinase in budding yeast. <i>Molecular Microbiology</i> , 2007, 66, 303-314.	2.5	128
47	Exploring the Mode-of-Action of Bioactive Compounds by Chemical-Genetic Profiling in Yeast. <i>Cell</i> , 2006, 126, 611-625.	28.9	447
48	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. <i>Molecular Cell</i> , 2006, 21, 319-330.	9.7	618
49	Revealing Hidden Relationships Among Yeast Genes Involved in Chromosome Segregation Using Systematic Synthetic Lethal and Synthetic Dosage Lethal Screens. <i>Cell Cycle</i> , 2006, 5, 592-595.	2.6	16
50	Comprehensive curation and analysis of global interaction networks in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biology</i> , 2006, 5, 11.	2.7	276
51	From worm genetic networks to complex human diseases. <i>Nature Genetics</i> , 2006, 38, 862-863.	21.4	13
52	Experimental approaches to identify genetic networks. <i>Current Opinion in Biotechnology</i> , 2006, 17, 472-480.	6.6	17
53	Characterization of the Yeast Amphiphysins Rvs161p and Rvs167p Reveals Roles for the Rvs Heterodimer In Vivo. <i>Molecular Biology of the Cell</i> , 2006, 17, 1306-1321.	2.1	54
54	Small open reading frames: Not so small anymore. <i>Genome Research</i> , 2006, 16, 314-315.	5.5	8

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55	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005, 438, 679-684.	27.8	915
56	Motifs, themes and thematic maps of an integrated <i>Saccharomyces cerevisiae</i> interaction network. <i>Journal of Biology</i> , 2005, 4, 6.	2.7	154
57	Systematic yeast synthetic lethal and synthetic dosage lethal screens identify genes required for chromosome segregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13956-13961.	7.1	126
58	Reverse recruitment: The Nup84 nuclear pore subcomplex mediates Rap1/Gcr1/Gcr2 transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5749-5754.	7.1	120
59	Interaction of the <i>Saccharomyces cerevisiae</i> Cortical Actin Patch Protein Rvs167p With Proteins Involved in ER to Golgi Vesicle Trafficking. <i>Genetics</i> , 2005, 170, 555-568.	2.9	20
60	Exploration of the Function and Organization of the Yeast Early Secretory Pathway through an Epistatic Miniarray Profile. <i>Cell</i> , 2005, 123, 507-519.	28.9	804
61	Late-G1 cyclin-CDK activity is essential for control of cell morphogenesis in budding yeast. <i>Nature Cell Biology</i> , 2004, 6, 59-66.	10.3	81
62	Global Mapping of the Yeast Genetic Interaction Network. <i>Science</i> , 2004, 303, 808-813.	12.6	1,908
63	Combining biological networks to predict genetic interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15682-15687.	7.1	225
64	CDK Activity Antagonizes Whi5, an Inhibitor of G1/S Transcription in Yeast. <i>Cell</i> , 2004, 117, 899-913.	28.9	414
65	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. <i>Trends in Cell Biology</i> , 2003, 13, 344-356.	7.9	126
66	Regulation of the Yeast Amphiphysin Homologue Rvs167p by Phosphorylation. <i>Molecular Biology of the Cell</i> , 2003, 14, 3027-3040.	2.1	33
67	G1 Transcription Factors Are Differentially Regulated in <i>Saccharomyces cerevisiae</i> by the Swi6-Binding Protein Stb1. <i>Molecular and Cellular Biology</i> , 2003, 23, 5064-5077.	2.3	60
68	Dissection of a Complex Phenotype by Functional Genomics Reveals Roles for the Yeast Cyclin-Dependent Protein Kinase Pho85 in Stress Adaptation and Cell Integrity. <i>Molecular and Cellular Biology</i> , 2002, 22, 5076-5088.	2.3	85
69	High-Resolution Genetic Mapping With Ordered Arrays of <i>Saccharomyces cerevisiae</i> Deletion Mutants. <i>Genetics</i> , 2002, 162, 1091-1099.	2.9	98
70	The protein kinase Pho85 is required for asymmetric accumulation of the Ash1 protein in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2001, 42, 345-353.	2.5	21
71	Systematic Genetic Analysis with Ordered Arrays of Yeast Deletion Mutants. <i>Science</i> , 2001, 294, 2364-2368.	12.6	1,946
72	Transcriptional Coregulation by the Cell Integrity Mitogen-Activated Protein Kinase Slt2 and the Cell Cycle Regulator Swi4. <i>Molecular and Cellular Biology</i> , 2001, 21, 6515-6528.	2.3	109

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73	Functions of Pho85 cyclin-dependent kinases in budding yeast. , 2000, 4, 97-106.		55
74	A Yeast taf17 Mutant Requires the Swi6 Transcriptional Activator for Viability and Shows Defects in Cell Cycle-Regulated Transcription. Genetics, 2000, 154, 1561-1576.	2.9	14
75	The cyclin family of budding yeast:abundant use of a good idea. Trends in Genetics, 1998, 14, 66-72.	6.7	138
76	SBF Cell Cycle Regulator as a Target of the Yeast PKC-MAP Kinase Pathway. Science, 1997, 275, 1781-1784.	12.6	234