

Charles Boone

List of Publications by Year in descending order

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Version: 2024-02-01

220
papers

35,499
citations

3930

88
h-index

3822

178
g-index

225
all docs

225
docs citations

225
times ranked

29434
citing authors

#	ARTICLE	IF	CITATIONS
1	Retention of duplicated genes in evolution. <i>Trends in Genetics</i> , 2022, 38, 59-72.	2.9	76
2	Clonamines stimulate autophagy, inhibit <i>Mycobacterium tuberculosis</i> survival in macrophages, and target Pik1. <i>Cell Chemical Biology</i> , 2022, 29, 870-882.e11.	2.5	7
3	Jerveratrum-Type Steroidal Alkaloids Inhibit β -1,6-Glucan Biosynthesis in Fungal Cell Walls. <i>Microbiology Spectrum</i> , 2022, 10, e0087321.	1.2	9
4	Genetic background and mistranslation frequency determine the impact of mistranslating tRNAs ^{er} UGG. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
5	Targeting fungal membrane homeostasis with imidazopyrazoindoles impairs azole resistance and biofilm formation. <i>Nature Communications</i> , 2022, 13, .	5.8	21
6	Context-dependent regulation of ferroptosis sensitivity. <i>Cell Chemical Biology</i> , 2022, 29, 1409-1418.e6.	2.5	42
7	Phenylboronic Ester-Activated Aryl Iodide-Selective Buchwald-Hartwig-Type Amination toward Bioactivity Assay. <i>ACS Omega</i> , 2022, 7, 24184-24189.	1.6	1
8	\tilde{I} -SGA: synthetic genetic array analysis for systematically screening and quantifying trigenic interactions in yeast. <i>Nature Protocols</i> , 2021, 16, 1219-1250.	5.5	6
9	Trigenic Synthetic Genetic Array (\tilde{I} -SGA) Technique for Complex Interaction Analysis. <i>Methods in Molecular Biology</i> , 2021, 2212, 377-400.	0.4	2
10	Reduced gene dosage of histone H4 prevents CENP-A mislocalization and chromosomal instability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2021, 218, .	1.2	8
11	Genome-wide screening of genes associated with momilactone B sensitivity in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
12	Environmental robustness of the global yeast genetic interaction network. <i>Science</i> , 2021, 372, .	6.0	40
13	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. <i>Molecular Systems Biology</i> , 2021, 17, e10013.	3.2	8
14	Single-cell image analysis to explore cell-to-cell heterogeneity in isogenic populations. <i>Cell Systems</i> , 2021, 12, 608-621.	2.9	15
15	A genome-scale yeast library with inducible expression of individual genes. <i>Molecular Systems Biology</i> , 2021, 17, e10207.	3.2	37
16	The amino acid substitution affects cellular response to mistranslation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	10
17	Timer-based proteomic profiling of the ubiquitin-proteasome system reveals a substrate receptor of the GID ubiquitin ligase. <i>Molecular Cell</i> , 2021, 81, 2460-2476.e11.	4.5	39
18	Improving Measures of Chemical Structural Similarity Using Machine Learning on Chemical-Genetic Interactions. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 4156-4172.	2.5	11

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19	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. <i>Nature Communications</i> , 2021, 12, 6497.	5.8	33
20	TheCellVision.org: A Database for Visualizing and Mining High-Content Cell Imaging Projects. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3969-3976.	0.8	4
21	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. <i>MBio</i> , 2020, 11, .	1.8	275
22	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. <i>Nature Metabolism</i> , 2020, 2, 499-513.	5.1	72
23	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. <i>Science</i> , 2020, 368, .	6.0	79
24	Skp, Cullin, F-box (SCF)-Met30 and SCF-Cdc4-Mediated Proteolysis of CENP-A Prevents Mislocalization of CENP-A for Chromosomal Stability in Budding Yeast. <i>PLoS Genetics</i> , 2020, 16, e1008597.	1.5	28
25	Dbf4-Dependent Kinase (DDK)-Mediated Proteolysis of CENP-A Prevents Mislocalization of CENP-A in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2057-2068.	0.8	11
26	Systematic genetics and single-cell imaging reveal widespread morphological pleiotropy and cell-to-cell variability. <i>Molecular Systems Biology</i> , 2020, 16, e9243.	3.2	37
27	Systematic analysis of bypass suppression of essential genes. <i>Molecular Systems Biology</i> , 2020, 16, e9828.	3.2	45
28	Genetic profiling of protein burden and nuclear export overload. <i>ELife</i> , 2020, 9, .	2.8	8
29	Decyl Gallate as a Possible Inhibitor of N-Glycosylation Process in <i>Paracoccidioides lutzii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	3
30	Discovering genetic interactions bridging pathways in genome-wide association studies. <i>Nature Communications</i> , 2019, 10, 4274.	5.8	52
31	Integrating yeast chemical genomics and mammalian cell pathway analysis. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 1245-1255.	2.8	2
32	Global Genetic Networks and the Genotype-to-Phenotype Relationship. <i>Cell</i> , 2019, 177, 85-100.	13.5	170
33	Genetic interaction networks in cancer cells. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 64-72.	1.5	28
34	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. <i>Journal of Molecular Biology</i> , 2019, 431, 1160-1171.	2.0	6
35	Complex modifier landscape underlying genetic background effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5045-5054.	3.3	41
36	Using BEAN-counter to quantify genetic interactions from multiplexed barcode sequencing experiments. <i>Nature Protocols</i> , 2019, 14, 415-440.	5.5	16

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37	Systematic analysis of complex genetic interactions. <i>Science</i> , 2018, 360, .	6.0	201
38	MOSAIC: a chemical-genetic interaction data repository and web resource for exploring chemical modes of action. <i>Bioinformatics</i> , 2018, 34, 1251-1252.	1.8	14
39	Predicting bioprocess targets of chemical compounds through integration of chemical-genetic and genetic interactions. <i>PLoS Computational Biology</i> , 2018, 14, e1006532.	1.5	13
40	Integrating genetic and protein-protein interaction networks maps a functional wiring diagram of a cell. <i>Current Opinion in Microbiology</i> , 2018, 45, 170-179.	2.3	31
41	A Genome-Wide Screen Reveals a Role for the HIR Histone Chaperone Complex in Preventing Mislocalization of Budding Yeast CENP-A. <i>Genetics</i> , 2018, 210, 203-218.	1.2	20
42	The budding yeast RSC complex maintains ploidy by promoting spindle pole body insertion. <i>Journal of Cell Biology</i> , 2018, 217, 2445-2462.	2.3	9
43	Global analysis of genetic circuitry and adaptive mechanisms enabling resistance to the azole antifungal drugs. <i>PLoS Genetics</i> , 2018, 14, e1007319.	1.5	37
44	Genetic Network Complexity Shapes Background-Dependent Phenotypic Expression. <i>Trends in Genetics</i> , 2018, 34, 578-586.	2.9	35
45	Automated analysis of high-content microscopy data with deep learning. <i>Molecular Systems Biology</i> , 2017, 13, 924.	3.2	220
46	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.	0.8	114
47	Machine learning and computer vision approaches for phenotypic profiling. <i>Journal of Cell Biology</i> , 2017, 216, 65-71.	2.3	130
48	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017, 20, 2735-2748.	2.9	47
49	The <i>Candida albicans</i> transcription factor Cas5 couples stress responses, drug resistance and cell cycle regulation. <i>Nature Communications</i> , 2017, 8, 499.	5.8	49
50	Functional annotation of chemical libraries across diverse biological processes. <i>Nature Chemical Biology</i> , 2017, 13, 982-993.	3.9	76
51	Mapping a diversity of genetic interactions in yeast. <i>Current Opinion in Systems Biology</i> , 2017, 6, 14-21.	1.3	20
52	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2719-2727.	0.8	417
53	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017, 13, e1006779.	1.5	30
54	Pathway-based discovery of genetic interactions in breast cancer. <i>PLoS Genetics</i> , 2017, 13, e1006973.	1.5	62

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55	Mechanisms of suppression: The wiring of genetic resilience. <i>BioEssays</i> , 2017, 39, 1700042.	1.2	31
56	Direct and Indirect Targeting of PP2A by Conserved Bacterial Type-III Effector Proteins. <i>PLoS Pathogens</i> , 2016, 12, e1005609.	2.1	51
57	Synthetic Genetic Array Analysis. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088807.	0.2	27
58	Synthetic Genetic Arrays: Automation of Yeast Genetics. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top086652.	0.2	11
59	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	2.4	116
60	High-Content Screening for Quantitative Cell Biology. <i>Trends in Cell Biology</i> , 2016, 26, 598-611.	3.6	214
61	Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. <i>Cell Systems</i> , 2016, 3, 264-277.e10.	2.9	26
62	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
63	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	6.0	157
64	Chromosome-Specific and Global Effects of Aneuploidy in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 202, 1395-1409.	1.2	37
65	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	13.5	479
66	Genetic Interactions Implicating Postreplicative Repair in Okazaki Fragment Processing. <i>PLoS Genetics</i> , 2015, 11, e1005659.	1.5	24
67	Yeast Proteome Dynamics from Single Cell Imaging and Automated Analysis. <i>Cell</i> , 2015, 161, 1413-1424.	13.5	254
68	Leveraging DNA Damage Response Signaling to Identify Yeast Genes Controlling Genome Stability. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 997-1006.	0.8	25
69	Plant-derived antifungal agent poaic acid targets β -1,3-glucan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1490-7.	3.3	91
70	Construction of Multifragment Plasmids by Homologous Recombination in Yeast. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top084111.	0.2	4
71	Rapid and Efficient Plasmid Construction by Homologous Recombination in Yeast. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot085100.	0.2	22
72	The indispensable genome. <i>Science</i> , 2015, 350, 1028-1029.	6.0	13

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73	CYCLoPs: A Comprehensive Database Constructed from Automated Analysis of Protein Abundance and Subcellular Localization Patterns in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1223-1232.	0.8	69
74	Heritability and genetic basis of protein level variation in an outbred population. <i>Genome Research</i> , 2014, 24, 1363-1370.	2.4	51
75	Yeast Systems Biology: Our Best Shot at Modeling a Cell. <i>Genetics</i> , 2014, 198, 435-437.	1.2	23
76	Protein quality control at the inner nuclear membrane. <i>Nature</i> , 2014, 516, 410-413.	13.7	188
77	Genome-wide Analysis Reveals Novel and Discrete Functions for Tubulin Carboxy-Terminal Tails. <i>Current Biology</i> , 2014, 24, 1295-1303.	1.8	26
78	Synthetic Genetic Array Analysis for Global Mapping of Genetic Networks in Yeast. <i>Methods in Molecular Biology</i> , 2014, 1205, 143-168.	0.4	30
79	Mapping the functional yeast ABC transporter interactome. <i>Nature Chemical Biology</i> , 2013, 9, 565-572.	3.9	93
80	Focus on chemical biology in Asia. <i>Molecular BioSystems</i> , 2013, 9, 825.	2.9	0
81	Simplifying the author and reader experience. <i>Molecular BioSystems</i> , 2013, 9, 9-9.	2.9	0
82	Systems-level antimicrobial drug and drug synergy discovery. <i>Nature Chemical Biology</i> , 2013, 9, 222-231.	3.9	146
83	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
84	Genetic Interaction Networks: Toward an Understanding of Heritability. <i>Annual Review of Genomics and Human Genetics</i> , 2013, 14, 111-133.	2.5	105
85	Actin Filament Elongation in Arp2/3-Derived Networks Is Controlled by Three Distinct Mechanisms. <i>Developmental Cell</i> , 2013, 24, 182-195.	3.1	41
86	A Comparative Genomic Approach for Identifying Synthetic Lethal Interactions in Human Cancer. <i>Cancer Research</i> , 2013, 73, 6128-6136.	0.4	56
87	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	3.2	90
88	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. <i>Journal of Cell Biology</i> , 2013, 201, 145-163.	2.3	58
89	Unligated Okazaki Fragments Induce PCNA Ubiquitination and a Requirement for Rad59-Dependent Replication Fork Progression. <i>PLoS ONE</i> , 2013, 8, e66379.	1.1	21
90	Network Evolution: Rewiring and Signatures of Conservation in Signaling. <i>PLoS Computational Biology</i> , 2012, 8, e1002411.	1.5	30

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91	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.	6.5	13
92	Regulatory circuitry governing morphogenesis in <i>Saccharomyces cerevisiae</i> and <i>Candida albicans</i> . <i>Cell Cycle</i> , 2012, 11, 4294-4295.	1.3	23
93	Functional Analysis With a Barcoder Yeast Gene Overexpression System. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1279-1289.	0.8	72
94	Genetic Variation in <i>Saccharomyces cerevisiae</i> : Circuit Diversification in a Signal Transduction Network. <i>Genetics</i> , 2012, 192, 1523-1532.	1.2	36
95	Conserved rules govern genetic interaction degree across species. <i>Genome Biology</i> , 2012, 13, R57.	13.9	48
96	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012, 14, 966-976.	4.6	431
97	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. <i>Science</i> , 2012, 337, 1353-1356.	6.0	186
98	Functional wiring of the yeast kinome revealed by global analysis of genetic network motifs. <i>Genome Research</i> , 2012, 22, 791-801.	2.4	65
99	Chemical-genomic profiling: Systematic analysis of the cellular targets of bioactive molecules. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 1952-1960.	1.4	36
100	Microarray-based target identification using drug hypersensitive fission yeast expressing ORFeome. <i>Molecular BioSystems</i> , 2011, 7, 1463.	2.9	21
101	Padanamides A and B, Highly Modified Linear Tetrapeptides Produced in Culture by a <i>Streptomyces</i> sp. Isolated from a Marine Sediment. <i>Organic Letters</i> , 2011, 13, 3936-3939.	2.4	46
102	From chemical genomics to personalized medicine—tackling the genotype to phenotype problem. <i>Molecular BioSystems</i> , 2011, 7, 13-13.	2.9	0
103	Systematic exploration of synergistic drug pairs. <i>Molecular Systems Biology</i> , 2011, 7, 544.	3.2	284
104	The TFIIH Subunit Tfb3 Regulates Cullin Neddylation. <i>Molecular Cell</i> , 2011, 43, 488-495.	4.5	39
105	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	9.4	194
106	The future of model organisms in human disease research. <i>Nature Reviews Genetics</i> , 2011, 12, 575-582.	7.7	66
107	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	9.4	352
108	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. <i>Nature Biotechnology</i> , 2011, 29, 505-511.	9.4	90

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109	New azole antifungal agents with novel modes of action: Synthesis and biological studies of new tridentate ligands based on pyrazole and triazole. <i>European Journal of Medicinal Chemistry</i> , 2011, 46, 4117-4124.	2.6	68
110	Combining functional genomics and chemical biology to identify targets of bioactive compounds. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 66-78.	2.8	72
111	Charting the genetic interaction map of a cell. <i>Current Opinion in Biotechnology</i> , 2011, 22, 66-74.	3.3	103
112	Nutrients and the Pkh1/2 and Pkc1 Protein Kinases Control mRNA Decay and P-body Assembly in Yeast. <i>Journal of Biological Chemistry</i> , 2011, 286, 8759-8770.	1.6	27
113	Histone modifications influence mediator interactions with chromatin. <i>Nucleic Acids Research</i> , 2011, 39, 8342-8354.	6.5	39
114	Uncoupling of GTP hydrolysis from eIF6 release on the ribosome causes Shwachman-Diamond syndrome. <i>Genes and Development</i> , 2011, 25, 917-929.	2.7	247
115	Ubiquitin Ligase Ufd2 Is Required for Efficient Degradation of Mps1 Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 43660-43667.	1.6	22
116	An "Exacerbate-reverse" Strategy in Yeast Identifies Histone Deacetylase Inhibition as a Correction for Cholesterol and Sphingolipid Transport Defects in Human Niemann-Pick Type C Disease. <i>Journal of Biological Chemistry</i> , 2011, 286, 23842-23851.	1.6	67
117	Drug-Sensitive DNA Polymerase ϵ Reveals a Role for Mismatch Repair in Checkpoint Activation in Yeast. <i>Genetics</i> , 2011, 189, 1211-1224.	1.2	9
118	Putting genetic interactions in context through a global modular decomposition. <i>Genome Research</i> , 2011, 21, 1375-1387.	2.4	61
119	Protein Complexes are Central in the Yeast Genetic Landscape. <i>PLoS Computational Biology</i> , 2011, 7, e1001092.	1.5	57
120	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	6.0	1,937
121	Reconstitution and Protein Composition Analysis of Endocytic Actin Patches. <i>Current Biology</i> , 2010, 20, 1890-1899.	1.8	59
122	The Awesome Power of Synergy from Chemical-Chemical Profiling. <i>Chemistry and Biology</i> , 2010, 17, 789-790.	6.2	1
123	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010, 7, 1017-1024.	9.0	319
124	Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. <i>Journal of Cell Biology</i> , 2010, 188, 69-81.	2.3	100
125	The DNA Damage Response Pathway Contributes to the Stability of Chromosome III Derivatives Lacking Efficient Replicators. <i>PLoS Genetics</i> , 2010, 6, e1001227.	1.5	29
126	Genetic interactions reveal the evolutionary trajectories of duplicate genes. <i>Molecular Systems Biology</i> , 2010, 6, 429.	3.2	97

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127	Synthetic Genetic Array (SGA) Analysis in <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>Methods in Enzymology</i> , 2010, 470, 145-179.	0.4	175
128	Genotype to Phenotype: A Complex Problem. <i>Science</i> , 2010, 328, 469-469.	6.0	358
129	Identification of <i>Saccharomyces cerevisiae</i> Spindle Pole Body Remodeling Factors. <i>PLoS ONE</i> , 2010, 5, e15426.	1.1	12
130	Shifted Transversal Design smart-pooling for high coverage interactome mapping. <i>Genome Research</i> , 2009, 19, 1262-1269.	2.4	36
131	Exploring the conservation of synthetic lethal genetic interaction networks. <i>Communicative and Integrative Biology</i> , 2009, 2, 78-81.	0.6	22
132	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	2.6	172
133	Rex1p deficiency leads to accumulation of precursor initiator tRNA ^{Met} and polyadenylation of substrate RNAs in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2009, 37, 298-308.	6.5	63
134	A picture is worth a thousand words: Genomics to phenomics in the yeast <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2009, 583, 1656-1661.	1.3	32
135	The yeast Shu complex couples error-free post-replication repair to homologous recombination. <i>Molecular Microbiology</i> , 2009, 73, 89-102.	1.2	88
136	A molecular barcoded yeast ORF library enables mode-of-action analysis of bioactive compounds. <i>Nature Biotechnology</i> , 2009, 27, 369-377.	9.4	254
137	An empirical framework for binary interactome mapping. <i>Nature Methods</i> , 2009, 6, 83-90.	9.0	800
138	You too can play with an edge. <i>Nature Methods</i> , 2009, 6, 797-798.	9.0	3
139	Global Map of SUMO Function Revealed by Protein-Protein Interaction and Genetic Networks. <i>Molecular Cell</i> , 2009, 33, 124-135.	4.5	109
140	Systematic Mapping of Genetic Interaction Networks. <i>Annual Review of Genetics</i> , 2009, 43, 601-625.	3.2	250
141	Ubiquitin-related modifier Urm1 acts as a sulphur carrier in thiolation of eukaryotic transfer RNA. <i>Nature</i> , 2009, 458, 228-232.	13.7	245
142	ITSN1 Controls Vesicle Recycling at the Neuromuscular Junction and Functions in Parallel with DAB1. <i>Traffic</i> , 2008, 9, 742-754.	1.3	43
143	The interaction network of the chaperonin CCT. <i>EMBO Journal</i> , 2008, 27, 1827-1839.	3.5	182
144	Yeast Barcoders: a chemogenomic application of a universal donor-strain collection carrying bar-code identifiers. <i>Nature Methods</i> , 2008, 5, 719-725.	9.0	99

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145	eSGA: E. coli synthetic genetic array analysis. <i>Nature Methods</i> , 2008, 5, 789-795.	9.0	231
146	Significant conservation of synthetic lethal genetic interaction networks between distantly related eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16653-16658.	3.3	165
147	Genetic and Biochemical Analysis of Yeast and Human Cap Trimethylguanosine Synthase. <i>Journal of Biological Chemistry</i> , 2008, 283, 31706-31718.	1.6	65
148	The <i>Saccharomyces cerevisiae</i> Homolog of p24 Is Essential for Maintaining the Association of p150 Glued With the Dynactin Complex. <i>Genetics</i> , 2008, 178, 703-709.	1.2	17
149	A Specificity Map for the PDZ Domain Family. <i>PLoS Biology</i> , 2008, 6, e239.	2.6	410
150	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. <i>Genome Research</i> , 2008, 18, 1092-1099.	2.4	105
151	Genetic Interactions of MAF1 Identify a Role for Med20 in Transcriptional Repression of Ribosomal Protein Genes. <i>PLoS Genetics</i> , 2008, 4, e1000112.	1.5	12
152	Molecular chaperone Hsp90 stabilizes Pih1/Nop17 to maintain R2TP complex activity that regulates snoRNA accumulation. <i>Journal of Cell Biology</i> , 2008, 180, 563-578.	2.3	159
153	Chemical Genetic Profiling of Imidazo[1,2-a]pyridines and -Pyrimidines Reveals Target Pathways Conserved between Yeast and Human Cells. <i>PLoS Genetics</i> , 2008, 4, e1000284.	1.5	37
154	Ybp2 Associates with the Central Kinetochore of <i>Saccharomyces cerevisiae</i> and Mediates Proper Mitotic Progression. <i>PLoS ONE</i> , 2008, 3, e1617.	1.1	13
155	Identification of a Novel Lysophospholipid Acyltransferase in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 30562-30569.	1.6	103
156	Inorganic Phosphate Deprivation Causes tRNA Nuclear Accumulation via Retrograde Transport in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2007, 176, 841-852.	1.2	43
157	The type III effector EspF coordinates membrane trafficking by the spatiotemporal activation of two eukaryotic signaling pathways. <i>Journal of Cell Biology</i> , 2007, 178, 1265-1278.	2.3	112
158	Genetic Dissection of Parallel Sister-Chromatid Cohesion Pathways. <i>Genetics</i> , 2007, 176, 1417-1429.	1.2	102
159	The Shwachman-Bodian-Diamond syndrome protein mediates translational activation of ribosomes in yeast. <i>Nature Genetics</i> , 2007, 39, 486-495.	9.4	290
160	Identifying specificity profiles for peptide recognition modules from phage-displayed peptide libraries. <i>Nature Protocols</i> , 2007, 2, 1368-1386.	5.5	174
161	Exploring genetic interactions and networks with yeast. <i>Nature Reviews Genetics</i> , 2007, 8, 437-449.	7.7	541
162	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	13.7	806

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163	16 High-Throughput Strain Construction and Systematic Synthetic Lethal Screening in. <i>Methods in Microbiology</i> , 2007, 36, 369-707.	0.4	87
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