Corey Nislow

List of Publications by Year in descending order

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197	21,395	65	138
papers	citations	h-index	g-index
220	220	220	31086
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Beta-cell specific Insr deletion promotes insulin hypersecretion and improves glucose tolerance prior to global insulin resistance. Nature Communications, 2022, 13, 735.	12.8	20
2	The cellular response to drug perturbation is limited: comparison of large-scale chemogenomic fitness signatures. BMC Genomics, 2022, 23, 197.	2.8	5
3	Experiment verification test of the Artemis I â€~Deep Space Radiation Genomics' experiment. Acta Astronautica, 2022, 198, 702-706.	3.2	4
4	Chemical–Genetic Interactions as a Means to Characterize Drug Synergy. Methods in Molecular Biology, 2021, 2381, 243-263.	0.9	2
5	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. Nature Communications, 2021, 12, 1054.	12.8	29
6	A genome-wide portrait of pervasive drug contaminants. Scientific Reports, 2021, 11, 12487.	3.3	4
7	Systematic Prediction of Antifungal Drug Synergy by Chemogenomic Screening in Saccharomyces cerevisiae. Frontiers in Fungal Biology, 2021, 2, .	2.0	3
8	Effects of Inhaled Corticosteroid/Long-Acting \hat{l}^2 sub>2-Agonist Combination on the Airway Microbiome of Patients with Chronic Obstructive Pulmonary Disease: A Randomized Controlled Clinical Trial (DISARM). American Journal of Respiratory and Critical Care Medicine, 2021, 204, 1143-1152.	5.6	44
9	Seven Years at High Salinity—Experimental Evolution of the Extremely Halotolerant Black Yeast Hortaea werneckii. Journal of Fungi (Basel, Switzerland), 2021, 7, 723.	3.5	8
10	Pharmacogenomics at the Point of Care: A Community Pharmacy Project in British Columbia. Journal of Personalized Medicine, 2021, 11, 11.	2.5	14
11	Characterization of the gut microbiome in a porcine model of thoracic spinal cord injury. BMC Genomics, 2021, 22, 775.	2.8	12
12	Interactively AUDIT Your Growth Curves with a Suite of R Packages. G3: Genes, Genomes, Genetics, 2020, 10, 933-943.	1.8	7
13	A competence-regulated toxin-antitoxin system in Haemophilus influenzae. PLoS ONE, 2020, 15, e0217255.	2.5	5
14	Broad-spectrum antifungal activities and mechanism of drimane sesquiterpenoids. Microbial Cell, 2020, 7, 146-159.	3.2	13
15	Moonshot: Affordable, Simple, Flight Hardware for the Artemis-1 Mission and Beyond. Frontiers in Space Technologies, 2020, 1 , .	1.4	2
16	Pharmacogenomic Testing: Clinical Evidence and Implementation Challenges. Journal of Personalized Medicine, 2019, 9, 40.	2.5	55
17	De novo pathogenic <i>DNM1L</i> variant in a patient diagnosed with atypical hereditary sensory and autonomic neuropathy. Molecular Genetics & Genomic Medicine, 2019, 7, e00961.	1.2	12
18	Heparanase protects the heart against chemical or ischemia/reperfusion injury. Journal of Molecular and Cellular Cardiology, 2019, 131, 29-40.	1.9	13

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19	MicroRNA Biomarkers in Cerebrospinal Fluid and Serum Reflect Injury Severity in Human Acute Traumatic Spinal Cord Injury. Journal of Neurotrauma, 2019, 36, 2358-2371.	3.4	46
20	PH-domain-binding inhibitors of nucleotide exchange factor BRAG2 disrupt Arf GTPase signaling. Nature Chemical Biology, 2019, 15, 358-366.	8.0	22
21	The Paf1 Complex Broadly Impacts the Transcriptome of <i>Saccharomyces cerevisiae</i> . Genetics, 2019, 212, 711-728.	2.9	10
22	Single-cell analysis for drug development using convex lens-induced confinement imaging. BioTechniques, 2019, 67, 210-217.	1.8	5
23	Sputum Microbiome Is Associated with 1-Year Mortality after Chronic Obstructive Pulmonary Disease Hospitalizations. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 1205-1213.	5.6	95
24	Network dynamics of the yeast methyltransferome. Microbial Cell, 2019, 6, 356-369.	3.2	1
25	Physical Forces Modulate Oxidative Status and Stress Defense Meditated Metabolic Adaptation of Yeast Colonies: Spaceflight and Microgravity Simulations. Microgravity Science and Technology, 2018, 30, 195-208.	1.4	10
26	Reducing insulin via conditional partial gene ablation in adults reverses dietâ€induced weight gain. FASEB Journal, 2018, 32, 1196-1206.	0.5	39
27	Idebenone and coenzyme Q10 are novel PPARÎ \pm Ĵ 3 ligands, with potential for treatment of fatty liver diseases. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	26
28	Insight into the Recent Genome Duplication of the Halophilic Yeast <i>Hortaea werneckii</i> Combining an Improved Genome with Gene Expression and Chromatin Structure. G3: Genes, Genomes, Genetics, 2017, 7, 2015-2022.	1.8	39
29	Serum MicroRNAs Reflect Injury Severity in a Large Animal Model of Thoracic Spinal Cord Injury. Scientific Reports, 2017, 7, 1376.	3.3	52
30	Comparative functional genomic screens of three yeast deletion collections reveal unexpected effects of genotype in response to diverse stress. Open Biology, 2017, 7, 160330.	3.6	12
31	Phenotypic diversity and genotypic flexibility of <i>Burkholderia cenocepacia</i> during long-term chronic infection of cystic fibrosis lungs. Genome Research, 2017, 27, 650-662.	5.5	64
32	Genome-Wide Screen Reveals sec21 Mutants of Saccharomyces cerevisiae Are Methotrexate-Resistant. G3: Genes, Genomes, Genetics, 2017, 7, 1251-1257.	1.8	3
33	Caryolan-1-ol, an antifungal volatile produced by <i>Streptomyces</i> spp., inhibits the endomembrane system of fungi. Open Biology, 2017, 7, 170075.	3.6	40
34	Reduced Circulating Insulin Enhances Insulin Sensitivity in Old Mice and Extends Lifespan. Cell Reports, 2017, 20, 451-463.	6.4	112
35	Heparanase Overexpression Induces Glucagon Resistance and Protects Animals From Chemically Induced Diabetes. Diabetes, 2017, 66, 45-57.	0.6	12
36	Novel Anti-Campylobacter Compounds Identified Using High Throughput Screening of a Pre-selected Enriched Small Molecules Library. Frontiers in Microbiology, 2016, 7, 405.	3.5	24

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37	Transformed Recombinant Enrichment Profiling Rapidly Identifies HMW1 as an Intracellular Invasion Locus in Haemophilus influenzae. PLoS Pathogens, 2016, 12, e1005576.	4.7	16
38	A Signaling Lipid Associated with Alzheimer's Disease Promotes Mitochondrial Dysfunction. Scientific Reports, 2016, 6, 19332.	3.3	25
39	Lichen-forming fungusCaloplaca flavoruscensinhibits transcription factors and chromatin remodeling system in fungi. FEMS Microbiology Letters, 2016, 363, fnw113.	1.8	0
40	Functional Genomics Using the Saccharomyces cerevisiae Yeast Deletion Collections. Cold Spring Harbor Protocols, 2016, 2016, pdb.top080945.	0.3	2
41	Identification of Chemical–Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088054.	0.3	4
42	Systematic Mapping of Chemical–Genetic Interactions in Saccharomyces cerevisiae. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077701.	0.3	5
43	Functional Profiling Using the Saccharomyces Genome Deletion Project Collections. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088039.	0.3	1
44	A chemogenomic approach to understand the antifungal action of Lichen-derived vulpinic acid. Journal of Applied Microbiology, 2016, 121, 1580-1591.	3.1	7
45	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. Nature Chemical Biology, 2016, 12, 867-875.	8.0	79
46	Signaling pathways coordinating the alkaline pH response confer resistance to the hevein-type plant antimicrobial peptide Pn-AMP1 in Saccharomyces cerevisiae. Planta, 2016, 244, 1229-1240.	3.2	3
47	The bronchial epithelial cell bacterial microbiome and host response in patients infected with human immunodeficiency virus. BMC Pulmonary Medicine, 2016, 16, 142.	2.0	8
48	Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles. ACS Central Science, 2016, 2, 687-701.	11.3	68
49	Microbial and biochemical basis of a Fusarium wilt-suppressive soil. ISME Journal, 2016, 10, 119-129.	9.8	355
50	Chromosome-wide histone deacetylation by sirtuins prevents hyperactivation of DNA damage-induced signaling upon replicative stress. Nucleic Acids Research, 2016, 44, 2706-2726.	14.5	27
51	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces \hat{l}^2 Cell Proliferation. Cell Metabolism, 2016, 23, 179-193.	16.2	160
52	Reverse Chemical Genetics: Comprehensive Fitness Profiling Reveals the Spectrum of Drug Target Interactions. PLoS Genetics, 2016, 12, e1006275.	3.5	13
53	Using C. elegans Forward and Reverse Genetics to Identify New Compounds with Anthelmintic Activity. PLoS Neglected Tropical Diseases, 2016, 10, e0005058.	3.0	45
54	Discovery of novel small molecule modulators of Clavibacter michiganensis subsp. michiganensis. Frontiers in Microbiology, 2015, 6, 1127.	3.5	18

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55	Genes Required for Survival in Microgravity Revealed by Genome-Wide Yeast Deletion Collections Cultured during Spaceflight. BioMed Research International, 2015, 2015, 1-10.	1.9	23
56	Endophytic colonization of barley (Hordeum vulgare) roots by the nematophagous fungus Pochonia chlamydosporia reveals plant growth promotion and a general defense and stress transcriptomic response. Journal of Plant Research, 2015, 128, 665-678.	2.4	73
57	Identification of a New Class of Antifungals Targeting the Synthesis of Fungal Sphingolipids. MBio, 2015, 6, e00647.	4.1	124
58	Select microtubule inhibitors increase lysosome acidity and promote lysosomal disruption in acute myeloid leukemia (AML) cells. Apoptosis: an International Journal on Programmed Cell Death, 2015, 20, 948-959.	4.9	22
59	Complementation of Yeast Genes with Human Genes as an Experimental Platform for Functional Testing of Human Genetic Variants. Genetics, 2015, 201, 1263-1274.	2.9	77
60	Caenorhabditis elegans is a useful model for anthelmintic discovery. Nature Communications, 2015, 6, 7485.	12.8	163
61	14-3-3ζ coordinates adipogenesis of visceral fat. Nature Communications, 2015, 6, 7671.	12.8	62
62	An Updated Collection of Sequence Barcoded Temperature-Sensitive Alleles of Yeast Essential Genes. G3: Genes, Genomes, Genetics, 2015, 5, 1879-1887.	1.8	38
63	Absence of Activation of DNA Repair Genes and Excellent Efficacy of Phosphaplatins against Human Ovarian Cancers: Implications To Treat Resistant Cancers. Journal of Medicinal Chemistry, 2015, 58, 8387-8401.	6.4	18
64	Transcriptome analysis of <i>Campylobacter jejuni </i> polyphosphate kinase (<i>ppk1 </i> and <i>ppk2 </i> mutants. Virulence, 2015, 6, 814-818.	4.4	14
65	Global Analysis of the Fungal Microbiome in Cystic Fibrosis Patients Reveals Loss of Function of the Transcriptional Repressor Nrg1 as a Mechanism of Pathogen Adaptation. PLoS Pathogens, 2015, 11, e1005308.	4.7	74
66	Genome-wide RNAi analysis reveals that simultaneous inhibition of specific mevalonate pathway genes potentiates tumor cell death. Oncotarget, 2015, 6, 26909-26921.	1.8	52
67	GC-Rich DNA Elements Enable Replication Origin Activity in the Methylotrophic Yeast Pichia pastoris. PLoS Genetics, 2014, 10, e1004169.	3 . 5	44
68	Complete Genome Sequence of Haemophilus influenzae Strain 375 from the Middle Ear of a Pediatric Patient with Otitis Media. Genome Announcements, 2014 , 2 , .	0.8	14
69	A unified model for yeast transcript definition. Genome Research, 2014, 24, 154-166.	5. 5	20
70	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. Genome Biology, 2014, 15, R64.	9.6	57
71	Sequencing and functional analysis of the genome of a nematode egg-parasitic fungus, Pochonia chlamydosporia. Fungal Genetics and Biology, 2014, 65, 69-80.	2.1	105
72	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. Science, 2014, 344, 208-211.	12.6	217

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73	CHIP-MYTH: A novel interactive proteomics method for the assessment of agonist-dependent interactions of the human \hat{l}^2 2-adrenergic receptor. Biochemical and Biophysical Research Communications, 2014, 445, 746-756.	2.1	17
74	Large-Scale Identification and Analysis of Suppressive Drug Interactions. Chemistry and Biology, 2014, 21, 541-551.	6.0	27
75	The Yeast Deletion Collection: A Decade of Functional Genomics. Genetics, 2014, 197, 451-465.	2.9	402
76	A genome scale overexpression screen to reveal drug activity in human cells. Genome Medicine, 2014, 6, 32.	8.2	29
77	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. Nature Chemical Biology, 2014, 10, 76-84.	8.0	39
78	DNA-Damaging Agents in Cancer Chemotherapy: Serendipity and Chemical Biology. Chemistry and Biology, 2013, 20, 648-659.	6.0	465
79	A High-Throughput Yeast Assay Identifies Synergistic Drug Combinations. Assay and Drug Development Technologies, 2013, 11, 299-307.	1.2	18
80	Effects of the Paf1 Complex and Histone Modifications on snoRNA 3′-End Formation Reveal Broad and Locus-Specific Regulation. Molecular and Cellular Biology, 2013, 33, 170-182.	2.3	22
81	Chemogenomic Profiling. , 2013, , 153-176.		3
82	A Novel Small Molecule Methyltransferase Is Important for Virulence in Candida albicans. ACS Chemical Biology, 2013, 8, 2785-2793.	3.4	7
83	A Compendium of Nucleosome and Transcript Profiles Reveals Determinants of Chromatin Architecture and Transcription. PLoS Genetics, 2013, 9, e1003479.	3.5	125
84	Genetic and Genomic Architecture of the Evolution of Resistance to Antifungal Drug Combinations. PLoS Genetics, 2013, 9, e1003390.	3.5	90
85	Conserved Substitution Patterns around Nucleosome Footprints in Eukaryotes and Archaea Derive from Frequent Nucleosome Repositioning through Evolution. PLoS Computational Biology, 2013, 9, e1003373.	3.2	13
86	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. G3: Genes, Genomes, Genetics, 2013, 3, 1375-1387.	1.8	5
87	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. Nucleic Acids Research, 2013, 41, 6332-6346.	14.5	68
88	Chemical Genomic Screening of a Saccharomyces cerevisiae Genomewide Mutant Collection Reveals Genes Required for Defense against Four Antimicrobial Peptides Derived from Proteins Found in Human Saliva. Antimicrobial Agents and Chemotherapy, 2013, 57, 840-847.	3.2	13
89	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. Journal of Cell Biology, 2013, 201, 145-163.	5.2	58
90	Lysosomal disruption preferentially targets acute myeloid leukemia cells and progenitors. Journal of Clinical Investigation, 2013, 123, 315-328.	8.2	117

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91	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast Hortaea werneckii. PLoS ONE, 2013, 8, e71328.	2.5	96
92	The role of the Paf1 complex in controlling transcriptioncoupled histone modifications. FASEB Journal, 2013, 27, 324.3.	0.5	0
93	Characterization of snoRNA 3'â€end formation in Saccharomyces cerevisiae reveals a broad role for the Paf1 complex and locusâ€specific roles for histone postâ€translational modifications. FASEB Journal, 2013, 27, lb97.	0.5	0
94	Functional Analysis With a Barcoder Yeast Gene Overexpression System. G3: Genes, Genomes, Genetics, 2012, 2, 1279-1289.	1.8	72
95	Genome Sequence of Shigella flexneri Serotype 5a Strain M90T Sm. Journal of Bacteriology, 2012, 194, 3022-3022.	2.2	38
96	Barcode Sequencing for Understanding Drug–Gene Interactions. Methods in Molecular Biology, 2012, 910, 55-69.	0.9	14
97	Genome-wide analysis of intracellular pH reveals quantitative control of cell division rate by pHc in Saccharomyces cerevisiae. Genome Biology, 2012, 13, R80.	9.6	139
98	A novel calcineurin-independent activity of cyclosporin A in Saccharomyces cerevisiae. Molecular BioSystems, 2012, 8, 2575.	2.9	6
99	Target Identification by Chromatographic Co-elution: Monitoring of Drug-Protein Interactions without Immobilization or Chemical Derivatization. Molecular and Cellular Proteomics, 2012, 11, M111.016642-1-M111.016642-14.	3.8	43
100	Comparative Chemogenomics To Examine the Mechanism of Action of DNA-Targeted Platinum-Acridine Anticancer Agents. ACS Chemical Biology, 2012, 7, 1892-1901.	3.4	39
101	Dissecting DNA damage response pathways by analysing protein localization and abundance changes Aduring DNA replication stress. Nature Cell Biology, 2012, 14, 966-976.	10.3	431
102	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. Science, 2012, 337, 1353-1356.	12.6	186
103	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
104	Timing of Transcriptional Quiescence during Gametogenesis Is Controlled by Global Histone H3K4 Demethylation. Developmental Cell, 2012, 23, 1059-1071.	7.0	29
105	An algorithm for chemical genomic profiling that minimizes batch effects: bucket evaluations. BMC Bioinformatics, 2012, 13, 245.	2.6	2
106	A phenotypic screening platform to identify small molecule modulators of Chlamydomonas reinhardtii growth, motility and photosynthesis. Genome Biology, 2012, 13, R105.	9.6	15
107	Chromatin is an ancient innovation conserved between Archaea and Eukarya. ELife, 2012, 1, e00078.	6.0	78
108	Bugs, drugs and chemical genomics. Nature Chemical Biology, 2012, 8, 46-56.	8.0	130

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109	Identification of yeast genes that confer resistance to chitosan oligosaccharide (COS) using chemogenomics. BMC Genomics, 2012, 13, 267.	2.8	50
110	Genomic Approaches for Determining Nucleosome Occupancy in Yeast. Methods in Molecular Biology, 2012, 833, 389-411.	0.9	6
111	Mitochondrial Electron Transport Is the Cellular Target of the Oncology Drug Elesclomol. PLoS ONE, 2012, 7, e29798.	2.5	105
112	The synthetic genetic interaction network reveals small molecules that target specific pathways in Sacchromyces cerevisiae. Molecular BioSystems, 2011, 7, 2019.	2.9	8
113	Displaying Chemical Information on a Biological Network Using Cytoscape. Methods in Molecular Biology, 2011, 781, 363-376.	0.9	7
114	Systematic exploration of synergistic drug pairs. Molecular Systems Biology, 2011, 7, 544.	7.2	284
115	Dafadine inhibits DAF-9 to promote dauer formation and longevity of Caenorhabditis elegans. Nature Chemical Biology, 2011, 7, 891-893.	8.0	27
116	Design, Synthesis and Characterization of a Highly Effective Inhibitor for Analog-Sensitive (as) Kinases. PLoS ONE, 2011, 6, e20789.	2.5	7
117	Competitive Genomic Screens of Barcoded Yeast Libraries. Journal of Visualized Experiments, 2011, , .	0.3	28
118	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. Nature Methods, 2011, 8, 159-164.	19.0	74
119	The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4. EMBO Journal, 2011, 30, 1919-1927.	7.8	47
120	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. Nature Biotechnology, 2011, 29, 361-367.	17.5	352
121	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. Nature Biotechnology, 2011, 29, 505-511.	17.5	90
122	New azole antifungal agents with novel modes of action: Synthesis and biological studies of new tridentate ligands based on pyrazole and triazole. European Journal of Medicinal Chemistry, 2011, 46, 4117-4124.	5.5	68
123	Inhibition of Mitochondrial Translation as a Therapeutic Strategy for Human Acute Myeloid Leukemia. Cancer Cell, 2011, 20, 674-688.	16.8	546
124	Compound Prioritization Methods Increase Rates of Chemical Probe Discovery in Model Organisms. Chemistry and Biology, 2011, 18, 1273-1283.	6.0	41
125	A comprehensive platform for highly multiplexed mammalian functional genetic screens. BMC Genomics, 2011, 12, 213.	2.8	31
126	Nucleosome-coupled expression differences in closely-related species. BMC Genomics, 2011, 12, 466.	2.8	7

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127	Curcumin Inhibits Growth of Saccharomyces cerevisiae through Iron Chelation. Eukaryotic Cell, 2011, 10, 1574-1581.	3.4	40
128	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	1.8	25
129	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. Genes and Development, 2011, 25, 2489-2501.	5.9	40
130	Evolution of Nucleosome Occupancy: Conservation of Global Properties and Divergence of Gene-Specific Patterns. Molecular and Cellular Biology, 2011, 31, 4348-4355.	2.3	28
131	Extensive role of the general regulatory factors, Abf1 and Rap1, in determining genome-wide chromatin structure in budding yeast. Nucleic Acids Research, 2011, 39, 2032-2044.	14.5	107
132	Multiple Means to the Same End: The Genetic Basis of Acquired Stress Resistance in Yeast. PLoS Genetics, 2011, 7, e1002353.	3.5	91
133	A Systems Biology Approach Reveals the Role of a Novel Methyltransferase in Response to Chemical Stress and Lipid Homeostasis. PLoS Genetics, 2011, 7, e1002332.	3.5	21
134	Response to "The Reality of Pervasive Transcription― PLoS Biology, 2011, 9, e1001102.	5.6	30
135	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.9	25
136	Signature-tagged Mutagenesis to Characterize Genes Through Competitive Selection of Bar-coded Genome Libraries. Methods in Molecular Biology, 2011, 765, 225-252.	0.9	4
137	Design, Synthesis, and Characterization of a Highly Effective Hog1 Inhibitor: A Powerful Tool for Analyzing MAP Kinase Signaling in Yeast. PLoS ONE, 2011, 6, e20012.	2.5	23
138	Lysosomal Disruption Selectively Targets Leukemia Cells and Leukemia Stem Cells Through A Mechanism Related to Increased Reactive Oxygen Species Production. Blood, 2011, 118, 61-61.	1.4	5
139	Inhibition of Mitochondrial Translation As a Therapeutic Strategy for Acute Myeloid Leukemia (AML). Blood, 2011, 118, 233-233.	1.4	0
140	The Genetic Landscape of a Cell. Science, 2010, 327, 425-431.	12.6	1,937
141	A survey of yeast genomic assays for drug and target discovery. , 2010, 127, 156-164.		108
142	A predictive model for drug bioaccumulation and bioactivity in Caenorhabditis elegans. Nature Chemical Biology, 2010, 6, 549-557.	8.0	164
143	Diversity of Eukaryotic DNA Replication Origins Revealed by Genome-Wide Analysis of Chromatin Structure. PLoS Genetics, 2010, 6, e1001092.	3.5	133
144	Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. Journal of Cell Biology, 2010, 188, 69-81.	5.2	100

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145	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	14.5	54
146	Highly-multiplexed barcode sequencing: an efficient method for parallel analysis of pooled samples. Nucleic Acids Research, 2010, 38, e142-e142.	14.5	184
147	Genome-Wide Screen in Saccharomyces cerevisiae Identifies Vacuolar Protein Sorting, Autophagy, Biosynthetic, and tRNA Methylation Genes Involved in Life Span Regulation. PLoS Genetics, 2010, 6, e1001024.	3.5	144
148	Gene Annotation and Drug Target Discovery in Candida albicans with a Tagged Transposon Mutant Collection. PLoS Pathogens, 2010, 6, e1001140.	4.7	85
149	Endosomal protein sorting and autophagy genes contribute to the regulation of yeast life span. Autophagy, 2010, 6, 1227-1228.	9.1	7
150	Exploring Gene Function and Drug Action Using Chemogenomic Dosage Assays. Methods in Enzymology, 2010, 470, 233-255.	1.0	27
151	Recent advances and method development for drug target identification. Trends in Pharmacological Sciences, 2010, 31, 82-88.	8.7	102
152	Genotype to Phenotype: A Complex Problem. Science, 2010, 328, 469-469.	12.6	358
153	Systematic analysis of genome-wide fitness data in yeast reveals novel gene function and drug action. Genome Biology, 2010, 11, R30.	9.6	94
154	Most "Dark Matter―Transcripts Are Associated With Known Genes. PLoS Biology, 2010, 8, e1000371.	5.6	377
155	Self-reporting cells. BioTechniques, 2009, 46, 356-357.	1.8	0
156	Quantitative phenotyping via deep barcode sequencing. Genome Research, 2009, 19, 1836-1842.	5.5	275
157	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. PLoS Genetics, 2009, 5, e1000407.	3.5	129
158	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	2.9	71
159	Precise Gene-Dose Alleles for Chemical Genetics. Genetics, 2009, 182, 623-626.	2.9	14
160	Novel insights into iron metabolism by integrating deletome and transcriptome analysis in an iron deficiency model of the yeast Saccharomyces cerevisiae. BMC Genomics, 2009, 10, 130.	2.8	35
161	A comparative analysis of DNA barcode microarray feature size. BMC Genomics, 2009, 10, 471.	2.8	13
162	Combining chemical genomics screens in yeast to reveal spectrum of effects of chemical inhibition of sphingolipid biosynthesis. BMC Microbiology, 2009, 9, 9.	3.3	27

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163	A molecular barcoded yeast ORF library enables mode-of-action analysis of bioactive compounds. Nature Biotechnology, 2009, 27, 369-377.	17.5	254
164	Knocking sense into regulatory pathways. Nature Biotechnology, 2009, 27, 149-150.	17.5	2
165	You too can play with an edge. Nature Methods, 2009, 6, 797-798.	19.0	3
166	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. Molecular Cell, 2009, 35, 340-351.	9.7	88
167	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. Methods in Molecular Biology, 2009, 548, 115-143.	0.9	12
168	Chemical-genetic approaches for exploring the mode of action of natural products., 2008, 66, 237-271.		20
169	An integrated platform of genomic assays reveals small-molecule bioactivities. Nature Chemical Biology, 2008, 4, 498-506.	8.0	178
170	Combination chemical genetics. Nature Chemical Biology, 2008, 4, 674-681.	8.0	158
171	Yeast Barcoders: a chemogenomic application of a universal donor-strain collection carrying bar-code identifiers. Nature Methods, 2008, 5, 719-725.	19.0	99
172	A Library of Yeast Transcription Factor Motifs Reveals a Widespread Function for Rsc3 in Targeting Nucleosome Exclusion at Promoters. Molecular Cell, 2008, 32, 878-887.	9.7	415
173	Yeast chemical genomics and drug discovery: an update. Trends in Pharmacological Sciences, 2008, 29, 499-504.	8.7	87
174	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. Science, 2008, 320, 362-365.	12.6	892
175	Identification of Genes Involved in the Toxic Response of Saccharomyces cerevisiae against Iron and Copper Overload by Parallel Analysis of Deletion Mutants. Toxicological Sciences, 2008, 101, 140-151.	3.1	81
176	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. Genome Research, 2008, 18, 1092-1099.	5.5	105
177	Identification of Small Molecule Inhibitors of Pseudomonas aeruginosa Exoenzyme S Using a Yeast Phenotypic Screen. PLoS Genetics, 2008, 4, e1000005.	3.5	84
178	Off-Target Effects of Psychoactive Drugs Revealed by Genome-Wide Assays in Yeast. PLoS Genetics, 2008, 4, e1000151.	3.5	79
179	Chemical–Genetic Profiling of Imidazo[1,2-a]pyridines and -Pyrimidines Reveals Target Pathways Conserved between Yeast and Human Cells. PLoS Genetics, 2008, 4, e1000284.	3.5	37
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#	Article	IF	CITATIONS
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