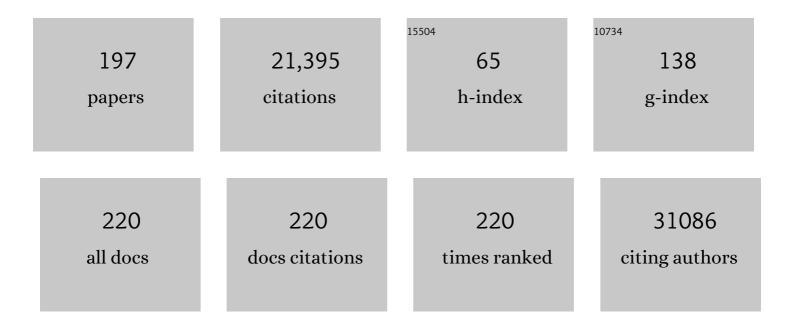
Corey Nislow

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
2	The Genetic Landscape of a Cell. Science, 2010, 327, 425-431.	12.6	1,937
3	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. Science, 2008, 320, 362-365.	12.6	892
4	A high-resolution atlas of nucleosome occupancy in yeast. Nature Genetics, 2007, 39, 1235-1244.	21.4	765
5	Inhibition of Mitochondrial Translation as a Therapeutic Strategy for Human Acute Myeloid Leukemia. Cancer Cell, 2011, 20, 674-688.	16.8	546
6	DNA-Damaging Agents in Cancer Chemotherapy: Serendipity and Chemical Biology. Chemistry and Biology, 2013, 20, 648-659.	6.0	465
7	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 793-798.	7.1	460
8	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. Genetics, 2005, 169, 1915-1925.	2.9	460
9	Dissecting DNA damage response pathways by analysing protein localization and abundance changesAduring DNA replication stress. Nature Cell Biology, 2012, 14, 966-976.	10.3	431
10	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
11	The Yeast Deletion Collection: A Decade of Functional Genomics. Genetics, 2014, 197, 451-465.	2.9	402
12	Most "Dark Matter―Transcripts Are Associated With Known Genes. PLoS Biology, 2010, 8, e1000371.	5.6	377
13	Genotype to Phenotype: A Complex Problem. Science, 2010, 328, 469-469.	12.6	358
14	Microbial and biochemical basis of a Fusarium wilt-suppressive soil. ISME Journal, 2016, 10, 119-129.	9.8	355
15	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. Nature Biotechnology, 2011, 29, 361-367.	17.5	352
16	A plus-end-directed motor enzyme that moves antiparallel microtubules in vitro localizes to the interzone of mitotic spindles. Nature, 1992, 359, 543-547.	27.8	345
17	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. Nature Genetics, 2007, 39, 199-206.	21.4	294
18	Systematic exploration of synergistic drug pairs. Molecular Systems Biology, 2011, 7, 544.	7.2	284

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19	Quantitative phenotyping via deep barcode sequencing. Genome Research, 2009, 19, 1836-1842.	5.5	275
20	A molecular barcoded yeast ORF library enables mode-of-action analysis of bioactive compounds. Nature Biotechnology, 2009, 27, 369-377.	17.5	254
21	<i>SET1</i> , A Yeast Member of the <i>Trithorax</i> Family, Functions in Transcriptional Silencing and Diverse Cellular Processes. Molecular Biology of the Cell, 1997, 8, 2421-2436.	2.1	217
22	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. Science, 2014, 344, 208-211.	12.6	217
23	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. Science, 2012, 337, 1353-1356.	12.6	186
24	Highly-multiplexed barcode sequencing: an efficient method for parallel analysis of pooled samples. Nucleic Acids Research, 2010, 38, e142-e142.	14.5	184
25	Genome-wide analysis of barcoded Saccharomyces cerevisiae gene-deletion mutants in pooled cultures. Nature Protocols, 2007, 2, 2958-2974.	12.0	179
26	An integrated platform of genomic assays reveals small-molecule bioactivities. Nature Chemical Biology, 2008, 4, 498-506.	8.0	178
27	A predictive model for drug bioaccumulation and bioactivity in Caenorhabditis elegans. Nature Chemical Biology, 2010, 6, 549-557.	8.0	164
28	Caenorhabditis elegans is a useful model for anthelmintic discovery. Nature Communications, 2015, 6, 7485.	12.8	163
29	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces Î ² Cell Proliferation. Cell Metabolism, 2016, 23, 179-193.	16.2	160
30	Combination chemical genetics. Nature Chemical Biology, 2008, 4, 674-681.	8.0	158
31	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. PLoS Genetics, 2005, 1, e24.	3.5	144
32	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
33	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
34	Diversity of Eukaryotic DNA Replication Origins Revealed by Genome-Wide Analysis of Chromatin Structure. PLoS Genetics, 2010, 6, e1001092.	3.5	133
35	Bugs, drugs and chemical genomics. Nature Chemical Biology, 2012, 8, 46-56.	8.0	130
36	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. PLoS Genetics, 2009, 5, e1000407.	3.5	129

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37	A Compendium of Nucleosome and Transcript Profiles Reveals Determinants of Chromatin Architecture and Transcription. PLoS Genetics, 2013, 9, e1003479.	3.5	125
38	Identification of a New Class of Antifungals Targeting the Synthesis of Fungal Sphingolipids. MBio, 2015, 6, e00647.	4.1	124
39	Lysosomal disruption preferentially targets acute myeloid leukemia cells and progenitors. Journal of Clinical Investigation, 2013, 123, 315-328.	8.2	117
40	Reduced Circulating Insulin Enhances Insulin Sensitivity in Old Mice and Extends Lifespan. Cell Reports, 2017, 20, 451-463.	6.4	112
41	A survey of yeast genomic assays for drug and target discovery. , 2010, 127, 156-164.		108
42	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
43	A unique and universal molecular barcode array. Nature Methods, 2006, 3, 601-603.	19.0	105
44	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. Genome Research, 2008, 18, 1092-1099.	5.5	105
45	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
46	Mitochondrial Electron Transport Is the Cellular Target of the Oncology Drug Elesclomol. PLoS ONE, 2012, 7, e29798.	2.5	105
47	Recent advances and method development for drug target identification. Trends in Pharmacological Sciences, 2010, 31, 82-88.	8.7	102
48	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
49	Introns Regulate RNA and Protein Abundance in Yeast. Genetics, 2006, 174, 511-518.	2.9	99
50	Yeast Barcoders: a chemogenomic application of a universal donor-strain collection carrying bar-code identifiers. Nature Methods, 2008, 5, 719-725.	19.0	99
51	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
52	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
53	Systematic analysis of genome-wide fitness data in yeast reveals novel gene function and drug action. Genome Biology, 2010, 11, R30.	9.6	94
54	Multiple Means to the Same End: The Genetic Basis of Acquired Stress Resistance in Yeast. PLoS Genetics, 2011, 7, e1002353.	3.5	91

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55	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. Nature Biotechnology, 2011, 29, 505-511.	17.5	90
56	Genetic and Genomic Architecture of the Evolution of Resistance to Antifungal Drug Combinations. PLoS Genetics, 2013, 9, e1003390.	3.5	90
57	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
58	Yeast chemical genomics and drug discovery: an update. Trends in Pharmacological Sciences, 2008, 29, 499-504.	8.7	87
59	Gene Annotation and Drug Target Discovery in Candida albicans with a Tagged Transposon Mutant Collection. PLoS Pathogens, 2010, 6, e1001140.	4.7	85
60	Identification of Small Molecule Inhibitors of Pseudomonas aeruginosa Exoenzyme S Using a Yeast Phenotypic Screen. PLoS Genetics, 2008, 4, e1000005.	3.5	84
61	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
62	Off-Target Effects of Psychoactive Drugs Revealed by Genome-Wide Assays in Yeast. PLoS Genetics, 2008, 4, e1000151.	3.5	79
63	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. Nature Chemical Biology, 2016, 12, 867-875.	8.0	79
64	Chromatin is an ancient innovation conserved between Archaea and Eukarya. ELife, 2012, 1, e00078.	6.0	78
65	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
66	Knocking out multigene redundancies via cycles of sexual assortment and fluorescence selection. Nature Methods, 2011, 8, 159-164.	19.0	74
67	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
68	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
69	Functional Analysis With a Barcoder Yeast Gene Overexpression System. G3: Genes, Genomes, Genetics, 2012, 2, 1279-1289.	1.8	72
70	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	2.9	71
71	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
72	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. Nucleic Acids Research, 2013, 41, 6332-6346.	14.5	68

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73	Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles. ACS Central Science, 2016, 2, 687-701.	11.3	68
74	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
75	14-3-3ζ coordinates adipogenesis of visceral fat. Nature Communications, 2015, 6, 7671.	12.8	62
76	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. Journal of Cell Biology, 2013, 201, 145-163.	5.2	58
77	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. Genome Biology, 2014, 15, R64.	9.6	57
78	Accelerating the Discovery of Biologically Active Small Molecules Using a High-Throughput Yeast Halo Assay⊥. Journal of Natural Products, 2007, 70, 383-390.	3.0	56
79	Pharmacogenomic Testing: Clinical Evidence and Implementation Challenges. Journal of Personalized Medicine, 2019, 9, 40.	2.5	55
80	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	14.5	54
81	Serum MicroRNAs Reflect Injury Severity in a Large Animal Model of Thoracic Spinal Cord Injury. Scientific Reports, 2017, 7, 1376.	3.3	52
82	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
83	Identification of yeast genes that confer resistance to chitosan oligosaccharide (COS) using chemogenomics. BMC Genomics, 2012, 13, 267.	2.8	50
84	The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4. EMBO Journal, 2011, 30, 1919-1927.	7.8	47
85	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
86	Using C. elegans Forward and Reverse Genetics to Identify New Compounds with Anthelmintic Activity. PLoS Neglected Tropical Diseases, 2016, 10, e0005058.	3.0	45
87	GC-Rich DNA Elements Enable Replication Origin Activity in the Methylotrophic Yeast Pichia pastoris. PLoS Genetics, 2014, 10, e1004169.	3.5	44
88	Effects of Inhaled Corticosteroid/Long-Acting β 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
89	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
90	Compound Prioritization Methods Increase Rates of Chemical Probe Discovery in Model Organisms. Chemistry and Biology, 2011, 18, 1273-1283.	6.0	41

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91	Curcumin Inhibits Growth of Saccharomyces cerevisiae through Iron Chelation. Eukaryotic Cell, 2011, 10, 1574-1581.	3.4	40
92	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
93	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
94	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
95	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. Nature Chemical Biology, 2014, 10, 76-84.	8.0	39
96	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
97	Reducing insulin via conditional partial gene ablation in adults reverses dietâ€induced weight gain. FASEB Journal, 2018, 32, 1196-1206.	0.5	39
98	Genome Sequence of Shigella flexneri Serotype 5a Strain M90T Sm. Journal of Bacteriology, 2012, 194, 3022-3022.	2.2	38
99	An Updated Collection of Sequence Barcoded Temperature-Sensitive Alleles of Yeast Essential Genes. G3: Genes, Genomes, Genetics, 2015, 5, 1879-1887.	1.8	38
100	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
101	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
102	Molecular components of the mitotic spindle. BioEssays, 1992, 14, 81-88.	2.5	34
103	Regionalized Cell Division during Sea Urchin Gastrulation Contributes to Archenteron Formation and Is Correlated with the Establishment of Larval Symmetry. (sea urchin/gastrulation/cell) Tj ETQq1 1 0.784314	4 rg B፮ /Ov	erlæck 10 Tf 5
104	A comprehensive platform for highly multiplexed mammalian functional genetic screens. BMC Genomics, 2011, 12, 213.	2.8	31
105	Response to "The Reality of Pervasive Transcription― PLoS Biology, 2011, 9, e1001102.	5.6	30
106	Timing of Transcriptional Quiescence during Gametogenesis Is Controlled by Global Histone H3K4 Demethylation. Developmental Cell, 2012, 23, 1059-1071.	7.0	29
107	A genome scale overexpression screen to reveal drug activity in human cells. Genome Medicine, 2014, 6, 32.	8.2	29
108	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. Nature Communications, 2021, 12, 1054.	12.8	29

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109	Competitive Genomic Screens of Barcoded Yeast Libraries. Journal of Visualized Experiments, 2011, , .	0.3	28
110	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
111	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
112	Exploring Gene Function and Drug Action Using Chemogenomic Dosage Assays. Methods in Enzymology, 2010, 470, 233-255.	1.0	27
113	Dafadine inhibits DAF-9 to promote dauer formation and longevity of Caenorhabditis elegans. Nature Chemical Biology, 2011, 7, 891-893.	8.0	27
114	Large-Scale Identification and Analysis of Suppressive Drug Interactions. Chemistry and Biology, 2014, 21, 541-551.	6.0	27
115	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
116	Idebenone and coenzyme Q10 are novel PPARÎ $\pm/$ Î ³ ligands, with potential for treatment of fatty liver diseases. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	26
117	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	1.8	25
118	A Signaling Lipid Associated with Alzheimer's Disease Promotes Mitochondrial Dysfunction. Scientific Reports, 2016, 6, 19332.	3.3	25
119	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.9	25
120	Examining protein protein interactions using endogenously tagged yeast arrays: The Cross-and-Capture system. Genome Research, 2007, 17, 1774-1782.	5.5	24
121	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
122	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
123	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
124	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
125	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
126	PH-domain-binding inhibitors of nucleotide exchange factor BRAG2 disrupt Arf GTPase signaling. Nature Chemical Biology, 2019, 15, 358-366.	8.0	22

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127	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
128	Chemical-genetic approaches for exploring the mode of action of natural products. , 2008, 66, 237-271.		20
129	A unified model for yeast transcript definition. Genome Research, 2014, 24, 154-166.	5.5	20
130	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
131	A High-Throughput Yeast Assay Identifies Synergistic Drug Combinations. Assay and Drug Development Technologies, 2013, 11, 299-307.	1.2	18
132	Discovery of novel small molecule modulators of Clavibacter michiganensis subsp. michiganensis. Frontiers in Microbiology, 2015, 6, 1127.	3.5	18
133	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
134	Experimental approaches to identify genetic networks. Current Opinion in Biotechnology, 2006, 17, 472-480.	6.6	17
135	CHIP-MYTH: A novel interactive proteomics method for the assessment of agonist-dependent interactions of the human l²2-adrenergic receptor. Biochemical and Biophysical Research Communications, 2014, 445, 746-756.	2.1	17
136	Chemical Genomic Profiling for Identifying Intracellular Targets of Toxicants Producing Parkinson's Disease. Toxicological Sciences, 2007, 95, 182-187.	3.1	16
137	Transformed Recombinant Enrichment Profiling Rapidly Identifies HMW1 as an Intracellular Invasion Locus in Haemophilus influenzae. PLoS Pathogens, 2016, 12, e1005576.	4.7	16
138	A phenotypic screening platform to identify small molecule modulators of Chlamydomonas reinhardtii growth, motility and photosynthesis. Genome Biology, 2012, 13, R105.	9.6	15
139	Precise Gene-Dose Alleles for Chemical Genetics. Genetics, 2009, 182, 623-626.	2.9	14
140	Barcode Sequencing for Understanding Drug–Gene Interactions. Methods in Molecular Biology, 2012, 910, 55-69.	0.9	14
141	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
142	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
143	Pharmacogenomics at the Point of Care: A Community Pharmacy Project in British Columbia. Journal of Personalized Medicine, 2021, 11, 11.	2.5	14
144	A comparative analysis of DNA barcode microarray feature size. BMC Genomics, 2009, 10, 471.	2.8	13

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145	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
146	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
147	Heparanase protects the heart against chemical or ischemia/reperfusion injury. Journal of Molecular and Cellular Cardiology, 2019, 131, 29-40.	1.9	13
148	Reverse Chemical Genetics: Comprehensive Fitness Profiling Reveals the Spectrum of Drug Target Interactions. PLoS Genetics, 2016, 12, e1006275.	3.5	13
149	Broad-spectrum antifungal activities and mechanism of drimane sesquiterpenoids. Microbial Cell, 2020, 7, 146-159.	3.2	13
150	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
151	Heparanase Overexpression Induces Glucagon Resistance and Protects Animals From Chemically Induced Diabetes. Diabetes, 2017, 66, 45-57.	0.6	12
152	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
153	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. Methods in Molecular Biology, 2009, 548, 115-143.	0.9	12
154	Characterization of the gut microbiome in a porcine model of thoracic spinal cord injury. BMC Genomics, 2021, 22, 775.	2.8	12
155	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
156	The Paf1 Complex Broadly Impacts the Transcriptome of <i>Saccharomyces cerevisiae</i> . Genetics, 2019, 212, 711-728.	2.9	10
157	The synthetic genetic interaction network reveals small molecules that target specific pathways in Sacchromyces cerevisiae. Molecular BioSystems, 2011, 7, 2019.	2.9	8
158	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
159	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
160	The origin of skeleton forming cells in the sea urchin embryo. Roux's Archives of Developmental Biology, 1988, 197, 447-456.	1.2	7
161	17 Chemical Genomic Tools for Understanding Gene Function and Drug Action. Methods in Microbiology, 2007, , 387-709.	0.8	7
162	Endosomal protein sorting and autophagy genes contribute to the regulation of yeast life span. Autophagy, 2010, 6, 1227-1228.	9.1	7

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163	Displaying Chemical Information on a Biological Network Using Cytoscape. Methods in Molecular Biology, 2011, 781, 363-376.	0.9	7
164	Design, Synthesis and Characterization of a Highly Effective Inhibitor for Analog-Sensitive (as) Kinases. PLoS ONE, 2011, 6, e20789.	2.5	7
165	Nucleosome-coupled expression differences in closely-related species. BMC Genomics, 2011, 12, 466.	2.8	7
166	A Novel Small Molecule Methyltransferase Is Important for Virulence in Candida albicans. ACS Chemical Biology, 2013, 8, 2785-2793.	3.4	7
167	A chemogenomic approach to understand the antifungal action of Lichen-derived vulpinic acid. Journal of Applied Microbiology, 2016, 121, 1580-1591.	3.1	7
168	Interactively AUDIT Your Growth Curves with a Suite of R Packages. G3: Genes, Genomes, Genetics, 2020, 10, 933-943.	1.8	7
169	A novel calcineurin-independent activity of cyclosporin A in Saccharomyces cerevisiae. Molecular BioSystems, 2012, 8, 2575.	2.9	6
170	Genomic Approaches for Determining Nucleosome Occupancy in Yeast. Methods in Molecular Biology, 2012, 833, 389-411.	0.9	6
171	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. G3: Genes, Genomes, Genetics, 2013, 3, 1375-1387.	1.8	5
172	Systematic Mapping of Chemical–Genetic Interactions in Saccharomyces cerevisiae. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077701.	0.3	5
173	Single-cell analysis for drug development using convex lens-induced confinement imaging. BioTechniques, 2019, 67, 210-217.	1.8	5
174	A competence-regulated toxin-antitoxin system in Haemophilus influenzae. PLoS ONE, 2020, 15, e0217255.	2.5	5
175	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
176	The cellular response to drug perturbation is limited: comparison of large-scale chemogenomic fitness signatures. BMC Genomics, 2022, 23, 197.	2.8	5
177	Identification of Chemical–Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088054.	0.3	4
178	A genome-wide portrait of pervasive drug contaminants. Scientific Reports, 2021, 11, 12487.	3.3	4
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