

Stephen G Oliver

List of Publications by Year in descending order

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314
papers

33,393
citations

9264
74
h-index

4991
167
g-index

330
all docs

330
docs citations

330
times ranked

41283
citing authors

#	ARTICLE	IF	CITATIONS
1	The Neighborhood of the Spike Gene Is a Hotspot for Modular Intertypic Homologous and Nonhomologous Recombination in Coronavirus Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	30
2	The Remarkable Evolutionary Plasticity of Coronaviruses by Mutation and Recombination: Insights for the COVID-19 Pandemic and the Future Evolutionary Paths of SARS-CoV-2. <i>Viruses</i> , 2022, 14, 78.	3.3	64
3	From Petri Plates to Petri Nets, a revolution in yeast biology. <i>FEMS Yeast Research</i> , 2022, , .	2.3	0
4	Comparative Analysis of SARS-CoV-2 Variants of Concern, Including Omicron, Highlights Their Common and Distinctive Amino Acid Substitution Patterns, Especially at the Spike ORF. <i>Viruses</i> , 2022, 14, 707.	3.3	30
5	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	2.9	60
6	Combination of Genome-Scale Models and Bioreactor Dynamics to Optimize the Production of Commodity Chemicals. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 855735.	3.5	0
7	Data intelligence for process performance prediction in biologics manufacturing. <i>Computers and Chemical Engineering</i> , 2021, 146, 107226.	3.8	9
8	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
9	Yeast Double Transporter Gene Deletion Library for Identification of Xenobiotic Carriers in Low or High Throughput. <i>MBio</i> , 2021, 12, e0322121.	4.1	5
10	Extending the Modeling and Analysis Capabilities of Continuous Petri Nets by Flexible Nets. , 2021, , .		2
11	Steady State Analysis of Flexible Nets. <i>IEEE Transactions on Automatic Control</i> , 2020, 65, 2510-2525.	5.7	5
12	A unifying modelling formalism for the integration of stoichiometric and kinetic models. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200341.	3.4	3
13	Comparative Analysis of the Core Proteomes among the Pseudomonas Major Evolutionary Groups Reveals Species-Specific Adaptations for Pseudomonas aeruginosa and Pseudomonas chlororaphis. <i>Diversity</i> , 2020, 12, 289.	1.7	37
14	fnyzer: A Python Package for the Analysis of Flexible Nets. <i>Lecture Notes in Computer Science</i> , 2020, , 349-355.	1.3	2
15	Metaheuristic approaches in biopharmaceutical process development data analysis. <i>Bioprocess and Biosystems Engineering</i> , 2019, 42, 1399-1408.	3.4	9
16	Metabolic response to Parkinson's disease recapitulated by the haploinsufficient diploid yeast cells hemizygous for the adrenodoxin reductase gene. <i>Molecular Omics</i> , 2019, 15, 340-347.	2.8	0
17	Flexible Nets: a modeling formalism for dynamic systems with uncertain parameters. <i>Discrete Event Dynamic Systems: Theory and Applications</i> , 2019, 29, 367-392.	1.5	4
18	Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. <i>Nucleic Acids Research</i> , 2019, 47, 9998-10009.	14.5	44

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19	Determination of the Global Pattern of Gene Expression in Yeast Cells by Intracellular Levels of Guanine Nucleotides. MBio, 2019, 10, .	4.1	9
20	PomBase 2018: user-driven reimplementaion of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. Nucleic Acids Research, 2019, 47, D821-D827.	14.5	157
21	High-energy guanine nucleotides as a signal capable of linking growth to cellular energy status via the control of gene transcription. Current Genetics, 2019, 65, 893-897.	1.7	10
22	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. Open Biology, 2019, 9, 180241.	3.6	80
23	Enhancing the functionality of a microscale bioreactor system as an industrial process development tool for mammalian perfusion culture. Biotechnology and Bioengineering, 2019, 116, 1315-1325.	3.3	16
24	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2019, 19, .	2.3	1
25	Extension of the yeast metabolic model to include iron metabolism and its use to estimate global levels of iron-recruiting enzyme abundance from cofactor requirements. Biotechnology and Bioengineering, 2019, 116, 610-621.	3.3	15
26	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	14.5	3,474
27	A heuristic approach to handling missing data in biologics manufacturing databases. Bioprocess and Biosystems Engineering, 2019, 42, 657-663.	3.4	9
28	Modeling, analyzing and controlling hybrid systems by Guarded Flexible Nets. Nonlinear Analysis: Hybrid Systems, 2019, 32, 131-146.	3.5	6
29	The subcellular organisation of <i>Saccharomyces cerevisiae</i> . Current Opinion in Chemical Biology, 2019, 48, 86-95.	6.1	26
30	Yeast Systems Biology: The Continuing Challenge of Eukaryotic Complexity. Methods in Molecular Biology, 2019, 2049, 3-13.	0.9	1
31	Mapping the <i>Saccharomyces cerevisiae</i> Spatial Proteome with High Resolution Using hyperLOPIT. Methods in Molecular Biology, 2019, 2049, 165-190.	0.9	8
32	A Protocol to Map the Spatial Proteome Using HyperLOPIT in <i>Saccharomyces cerevisiae</i> . Bio-protocol, 2019, 9, e3303.	0.4	2
33	Evaluation of the ability of commercial wine yeasts to form biofilms (mats) and adhere to plastic: implications for the microbiota of the winery environment. FEMS Microbiology Ecology, 2018, 94, .	2.7	10
34	Handling variability and incompleteness of biological data by flexible nets: a case study for Wilson disease. Npj Systems Biology and Applications, 2018, 4, 7.	3.0	13
35	Plasmodium dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. Scientific Reports, 2018, 8, 1038.	3.3	31
36	Diffusion-Limited Growth of Microbial Colonies. Scientific Reports, 2018, 8, 5992.	3.3	26

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37	TAMMiCol: Tool for analysis of the morphology of microbial colonies. PLoS Computational Biology, 2018, 14, e1006629.	3.2	7
38	Saccharomyces cerevisiae adapted to grow in the presence of low-dose rapamycin exhibit altered amino acid metabolism. Cell Communication and Signaling, 2018, 16, 85.	6.5	13
39	Process development for the continuous production of heterologous proteins by the industrial yeast, <i>Komagataella phaffii</i> . Biotechnology and Bioengineering, 2018, 115, 2962-2973.	3.3	16
40	Antiplasmodial and trypanocidal activity of violacein and deoxyviolacein produced from synthetic operons. BMC Biotechnology, 2018, 18, 22.	3.3	32
41	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	14.5	1,838
42	The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. G3: Genes, Genomes, Genetics, 2017, 7, 1239-1249.	1.8	18
43	Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3935-E3943.	7.1	91
44	Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. Neurobiology of Aging, 2017, 57, 104-119.	3.1	24
45	Quantifying the dominant growth mechanisms of dimorphic yeast using a lattice-based model. Journal of the Royal Society Interface, 2017, 14, 20170314.	3.4	16
46	Metabolic modeling to identify engineering targets for <i>Komagataella phaffii</i> : The effect of biomass composition on gene target identification. Biotechnology and Bioengineering, 2017, 114, 2605-2615.	3.3	16
47	Bacterial Signaling Nucleotides Inhibit Yeast Cell Growth by Impacting Mitochondrial and Other Specifically Eukaryotic Functions. MBio, 2017, 8, .	4.1	10
48	Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. GigaScience, 2017, 6, 1-11.	6.4	602
49	CamOptimus: a tool for exploiting complex adaptive evolution to optimize experiments and processes in biotechnology. Microbiology (United Kingdom), 2017, 163, 829-839.	1.8	9
50	Model organism databases: essential resources that need the support of both funders and users. BMC Biology, 2016, 14, 49.	3.8	46
51	Yeast-Based High-Throughput Screens to Identify Novel Compounds Active against <i>Brugia malayi</i> . PLoS Neglected Tropical Diseases, 2016, 10, e0004401.	3.0	24
52	Response to "The Need for Speed"™, by Matsson et al .. Trends in Pharmacological Sciences, 2016, 37, 245-246.	8.7	2
53	The metabolome 18 years on: a concept comes of age. Metabolomics, 2016, 12, 148.	3.0	95
54	The Challenges of Interpreting Phosphoproteomics Data: A Critical View Through the Bioinformatics Lens. Lecture Notes in Computer Science, 2016, , 196-204.	1.3	3

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55	CLUSTERnGO: a user-defined modelling platform for two-stage clustering of time-series data. <i>Bioinformatics</i> , 2016, 32, 388-397.	4.1	7
56	Alzheimer's as a Systems-Level Disease Involving the Interplay of Multiple Cellular Networks. <i>Methods in Molecular Biology</i> , 2016, 1303, 3-48.	0.9	33
57	Chronological Lifespan in Yeast Is Dependent on the Accumulation of Storage Carbohydrates Mediated by Yak1, Mck1 and Rim15 Kinases. <i>PLoS Genetics</i> , 2016, 12, e1006458.	3.5	51
58	A Tool for Multiple Targeted Genome Deletions that Is Precise, Scar-Free, and Suitable for Automation. <i>PLoS ONE</i> , 2015, 10, e0142494.	2.5	1
59	Fitting Transporter Activities to Cellular Drug Concentrations and Fluxes: Why the Bumblebee Can Fly. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 710-723.	8.7	24
60	Biomass composition: the 'elephant in the room' of metabolic modelling. <i>Metabolomics</i> , 2015, 11, 1690-1701.	3.0	58
61	Identification and Deconvolution of Cross-Resistance Signals from Antimalarial Compounds Using Multidrug-Resistant <i>Plasmodium falciparum</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1110-1118.	3.2	34
62	Quantifying Two-Dimensional Filamentous and Invasive Growth Spatial Patterns in Yeast Colonies. <i>PLoS Computational Biology</i> , 2015, 11, e1004070.	3.2	14
63	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	14.5	95
64	Cheaper faster drug development validated by the repositioning of drugs against neglected tropical diseases. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20141289.	3.4	97
65	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. <i>Trends in Biotechnology</i> , 2015, 33, 237-246.	9.3	167
66	The Yeast GSK-3 Homologue Mck1 Is a Key Controller of Quiescence Entry and Chronological Lifespan. <i>PLoS Genetics</i> , 2015, 11, e1005282.	3.5	18
67	The TRiC/CCT Chaperone Is Implicated in Alzheimer's Disease Based on Patient GWAS and an RNAi Screen in <i>Aβ2</i> -Expressing <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2014, 9, e102985.	2.5	34
68	How drugs get into cells: tested and testable predictions to help discriminate between transporter-mediated uptake and lipoidal bilayer diffusion. <i>Frontiers in Pharmacology</i> , 2014, 5, 231.	3.5	136
69	The harder we work â€¦. <i>Yeast</i> , 2014, 31, 81-82.	1.7	0
70	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014, 30, 1791-1792.	4.1	41
71	A protocol for the subcellular fractionation of <i>Saccharomyces cerevisiae</i> using nitrogen cavitation and density gradient centrifugation. <i>Yeast</i> , 2014, 31, 127-135.	1.7	12
72	Yeast cells with impaired drug resistance accumulate glycerol and glucose. <i>Molecular BioSystems</i> , 2014, 10, 93-102.	2.9	12

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73	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . Trends in Biotechnology, 2014, 32, 396-399.	9.3	23
74	1 Yeast as a Model for Systems Biology Studies on Complex Diseases. , 2014, , 3-30.		2
75	esyN: Network Building, Sharing and Publishing. PLoS ONE, 2014, 9, e106035.	2.5	59
76	Investigating the physiological response of <i>Pichia</i> (<i>Komagataella</i>) <i>pastoris</i> GS115 to the heterologous expression of misfolded proteins using chemostat cultures. Applied Microbiology and Biotechnology, 2013, 97, 9747-9762.	3.6	47
77	Predicting complex phenotype–genotype interactions to enable yeast engineering: <i>Saccharomyces cerevisiae</i> as a model organism and a cell factory. Biotechnology Journal, 2013, 8, 1017-1034.	3.5	20
78	The promiscuous binding of pharmaceutical drugs and their transporter-mediated uptake into cells: what we (need to) know and how we can do so. Drug Discovery Today, 2013, 18, 218-239.	6.4	130
79	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. FEBS Letters, 2013, 587, 2832-2841.	2.8	113
80	Copy-number variation of cancer-gene orthologs is sufficient to induce cancer-like symptoms in <i>Saccharomyces cerevisiae</i> . BMC Biology, 2013, 11, 24.	3.8	16
81	Yeast Systems Biology. , 2013, , 343-365.		6
82	FYPO: the fission yeast phenotype ontology. Bioinformatics, 2013, 29, 1671-1678.	4.1	53
83	Control analysis of the eukaryotic cell cycle using gene copy-number series in yeast tetraploids. BMC Genomics, 2013, 14, 744.	2.8	4
84	Synergistic effects of TOR and proteasome pathways on the yeast transcriptome and cell growth. Open Biology, 2013, 3, 120137.	3.6	21
85	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. Open Biology, 2013, 3, 120158.	3.6	32
86	Evaluation and Properties of the Budding Yeast Phosphoproteome. Molecular and Cellular Proteomics, 2012, 11, M111.009555.	3.8	44
87	PomBase: a comprehensive online resource for fission yeast. Nucleic Acids Research, 2012, 40, D695-D699.	14.5	288
88	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. Nature Biotechnology, 2012, 30, 1176-1178.	17.5	107
89	Evaluation of industrial <i>Saccharomyces cerevisiae</i> strains for ethanol production from biomass. Biomass and Bioenergy, 2012, 45, 230-238.	5.7	63
90	The genetic control of growth rate: a systems biology study in yeast. BMC Systems Biology, 2012, 6, 4.	3.0	49

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91	Short- and long-term dynamic responses of the metabolic network and gene expression in yeast to a transient change in the nutrient environment. <i>Molecular BioSystems</i> , 2012, 8, 1760.	2.9	6
92	Genome-wide analysis of longevity in nutrient-deprived <i>Saccharomyces cerevisiae</i> reveals importance of recycling in maintaining cell viability. <i>Environmental Microbiology</i> , 2012, 14, 1249-1260.	3.8	21
93	Phenomic and transcriptomic analyses reveal that autophagy plays a major role in desiccation tolerance in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2011, 7, 139-149.	2.9	35
94	Protein Production in <i>Saccharomyces cerevisiae</i> for Systems Biology Studies. <i>Methods in Enzymology</i> , 2011, 500, 197-212.	1.0	6
95	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	21.4	194
96	Haploinsufficiency and the sex chromosomes from yeasts to humans. <i>BMC Biology</i> , 2011, 9, 15.	3.8	26
97	Genome-wide assessment of the carriers involved in the cellular uptake of drugs: a model system in yeast. <i>BMC Biology</i> , 2011, 9, 70.	3.8	59
98	Pharmaceutical drug transport: the issues and the implications that it is essentially carrier-mediated only. <i>Drug Discovery Today</i> , 2011, 16, 704-714.	6.4	160
99	The yin and yang of yeast: biodiversity research and systems biology as complementary forces driving innovation in biotechnology. <i>Biotechnology Letters</i> , 2011, 33, 477-487.	2.2	5
100	How yeast re-programmes its transcriptional profile in response to different nutrient impulses. <i>BMC Systems Biology</i> , 2011, 5, 148.	3.0	37
101	On the formalization and reuse of scientific research. <i>Journal of the Royal Society Interface</i> , 2011, 8, 1440-1448.	3.4	15
102	Absolute Quantification of the Glycolytic Pathway in Yeast. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007633.	3.8	70
103	The role of proteasome-mediated proteolysis in modulating potentially harmful transcription factor activity in <i>Saccharomyces cerevisiae</i> . <i>Bioinformatics</i> , 2011, 27, i283-i287.	4.1	3
104	JmjN interacts with JmjC to ensure selective proteolysis of Gis1 by the proteasome. <i>Microbiology (United Kingdom)</i> , 2011, 157, 2694-2701.	1.8	28
105	Genome-wide analysis of yeast stress survival and tolerance acquisition to analyze the central trade-off between growth rate and cellular robustness. <i>Molecular Biology of the Cell</i> , 2011, 22, 4435-4446.	2.1	138
106	Functional Expression of Parasite Drug Targets and Their Human Orthologs in Yeast. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1320.	3.0	29
107	Yeast Systems Biology: The Challenge of Eukaryotic Complexity. <i>Methods in Molecular Biology</i> , 2011, 759, 3-28.	0.9	10
108	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	12.8	100

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109	Metabolic flux analysis for recombinant protein production by <i>Pichia pastoris</i> using dual carbon sources: Effects of methanol feeding rate. <i>Biotechnology and Bioengineering</i> , 2010, 105, 317-329.	3.3	60
110	Conditional cell-wall mutants of <i>Saccharomyces cerevisiae</i> as delivery vehicles for therapeutic agents in vivo to the GI tract. <i>Journal of Biotechnology</i> , 2010, 147, 136-143.	3.8	9
111	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	3.8	89
112	Evolutionary Systems Biology of Amino Acid Biosynthetic Cost in Yeast. <i>PLoS ONE</i> , 2010, 5, e11935.	2.5	57
113	Posttranslational regulation impacts the fate of duplicated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2967-2971.	7.1	65
114	The Transcription Activity of Gis1 Is Negatively Modulated by Proteasome-mediated Limited Proteolysis. <i>Journal of Biological Chemistry</i> , 2010, 285, 6465-6476.	3.4	22
115	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
116	Make Way for Robot Scientists. <i>Science</i> , 2009, 325, 945-945.	12.6	10
117	Gis1 is required for transcriptional reprogramming of carbon metabolism and the stress response during transition into stationary phase in yeast. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1690-1698.	1.8	58
118	Information management for high content live cell imaging. <i>BMC Bioinformatics</i> , 2009, 10, 226.	2.6	4
119	The Robot Scientist Adam. <i>Computer</i> , 2009, 42, 46-54.	1.1	28
120	Global gene expression in recombinant and non-recombinant yeast <i>Saccharomyces cerevisiae</i> in three different metabolic states. <i>Biotechnology Advances</i> , 2009, 27, 1092-1117.	11.7	14
121	Fed-batch methanol feeding strategy for recombinant protein production by <i>Pichia pastoris</i> in the presence of co-substrate sorbitol. <i>Yeast</i> , 2009, 26, 473-484.	1.7	102
122	A structured kinetic model for recombinant protein production by Mut+ strain of <i>Pichia pastoris</i> . <i>Chemical Engineering Science</i> , 2009, 64, 5028-5035.	3.8	20
123	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	2.1	99
124	The Automation of Science. <i>Science</i> , 2009, 324, 85-89.	12.6	458
125	A metabolomic and multivariate statistical process to assess the effects of genotoxins in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2009, 5, 1913.	2.9	9
126	Implications of the Dominant Role of Transporters in Drug Uptake by Cells (Supplementary Material). <i>Current Topics in Medicinal Chemistry</i> , 2009, 9, 163-181.	2.1	81

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127	Exometabolic and transcriptional response in relation to phenotype and gene copy number in respiration-related deletion mutants of <i>S. cerevisiae</i> . <i>Yeast</i> , 2008, 25, 661-672.	1.7	7
128	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	17.5	530
129	Identification and characterization of high-flux-control genes of yeast through competition analyses in continuous cultures. <i>Nature Genetics</i> , 2008, 40, 113-117.	21.4	93
130	Data capture in bioinformatics: requirements and experiences with Pedro. <i>BMC Bioinformatics</i> , 2008, 9, 183.	2.6	13
131	Performing statistical analyses on quantitative data in Taverna workflows: An example using R and maxdBrowse to identify differentially-expressed genes from microarray data. <i>BMC Bioinformatics</i> , 2008, 9, 334.	2.6	38
132	Choose your partners: dimerization in eukaryotic transcription factors. <i>Trends in Biochemical Sciences</i> , 2008, 33, 220-229.	7.5	229
133	ISPIDER Central: an integrated database web-server for proteomics. <i>Nucleic Acids Research</i> , 2008, 36, W485-W490.	14.5	18
134	Integration of Metabolic Modeling and Phenotypic Data in Evaluation and Improvement of Ethanol Production Using Respiration-Deficient Mutants of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 5809-5816.	3.1	23
135	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008, , .	0.1	2
136	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008, , .	0.1	3
137	Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated with Fungal Pathogenesis. <i>PLoS ONE</i> , 2008, 3, e2300.	2.5	169
138	9 Transcript Analysis: A Microarray Approach. <i>Methods in Microbiology</i> , 2007, , 189-703.	0.8	2
139	Global Phenotype Screening and Transcript Analysis Outlines the Inhibitory Mode(s) of Action of Two Amphibian-Derived, α -Helical, Cationic Peptides on <i>Saccharomyces cerevisiae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3948-3959.	3.2	34
140	Plasticity of genetic interactions in metabolic networks of yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2307-2312.	7.1	185
141	Genotypic and Physiological Characterization of <i>Saccharomyces boulardii</i> , the Probiotic Strain of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 2458-2467.	3.1	151
142	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. <i>Genome Research</i> , 2007, 17, 510-519.	5.5	64
143	Comparative genome analysis across a kingdom of eukaryotic organisms: Specialization and diversification in the Fungi. <i>Genome Research</i> , 2007, 17, 1809-1822.	5.5	94
144	Cellular Processes and Pathways That Protect <i>Saccharomyces cerevisiae</i> Cells against the Plasma Membrane-Perturbing Compound Chitosan. <i>Eukaryotic Cell</i> , 2007, 6, 600-608.	3.4	62

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145	Specificity in protein interactions and its relationship with sequence diversity and coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7999-8004.	7.1	114
146	21 Metabolic Control in the Eukaryotic Cell, a Systems Biology Perspective. Methods in Microbiology, 2007, , 527-549.	0.8	3
147	1 Introduction to Functional Analysis in Yeast. Methods in Microbiology, 2007, 36, 1-21.	0.8	2
148	Protein Interactions from Complexes: A Structural Perspective. Comparative and Functional Genomics, 2007, 2007, 1-5.	2.0	16
149	A Methodology for Comparative Functional Genomics. Journal of Integrative Bioinformatics, 2007, 4, 112-122.	1.5	1
150	Transcriptional and metabolic response of <i>Saccharomyces cerevisiae</i> to a nutritional perturbation when under stress. Journal of Biotechnology, 2007, 131, S14-S15.	3.8	0
151	Application of the comprehensive set of heterozygous yeast deletion mutants to elucidate the molecular basis of cellular chromium toxicity. Genome Biology, 2007, 8, R268.	9.6	57
152	All duplicates are not equal: the difference between small-scale and genome duplication. Genome Biology, 2007, 8, R209.	9.6	163
153	Growth control of the eukaryote cell: a systems biology study in yeast. Journal of Biology, 2007, 6, 4.	2.7	234
154	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	17.5	1,047
155	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. Nature Biotechnology, 2007, 25, 1127-1133.	17.5	96
156	Flux Balance Analysis of a Genome-Scale Yeast Model Constrained by Exometabolomic Data Allows Metabolic System Identification of Genetically Different Strains. Biotechnology Progress, 2007, 23, 320-326.	2.6	30
157	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. BMC Systems Biology, 2007, 1, 34.	3.0	38
158	e-Fungi: a data resource for comparative analysis of fungal genomes. BMC Genomics, 2007, 8, 426.	2.8	32
159	A kingdom-specific protein domain HMM library for improved annotation of fungal genomes. BMC Genomics, 2007, 8, 97.	2.8	12
160	Storing, Searching, and Disseminating Experimental Proteomics Data. , 2007, , 472-483.		0
161	Automated tracking of gene expression in individual cells and cell compartments. Journal of the Royal Society Interface, 2006, 3, 787-794.	3.4	59
162	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. Molecular Cell, 2006, 21, 319-330.	9.7	618

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163	The relative merits of the tetO2 and tetO7 promoter systems for the functional analysis of heterologous genes in yeast and a compilation of essential yeast genes with tetO2 promoter substitutions. <i>Yeast</i> , 2006, 23, 325-331.	1.7	17
164	Annotation of unknown yeast ORFs by correlation analysis of microarray data and extensive literature searches. <i>Yeast</i> , 2006, 23, 553-571.	1.7	9
165	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
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