

# 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 Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
2	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
3	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002, 417, 399-403.	27.8	2,137
4	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
5	Systematic functional analysis of the yeast genome. <i>Trends in Biotechnology</i> , 1998, 16, 373-378.	9.3	1,059
6	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	17.5	1,047
7	A functional genomics strategy that uses metabolome data to reveal the phenotype of silent mutations. <i>Nature Biotechnology</i> , 2001, 19, 45-50.	17.5	948
8	The complete DNA sequence of yeast chromosome III. <i>Nature</i> , 1992, 357, 38-46.	27.8	924
9	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466.	17.5	724
10	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. <i>Molecular Cell</i> , 2006, 21, 319-330.	9.7	618
11	Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	602
12	Guilt-by-association goes global. <i>Nature</i> , 2000, 403, 601-602.	27.8	544
13	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
14	High-throughput classification of yeast mutants for functional genomics using metabolic footprinting. <i>Nature Biotechnology</i> , 2003, 21, 692-696.	17.5	500
15	Functional genomic hypothesis generation and experimentation by a robot scientist. <i>Nature</i> , 2004, 427, 247-252.	27.8	481
16	The Automation of Science. <i>Science</i> , 2009, 324, 85-89.	12.6	458
17	Here is the evidence, now what is the hypothesis? The complementary roles of inductive and hypothesis-driven science in the post-genomic era. <i>BioEssays</i> , 2004, 26, 99-105.	2.5	451
18	Metabolic footprinting and systems biology: the medium is the message. <i>Nature Reviews Microbiology</i> , 2005, 3, 557-565.	28.6	373

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19	Dynamics of Protein Turnover, a Missing Dimension in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 579-591.	3.8	369
20	From DNA sequence to biological function. <i>Nature</i> , 1996, 379, 597-600.	27.8	308
21	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012, 40, D695-D699.	14.5	288
22	A proposed framework for the description of plant metabolomics experiments and their results. <i>Nature Biotechnology</i> , 2004, 22, 1601-1606.	17.5	283
23	Dispersed growth of <i>Streptomyces</i> in liquid culture. <i>Applied Microbiology and Biotechnology</i> , 1989, 31, 272.	3.6	246
24	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003, 21, 247-254.	17.5	246
25	Chromosome evolution in eukaryotes: a multi-kingdom perspective. <i>Trends in Genetics</i> , 2005, 21, 673-682.	6.7	238
26	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , 2007, 6, 4.	2.7	234
27	Engineering evolution to study speciation in yeasts. <i>Nature</i> , 2003, 422, 68-72.	27.8	232
28	Choose your partners: dimerization in eukaryotic transcription factors. <i>Trends in Biochemical Sciences</i> , 2008, 33, 220-229.	7.5	229
29	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
30	An optimized protocol for metabolome analysis in yeast using direct infusion electrospray mass spectrometry. <i>Phytochemistry</i> , 2003, 62, 929-937.	2.9	207
31	The next wave in metabolome analysis. <i>Trends in Biotechnology</i> , 2005, 23, 544-546.	9.3	204
32	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	21.4	194
33	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
34	Improved matrix-assisted laser desorption/ionization mass spectrometric analysis of tryptic hydrolysates of proteins following guanidination of lysine-containing peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 2070-2073.	1.5	169
35	Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated with Fungal Pathogenesis. <i>PLoS ONE</i> , 2008, 3, e2300.	2.5	169
36	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. <i>Trends in Biotechnology</i> , 2015, 33, 237-246.	9.3	167

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37	All duplicates are not equal: the difference between small-scale and genome duplication. <i>Genome Biology</i> , 2007, 8, R209.	9.6	163
38	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
39	PomBase 2018: user-driven reimplementaion of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019, 47, D821-D827.	14.5	157
40	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
41	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
42	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
43	A network approach to the systematic analysis of yeast gene function. <i>Trends in Genetics</i> , 1996, 12, 241-242.	6.7	134
44	Ethanol inhibition of yeast growth and fermentation: Differences in the magnitude and complexity of the effect. <i>European Journal of Applied Microbiology and Biotechnology</i> , 1981, 11, 151-155.	1.3	132
45	The promiscuous binding of pharmaceutical drugs and their transporter-mediated uptake into cells: what we (need to) know and how we can do so. <i>Drug Discovery Today</i> , 2013, 18, 218-239.	6.4	130
46	Suitability of replacement markers for functional analysis studies in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1997, 13, 1563-1573.	1.7	125
47	Exploring redundancy in the yeast genome: an improved strategy for use of the cre-loxP system. <i>Gene</i> , 2000, 252, 127-135.	2.2	120
48	Global analysis of nutrient control of gene expression in <i>Saccharomyces cerevisiae</i> during growth and starvation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3148-3153.	7.1	120
49	Specificity in protein interactions and its relationship with sequence diversity and coevolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7999-8004.	7.1	114
50	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	2.8	113
51	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	17.5	107
52	Functional genomics: lessons from yeast. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 17-23.	4.0	104
53	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
54	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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55	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
56	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
57	Conceptual modelling of genomic information. <i>Bioinformatics</i> , 2000, 16, 548-557.	4.1	96
58	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	17.5	96
59	Proteomic response to amino acid starvation in <i>Candida albicans</i> and <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2004, 4, 2425-2436.	2.2	95
60	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
61	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	14.5	95
62	The metabolome 18 years on: a concept comes of age. <i>Metabolomics</i> , 2016, 12, 148.	3.0	95
63	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
64	The yeast 2 $\frac{1}{4}$ plasmid: strategies for the survival of a selfish DNA. <i>Molecular Genetics and Genomics</i> , 1986, 205, 417-421.	2.4	93
65	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
66	Isolation of ethanol-tolerant mutants of yeast by continuous selection. <i>European Journal of Applied Microbiology and Biotechnology</i> , 1982, 16, 119-122.	1.3	92
67	DNA sequence analysis of ARSelements from chromosome III of <i>Saccharomyces cerevisiae</i> : identification of a new conserved sequence. <i>Nucleic Acids Research</i> , 1986, 14, 6247-6264.	14.5	92
68	Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3935-E3943.	7.1	91
69	Development of yeast strains for the efficient utilisation of starch: evaluation of constructs that express $\alpha$ -amylase and glucoamylase separately or as bifunctional fusion proteins. <i>Applied Microbiology and Biotechnology</i> , 1995, 43, 1067-1076.	3.6	90
70	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	3.8	89
71	Convergent evolution of gene networks by single gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004, 5, 274-279.	4.5	83
72	Transcriptome Analysis of Recombinant Protein Secretion by <i>Aspergillus nidulans</i> and the Unfolded-Protein Response In Vivo. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2737-2747.	3.1	83

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73	Stability of a cloned gene in yeast grown in chemostat culture. <i>Molecular Genetics and Genomics</i> , 1983, 192, 361-365.	2.4	81
74	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
75	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. <i>Open Biology</i> , 2019, 9, 180241.	3.6	80
76	Hybridization array technology coupled with chemostat culture: Tools to interrogate gene expression in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2002, 26, 281-290.	3.8	79
77	Towards a truly integrative biology through the functional genomics of yeast. <i>Current Opinion in Biotechnology</i> , 2001, 12, 87-91.	6.6	75
78	Discrimination of Modes of Action of Antifungal Substances by Use of Metabolic Footprinting. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6157-6165.	3.1	73
79	Chromatographic separations as a prelude to two-dimensional electrophoresis in proteomics analysis. <i>Proteomics</i> , 2001, 1, 42-53.	2.2	70
80	Absolute Quantification of the Glycolytic Pathway in Yeast:. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007633.	3.8	70
81	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
82	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. <i>Genome Research</i> , 2007, 17, 510-519.	5.5	64
83	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
84	Evaluation of industrial <i>Saccharomyces cerevisiae</i> strains for ethanol production from biomass. <i>Biomass and Bioenergy</i> , 2012, 45, 230-238.	5.7	63
85	Comparative Genomic Hybridization Provides New Insights Into the Molecular Taxonomy of the <i>Saccharomyces Sensu Stricto</i> Complex. <i>Genome Research</i> , 2004, 14, 1043-1051.	5.5	62
86	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
87	Analysis of the Seven-Member AAD Gene Set Demonstrates That Genetic Redundancy in Yeast May Be More Apparent Than Real. <i>Genetics</i> , 1999, 153, 1591-1600.	2.9	62
88	A combination of chemical derivatisation and improved bioinformatic tools optimises protein identification for proteomics. <i>Electrophoresis</i> , 2001, 22, 552-559.	2.4	61
89	Ethanol production and fermentation characteristics of recombinant <i>saccharomyces cerevisiae</i> strains grown on starch. <i>Enzyme and Microbial Technology</i> , 1998, 22, 672-677.	3.2	60
90	Disruption of seven hypothetical aryl alcohol dehydrogenase genes from <i>Saccharomyces cerevisiae</i> and construction of a multiple knock-out strain. <i>Yeast</i> , 1999, 15, 1681-1689.	1.7	60

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91	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
92	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	2.9	60
93	A "hot-spot"™ for Ty transposition on the left arm of yeast chromosome III. <i>Nucleic Acids Research</i> , 1986, 14, 3475-3485.	14.5	59
94	A physical comparison of chromosome III in six strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1994, 10, 39-57.	1.7	59
95	Automated tracking of gene expression in individual cells and cell compartments. <i>Journal of the Royal Society Interface</i> , 2006, 3, 787-794.	3.4	59
96	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
97	esyN: Network Building, Sharing and Publishing. <i>PLoS ONE</i> , 2014, 9, e106035.	2.5	59
98	Stable isotope labelling in vivo as an aid to protein identification in peptide mass fingerprinting. <i>Proteomics</i> , 2002, 2, 157-163.	2.2	58
99	PEDRo: A database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004, 5, 68.	2.8	58
100	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
101	Biomass composition: the "elephant in the room" of metabolic modelling. <i>Metabolomics</i> , 2015, 11, 1690-1701.	3.0	58
102	Glycosylation deficiency phenotypes resulting from depletion of GDP-mannose pyrophosphorylase in two yeast species. <i>Molecular Microbiology</i> , 2000, 36, 1156-1166.	2.5	57
103	Application of the comprehensive set of heterozygous yeast deletion mutants to elucidate the molecular basis of cellular chromium toxicity. <i>Genome Biology</i> , 2007, 8, R268.	9.6	57
104	Evolutionary Systems Biology of Amino Acid Biosynthetic Cost in Yeast. <i>PLoS ONE</i> , 2010, 5, e11935.	2.5	57
105	Application of TOF-SIMS with Chemometrics To Discriminate between Four Different Yeast Strains from the Species <i>Candida glabrata</i> and <i>Saccharomyces cerevisiae</i> . <i>Analytical Chemistry</i> , 2005, 77, 1740-1745.	6.5	55
106	FYPO: the fission yeast phenotype ontology. <i>Bioinformatics</i> , 2013, 29, 1671-1678.	4.1	53
107	Yeast as a Touchstone in Post-genomic Research: Strategies for Integrative Analysis in Functional Genomics. <i>BMB Reports</i> , 2004, 37, 93-106.	2.4	52
108	Doxycycline, the drug used to control the tet-regulatable promoter system, has no effect on global gene expression in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2005, 22, 565-569.	1.7	51

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109	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
110	Quantitative analysis of yeast gene function using competition experiments in continuous culture. , 1998, 14, 1417-1427.		49
111	The genetic control of growth rate: a systems biology study in yeast. <i>BMC Systems Biology</i> , 2012, 6, 4.	3.0	49
112	Using yeast to place human genes in functional categories. <i>Gene</i> , 2003, 303, 121-129.	2.2	48
113	Ethanol production using nuclear petite yeast mutants. <i>Applied Microbiology and Biotechnology</i> , 1998, 49, 511-516.	3.6	47
114	Production of Ethanol from Starch by Respiration-Deficient Recombinant <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 6443-6445.	3.1	47
115	Investigating the physiological response of <i>Pichia (Komagataella) pastoris</i> GS115 to the heterologous expression of misfolded proteins using chemostat cultures. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9747-9762.	3.6	47
116	Transcriptome profiling of a <i>Saccharomyces cerevisiae</i> mutant with a constitutively activated Ras/cAMP pathway. <i>Physiological Genomics</i> , 2003, 16, 107-118.	2.3	46
117	Use of expressed sequence tag analysis and cDNA microarrays of the filamentous fungus <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2004, 41, 199-212.	2.1	46
118	Model organism databases: essential resources that need the support of both funders and users. <i>BMC Biology</i> , 2016, 14, 49.	3.8	46
119	Improvement of antibiotic titers from <i>Streptomyces</i> bacteria by interactive continuous selection. <i>Biotechnology and Bioengineering</i> , 1996, 49, 185-196.	3.3	45
120	Transcript analysis of 1003 novel yeast genes using high-throughput northern hybridizations. <i>EMBO Journal</i> , 2001, 20, 3177-3186.	7.8	45
121	Effects of reciprocal chromosomal translocations on the fitness of <i>Saccharomyces cerevisiae</i> . <i>EMBO Reports</i> , 2004, 5, 392-398.	4.5	45
122	Yeast as a navigational aid in genome analysis. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1483-1487.	1.8	45
123	Polymorphisms on the right arm of yeast chromosome III associated with Ty transposition and recombination events. <i>Nucleic Acids Research</i> , 1987, 15, 8963-8982.	14.5	44
124	Evaluation and Properties of the Budding Yeast Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M1111.009555.	3.8	44
125	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
126	Glutamic protease distribution is limited to filamentous fungi. <i>FEMS Microbiology Letters</i> , 2004, 239, 95-101.	1.8	42



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127	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014, 30, 1791-1792.	4.1	41
128	The effect of temperature on the ethanol tolerance of the yeast, <i>Saccharomyces uvarum</i> . <i>Biotechnology Letters</i> , 1982, 4, 269-273.	2.2	39
129	From gene to screen with yeast. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 405-409.	3.3	39
130	GIMS: an integrated data storage and analysis environment for genomic and functional data. <i>Yeast</i> , 2003, 20, 1291-1306.	1.7	39
131	An improved tetO promoter replacement system for regulating the expression of yeast genes. <i>Yeast</i> , 2003, 20, 1255-1262.	1.7	38
132	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. <i>BMC Systems Biology</i> , 2007, 1, 34.	3.0	38
133	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
134	MeMo: a hybrid SQL/XML approach to metabolomic data management for functional genomics. <i>BMC Bioinformatics</i> , 2006, 7, 281.	2.6	37
135	From genomes to systems: the path with yeast. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 477-482.	4.0	37
136	How yeast re-programmes its transcriptional profile in response to different nutrient impulses. <i>BMC Systems Biology</i> , 2011, 5, 148.	3.0	37
137	Comparative Analysis of the Core Proteomes among the <i>Pseudomonas</i> Major Evolutionary Groups Reveals Species-Specific Adaptations for <i>Pseudomonas aeruginosa</i> and <i>Pseudomonas chlororaphis</i> . <i>Diversity</i> , 2020, 12, 289.	1.7	37
138	Improvement of ethanol production from starch by recombinant yeast through manipulation of environmental factors. <i>Enzyme and Microbial Technology</i> , 2002, 31, 640-647.	3.2	36
139	A model-based analysis of microarray experimental error and normalisation. <i>Nucleic Acids Research</i> , 2003, 31, 96e-96.	14.5	35
140	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
141	Global Phenotype Screening and Transcript Analysis Outlines the Inhibitory Mode(s) of Action of Two Amphibian-Derived, $\alpha$ -Helical, Cationic Peptides on <i>Saccharomyces cerevisiae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3948-3959.	3.2	34
142	The TRiC/CCT Chaperone Is Implicated in Alzheimer's Disease Based on Patient GWAS and an RNAi Screen in $A\beta$ -Expressing <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2014, 9, e102985.	2.5	34
143	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
144	Environmental signals triggering methylenomycin production by <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 1997, 179, 5511-5515.	2.2	33

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145	Transcript analysis of 250 novel yeast genes from chromosome XIV. , 1999, 15, 329-350.		33
146	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
147	Mcm1p-Induced DNA Bending Regulates the Formation of Ternary Transcription Factor Complexes. <i>Molecular and Cellular Biology</i> , 2003, 23, 450-461.	2.3	32
148	e-Fungi: a data resource for comparative analysis of fungal genomes. <i>BMC Genomics</i> , 2007, 8, 426.	2.8	32
149	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. <i>Open Biology</i> , 2013, 3, 120158.	3.6	32
150	Antiplasmodial and trypanocidal activity of violacein and deoxyviolacein produced from synthetic operons. <i>BMC Biotechnology</i> , 2018, 18, 22.	3.3	32
151	Automation of DNA Sequencing: A System to Perform the Sanger Dideoxysequencing Reactions. <i>Bio/technology</i> , 1985, 3, 911-915.	1.5	31
152	Cloning and characterisation of the ribosomal RNA genes of the dimorphic yeast, <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1986, 10, 449-452.	1.7	31
153	17 Metabolic Control Analysis as a Tool in the Elucidation of the Function of Novel Genes. <i>Methods in Microbiology</i> , 1998, , 297-336.	0.8	31
154	Integrative investigation of metabolic and transcriptomic data. <i>BMC Bioinformatics</i> , 2006, 7, 203.	2.6	31
155	<i>Plasmodium</i> dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. <i>Scientific Reports</i> , 2018, 8, 1038.	3.3	31
156	Flux Balance Analysis of a Genome-Scale Yeast Model Constrained by Exometabolomic Data Allows Metabolic System Identification of Genetically Different Strains. <i>Biotechnology Progress</i> , 2007, 23, 320-326.	2.6	30
157	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
158	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
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