

Stephen G Oliver

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8813550/stephen-g-oliver-publications-by-citations.pdf>
Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

303 papers	24,754 citations	71 h-index	152 g-index
330 ext. papers	30,131 ext. citations	9.3 avg, IF	8.05 L-index

#	Paper	IF	Citations
303	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019 , 47, D330-D338.	18.1	1962
302	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002 , 417, 399-403.	40.1	1856
301	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017 , 45, D331-D338.	12.38	1258
300	Systematic functional analysis of the yeast genome. <i>Trends in Biotechnology</i> , 1998 , 16, 373-8	15.1	906
299	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007 , 25, 221-31	44.5	889
298	A functional genomics strategy that uses metabolome data to reveal the phenotype of silent mutations. <i>Nature Biotechnology</i> , 2001 , 19, 45-50	44.5	839
297	The complete DNA sequence of yeast chromosome III. <i>Nature</i> , 1992 , 357, 38-46	50.4	812
296	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004 , 22, 1459-66	44.5	632
295	Mapping pathways and phenotypes by systematic gene overexpression. <i>Molecular Cell</i> , 2006 , 21, 319-301.	17.6	502
294	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021 , 49, D325-D334	20.1	494
293	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008 , 26, 1155-60	44.5	471
292	High-throughput classification of yeast mutants for functional genomics using metabolic footprinting. <i>Nature Biotechnology</i> , 2003 , 21, 692-6	44.5	439
291	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	4.1	404
290	Functional genomic hypothesis generation and experimentation by a robot scientist. <i>Nature</i> , 2004 , 427, 247-52	50.4	341
289	The automation of science. <i>Science</i> , 2009 , 324, 85-9	33.3	324
288	Metabolic footprinting and systems biology: the medium is the message. <i>Nature Reviews Microbiology</i> , 2005 , 3, 557-65	22.2	310
287	Dynamics of protein turnover, a missing dimension in proteomics. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 579-91	7.6	307

286	Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	291
285	From DNA sequence to biological function. <i>Nature</i> , 1996 , 379, 597-600	50.4	270
284	A proposed framework for the description of plant metabolomics experiments and their results. <i>Nature Biotechnology</i> , 2004 , 22, 1601-6	44.5	260
283	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012 , 40, D695-9	20.1	221
282	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003 , 21, 247-54	44.5	220
281	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , 2007 , 6, 4		208
280	Engineering evolution to study speciation in yeasts. <i>Nature</i> , 2003 , 422, 68-72	50.4	198
279	An optimized protocol for metabolome analysis in yeast using direct infusion electrospray mass spectrometry. <i>Phytochemistry</i> , 2003 , 62, 929-37	4	192
278	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006 , 440, 667-70	50.4	189
277	Chromosome evolution in eukaryotes: a multi-kingdom perspective. <i>Trends in Genetics</i> , 2005 , 21, 673-82	8.5	188
276	The next wave in metabolome analysis. <i>Trends in Biotechnology</i> , 2005 , 23, 544-6	15.1	182
275	Dispersed growth of <i>Streptomyces</i> in liquid culture. <i>Applied Microbiology and Biotechnology</i> , 1989 , 31, 272	5.7	179
274	Choose your partners: dimerization in eukaryotic transcription factors. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 220-9	10.3	168
273	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, 2307-12	11.5	160
272	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011 , 43, 656-62	36.3	156
271	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, 2070-3	2.2	155
270	Pharmaceutical drug transport: the issues and the implications that it is essentially carrier-mediated only. <i>Drug Discovery Today</i> , 2011 , 16, 704-14	8.8	145
269	Comparative genome analysis of filamentous fungi reveals gene family expansions associated with fungal pathogenesis. <i>PLoS ONE</i> , 2008 , 3, e2300	3.7	140

268	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. <i>Trends in Biotechnology</i> , 2015 , 33, 237-46	15.1	136
267	All duplicates are not equal: the difference between small-scale and genome duplication. <i>Genome Biology</i> , 2007 , 8, R209	18.3	123
266	A network approach to the systematic analysis of yeast gene function. <i>Trends in Genetics</i> , 1996 , 12, 241-255	28.5	121
265	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, 218-39	8.8	120
264	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		116
263	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	5.6	114
262	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, 2458-67	4.8	111
261	Suitability of replacement markers for functional analysis studies in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1997 , 13, 1563-73	3.4	105
260	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, 3148-53	11.5	103
259	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	11.5	100
258	Exploring redundancy in the yeast genome: an improved strategy for use of the cre-loxP system. <i>Gene</i> , 2000 , 252, 127-35	3.8	100
257	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, 4435-46	3.5	97
256	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013 , 587, 2832-41	3.8	91
255	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, 473-84	3.4	91
254	PomBase 2018: user-driven reimplementations of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019 , 47, D821-D827	20.1	89
253	DNA sequence analysis of ARS elements from chromosome III of <i>Saccharomyces cerevisiae</i> : identification of a new conserved sequence. <i>Nucleic Acids Research</i> , 1986 , 14, 6247-64	20.1	87
252	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, 1067-76	5.7	84
251	Conceptual modelling of genomic information. <i>Bioinformatics</i> , 2000 , 16, 548-57	7.2	83

250	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: a community effort. <i>Fungal Genetics and Biology</i> , 2009 , 46 Suppl 1, S2-13	3.9	82
249	Identification and characterization of high-flux-control genes of yeast through competition analyses in continuous cultures. <i>Nature Genetics</i> , 2008 , 40, 113-7	36.3	82
248	Proteomic response to amino acid starvation in <i>Candida albicans</i> and <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2004 , 4, 2425-36	4.8	82
247	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010 , 4, 145	3.5	81
246	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007 , 25, 1127-33	44.5	81
245	The yeast 2 micron plasmid: strategies for the survival of a selfish DNA. <i>Molecular Genetics and Genomics</i> , 1986 , 205, 417-21		79
244	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010 , 1, 145	17.4	78
243	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, 2737-47	4.8	78
242	Hybridization array technology coupled with chemostat culture: Tools to interrogate gene expression in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2002 , 26, 281-90	4.6	77
241	Implications of the dominant role of transporters in drug uptake by cells. <i>Current Topics in Medicinal Chemistry</i> , 2009 , 9, 163-81	3	76
240	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012 , 30, 1176-8	44.5	75
239	Comparative genome analysis across a kingdom of eukaryotic organisms: specialization and diversification in the fungi. <i>Genome Research</i> , 2007 , 17, 1809-22	9.7	75
238	Convergent evolution of gene networks by single-gene duplications in higher eukaryotes. <i>EMBO Reports</i> , 2004 , 5, 274-9	6.5	75
237	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015 , 43, D656-61	20.1	74
236	Functional genomics: lessons from yeast. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002 , 357, 17-23	5.8	74
235	Isolation of ethanol-tolerant mutants of yeast by continuous selection. <i>European Journal of Applied Microbiology and Biotechnology</i> , 1982 , 16, 119-122		74
234	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	11.5	72
233	Discrimination of modes of action of antifungal substances by use of metabolic footprinting. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 6157-65	4.8	69

232	Stability of a cloned gene in yeast grown in chemostat culture. <i>Molecular Genetics and Genomics</i> , 1983 , 192, 361-5		67
231	The metabolome 18 years on: a concept comes of age. <i>Metabolomics</i> , 2016 , 12, 148	4.7	65
230	Towards a truly integrative biology through the functional genomics of yeast. <i>Current Opinion in Biotechnology</i> , 2001 , 12, 87-91	11.4	63
229	Chromatographic separations as a prelude to two-dimensional electrophoresis in proteomics analysis. <i>Proteomics</i> , 2001 , 1, 42-53	4.8	63
228	Absolute quantification of the glycolytic pathway in yeast: deployment of a complete QconCAT approach. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.007633	7.6	61
227	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. <i>Genome Research</i> , 2007 , 17, 510-9	9.7	61
226	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	4.1	59
225	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010 , 8, 68	7.3	58
224	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, 1681-9	3.4	57
223	Comparative genomic hybridization provides new insights into the molecular taxonomy of the <i>Saccharomyces sensu stricto</i> complex. <i>Genome Research</i> , 2004 , 14, 1043-51	9.7	56
222	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	7.3	54
221	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, 317-29	4.9	54
220	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	3.8	53
219	A physical comparison of chromosome III in six strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1994 , 10, 39-53	3.4	53
218	Glycosylation deficiency phenotypes resulting from depletion of GDP-mannose pyrophosphorylase in two yeast species. <i>Molecular Microbiology</i> , 2000 , 36, 1156-66	4.1	52
217	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, 1591-600	4	52
216	Evaluation of industrial <i>Saccharomyces cerevisiae</i> strains for ethanol production from biomass. <i>Biomass and Bioenergy</i> , 2012 , 45, 230-238	5.3	51
215	Cellular processes and pathways that protect <i>Saccharomyces cerevisiae</i> cells against the plasma membrane-perturbing compound chitosan. <i>Eukaryotic Cell</i> , 2007 , 6, 600-8		51

214	Automated tracking of gene expression in individual cells and cell compartments. <i>Journal of the Royal Society Interface</i> , 2006 , 3, 787-94	4.1	51
213	Stable isotope labelling in vivo as an aid to protein identification in peptide mass fingerprinting. <i>Proteomics</i> , 2002 , 2, 157-63	4.8	51
212	A combination of chemical derivatisation and improved bioinformatic tools optimises protein identification for proteomics. <i>Electrophoresis</i> , 2001 , 22, 552-9	3.6	51
211	A 'hot-spot' for Ty transposition on the left arm of yeast chromosome III. <i>Nucleic Acids Research</i> , 1986 , 14, 3475-85	20.1	51
210	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	2.9	50
209	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, 1740-5	7.8	49
208	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, 2967-71	11.5	48
207	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	18.3	47
206	PEDRo: a database for storing, searching and disseminating experimental proteomics data. <i>BMC Genomics</i> , 2004 , 5, 68	4.5	47
205	Yeast as a touchstone in post-genomic research: strategies for integrative analysis in functional genomics. <i>BMB Reports</i> , 2004 , 37, 93-106	5.5	46
204	Evolutionary systems biology of amino acid biosynthetic cost in yeast. <i>PLoS ONE</i> , 2010 , 5, e11935	3.7	45
203	Using yeast to place human genes in functional categories. <i>Gene</i> , 2003 , 303, 121-9	3.8	45
202	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, 565-9	3.4	45
201	Quantitative analysis of yeast gene function using competition experiments in continuous culture. <i>Yeast</i> , 1998 , 14, 1417-27	3.4	43
200	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	3.9	43
199	Biomass composition: the "elephant in the room" of metabolic modelling. <i>Metabolomics</i> , 2015 , 11, 1690-1701	17.01	42
198	Ethanol production using nuclear petite yeast mutants. <i>Applied Microbiology and Biotechnology</i> , 1998 , 49, 511-6	5.7	42
197	Transcriptome profiling of a <i>Saccharomyces cerevisiae</i> mutant with a constitutively activated Ras/cAMP pathway. <i>Physiological Genomics</i> , 2003 , 16, 107-18	3.6	42

196	esyN: network building, sharing and publishing. <i>PLoS ONE</i> , 2014 , 9, e106035	3.7	41
195	Evaluation and properties of the budding yeast phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.009555	7.6	40
194	Effects of reciprocal chromosomal translocations on the fitness of <i>Saccharomyces cerevisiae</i> . <i>EMBO Reports</i> , 2004 , 5, 392-8	6.5	40
193	Improvement of antibiotic titers from <i>Streptomyces</i> bacteria by interactive continuous selection. <i>Biotechnology and Bioengineering</i> , 1996 , 49, 185-96	4.9	40
192	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. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 9747-9762	5.7	39
191	The genetic control of growth rate: a systems biology study in yeast. <i>BMC Systems Biology</i> , 2012 , 6, 4	3.5	39
190	Production of ethanol from starch by respiration-deficient recombinant <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6443-5	4.8	38
189	Transcript analysis of 1003 novel yeast genes using high-throughput northern hybridizations. <i>EMBO Journal</i> , 2001 , 20, 3177-86	13	38
188	Glutamic protease distribution is limited to filamentous fungi. <i>FEMS Microbiology Letters</i> , 2004 , 239, 95-101	2.9	37
187	An improved tetO promoter replacement system for regulating the expression of yeast genes. <i>Yeast</i> , 2003 , 20, 1255-62	3.4	36
186	Polymorphisms on the right arm of yeast chromosome III associated with Ty transposition and recombination events. <i>Nucleic Acids Research</i> , 1987 , 15, 8963-82	20.1	36
185	FYPO: the fission yeast phenotype ontology. <i>Bioinformatics</i> , 2013 , 29, 1671-8	7.2	35
184	GIMS: an integrated data storage and analysis environment for genomic and functional data. <i>Yeast</i> , 2003 , 20, 1291-306	3.4	35
183	The effect of temperature on the ethanol tolerance of the yeast, <i>Saccharomyces uvarum</i> . <i>Biotechnology Letters</i> , 1982 , 4, 269-273	3	34
182	Yeast as a navigational aid in genome analysis. 1996 Kathleen Barton-Wright Memorial Lecture. <i>Microbiology (United Kingdom)</i> , 1997 , 143 (Pt 5), 1483-1487	2.9	34
181	From gene to screen with yeast. <i>Current Opinion in Genetics and Development</i> , 1997 , 7, 405-9	4.9	33
180	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	3.6	33
179	MeMo: a hybrid SQL/XML approach to metabolomic data management for functional genomics. <i>BMC Bioinformatics</i> , 2006 , 7, 281	3.6	33

178	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	6	33
177	Mcm1p-induced DNA bending regulates the formation of ternary transcription factor complexes. <i>Molecular and Cellular Biology</i> , 2003 , 23, 450-61	4.8	31
176	A model-based analysis of microarray experimental error and normalisation. <i>Nucleic Acids Research</i> , 2003 , 31, e96	20.1	31
175	Cloning and characterisation of the ribosomal RNA genes of the dimorphic yeast, <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1986 , 10, 449-52	2.9	31
174	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. <i>Open Biology</i> , 2019 , 9, 180241	7	30
173	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014 , 30, 1791-2	7.2	30
172	How yeast re-programmes its transcriptional profile in response to different nutrient impulses. <i>BMC Systems Biology</i> , 2011 , 5, 148	3.5	30
171	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, 3948-59	5.9	30
170	Model organism databases: essential resources that need the support of both funders and users. <i>BMC Biology</i> , 2016 , 14, 49	7.3	30
169	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, 139-49		29
168	Automation of DNA Sequencing: A System to Perform the Sanger Dideoxysequencing Reactions. <i>Bio/technology</i> , 1985 , 3, 911-915		29
167	Environmental signals triggering methylenomycin production by <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 1997 , 179, 5511-5	3.5	28
166	Integrative investigation of metabolic and transcriptomic data. <i>BMC Bioinformatics</i> , 2006 , 7, 203	3.6	28
165	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, 320-6	2.8	27
164	Improvement of ethanol production from starch by recombinant yeast through manipulation of environmental factors. <i>Enzyme and Microbial Technology</i> , 2002 , 31, 640-647	3.8	27
163	A laser desorption ionisation mass spectrometry approach for high throughput metabolomics. <i>Metabolomics</i> , 2005 , 1, 243-250	4.7	27
162	The exploitation of selective cleavage of singly protonated peptide ions adjacent to aspartic acid residues using a quadrupole orthogonal time-of-flight mass spectrometer equipped with a matrix-assisted laser desorption/ionization source. <i>International Journal of Mass Spectrometry</i> , 2001 , 210-211, 665-676	1.9	27
161	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. <i>Open Biology</i> , 2013 , 3, 120158	7	26

160	From genomes to systems: the path with yeast. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 477-82	5.8	26
159	Suppression of sorbitol dependence in a strain bearing a mutation in the SRB1/PSA1/VIG9 gene encoding GDP-mannose pyrophosphorylase by PDE2 overexpression suggests a role for the Ras/cAMP signal-transduction pathway in the control of yeast cell-wall biogenesis. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 9), 2133-2146	2.9	26
158	17 Metabolic Control Analysis as a Tool in the Elucidation of the Function of Novel Genes. <i>Methods in Microbiology</i> , 1998 , 297-336	2.8	25
157	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	3.5	25
156	Alzheimer's as a Systems-Level Disease Involving the Interplay of Multiple Cellular Networks. <i>Methods in Molecular Biology</i> , 2016 , 1303, 3-48	1.4	24
155	e-Fungi: a data resource for comparative analysis of fungal genomes. <i>BMC Genomics</i> , 2007 , 8, 426	4.5	24
154	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. <i>BMC Genomics</i> , 2006 , 7, 107	4.5	24
153	Transcript analysis of 250 novel yeast genes from chromosome XIV. <i>Yeast</i> , 1999 , 15, 329-50	3.4	24
152	Characterization of morphological mutants generated spontaneously in glucose-limited, continuous flow cultures of <i>Fusarium graminearum</i> A3/5. <i>Mycological Research</i> , 1992 , 96, 555-562		24
151	Appearance of morphological (colonial) mutants in glucose-limited, continuous flow cultures of <i>Fusarium graminearum</i> A3/5. <i>Mycological Research</i> , 1991 , 95, 1284-1288		24
150	Antiplasmodial and trypanocidal activity of violacein and deoxyviolacein produced from synthetic operons. <i>BMC Biotechnology</i> , 2018 , 18, 22	3.5	23
149	Haploinsufficiency and the sex chromosomes from yeasts to humans. <i>BMC Biology</i> , 2011 , 9, 15	7.3	23
148	JmjN interacts with JmjC to ensure selective proteolysis of Gis1 by the proteasome. <i>Microbiology (United Kingdom)</i> , 2011 , 157, 2694-2701	2.9	23
147	Functional expression of parasite drug targets and their human orthologs in yeast. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1320	4.8	23
146	Nutrient-dependent selection of morphological mutants of <i>Fusarium graminearum</i> A3/5 isolated from long-term continuous flow cultures. <i>Biotechnology and Bioengineering</i> , 1992 , 40, 1181-9	4.9	23
145	Treatment of yeast cells with wall lytic enzymes is not required to prepare chromosomes for pulsed-field gel analysis. <i>Yeast</i> , 1993 , 9, 1053-5	3.4	23
144	Fitting Transporter Activities to Cellular Drug Concentrations and Fluxes: Why the Bumblebee Can Fly. <i>Trends in Pharmacological Sciences</i> , 2015 , 36, 710-723	13.2	22
143	The TRiC/CCT chaperone is implicated in Alzheimer's disease based on patient GWAS and an RNAi screen in Aβ-expressing <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2014 , 9, e102985	3.7	22

142	Pedro: a configurable data entry tool for XML. <i>Bioinformatics</i> , 2004 , 20, 2463-5	7.2	22
141	Combining transcriptome data with genomic and cDNA sequence alignments to make confident functional assignments for <i>Aspergillus nidulans</i> genes. <i>Mycological Research</i> , 2004 , 108, 853-7		22
140	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, 1110-8	5.9	21
139	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, 5809-16	4.8	21
138	Genome-wide analysis of the effects of heat shock on a <i>Saccharomyces cerevisiae</i> mutant with a constitutively activated cAMP-dependent pathway. <i>Comparative and Functional Genomics</i> , 2004 , 5, 419-31		21
137	Bioinformatic assessment of mass spectrometric chemical derivatisation techniques for proteome database searching. <i>Proteomics</i> , 2001 , 1, 1368-77	4.8	20
136	The transcription activity of Gis1 is negatively modulated by proteasome-mediated limited proteolysis. <i>Journal of Biological Chemistry</i> , 2010 , 285, 6465-76	5.4	19
135	Enhancement of Ty transposition at the ADH4 and ADH2 loci in meiotic yeast cells. <i>Molecular Genetics and Genomics</i> , 1997 , 254, 555-61		19
134	Formation of intergeneric hybrids of yeast by protoplast fusion of <i>Yarrowia</i> and <i>Kluyveromyces</i> species. <i>Current Genetics</i> , 1984 , 8, 49-55	2.9	19
133	Yeast-Based High-Throughput Screens to Identify Novel Compounds Active against <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004401	4.8	19
132	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	20.1	18
131	<i>Plasmodium</i> dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. <i>Scientific Reports</i> , 2018 , 8, 1038	4.9	18
130	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . <i>Trends in Biotechnology</i> , 2014 , 32, 396-9	15.1	18
129	The Robot Scientist Adam. <i>Computer</i> , 2009 , 42, 46-54	1.6	18
128	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	4.4	18
127	Effect of dataset selection on the topological interpretation of protein interaction networks. <i>BMC Genomics</i> , 2005 , 6, 131	4.5	18
126	Physical separation and functional interaction of <i>Kluyveromyces lactis</i> and <i>Saccharomyces cerevisiae</i> ARS elements derived from killer plasmid DNA. <i>Yeast</i> , 1986 , 2, 179-91	3.4	18
125	ISPIDER Central: an integrated database web-server for proteomics. <i>Nucleic Acids Research</i> , 2008 , 36, W485-90	20.1	17

124	Phenotypic activation to discover biological pathways and kinase substrates. <i>Cell Cycle</i> , 2006 , 5, 1397-402.	4.7	17
123	Heritable damage to yeast caused by transformation. <i>Nature Biotechnology</i> , 1991 , 9, 179-82	44.5	17
122	Complementation of the <i>Saccharomyces cerevisiae</i> srb1-1 mutation: an autoselection system for stable plasmid maintenance. <i>Current Genetics</i> , 1992 , 21, 339-44	2.9	17
121	Isolation and characterisation of a double-stranded RNA virus-like particle from the yeast <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1983 , 7, 185-90	2.9	17
120	Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. <i>Neurobiology of Aging</i> , 2017 , 57, 104-119	5.6	16
119	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, 1249-60	5.2	16
118	Predicting complex phenotype-genotype interactions to enable yeast engineering: <i>Saccharomyces cerevisiae</i> as a model organism and a cell factory. <i>Biotechnology Journal</i> , 2013 , 8, 1017-34	5.6	16
117	Down-regulation of the expression of PKC1 and SRB1/PSA1/VIG9, two genes involved in cell wall integrity in <i>Saccharomyces cerevisiae</i> , causes flocculation. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 2), 309-316	2.9	16
116	Genetically controlled cell lysis in the yeast <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 1999 , 64, 607-15	4.9	16
115	The regulation of RNA synthesis in yeast IV. Synthesis of double-stranded RNA. <i>Molecular Genetics and Genomics</i> , 1979 , 171, 161-6		16
114	Diffusion-Limited Growth of Microbial Colonies. <i>Scientific Reports</i> , 2018 , 8, 5992	4.9	15
113	Copy-number variation of cancer-gene orthologs is sufficient to induce cancer-like symptoms in <i>Saccharomyces cerevisiae</i> . <i>BMC Biology</i> , 2013 , 11, 24	7.3	15
112	Synergistic effects of TOR and proteasome pathways on the yeast transcriptome and cell growth. <i>Open Biology</i> , 2013 , 3, 120137	7	15
111	Analysis of a continuous-culture technique for the selection of mutants tolerant to extreme environmental stress. <i>Biotechnology and Bioengineering</i> , 1999 , 65, 397-406	4.9	15
110	The subcellular organisation of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , 2019 , 48, 86-95	9.7	15
109	The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1239-1249	3.2	14
108	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, 325-31	3.4	14
107	A critical and integrated view of the yeast interactome. <i>Comparative and Functional Genomics</i> , 2004 , 5, 382-402		14

106	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	17.8	13
105	On the formalization and reuse of scientific research. <i>Journal of the Royal Society Interface</i> , 2011 , 8, 1440-1448	4.8	13
104	SiteSeer: Visualisation and analysis of transcription factor binding sites in nucleotide sequences. <i>Nucleic Acids Research</i> , 2003 , 31, 3572-5	20.1	13
103	Overexpression of a serine alkaline protease gene in <i>Bacillus licheniformis</i> and its impact on the metabolic reaction network. <i>Enzyme and Microbial Technology</i> , 2003 , 32, 706-720	3.8	13
102	pH oscillations and constant low pH delay the appearance of highly branched (colonial) mutants in chemostat cultures of the quorn(R) myco-protein fungus, <i>Fusarium graminearum</i> A3/5. <i>Biotechnology and Bioengineering</i> , 1996 , 51, 61-8	4.9	13
101	DNA sequence analysis of a 35 kb segment from <i>Saccharomyces cerevisiae</i> chromosome VII reveals 19 open reading frames including RAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43. <i>Yeast</i> , 1995 , 11, 1413-9	3.4	13
100	Enhancing the functionality of a microscale bioreactor system as an industrial process development tool for mammalian perfusion culture. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 1315-1325	4.9	12
99	Metabolic modeling to identify engineering targets for <i>Komagataella phaffii</i> : The effect of biomass composition on gene target identification. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 2605-2615	4.9	12
98	1 Introduction to Functional Analysis of the Yeast Genome. <i>Methods in Microbiology</i> , 1998 , 26, 1-13	2.8	12
97	Protein interactions from complexes: a structural perspective. <i>Comparative and Functional Genomics</i> , 2007 , 2007, 49356		12
96	Genome-wide analysis of the context-dependence of regulatory networks. <i>Genome Biology</i> , 2005 , 6, 206	18.3	12
95	Introduction of YACs into intact yeast cells by a procedure which shows low levels of recombination and co-transformation. <i>Nucleic Acids Research</i> , 1994 , 22, 5011-5	20.1	12
94	Enhanced stability of a 2 μ -based recombinant plasmid in diploid yeast. <i>Biotechnology Letters</i> , 1986 , 8, 391-396	3	12
93	Purification and properties of a double-stranded ribonuclease from the yeast <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 1983 , 137, 501-7		12
92	The Yeast GSK-3 Homologue Mck1 Is a Key Controller of Quiescence Entry and Chronological Lifespan. <i>PLoS Genetics</i> , 2015 , 11, e1005282	6	12
91	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	2.5	12
90	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. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 610-621	4.9	12
89	Quantifying two-dimensional filamentous and invasive growth spatial patterns in yeast colonies. <i>PLoS Computational Biology</i> , 2015 , 11, e1004070	5	11

88	Yeast cells with impaired drug resistance accumulate glycerol and glucose. <i>Molecular BioSystems</i> , 2014 , 10, 93-102		11
87	Evolution of <i>Fusarium graminearum</i> A3/5 grown in a series of glucose-limited chemostat cultures at a high dilution rate. <i>Mycological Research</i> , 1995 , 99, 173-178		11
86	Handling variability and incompleteness of biological data by flexible nets: a case study for Wilson disease. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 7	5	10
85	A protocol for the subcellular fractionation of <i>Saccharomyces cerevisiae</i> using nitrogen cavitation and density gradient centrifugation. <i>Yeast</i> , 2014 , 31, 127-35	3.4	10
84	Data capture in bioinformatics: requirements and experiences with Pedro. <i>BMC Bioinformatics</i> , 2008 , 9, 183	3.6	10
83	Functional expression of the yeast Mn-superoxide dismutase gene in <i>Escherichia coli</i> requires deletion of the signal peptide sequence. <i>Gene</i> , 1988 , 73, 121-30	3.8	10
82	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,	6.2	10
81	Yeast systems biology: the challenge of eukaryotic complexity. <i>Methods in Molecular Biology</i> , 2011 , 759, 3-28	1.4	10
80	Quantifying the dominant growth mechanisms of dimorphic yeast using a lattice-based model. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	9
79	Ethanol production and tolerance in grande and petite yeasts. <i>Journal of Chemical Technology and Biotechnology Biotechnology</i> , 2008 , 34, 116-120		9
78	Model-driven user interfaces for bioinformatics data resources: regenerating the wheel as an alternative to reinventing it. <i>BMC Bioinformatics</i> , 2006 , 7, 532	3.6	9
77	Optimal substrate feeding policy for fed-batch cultures of <i>S. cerevisiae</i> expressing bifunctional fusion protein displaying amylolytic activities. <i>Enzyme and Microbial Technology</i> , 2003 , 33, 262-269	3.8	9
76	Characterization of recombinant <i>Saccharomyces cerevisiae</i> manganese-containing superoxide dismutase and its H30A and K170R mutants expressed in <i>Escherichia coli</i> . <i>Biochemistry</i> , 1998 , 37, 11323-31	3.2	9
75	Phenotypic differences between induced and spontaneous 2 μ plasmid-free segregants of <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1987 , 11, 415-418	2.9	9
74	Process development for the continuous production of heterologous proteins by the industrial yeast, <i>Komagataella phaffii</i> . <i>Biotechnology and Bioengineering</i> , 2018 , 115, 2962-2973	4.9	9
73	Evaluation of the ability of commercial wine yeasts to form biofilms (mats) and adhere to plastic: implications for the microbiota of the winery environment. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	8
72	Bacterial Signaling Nucleotides Inhibit Yeast Cell Growth by Impacting Mitochondrial and Other Specifically Eukaryotic Functions. <i>MBio</i> , 2017 , 8,	7.8	8
71	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, 136-43	3.7	8

70	A kingdom-specific protein domain HMM library for improved annotation of fungal genomes. <i>BMC Genomics</i> , 2007 , 8, 97	4.5	8
69	Annotation of unknown yeast ORFs by correlation analysis of microarray data and extensive literature searches. <i>Yeast</i> , 2006 , 23, 553-71	3.4	8
68	A new family of yeast vectors and S288C-derived strains for the systematic analysis of gene function. <i>Yeast</i> , 2001 , 18, 563-75	3.4	8
67	Molecular and Genetic Approaches to Alcohol Biotechnology in Brazil. <i>Critical Reviews in Biotechnology</i> , 1987 , 6, 323-355	9.4	8
66	Reduced ethanol tolerance: One of the pleiotropic effects of the pep4.3 mutation in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology Letters</i> , 1983 , 5, 419-422	3	8
65	Determination of the Global Pattern of Gene Expression in Yeast Cells by Intracellular Levels of Guanine Nucleotides. <i>MBio</i> , 2019 , 10,	7.8	7
64	Make way for robot scientists. <i>Science</i> , 2009 , 325, 945	33.3	7
63	Functional Analysis of six novel ORFs on the left arm of Chromosome XII of <i>Saccharomyces cerevisiae</i> reveals three of them responding to S-starvation. <i>Yeast</i> , 2001 , 18, 325-34	3.4	7
62	Functional analysis of six novel ORFs on the left arm of chromosome XII in <i>Saccharomyces cerevisiae</i> reveals two essential genes, one of which is under cell-cycle control. <i>Yeast</i> , 2000 , 16, 277-88	3.4	7
61	Functional analysis of eight open reading frames on chromosomes XII and XIV of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2000 , 16, 1457-68	3.4	7
60	The maintenance of self-replicating plasmids in <i>Saccharomyces cerevisiae</i> : mathematical modelling, computer simulations and experimental tests. <i>Yeast</i> , 1995 , 11, 641-58	3.4	7
59	An apparatus for the fluorescence scanning of ethidium bromide-stained gels. <i>Analytical Biochemistry</i> , 1977 , 82, 271-7	3.1	7
58	CamOptimus: a tool for exploiting complex adaptive evolution to optimize experiments and processes in biotechnology. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 829-839	2.9	7
57	<i>Saccharomyces cerevisiae</i> adapted to grow in the presence of low-dose rapamycin exhibit altered amino acid metabolism. <i>Cell Communication and Signaling</i> , 2018 , 16, 85	7.5	7
56	The neighborhood of the Spike gene is a hotspot for modular intertypic homologous and non-homologous recombination in Coronavirus genomes. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	7
55	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, 1760-74		6
54	Yeast Systems Biology 2013 , 343-365		6
53	Protein production in <i>Saccharomyces cerevisiae</i> for systems biology studies. <i>Methods in Enzymology</i> , 2011 , 500, 197-212	1.7	6

52	A metabolomic and multivariate statistical process to assess the effects of genotoxins in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2009 , 5, 1913-24		6
51	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, 661-72	3.4	6
50	Studies on plasmid stability, cell metabolism and superoxide dismutase production by P _{gk} - strains of <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 1992 , 37, 615-20	5.7	6
49	Classical Yeast Biotechnology 1991 , 213-248		6
48	A heuristic approach to handling missing data in biologics manufacturing databases. <i>Bioprocess and Biosystems Engineering</i> , 2019 , 42, 657-663	3.7	6
47	CLUSTERnGO: a user-defined modelling platform for two-stage clustering of time-series data. <i>Bioinformatics</i> , 2016 , 32, 388-97	7.2	5
46	Selection of microbial mutants tolerant to extreme environmental stress using continuous culture-control design. <i>Biotechnology Progress</i> , 1999 , 15, 1115-24	2.8	5
45	Cell physiology and antibiotic production of <i>Streptomyces coelicolor</i> grown on solid medium. <i>Biotechnology Letters</i> , 1994 , 16, 1015-1020	3	5
44	A microculture hybridization technique for the detection of specific DNA sequences in filamentous fungi. <i>Experimental Mycology</i> , 1987 , 11, 70-73		5
43	A downstream activator sequence regulates the expression of the yeast transposon. <i>Current Genetics</i> , 1988 , 13, 357-62	2.9	5
42	Mapping the <i>Saccharomyces cerevisiae</i> Spatial Proteome with High Resolution Using hyperLOPIT. <i>Methods in Molecular Biology</i> , 2019 , 2049, 165-190	1.4	5
41	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,	6.2	5
40	High-energy guanine nucleotides as a signal capable of linking growth to cellular energy status via the control of gene transcription. <i>Current Genetics</i> , 2019 , 65, 893-897	2.9	4
39	Metaheuristic approaches in biopharmaceutical process development data analysis. <i>Bioprocess and Biosystems Engineering</i> , 2019 , 42, 1399-1408	3.7	4
38	Control analysis of the eukaryotic cell cycle using gene copy-number series in yeast tetraploids. <i>BMC Genomics</i> , 2013 , 14, 744	4.5	4
37	The yin and yang of yeast: biodiversity research and systems biology as complementary forces driving innovation in biotechnology. <i>Biotechnology Letters</i> , 2011 , 33, 477-87	3	4
36	Information management for high content live cell imaging. <i>BMC Bioinformatics</i> , 2009 , 10, 226	3.6	4
35	Functional Genomics: all the king's horses and all the king's men can put Humpty together again. <i>Molecular Cell</i> , 2003 , 12, 1343-4	17.6	4

34	Sequence search algorithms for single pass sequence identification: does one size fit all?. <i>Comparative and Functional Genomics</i> , 2001 , 2, 4-9		4
33	From DNA sequence to biological function: the new "Voyage of the Beagle". <i>Biochemical Society Transactions</i> , 1996 , 24, 291-2	5.1	4
32	Modeling, analyzing and controlling hybrid systems by Guarded Flexible Nets. <i>Nonlinear Analysis: Hybrid Systems</i> , 2019 , 32, 131-146	4.5	4
31	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	3
30	21 Metabolic Control in the Eukaryotic Cell, a Systems Biology Perspective. <i>Methods in Microbiology</i> , 2007 , 527-549	2.8	3
29	Tools for the study of genome rearrangements in laboratory and industrial yeast strains. <i>Yeast</i> , 2002 , 19, 441-8	3.4	3
28	Sequence analysis of a 10 kb fragment of yeast chromosome XI identifies the SMY1 locus and reveals sequences related to a pre-mRNA splicing factor and vacuolar ATPase subunit C plus a number of unidentified open reading frames. <i>Yeast</i> , 1994 , 10, 247-55	3.4	3
27	Sequence analysis of a 3.5 Kb EcoRI fragment from the left arm of <i>Saccharomyces cerevisiae</i> chromosome XI reveals the location of the MBR1 gene and a sequence related to a GTPase-activating protein. <i>Yeast</i> , 1994 , 10, 257-64	3.4	3
26	Data intelligence for process performance prediction in biologics manufacturing. <i>Computers and Chemical Engineering</i> , 2021 , 146, 107226	4	3
25	The Challenges of Interpreting Phosphoproteomics Data: A Critical View Through the Bioinformatics Lens. <i>Lecture Notes in Computer Science</i> , 2016 , 196-204	0.9	3
24	. <i>IEEE Transactions on Automatic Control</i> , 2020 , 65, 2510-2525	5.9	3
23	TAMMiCol: Tool for analysis of the morphology of microbial colonies. <i>PLoS Computational Biology</i> , 2018 , 14, e1006629	5	3
22	Yeast Double Transporter Gene Deletion Library for Identification of Xenobiotic Carriers in Low or High Throughput.. <i>MBio</i> , 2021 , 12, e0322121	7.8	3
21	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. <i>Nature Precedings</i> , 2008 ,		2
20	9 Transcript Analysis: A Microarray Approach. <i>Methods in Microbiology</i> , 2007 , 189-703	2.8	2
19	Replication and recombination in gene establishment in non- <i>Saccharomyces</i> yeasts. <i>Journal of Basic Microbiology</i> , 1988 , 28, 197-208	2.7	2
18	An <i>E. coli</i> -yeast shuttle cosmid with positive selection for inserted fragments. <i>Current Genetics</i> , 1985 , 10, 29-33	2.9	2
17	A unifying modelling formalism for the integration of stoichiometric and kinetic models. <i>Journal of the Royal Society Interface</i> , 2020 , 17, 20200341	4.1	2

16	Response to 'The Need for Speed', by Matsson et al. <i>Trends in Pharmacological Sciences</i> , 2016 , 37, 245-246, 2	4.2	2
15	A Tool for Multiple Targeted Genome Deletions that Is Precise, Scar-Free, and Suitable for Automation. <i>PLoS ONE</i> , 2015 , 10, e0142494	3.7	1
14	The role of proteasome-mediated proteolysis in modulating potentially harmful transcription factor activity in <i>Saccharomyces cerevisiae</i> . <i>Bioinformatics</i> , 2011 , 27, i283-7	7.2	1
13	1 Introduction to Functional Analysis in Yeast. <i>Methods in Microbiology</i> , 2007 , 36, 1-21	2.8	1
12	A Methodology for Comparative Functional Genomics. <i>Journal of Integrative Bioinformatics</i> , 2007 , 4, 112-122	3.2	1
11	Towards Integrative Functional Genomics Using Yeast as a Reference Model 2005 , 9-29		1
10	A Protocol to Map the Spatial Proteome Using HyperLOPIT in. <i>Bio-protocol</i> , 2019 , 9, e3303	0.9	1
9	fnyzer: A Python Package for the Analysis of Flexible Nets. <i>Lecture Notes in Computer Science</i> , 2020 , 349-355	3.5	1
8	Yeast Systems Biology: The Continuing Challenge of Eukaryotic Complexity. <i>Methods in Molecular Biology</i> , 2019 , 2049, 3-13	1.4	1
7	1 Yeast as a Model for Systems Biology Studies on Complex Diseases 2014 , 3-30		1
6	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	1
5	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	4.4	
4	Transcriptional and metabolic response of <i>Saccharomyces cerevisiae</i> to a nutritional perturbation when under stress. <i>Journal of Biotechnology</i> , 2007 , 131, S14-S15	3.7	
3	Current awarenessRecent symposia and seminars. <i>Luminescence</i> , 1992 , 7, 215-222		
2	Storing, Searching, and Disseminating Experimental Proteomics Data 2007 , 472-483		
1	Combination of Genome-Scale Models and Bioreactor Dynamics to Optimize the Production of Commodity Chemicals.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 855735	5.6	