Stephen G Oliver

List of Publications by Year in Descending Order

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 Remarkable Evolutionary Plasticity of Coronaviruses by Mutation and Recombination: Insights for the COVID-19 Pandemic and the Future Evolutionary Paths of SARS-CoV-2.. *Viruses*, **2022**, 14,	6.2	10
302	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.. *Viruses*, **2022**, 14,	6.2	5
301	Combination of Genome-Scale Models and Bioreactor Dynamics to Optimize the Production of Commodity Chemicals.. *Frontiers in Molecular Biosciences*, **2022**, 9, 855735	5.6	
300	The Gene Ontology resource: enriching a GOld mine. *Nucleic Acids Research*, **2021**, 49, D325-D334	20.1	494
299	Data intelligence for process performance prediction in biologics manufacturing. *Computers and Chemical Engineering*, **2021**, 146, 107226	4	3
298	The neighborhood of the Spike gene is a hotspot for modular intertypic homologous and non-homologous recombination in Coronavirus genomes. *Molecular Biology and Evolution*, **2021**,	8.3	7
297	Yeast Double Transporter Gene Deletion Library for Identification of Xenobiotic Carriers in Low or High Throughput.. *MBio*, **2021**, 12, e0322121	7.8	3
296	fnyzer: A Python Package for the Analysis of Flexible Nets. *Lecture Notes in Computer Science*, **2020**, 349-355	3.5	1
295	A unifying modelling formalism for the integration of stoichiometric and kinetic models. *Journal of the Royal Society Interface*, **2020**, 17, 20200341	4.1	2
294	Comparative Analysis of the Core Proteomes among the Pseudomonas Major Evolutionary Groups Reveals Species-Specific Adaptations for Pseudomonas aeruginosa and Pseudomonas chlororaphis. *Diversity*, **2020**, 12, 289	2.5	12
293	. *IEEE Transactions on Automatic Control*, **2020**, 65, 2510-2525	5.9	3
292	Metabolic response to Parkinson's disease recapitulated by the haploinsufficient diploid yeast cells hemizygous for the adrenodoxin reductase gene. *Molecular Omics*, **2019**, 15, 340-347	4.4	
291	Flexible Nets: a modeling formalism for dynamic systems with uncertain parameters. *Discrete Event Dynamic Systems: Theory and Applications*, **2019**, 29, 367-392	1	3
290	Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. *Nucleic Acids Research*, **2019**, 47, 9998-10009	20.1	18
289	Determination of the Global Pattern of Gene Expression in Yeast Cells by Intracellular Levels of Guanine Nucleotides. *MBio*, **2019**, 10,	7.8	7
288	PomBase 2018: user-driven reimplementation of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. *Nucleic Acids Research*, **2019**, 47, D821-D827	20.1	89
287	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	2.9	4

286	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. *Open Biology*, **2019**, 9, 180241	7	30
285	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	4.9	12
284	Metaheuristic approaches in biopharmaceutical process development data analysis. *Bioprocess and Biosystems Engineering*, **2019**, 42, 1399-1408	3.7	4
283	A Protocol to Map the Spatial Proteome Using HyperLOPIT in. *Bio-protocol*, **2019**, 9, e3303	0.9	1
282	Yeast Systems Biology: The Continuing Challenge of Eukaryotic Complexity. *Methods in Molecular Biology*, **2019**, 2049, 3-13	1.4	1
281	Mapping the Saccharomyces cerevisiae Spatial Proteome with High Resolution Using hyperLOPIT. *Methods in Molecular Biology*, **2019**, 2049, 165-190	1.4	5
280	Transcriptional regulation of the genes involved in protein metabolism and processing in Saccharomyces cerevisiae. *FEMS Yeast Research*, **2019**, 19,	3.1	1
279	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	4.9	12
278	The Gene Ontology Resource: 20 years and still GOing strong. *Nucleic Acids Research*, **2019**, 47, D330-D338	19.1	1962
277	A heuristic approach to handling missing data in biologics manufacturing databases. *Bioprocess and Biosystems Engineering*, **2019**, 42, 657-663	3.7	6
276	Modeling, analyzing and controlling hybrid systems by Guarded Flexible Nets. *Nonlinear Analysis: Hybrid Systems*, **2019**, 32, 131-146	4.5	4
275	The subcellular organisation of Saccharomyces cerevisiae. *Current Opinion in Chemical Biology*, **2019**, 48, 86-95	9.7	15
274	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,	4.3	8
273	Handling variability and incompleteness of biological data by flexible nets: a case study for Wilson disease. *Npj Systems Biology and Applications*, **2018**, 4, 7	5	10
272	Plasmodium dihydrofolate reductase is a second enzyme target for the antimalarial action of triclosan. *Scientific Reports*, **2018**, 8, 1038	4.9	18
271	Diffusion-Limited Growth of Microbial Colonies. *Scientific Reports*, **2018**, 8, 5992	4.9	15
270	Antiplasmodial and trypanocidal activity of violacein and deoxyviolacein produced from synthetic operons. *BMC Biotechnology*, **2018**, 18, 22	3.5	23
269	TAMMiCol: Tool for analysis of the morphology of microbial colonies. *PLoS Computational Biology*, **2018**, 14, e1006629	5	3

268   Saccharomyces cerevisiae adapted to grow in the presence of low-dose rapamycin exhibit altered amino acid metabolism. *Cell Communication and Signaling*, **2018**, 16, 85   7.5   7

267   Process development for the continuous production of heterologous proteins by the industrial yeast, Komagataella phaffii. *Biotechnology and Bioengineering*, **2018**, 115, 2962-2973   4.9   9

266   Expansion of the Gene Ontology knowledgebase and resources. *Nucleic Acids Research*, **2017**, 45, D331-D338   23.3   1258

265   The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. *G3: Genes, Genomes, Genetics*, **2017**, 7, 1239-1249   3.2   14

264   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   11.5   72

263   Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. *Neurobiology of Aging*, **2017**, 57, 104-119   5.6   16

262   Quantifying the dominant growth mechanisms of dimorphic yeast using a lattice-based model. *Journal of the Royal Society Interface*, **2017**, 14,   4.1   9

261   Metabolic modeling to identify engineering targets for Komagataella phaffii: The effect of biomass composition on gene target identification. *Biotechnology and Bioengineering*, **2017**, 114, 2605-2615   4.9   12

260   Bacterial Signaling Nucleotides Inhibit Yeast Cell Growth by Impacting Mitochondrial and Other Specifically Eukaryotic Functions. *MBio*, **2017**, 8,   7.8   8

259   Estimating the total number of phosphoproteins and phosphorylation sites in eukaryotic proteomes. *GigaScience*, **2017**, 6, 1-11   7.6   291

258   CamOptimus: a tool for exploiting complex adaptive evolution to optimize experiments and processes in biotechnology. *Microbiology (United Kingdom)*, **2017**, 163, 829-839   2.9   7

257   Alzheimer's as a Systems-Level Disease Involving the Interplay of Multiple Cellular Networks. *Methods in Molecular Biology*, **2016**, 1303, 3-48   1.4   24

256   CLUSTERnGO: a user-defined modelling platform for two-stage clustering of time-series data. *Bioinformatics*, **2016**, 32, 388-97   7.2   5

255   Chronological Lifespan in Yeast Is Dependent on the Accumulation of Storage Carbohydrates Mediated by Yak1, Mck1 and Rim15 Kinases. *PLoS Genetics*, **2016**, 12, e1006458   6   33

254   Model organism databases: essential resources that need the support of both funders and users. *BMC Biology*, **2016**, 14, 49   7.3   30

253   Yeast-Based High-Throughput Screens to Identify Novel Compounds Active against Brugia malayi. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004401   4.8   19

252   Response to 'The Need for Speed', by Matsson et al. *Trends in Pharmacological Sciences*, **2016**, 37, 245-246   13.2   2

251   The metabolome 18 years on: a concept comes of age. *Metabolomics*, **2016**, 12, 148   4.7   65

250   The Challenges of Interpreting Phosphoproteomics Data: A Critical View Through the Bioinformatics Lens. *Lecture Notes in Computer Science*, **2016**, 196-204   0.9   3

249   Biomass composition: the "elephant in the room" of metabolic modelling. *Metabolomics*, **2015**, 11, 1690-1701   4.7   42

248   Identification and deconvolution of cross-resistance signals from antimalarial compounds using multidrug-resistant Plasmodium falciparum strains. *Antimicrobial Agents and Chemotherapy*, **2015**, 59, 1110-8   5.9   21

247   Quantifying two-dimensional filamentous and invasive growth spatial patterns in yeast colonies. *PLoS Computational Biology*, **2015**, 11, e1004070   5   11

246   PomBase 2015: updates to the fission yeast database. *Nucleic Acids Research*, **2015**, 43, D656-61   20.1   74

245   Cheaper faster drug development validated by the repositioning of drugs against neglected tropical diseases. *Journal of the Royal Society Interface*, **2015**, 12, 20141289   4.1   59

244   Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. *Trends in Biotechnology*, **2015**, 33, 237-46   15.1   136

243   A Tool for Multiple Targeted Genome Deletions that Is Precise, Scar-Free, and Suitable for Automation. *PLoS ONE*, **2015**, 10, e0142494   3.7   1

242   Fitting Transporter Activities to Cellular Drug Concentrations and Fluxes: Why the Bumblebee Can Fly. *Trends in Pharmacological Sciences*, **2015**, 36, 710-723   13.2   22

241   The Yeast GSK-3 Homologue Mck1 Is a Key Controller of Quiescence Entry and Chronological Lifespan. *PLoS Genetics*, **2015**, 11, e1005282   6   12

240   A protocol for the subcellular fractionation of Saccharomyces cerevisiae using nitrogen cavitation and density gradient centrifugation. *Yeast*, **2014**, 31, 127-35   3.4   10

239   Yeast cells with impaired drug resistance accumulate glycerol and glucose. *Molecular BioSystems*, **2014**, 10, 93-102   11

238   Improving functional annotation for industrial microbes: a case study with Pichia pastoris. *Trends in Biotechnology*, **2014**, 32, 396-9   15.1   18

237   The TRiC/CCT chaperone is implicated in Alzheimer's disease based on patient GWAS and an RNAi screen in Aβ-expressing Caenorhabditis elegans. *PLoS ONE*, **2014**, 9, e102985   3.7   22

236   How drugs get into cells: tested and testable predictions to help discriminate between transporter-mediated uptake and lipoidal bilayer diffusion. *Frontiers in Pharmacology*, **2014**, 5, 231   5.6   114

235   Canto: an online tool for community literature curation. *Bioinformatics*, **2014**, 30, 1791-2   7.2   30

234   esyN: network building, sharing and publishing. *PLoS ONE*, **2014**, 9, e106035   3.7   41

233   1 Yeast as a Model for Systems Biology Studies on Complex Diseases **2014**, 3-30   1

232	Investigating the physiological response of Pichia (Komagataella) pastoris GS115 to the heterologous expression of misfolded proteins using chemostat cultures. *Applied Microbiology and Biotechnology*, **2013**, 97, 9747-9762	5.7	39
231	Predicting complex phenotype-genotype interactions to enable yeast engineering: Saccharomyces cerevisiae as a model organism and a cell factory. *Biotechnology Journal*, **2013**, 8, 1017-34	5.6	16
230	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, 218-39	8.8	120
229	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. *FEBS Letters*, **2013**, 587, 2832-41	3.8	91
228	Copy-number variation of cancer-gene orthologs is sufficient to induce cancer-like symptoms in Saccharomyces cerevisiae. *BMC Biology*, **2013**, 11, 24	7.3	15
227	Yeast Systems Biology **2013**, 343-365		6
226	FYPO: the fission yeast phenotype ontology. *Bioinformatics*, **2013**, 29, 1671-8	7.2	35
225	Control analysis of the eukaryotic cell cycle using gene copy-number series in yeast tetraploids. *BMC Genomics*, **2013**, 14, 744	4.5	4
224	Synergistic effects of TOR and proteasome pathways on the yeast transcriptome and cell growth. *Open Biology*, **2013**, 3, 120137	7	15
223	Yeast-based automated high-throughput screens to identify anti-parasitic lead compounds. *Open Biology*, **2013**, 3, 120158	7	26
222	Genome-wide analysis of longevity in nutrient-deprived Saccharomyces cerevisiae reveals importance of recycling in maintaining cell viability. *Environmental Microbiology*, **2012**, 14, 1249-60	5.2	16
221	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. *Nature Biotechnology*, **2012**, 30, 1176-8	44.5	75
220	Evaluation of industrial Saccharomyces cerevisiae strains for ethanol production from biomass. *Biomass and Bioenergy*, **2012**, 45, 230-238	5.3	51
219	The genetic control of growth rate: a systems biology study in yeast. *BMC Systems Biology*, **2012**, 6, 4	3.5	39
218	Short- and long-term dynamic responses of the metabolic network and gene expression in yeast to a transient change in the nutrient environment. *Molecular BioSystems*, **2012**, 8, 1760-74		6
217	Evaluation and properties of the budding yeast phosphoproteome. *Molecular and Cellular Proteomics*, **2012**, 11, M111.009555	7.6	40
216	PomBase: a comprehensive online resource for fission yeast. *Nucleic Acids Research*, **2012**, 40, D695-9	20.1	221
215	Protein production in Saccharomyces cerevisiae for systems biology studies. *Methods in Enzymology*, **2011**, 500, 197-212	1.7	6

214	An integrated approach to characterize genetic interaction networks in yeast metabolism. *Nature Genetics*, **2011**, 43, 656-62	36.3	156
213	Haploinsufficiency and the sex chromosomes from yeasts to humans. *BMC Biology*, **2011**, 9, 15	7.3	23
212	Genome-wide assessment of the carriers involved in the cellular uptake of drugs: a model system in yeast. *BMC Biology*, **2011**, 9, 70	7.3	54
211	Pharmaceutical drug transport: the issues and the implications that it is essentially carrier-mediated only. *Drug Discovery Today*, **2011**, 16, 704-14	8.8	145
210	The yin and yang of yeast: biodiversity research and systems biology as complementary forces driving innovation in biotechnology. *Biotechnology Letters*, **2011**, 33, 477-87	3	4
209	How yeast re-programmes its transcriptional profile in response to different nutrient impulses. *BMC Systems Biology*, **2011**, 5, 148	3.5	30
208	Phenomic and transcriptomic analyses reveal that autophagy plays a major role in desiccation tolerance in Saccharomyces cerevisiae. *Molecular BioSystems*, **2011**, 7, 139-49		29
207	On the formalization and reuse of scientific research. *Journal of the Royal Society Interface*, **2011**, 8, 1440-8		13
206	Absolute quantification of the glycolytic pathway in yeast: deployment of a complete QconCAT approach. *Molecular and Cellular Proteomics*, **2011**, 10, M111.007633	7.6	61
205	The role of proteosome-mediated proteolysis in modulating potentially harmful transcription factor activity in Saccharomyces cerevisiae. *Bioinformatics*, **2011**, 27, i283-7	7.2	1
204	JmjN interacts with JmjC to ensure selective proteolysis of Gis1 by the proteasome. *Microbiology (United Kingdom)*, **2011**, 157, 2694-2701	2.9	23
203	Genome-wide analysis of yeast stress survival and tolerance acquisition to analyze the central trade-off between growth rate and cellular robustness. *Molecular Biology of the Cell*, **2011**, 22, 4435-46	3.5	97
202	Functional expression of parasite drug targets and their human orthologs in yeast. *PLoS Neglected Tropical Diseases*, **2011**, 5, e1320	4.8	23
201	Yeast systems biology: the challenge of eukaryotic complexity. *Methods in Molecular Biology*, **2011**, 759, 3-28	1.4	10
200	Evolutionary systems biology of amino acid biosynthetic cost in yeast. *PLoS ONE*, **2010**, 5, e11935	3.7	45
199	Posttranslational regulation impacts the fate of duplicated genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 2967-71	11.5	48
198	The transcription activity of Gis1 is negatively modulated by proteasome-mediated limited proteolysis. *Journal of Biological Chemistry*, **2010**, 285, 6465-76	5.4	19
197	Further developments towards a genome-scale metabolic model of yeast. *BMC Systems Biology*, **2010**, 4, 145	3.5	81

196	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. *Nature Communications*, **2010**, 1, 145	17.4	78
195	Metabolic flux analysis for recombinant protein production by Pichia pastoris using dual carbon sources: Effects of methanol feeding rate. *Biotechnology and Bioengineering*, **2010**, 105, 317-29	4.9	54
194	Conditional cell-wall mutants of Saccharomyces cerevisiae as delivery vehicles for therapeutic agents in vivo to the GI tract. *Journal of Biotechnology*, **2010**, 147, 136-43	3.7	8
193	Nutrient control of eukaryote cell growth: a systems biology study in yeast. *BMC Biology*, **2010**, 8, 68	7.3	58
192	Make way for robot scientists. *Science*, **2009**, 325, 945	33.3	7
191	Gis1 is required for transcriptional reprogramming of carbon metabolism and the stress response during transition into stationary phase in yeast. *Microbiology (United Kingdom)*, **2009**, 155, 1690-1698	2.9	50
190	Information management for high content live cell imaging. *BMC Bioinformatics*, **2009**, 10, 226	3.6	4
189	The Robot Scientist Adam. *Computer*, **2009**, 42, 46-54	1.6	18
188	Global gene expression in recombinant and non-recombinant yeast Saccharomyces cerevisiae in three different metabolic states. *Biotechnology Advances*, **2009**, 27, 1092-1117	17.8	13
187	Fed-batch methanol feeding strategy for recombinant protein production by Pichia pastoris in the presence of co-substrate sorbitol. *Yeast*, **2009**, 26, 473-84	3.4	91
186	A structured kinetic model for recombinant protein production by Mut+ strain of Pichia pastoris. *Chemical Engineering Science*, **2009**, 64, 5028-5035	4.4	18
185	The 2008 update of the Aspergillus nidulans genome annotation: a community effort. *Fungal Genetics and Biology*, **2009**, 46 Suppl 1, S2-13	3.9	82
184	The automation of science. *Science*, **2009**, 324, 85-9	33.3	324
183	A metabolomic and multivariate statistical process to assess the effects of genotoxins in Saccharomyces cerevisiae. *Molecular BioSystems*, **2009**, 5, 1913-24		6
182	Implications of the dominant role of transporters in drug uptake by cells. *Current Topics in Medicinal Chemistry*, **2009**, 9, 163-81	3	76
181	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology*, **2008**, 26, 1155-60	44.5	471
180	Identification and characterization of high-flux-control genes of yeast through competition analyses in continuous cultures. *Nature Genetics*, **2008**, 40, 113-7	36.3	82
179	Data capture in bioinformatics: requirements and experiences with Pedro. *BMC Bioinformatics*, **2008**, 9, 183	3.6	10

178	Performing statistical analyses on quantitative data in Taverna workflows: an example using R and maxdBrowse to identify differentially-expressed genes from microarray data. *BMC Bioinformatics*, **2008**, 9, 334	3.6	33
177	Choose your partners: dimerization in eukaryotic transcription factors. *Trends in Biochemical Sciences*, **2008**, 33, 220-9	10.3	168
176	ISPIDER Central: an integrated database web-server for proteomics. *Nucleic Acids Research*, **2008**, 36, W485-90	20.1	17
175	Integration of metabolic modeling and phenotypic data in evaluation and improvement of ethanol production using respiration-deficient mutants of Saccharomyces cerevisiae. *Applied and Environmental Microbiology*, **2008**, 74, 5809-16	4.8	21
174	Ethanol production and tolerance in grande and petite yeasts. *Journal of Chemical Technology and Biotechnology Biotechnology*, **2008**, 34, 116-120		9
173	Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome. *Nature Precedings*, **2008**,		2
172	Exometabolic and transcriptional response in relation to phenotype and gene copy number in respiration-related deletion mutants of S. cerevisiae. *Yeast*, **2008**, 25, 661-72	3.4	6
171	Comparative genome analysis of filamentous fungi reveals gene family expansions associated with fungal pathogenesis. *PLoS ONE*, **2008**, 3, e2300	3.7	140
170	Growth control of the eukaryote cell: a systems biology study in yeast. *Journal of Biology*, **2007**, 6, 4		208
169	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. *Nature Biotechnology*, **2007**, 25, 221-31	44.5	889
168	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. *Nature Biotechnology*, **2007**, 25, 1127-33	44.5	81
167	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, 320-6	2.8	27
166	A protein interaction atlas for the nuclear receptors: properties and quality of a hub-based dimerisation network. *BMC Systems Biology*, **2007**, 1, 34	3.5	25
165	e-Fungi: a data resource for comparative analysis of fungal genomes. *BMC Genomics*, **2007**, 8, 426	4.5	24
164	A kingdom-specific protein domain HMM library for improved annotation of fungal genomes. *BMC Genomics*, **2007**, 8, 97	4.5	8
163	9 Transcript Analysis: A Microarray Approach. *Methods in Microbiology*, **2007**, 189-703	2.8	2
162	Global phenotype screening and transcript analysis outlines the inhibitory mode(s) of action of two amphibian-derived, alpha-helical, cationic peptides on Saccharomyces cerevisiae. *Antimicrobial Agents and Chemotherapy*, **2007**, 51, 3948-59	5.9	30
161	Plasticity of genetic interactions in metabolic networks of yeast. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 2307-12	11.5	160

160	Genotypic and physiological characterization of Saccharomyces boulardii, the probiotic strain of Saccharomyces cerevisiae. *Applied and Environmental Microbiology*, **2007**, 73, 2458-67	4.8	111
159	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. *Genome Research*, **2007**, 17, 510-9	9.7	61
158	Comparative genome analysis across a kingdom of eukaryotic organisms: specialization and diversification in the fungi. *Genome Research*, **2007**, 17, 1809-22	9.7	75
157	Cellular processes and pathways that protect Saccharomyces cerevisiae cells against the plasma membrane-perturbing compound chitosan. *Eukaryotic Cell*, **2007**, 6, 600-8		51
156	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	11.5	100
155	21 Metabolic Control in the Eukaryotic Cell, a Systems Biology Perspective. *Methods in Microbiology*, **2007**, 527-549	2.8	3
154	1 Introduction to Functional Analysis in Yeast. *Methods in Microbiology*, **2007**, 36, 1-21	2.8	1
153	Protein interactions from complexes: a structural perspective. *Comparative and Functional Genomics*, **2007**, 2007, 49356		12
152	A Methodology for Comparative Functional Genomics. *Journal of Integrative Bioinformatics*, **2007**, 4, 112-122	3.1	1
151	Transcriptional and metabolic response of Saccharomyces cerevisiae to a nutritional perturbation when under stress. *Journal of Biotechnology*, **2007**, 131, S14-S15	3.7	
150	Application of the comprehensive set of heterozygous yeast deletion mutants to elucidate the molecular basis of cellular chromium toxicity. *Genome Biology*, **2007**, 8, R268	18.3	47
149	All duplicates are not equal: the difference between small-scale and genome duplication. *Genome Biology*, **2007**, 8, R209	18.3	123
148	Storing, Searching, and Disseminating Experimental Proteomics Data **2007**, 472-483		
147	Integrative investigation of metabolic and transcriptomic data. *BMC Bioinformatics*, **2006**, 7, 203	3.6	28
146	MeMo: a hybrid SQL/XML approach to metabolomic data management for functional genomics. *BMC Bioinformatics*, **2006**, 7, 281	3.6	33
145	Model-driven user interfaces for bioinformatics data resources: regenerating the wheel as an alternative to reinventing it. *BMC Bioinformatics*, **2006**, 7, 532	3.6	9
144	Reduction/oxidation-phosphorylation control of DNA binding in the bZIP dimerization network. *BMC Genomics*, **2006**, 7, 107	4.5	24
143	Phenotypic activation to discover biological pathways and kinase substrates. *Cell Cycle*, **2006**, 5, 1397-402	4.7	17

142	From genomes to systems: the path with yeast. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2006**, 361, 477-82	5.8	26
141	Automated tracking of gene expression in individual cells and cell compartments. *Journal of the Royal Society Interface*, **2006**, 3, 787-94	4.1	51
140	Mapping pathways and phenotypes by systematic gene overexpression. *Molecular Cell*, **2006**, 21, 319-30	17.6	502
139	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. *Yeast*, **2006**, 23, 325-31	3.4	14
138	Annotation of unknown yeast ORFs by correlation analysis of microarray data and extensive literature searches. *Yeast*, **2006**, 23, 553-71	3.4	8
137	Chance and necessity in the evolution of minimal metabolic networks. *Nature*, **2006**, 440, 667-70	50.4	189
136	Application of TOF-SIMS with chemometrics to discriminate between four different yeast strains from the species Candida glabrata and Saccharomyces cerevisiae. *Analytical Chemistry*, **2005**, 77, 1740-5	7.8	49
135	Genome-wide analysis of the context-dependence of regulatory networks. *Genome Biology*, **2005**, 6, 206	18.3	12
134	Metabolic footprinting and systems biology: the medium is the message. *Nature Reviews Microbiology*, **2005**, 3, 557-65	22.2	310
133	The next wave in metabolome analysis. *Trends in Biotechnology*, **2005**, 23, 544-6	15.1	182
132	Chromosome evolution in eukaryotes: a multi-kingdom perspective. *Trends in Genetics*, **2005**, 21, 673-82	8.5	188
131	Effect of dataset selection on the topological interpretation of protein interaction networks. *BMC Genomics*, **2005**, 6, 131	4.5	18
130	A laser desorption ionisation mass spectrometry approach for high throughput metabolomics. *Metabolomics*, **2005**, 1, 243-250	4.7	27
129	Doxycycline, the drug used to control the tet-regulatable promoter system, has no effect on global gene expression in Saccharomyces cerevisiae. *Yeast*, **2005**, 22, 565-9	3.4	45
128	Towards Integrative Functional Genomics Using Yeast as a Reference Model **2005**, 9-29		1
127	Transcriptome analysis of recombinant protein secretion by Aspergillus nidulans and the unfolded-protein response in vivo. *Applied and Environmental Microbiology*, **2005**, 71, 2737-47	4.8	78
126	Production of ethanol from starch by respiration-deficient recombinant Saccharomyces cerevisiae. *Applied and Environmental Microbiology*, **2005**, 71, 6443-5	4.8	38
125	Pedro: a configurable data entry tool for XML. *Bioinformatics*, **2004**, 20, 2463-5	7.2	22

124	Comparative genomic hybridization provides new insights into the molecular taxonomy of the Saccharomyces sensu stricto complex. *Genome Research*, **2004**, 14, 1043-51	9.7	56
123	Global analysis of nutrient control of gene expression in Saccharomyces cerevisiae during growth and starvation. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 3148-53	11.5	103
122	A common open representation of mass spectrometry data and its application to proteomics research. *Nature Biotechnology*, **2004**, 22, 1459-66	44.5	632
121	A proposed framework for the description of plant metabolomics experiments and their results. *Nature Biotechnology*, **2004**, 22, 1601-6	44.5	260
120	Convergent evolution of gene networks by single-gene duplications in higher eukaryotes. *EMBO Reports*, **2004**, 5, 274-9	6.5	75
119	Effects of reciprocal chromosomal translocations on the fitness of Saccharomyces cerevisiae. *EMBO Reports*, **2004**, 5, 392-8	6.5	40
118	Functional genomic hypothesis generation and experimentation by a robot scientist. *Nature*, **2004**, 427, 247-52	50.4	341
117	Combining transcriptome data with genomic and cDNA sequence alignments to make confident functional assignments for Aspergillus nidulans genes. *Mycological Research*, **2004**, 108, 853-7		22
116	PEDRo: a database for storing, searching and disseminating experimental proteomics data. *BMC Genomics*, **2004**, 5, 68	4.5	47
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