

Balázs Papp

List of Publications by Year in descending order

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71
papers

10,078
citations

66343

42
h-index

85541

71
g-index

93
all docs

93
docs citations

93
times ranked

12900
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
2	Dosage sensitivity and the evolution of gene families in yeast. <i>Nature</i> , 2003, 424, 194-197.	27.8	757
3	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. <i>Molecular Cell</i> , 2006, 21, 319-330.	9.7	618
4	Highly Expressed Genes in Yeast Evolve Slowly. <i>Genetics</i> , 2001, 158, 927-931.	2.9	556
5	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. <i>Nature Genetics</i> , 2005, 37, 1372-1375.	21.4	473
6	An integrated view of protein evolution. <i>Nature Reviews Genetics</i> , 2006, 7, 337-348.	16.3	460
7	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731.	13.3	325
8	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. <i>Nature</i> , 2004, 429, 661-664.	27.8	324
9	Bacterial evolution of antibiotic hypersensitivity. <i>Molecular Systems Biology</i> , 2013, 9, 700.	7.2	277
10	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. <i>Nature Communications</i> , 2019, 10, 4538.	12.8	222
11	Collateral sensitivity of antibiotic-resistant microbes. <i>Trends in Microbiology</i> , 2015, 23, 401-407.	7.7	220
12	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
13	Rate of evolution and gene dispensability. <i>Nature</i> , 2003, 421, 496-497.	27.8	205
14	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4573-4582.	3.2	198
15	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	12.8	195
16	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	21.4	194
17	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
18	The Genomic Landscape of Compensatory Evolution. <i>PLoS Biology</i> , 2014, 12, e1001935.	5.6	150

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19	Phenotypic heterogeneity promotes adaptive evolution. <i>PLoS Biology</i> , 2017, 15, e2000644.	5.6	128
20	Evolution of cis-regulatory elements in duplicated genes of yeast. <i>Trends in Genetics</i> , 2003, 19, 417-422.	6.7	127
21	Systems-biology approaches for predicting genomic evolution. <i>Nature Reviews Genetics</i> , 2011, 12, 591-602.	16.3	112
22	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	102
23	Network-level architecture and the evolutionary potential of underground metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11762-11767.	7.1	101
24	Genetic interactions reveal the evolutionary trajectories of duplicate genes. <i>Molecular Systems Biology</i> , 2010, 6, 429.	7.2	97
25	ModuLand plug-in for Cytoscape: determination of hierarchical layers of overlapping network modules and community centrality. <i>Bioinformatics</i> , 2012, 28, 2202-2204.	4.1	91
26	Erroneous energy-generating cycles in published genome scale metabolic networks: Identification and removal. <i>PLoS Computational Biology</i> , 2017, 13, e1005494.	3.2	88
27	Molecular chaperones as regulatory elements of cellular networks. <i>Current Opinion in Cell Biology</i> , 2005, 17, 210-215.	5.4	85
28	Co-Regulation of Metabolic Genes Is Better Explained by Flux Coupling Than by Network Distance. <i>PLoS Computational Biology</i> , 2008, 4, e26.	3.2	81
29	Indispensability of Horizontally Transferred Genes and Its Impact on Bacterial Genome Streamlining. <i>Molecular Biology and Evolution</i> , 2016, 33, 1257-1269.	8.9	80
30	Directed evolution of multiple genomic loci allows the prediction of antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5726-E5735.	7.1	74
31	A critical view of metabolic network adaptations. <i>HFSP Journal</i> , 2009, 3, 24-35.	2.5	68
32	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 447-458.	13.3	68
33	Functional wiring of the yeast kinome revealed by global analysis of genetic network motifs. <i>Genome Research</i> , 2012, 22, 791-801.	5.5	65
34	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. <i>Genome Research</i> , 2007, 17, 510-519.	5.5	64
35	Systematic Genome Reductions: A Theoretical and Experimental Approaches. <i>Chemical Reviews</i> , 2007, 107, 3498-3513.	47.7	60
36	Computational identification of obligatorily autocatalytic replicators embedded in metabolic networks. <i>Genome Biology</i> , 2008, 9, R51.	9.6	60

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37	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. <i>Nature Communications</i> , 2016, 7, 11607.	12.8	60
38	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. <i>Genome Biology</i> , 2014, 15, R64.	9.6	57
39	Pathogen diversity drives the evolution of generalist MHC-II alleles in human populations. <i>PLoS Biology</i> , 2019, 17, e3000131.	5.6	56
40	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. <i>Molecular Biology and Evolution</i> , 2014, 31, 2793-2804.	8.9	54
41	Rapid decline of bacterial drug-resistance in an antibiotic-free environment through phenotypic reversion. <i>ELife</i> , 2019, 8, .	6.0	54
42	Does the Recombination Rate Affect the Efficiency of Purifying Selection? The Yeast Genome Provides a Partial Answer. <i>Molecular Biology and Evolution</i> , 2001, 18, 2323-2326.	8.9	52
43	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	7.2	52
44	The dawn of evolutionary genome engineering. <i>Nature Reviews Genetics</i> , 2014, 15, 504-512.	16.3	45
45	Underground metabolism: network-level perspective and biotechnological potential. <i>Current Opinion in Biotechnology</i> , 2018, 49, 108-114.	6.6	45
46	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
47	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1601-1611.	8.9	37
48	Stochasticity in Protein Levels Drives Colinearity of Gene Order in Metabolic Operons of <i>Escherichia coli</i> . <i>PLoS Biology</i> , 2009, 7, e1000115.	5.6	35
49	Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159.	8.9	35
50	Metabolic modeling of endosymbiont genome reduction on a temporal scale. <i>Molecular Systems Biology</i> , 2011, 7, 479.	7.2	34
51	Metabolic reconstruction and analysis for parasite genomes. <i>Trends in Parasitology</i> , 2007, 23, 548-554.	3.3	33
52	Evolution of complex adaptations in molecular systems. <i>Nature Ecology and Evolution</i> , 2017, 1, 1084-1092.	7.8	31
53	Hsp70-associated chaperones have a critical role in buffering protein production costs. <i>ELife</i> , 2018, 7, .	6.0	29
54	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. <i>Nature Communications</i> , 2019, 10, 5731.	12.8	29

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55	Exploring the fitness benefits of genome reduction in <i>Escherichia coli</i> by a selection-driven approach. <i>Scientific Reports</i> , 2020, 10, 7345.	3.3	27
56	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2228-2240.	8.9	23
57	Cancer cell metabolism as new targets for novel designed therapies. <i>Future Medicinal Chemistry</i> , 2014, 6, 1791-1810.	2.3	22
58	Model-driven discovery of long-chain fatty acid metabolic reprogramming in heterogeneous prostate cancer cells. <i>PLoS Computational Biology</i> , 2018, 14, e1005914.	3.2	22
59	Phenotypic Activation to Discover Biological Pathways and Kinase Substrates. <i>Cell Cycle</i> , 2006, 5, 1397-1402.	2.6	18
60	Selfish cells threaten multicellular life. <i>Trends in Ecology and Evolution</i> , 2000, 15, 351-352.	8.7	16
61	Gene loss and compensatory evolution promotes the emergence of morphological novelties in budding yeast. <i>Nature Ecology and Evolution</i> , 2022, 6, 763-773.	7.8	16
62	Molecular mechanisms underlying COPD-muscle dysfunction unveiled through a systems medicine approach. <i>Bioinformatics</i> , 2017, 33, 95-103.	4.1	15
63	Genome-wide analysis of the context-dependence of regulatory networks. <i>Genome Biology</i> , 2005, 6, 206.	9.6	13
64	Negative trade-off between neoantigen repertoire breadth and the specificity of HLA-I molecules shapes antitumor immunity. <i>Nature Cancer</i> , 2021, 2, 950-961.	13.2	13
65	Use of Genome-Scale Metabolic Models in Evolutionary Systems Biology. <i>Methods in Molecular Biology</i> , 2011, 759, 483-497.	0.9	9
66	Systems biology of epistasis: Shedding light on genetic interaction network "hubs". <i>Cell Cycle</i> , 2011, 10, 3623-3624.	2.6	9
67	Suboptimal Global Transcriptional Response Increases the Harmful Effects of Loss-of-Function Mutations. <i>Molecular Biology and Evolution</i> , 2021, 38, 1137-1150.	8.9	9
68	From passengers to drivers. <i>Mobile Genetic Elements</i> , 2013, 3, e23617.	1.8	8
69	No Evidence That Protein Noise-Induced Epigenetic Epistasis Constrains Gene Expression Evolution. <i>Molecular Biology and Evolution</i> , 2016, 34, msw236.	8.9	2
70	New recipe for targeting resistance. <i>Nature Chemical Biology</i> , 2016, 12, 891-892.	8.0	2
71	Underground metabolism as a rich reservoir for pathway engineering. <i>Bioinformatics</i> , 2022, 38, 3070-3077.	4.1	2