

Balázs Papp

List of Publications by Year in descending order

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Version: 2024-02-01

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	Underground metabolism as a rich reservoir for pathway engineering. <i>Bioinformatics</i> , 2022, 38, 3070-3077.	4.1	2
2	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
3	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
4	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
5	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
6	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2228-2240.	8.9	23
7	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. <i>Nature Communications</i> , 2019, 10, 4538.	12.8	222
8	Pathogen diversity drives the evolution of generalist MHC-II alleles in human populations. <i>PLoS Biology</i> , 2019, 17, e3000131.	5.6	56
9	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1601-1611.	8.9	37
10	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	7.2	52
11	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
12	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
13	Rapid decline of bacterial drug-resistance in an antibiotic-free environment through phenotypic reversion. <i>ELife</i> , 2019, 8, .	6.0	54
14	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	102
15	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
16	Underground metabolism: network-level perspective and biotechnological potential. <i>Current Opinion in Biotechnology</i> , 2018, 49, 108-114.	6.6	45
17	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731.	13.3	325
18	Hsp70-associated chaperones have a critical role in buffering protein production costs. <i>ELife</i> , 2018, 7, .	6.0	29

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19	Directed evolution of multiple genomic loci allows the prediction of antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5726-E5735.	7.1	74
20	Model-driven discovery of long-chain fatty acid metabolic reprogramming in heterogeneous prostate cancer cells. PLoS Computational Biology, 2018, 14, e1005914.	3.2	22
21	Evolution of complex adaptations in molecular systems. Nature Ecology and Evolution, 2017, 1, 1084-1092.	7.8	31
22	Molecular mechanisms underlying COPD-muscle dysfunction unveiled through a systems medicine approach. Bioinformatics, 2017, 33, 95-103.	4.1	15
23	Phenotypic heterogeneity promotes adaptive evolution. PLoS Biology, 2017, 15, e2000644.	5.6	128
24	Erroneous energy-generating cycles in published genome scale metabolic networks: Identification and removal. PLoS Computational Biology, 2017, 13, e1005494.	3.2	88
25	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. Nature Communications, 2016, 7, 11607.	12.8	60
26	No Evidence That Protein Noise-Induced Epigenetic Epistasis Constrains Gene Expression Evolution. Molecular Biology and Evolution, 2016, 34, msw236.	8.9	2
27	New recipe for targeting resistance. Nature Chemical Biology, 2016, 12, 891-892.	8.0	2
28	Indispensability of Horizontally Transferred Genes and Its Impact on Bacterial Genome Streamlining. Molecular Biology and Evolution, 2016, 33, 1257-1269.	8.9	80
29	Collateral sensitivity of antibiotic-resistant microbes. Trends in Microbiology, 2015, 23, 401-407.	7.7	220
30	The Genomic Landscape of Compensatory Evolution. PLoS Biology, 2014, 12, e1001935.	5.6	150
31	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. Molecular Biology and Evolution, 2014, 31, 2793-2804.	8.9	54
32	Cancer cell metabolism as new targets for novel designed therapies. Future Medicinal Chemistry, 2014, 6, 1791-1810.	2.3	22
33	Network-level architecture and the evolutionary potential of underground metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11762-11767.	7.1	101
34	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. Genome Biology, 2014, 15, R64.	9.6	57
35	The dawn of evolutionary genome engineering. Nature Reviews Genetics, 2014, 15, 504-512.	16.3	45
36	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. Nature Communications, 2014, 5, 4352.	12.8	195

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37	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4573-4582.	3.2	198
38	Bacterial evolution of antibiotic hypersensitivity. <i>Molecular Systems Biology</i> , 2013, 9, 700.	7.2	277
39	From passengers to drivers. <i>Mobile Genetic Elements</i> , 2013, 3, e23617.	1.8	8
40	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
41	Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159.	8.9	35
42	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
43	Use of Genome-Scale Metabolic Models in Evolutionary Systems Biology. <i>Methods in Molecular Biology</i> , 2011, 759, 483-497.	0.9	9
44	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	21.4	194
45	Systems-biology approaches for predicting genomic evolution. <i>Nature Reviews Genetics</i> , 2011, 12, 591-602.	16.3	112
46	Systems biology of epistasis: Shedding light on genetic interaction network "hubs". <i>Cell Cycle</i> , 2011, 10, 3623-3624.	2.6	9
47	Metabolic modeling of endosymbiont genome reduction on a temporal scale. <i>Molecular Systems Biology</i> , 2011, 7, 479.	7.2	34
48	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
49	Genetic interactions reveal the evolutionary trajectories of duplicate genes. <i>Molecular Systems Biology</i> , 2010, 6, 429.	7.2	97
50	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
51	A critical view of metabolic network adaptations. <i>HFSP Journal</i> , 2009, 3, 24-35.	2.5	68
52	Computational identification of obligatorily autocatalytic replicators embedded in metabolic networks. <i>Genome Biology</i> , 2008, 9, R51.	9.6	60
53	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
54	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

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55	Evaluation of predicted network modules in yeast metabolism using NMR-based metabolite profiling. <i>Genome Research</i> , 2007, 17, 510-519.	5.5	64
56	Systematic Genome Reductions: A Theoretical and Experimental Approaches. <i>Chemical Reviews</i> , 2007, 107, 3498-3513.	47.7	60
57	Metabolic reconstruction and analysis for parasite genomes. <i>Trends in Parasitology</i> , 2007, 23, 548-554.	3.3	33
58	Mapping Pathways and Phenotypes by Systematic Gene Overexpression. <i>Molecular Cell</i> , 2006, 21, 319-330.	9.7	618
59	An integrated view of protein evolution. <i>Nature Reviews Genetics</i> , 2006, 7, 337-348.	16.3	460
60	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
61	Phenotypic Activation to Discover Biological Pathways and Kinase Substrates. <i>Cell Cycle</i> , 2006, 5, 1397-1402.	2.6	18
62	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. <i>Nature Genetics</i> , 2005, 37, 1372-1375.	21.4	473
63	Molecular chaperones as regulatory elements of cellular networks. <i>Current Opinion in Cell Biology</i> , 2005, 17, 210-215.	5.4	85
64	Genome-wide analysis of the context-dependence of regulatory networks. <i>Genome Biology</i> , 2005, 6, 206.	9.6	13
65	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. <i>Nature</i> , 2004, 429, 661-664.	27.8	324
66	Evolution of cis-regulatory elements in duplicated genes of yeast. <i>Trends in Genetics</i> , 2003, 19, 417-422.	6.7	127
67	Rate of evolution and gene dispensability. <i>Nature</i> , 2003, 421, 496-497.	27.8	205
68	Dosage sensitivity and the evolution of gene families in yeast. <i>Nature</i> , 2003, 424, 194-197.	27.8	757
69	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
70	Highly Expressed Genes in Yeast Evolve Slowly. <i>Genetics</i> , 2001, 158, 927-931.	2.9	556
71	Selfish cells threaten multicellular life. <i>Trends in Ecology and Evolution</i> , 2000, 15, 351-352.	8.7	16