

Csaba Pál

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

7,401
citations

136950

32
h-index

123424

61
g-index

71
all docs

71
docs citations

71
times ranked

10508
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	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. <i>Nature Genetics</i> , 2005, 37, 1372-1375.	21.4	473
4	An integrated view of protein evolution. <i>Nature Reviews Genetics</i> , 2006, 7, 337-348.	16.3	460
5	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731.	13.3	325
6	Bacterial evolution of antibiotic hypersensitivity. <i>Molecular Systems Biology</i> , 2013, 9, 700.	7.2	277
7	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. <i>Nature Communications</i> , 2019, 10, 4538.	12.8	222
8	Collateral sensitivity of antibiotic-resistant microbes. <i>Trends in Microbiology</i> , 2015, 23, 401-407.	7.7	220
9	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
10	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4573-4582.	3.2	198
11	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	12.8	195
12	A highly precise and portable genome engineering method allows comparison of mutational effects across bacterial species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2502-2507.	7.1	190
13	The Genomic Landscape of Compensatory Evolution. <i>PLoS Biology</i> , 2014, 12, e1001935.	5.6	150
14	Phenotypic heterogeneity promotes adaptive evolution. <i>PLoS Biology</i> , 2017, 15, e2000644.	5.6	128
15	Systems-biology approaches for predicting genomic evolution. <i>Nature Reviews Genetics</i> , 2011, 12, 591-602.	16.3	112
16	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
17	Improved bacterial recombineering by parallelized protein discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13689-13698.	7.1	82
18	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

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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	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. Nature Microbiology, 2019, 4, 447-458.	13.3	68
21	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. Nature Communications, 2016, 7, 11607.	12.8	60
22	Pathogen diversity drives the evolution of generalist MHC-II alleles in human populations. PLoS Biology, 2019, 17, e3000131.	5.6	56
23	Genome-Wide Abolishment of Mobile Genetic Elements Using Genome Shuffling and CRISPR/Cas-Assisted MAGE Allows the Efficient Stabilization of a Bacterial Chassis. ACS Synthetic Biology, 2017, 6, 1471-1483.	3.8	55
24	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. Molecular Biology and Evolution, 2014, 31, 2793-2804.	8.9	54
25	Rapid decline of bacterial drug-resistance in an antibiotic-free environment through phenotypic reversion. ELife, 2019, 8, .	6.0	54
26	Enzyme promiscuity shapes adaptation to novel growth substrates. Molecular Systems Biology, 2019, 15, e8462.	7.2	52
27	Recombineering and MAGE. Nature Reviews Methods Primers, 2021, 1, .	21.2	47
28	Conditional DNA repair mutants enable highly precise genome engineering. Nucleic Acids Research, 2014, 42, e62-e62.	14.5	46
29	Horizontal gene transfer depends on gene content of the host. Bioinformatics, 2005, 21, ii222-ii223.	4.1	45
30	The dawn of evolutionary genome engineering. Nature Reviews Genetics, 2014, 15, 504-512.	16.3	45
31	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. Nature Structural and Molecular Biology, 2018, 25, 279-288.	8.2	43
32	A standardized workflow for surveying recombinases expands bacterial genome editing capabilities. Microbial Biotechnology, 2018, 11, 176-188.	4.2	43
33	Dual Action of the PN159/KLAL/MAP Peptide: Increase of Drug Penetration across Caco-2 Intestinal Barrier Model by Modulation of Tight Junctions and Plasma Membrane Permeability. Pharmaceutics, 2019, 11, 73.	4.5	38
34	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. Molecular Biology and Evolution, 2019, 36, 1601-1611.	8.9	37
35	Competition between Transposable Elements and Mutator Genes in Bacteria. Molecular Biology and Evolution, 2012, 29, 3153-3159.	8.9	35
36	New N -phenylpyrrolamide DNA gyrase B inhibitors: Optimization of efficacy and antibacterial activity. European Journal of Medicinal Chemistry, 2018, 154, 117-132.	5.5	35

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37	Evolution of complex adaptations in molecular systems. <i>Nature Ecology and Evolution</i> , 2017, 1, 1084-1092.	7.8	31
38	Hsp70-associated chaperones have a critical role in buffering protein production costs. <i>ELife</i> , 2018, 7, .	6.0	29
39	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
40	Evolution of Robustness to Protein Mistranslation by Accelerated Protein Turnover. <i>PLoS Biology</i> , 2015, 13, e1002291.	5.6	29
41	Rapid Evolution of Reduced Susceptibility against a Balanced Dual-Targeting Antibiotic through Stepping-Stone Mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	23
42	Mismatch repair hierarchy of <i>Pseudomonas putida</i> revealed by mutagenic ssDNA recombineering of the <i>pyrF</i> gene. <i>Environmental Microbiology</i> , 2020, 22, 45-58.	3.8	22
43	Rational design of balanced dual-targeting antibiotics with limited resistance. <i>PLoS Biology</i> , 2020, 18, e3000819.	5.6	20
44	Efflux Pump Control Alters Synthetic Gene Circuit Function. <i>ACS Synthetic Biology</i> , 2016, 5, 619-631.	3.8	16
45	CRISPR-interference-based modulation of mobile genetic elements in bacteria. <i>Synthetic Biology</i> , 2019, 4, ysz008.	2.2	16
46	Dual <i>Escherichia coli</i> DNA Gyrase A and B Inhibitors with Antibacterial Activity. <i>ChemMedChem</i> , 2020, 15, 265-269.	3.2	16
47	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
48	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. <i>ACS Synthetic Biology</i> , 2020, 9, 104-114.	3.8	15
49	New dual ATP-competitive inhibitors of bacterial DNA gyrase and topoisomerase IV active against ESKAPE pathogens. <i>European Journal of Medicinal Chemistry</i> , 2021, 213, 113200.	5.5	15
50	Functional Anatomical Changes in Ulcerative Colitis Patients Determine Their Gut Microbiota Composition and Consequently the Possible Treatment Outcome. <i>Pharmaceuticals</i> , 2020, 13, 346.	3.8	13
51	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
52	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	5.6	10
53	Targeted mutagenesis of multiple chromosomal regions in microbes. <i>Current Opinion in Microbiology</i> , 2020, 57, 22-30.	5.1	10
54	Second-generation 4,5,6,7-tetrahydrobenzo[<i>d</i>]thiazoles as novel DNA gyrase inhibitors. <i>Future Medicinal Chemistry</i> , 2020, 12, 277-297.	2.3	9

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55	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
56	Hybrid Inhibitors of DNA Gyrase A and B: Design, Synthesis and Evaluation. <i>Pharmaceutics</i> , 2021, 13, 6.	4.5	9
57	From passengers to drivers. <i>Mobile Genetic Elements</i> , 2013, 3, e23617.	1.8	8
58	ssDNA recombineering boosts in vivo evolution of nanobodies displayed on bacterial surfaces. <i>Communications Biology</i> , 2021, 4, 1169.	4.4	6
59	Rationally designed foldameric adjuvants enhance antibiotic efficacy <i>via</i> promoting membrane hyperpolarization. <i>Molecular Systems Design and Engineering</i> , 2022, 7, 21-33.	3.4	5
60	Proteome-wide landscape of solubility limits in a bacterial cell. <i>Scientific Reports</i> , 2022, 12, 6547.	3.3	2