

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	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
2	Proteome-wide landscape of solubility limits in a bacterial cell. <i>Scientific Reports</i> , 2022, 12, 6547.	3.3	2
3	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
4	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
5	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
6	Recombineering and MAGE. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	47
7	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
8	ssDNA recombineering boosts in vivo evolution of nanobodies displayed on bacterial surfaces. <i>Communications Biology</i> , 2021, 4, 1169.	4.4	6
9	Hybrid Inhibitors of DNA Gyrase A and B: Design, Synthesis and Evaluation. <i>Pharmaceutics</i> , 2021, 13, 6.	4.5	9
10	Dual <i>Escherichia coli</i> DNA Gyrase A and B Inhibitors with Antibacterial Activity. <i>ChemMedChem</i> , 2020, 15, 265-269.	3.2	16
11	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
12	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. <i>ACS Synthetic Biology</i> , 2020, 9, 104-114.	3.8	15
13	Rational design of balanced dual-targeting antibiotics with limited resistance. <i>PLoS Biology</i> , 2020, 18, e3000819.	5.6	20
14	Functional Anatomical Changes in Ulcerative Colitis Patients Determine Their Gut Microbiota Composition and Consequently the Possible Treatment Outcome. <i>Pharmaceutics</i> , 2020, 13, 346.	3.8	13
15	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
16	Targeted mutagenesis of multiple chromosomal regions in microbes. <i>Current Opinion in Microbiology</i> , 2020, 57, 22-30.	5.1	10
17	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
18	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

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19	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. <i>Nature Communications</i> , 2019, 10, 4538.	12.8	222
20	Pathogen diversity drives the evolution of generalist MHC-II alleles in human populations. <i>PLoS Biology</i> , 2019, 17, e3000131.	5.6	56
21	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1601-1611.	8.9	37
22	CRISPR-interference-based modulation of mobile genetic elements in bacteria. <i>Synthetic Biology</i> , 2019, 4, ysz008.	2.2	16
23	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	7.2	52
24	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	5.6	10
25	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. <i>Pharmaceutics</i> , 2019, 11, 73.	4.5	38
26	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
27	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
28	Rapid decline of bacterial drug-resistance in an antibiotic-free environment through phenotypic reversion. <i>ELife</i> , 2019, 8, .	6.0	54
29	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
30	A standardized workflow for surveying recombinases expands bacterial genome editing capabilities. <i>Microbial Biotechnology</i> , 2018, 11, 176-188.	4.2	43
31	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731.	13.3	325
32	Hsp70-associated chaperones have a critical role in buffering protein production costs. <i>ELife</i> , 2018, 7, .	6.0	29
33	New N -phenylpyrrolamide DNA gyrase B inhibitors: Optimization of efficacy and antibacterial activity. <i>European Journal of Medicinal Chemistry</i> , 2018, 154, 117-132.	5.5	35
34	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
35	Genome-Wide Abolishment of Mobile Genetic Elements Using Genome Shuffling and CRISPR/Cas-Assisted MAGE Allows the Efficient Stabilization of a Bacterial Chassis. <i>ACS Synthetic Biology</i> , 2017, 6, 1471-1483.	3.8	55
36	Evolution of complex adaptations in molecular systems. <i>Nature Ecology and Evolution</i> , 2017, 1, 1084-1092.	7.8	31

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37	Phenotypic heterogeneity promotes adaptive evolution. PLoS Biology, 2017, 15, e2000644.	5.6	128
38	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. Nature Communications, 2016, 7, 11607.	12.8	60
39	Efflux Pump Control Alters Synthetic Gene Circuit Function. ACS Synthetic Biology, 2016, 5, 619-631.	3.8	16
40	Indispensability of Horizontally Transferred Genes and Its Impact on Bacterial Genome Streamlining. Molecular Biology and Evolution, 2016, 33, 1257-1269.	8.9	80
41	A highly precise and portable genome engineering method allows comparison of mutational effects across bacterial species. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2502-2507.	7.1	190
42	Collateral sensitivity of antibiotic-resistant microbes. Trends in Microbiology, 2015, 23, 401-407.	7.7	220
43	Evolution of Robustness to Protein Mistranslation by Accelerated Protein Turnover. PLoS Biology, 2015, 13, e1002291.	5.6	29
44	The Genomic Landscape of Compensatory Evolution. PLoS Biology, 2014, 12, e1001935.	5.6	150
45	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. Molecular Biology and Evolution, 2014, 31, 2793-2804.	8.9	54
46	Conditional DNA repair mutants enable highly precise genome engineering. Nucleic Acids Research, 2014, 42, e62-e62.	14.5	46
47	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
48	The dawn of evolutionary genome engineering. Nature Reviews Genetics, 2014, 15, 504-512.	16.3	45
49	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. Nature Communications, 2014, 5, 4352.	12.8	195
50	Antagonism between Bacteriostatic and Bactericidal Antibiotics Is Prevalent. Antimicrobial Agents and Chemotherapy, 2014, 58, 4573-4582.	3.2	198
51	Bacterial evolution of antibiotic hypersensitivity. Molecular Systems Biology, 2013, 9, 700.	7.2	277
52	From passengers to drivers. Mobile Genetic Elements, 2013, 3, e23617.	1.8	8
53	Competition between Transposable Elements and Mutator Genes in Bacteria. Molecular Biology and Evolution, 2012, 29, 3153-3159.	8.9	35
54	Systems-biology approaches for predicting genomic evolution. Nature Reviews Genetics, 2011, 12, 591-602.	16.3	112

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55	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
56	An integrated view of protein evolution. <i>Nature Reviews Genetics</i> , 2006, 7, 337-348.	16.3	460
57	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
58	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. <i>Nature Genetics</i> , 2005, 37, 1372-1375.	21.4	473
59	Horizontal gene transfer depends on gene content of the host. <i>Bioinformatics</i> , 2005, 21, ii222-ii223.	4.1	45
60	Dosage sensitivity and the evolution of gene families in yeast. <i>Nature</i> , 2003, 424, 194-197.	27.8	757