

Akos Nyerges

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,710
citations

394421

19
h-index

434195

31
g-index

45
all docs

45
docs citations

45
times ranked

2299
citing authors

#	ARTICLE	IF	CITATIONS
1	inPOSE: A Flexible Toolbox for Chromosomal Cloning and Amplification of Bacterial Transgenes. <i>Microorganisms</i> , 2022, 10, 236.	3.6	0
2	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
3	Recombineering and MAGE. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	47
4	ssDNA recombineering boosts in vivo evolution of nanobodies displayed on bacterial surfaces. <i>Communications Biology</i> , 2021, 4, 1169.	4.4	6
5	Hybrid Inhibitors of DNA Gyrase A and B: Design, Synthesis and Evaluation. <i>Pharmaceutics</i> , 2021, 13, 6.	4.5	9
6	Dual <i>Escherichia coli</i> DNA Gyrase A and B Inhibitors with Antibacterial Activity. <i>ChemMedChem</i> , 2020, 15, 265-269.	3.2	16
7	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
8	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. <i>ACS Synthetic Biology</i> , 2020, 9, 104-114.	3.8	15
9	Rational design of balanced dual-targeting antibiotics with limited resistance. <i>PLoS Biology</i> , 2020, 18, e3000819.	5.6	20
10	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
11	High-Efficiency Multi-site Genomic Editing of <i>Pseudomonas putida</i> through Thermoinducible ssDNA Recombineering. <i>IScience</i> , 2020, 23, 100946.	4.1	32
12	Targeted mutagenesis of multiple chromosomal regions in microbes. <i>Current Opinion in Microbiology</i> , 2020, 57, 22-30.	5.1	10
13	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
14	Synthetic genomes with altered genetic codes. <i>Current Opinion in Systems Biology</i> , 2020, 24, 32-40.	2.6	7
15	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
16	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1601-1611.	8.9	37
17	CRISPR-interference-based modulation of mobile genetic elements in bacteria. <i>Synthetic Biology</i> , 2019, 4, ysz008.	2.2	16
18	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	7.2	52

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19	An optimised series of substituted N-phenylpyrrolamides as DNA gyrase B inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2019, 167, 269-290.	5.5	36
20	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
21	A standardized workflow for surveying recombinases expands bacterial genome editing capabilities. <i>Microbial Biotechnology</i> , 2018, 11, 176-188.	4.2	43
22	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731.	13.3	325
23	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
24	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
25	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
26	Phenotypic heterogeneity promotes adaptive evolution. <i>PLoS Biology</i> , 2017, 15, e2000644.	5.6	128
27	System-level genome editing in microbes. <i>Current Opinion in Microbiology</i> , 2016, 33, 113-122.	5.1	23
28	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
29	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. <i>Molecular Biology and Evolution</i> , 2014, 31, 2793-2804.	8.9	54
30	Conditional DNA repair mutants enable highly precise genome engineering. <i>Nucleic Acids Research</i> , 2014, 42, e62-e62.	14.5	46
31	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	12.8	195