

Bjlint Csrg

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7371044/publications.pdf>

Version: 2024-02-01

25
papers

2,612
citations

361413

20
h-index

552781

26
g-index

29
all docs

29
docs citations

29
times ranked

3643
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Manipulation of a CAST of Characters in a Microbial Community. CRISPR Journal, 2022, , .	2.9	1
2	A compact Cascadeâ€“Cas3 system for targeted genome engineering. Nature Methods, 2020, 17, 1183-1190.	19.0	104
3	Anti-CRISPR protein applications: natural brakes for CRISPR-Cas technologies. Nature Methods, 2020, 17, 471-479.	19.0	158
4	Targeted mutagenesis of multiple chromosomal regions in microbes. Current Opinion in Microbiology, 2020, 57, 22-30.	5.1	10
5	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. Nature Communications, 2019, 10, 4538.	12.8	222
6	Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. Molecular Biology and Evolution, 2019, 36, 1601-1611.	8.9	37
7	Evolthon: A community endeavor to evolve lab evolution. PLoS Biology, 2019, 17, e3000182.	5.6	10
8	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. Nature Communications, 2019, 10, 5731.	12.8	29
9	Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. Nature Microbiology, 2018, 3, 718-731.	13.3	325
10	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
11	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
12	Phenotypic heterogeneity promotes adaptive evolution. PLoS Biology, 2017, 15, e2000644.	5.6	128
13	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. Nature Communications, 2016, 7, 11607.	12.8	60
14	System-level genome editing in microbes. Current Opinion in Microbiology, 2016, 33, 113-122.	5.1	23
15	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
16	Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. Molecular Biology and Evolution, 2014, 31, 2793-2804.	8.9	54
17	Conditional DNA repair mutants enable highly precise genome engineering. Nucleic Acids Research, 2014, 42, e62-e62.	14.5	46
18	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

#	ARTICLE	IF	CITATIONS
19	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	12.8	195
20	Bacterial evolution of antibiotic hypersensitivity. <i>Molecular Systems Biology</i> , 2013, 9, 700.	7.2	277
21	Genomewide Screen for Modulators of Evolvability under Toxic Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3453-3456.	3.2	9
22	Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159.	8.9	35
23	Low-mutation-rate, reduced-genome <i>Escherichia coli</i> : an improved host for faithful maintenance of engineered genetic constructs. <i>Microbial Cell Factories</i> , 2012, 11, 11.	4.0	108
24	Scarless Engineering of the <i>Escherichia coli</i> Genome. <i>Methods in Molecular Biology</i> , 2008, 416, 251-259.	0.9	22
25	The Complete Genome Sequence of <i>Escherichia coli</i> DH10B: Insights into the Biology of a Laboratory Workhorse. <i>Journal of Bacteriology</i> , 2008, 190, 2597-2606.	2.2	331