

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 | 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 |
| 2 | Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. <i>Nature Microbiology</i> , 2018, 3, 718-731. | 13.3 | 325 |
| 3 | Bacterial evolution of antibiotic hypersensitivity. <i>Molecular Systems Biology</i> , 2013, 9, 700. | 7.2 | 277 |
| 4 | Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. <i>Nature Communications</i> , 2019, 10, 4538. | 12.8 | 222 |
| 5 | Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352. | 12.8 | 195 |
| 6 | 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 |
| 7 | Anti-CRISPR protein applications: natural brakes for CRISPR-Cas technologies. <i>Nature Methods</i> , 2020, 17, 471-479. | 19.0 | 158 |
| 8 | Phenotypic heterogeneity promotes adaptive evolution. <i>PLoS Biology</i> , 2017, 15, e2000644. | 5.6 | 128 |
| 9 | 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 |
| 10 | A compact Cascade-Cas3 system for targeted genome engineering. <i>Nature Methods</i> , 2020, 17, 1183-1190. | 19.0 | 104 |
| 11 | 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 |
| 12 | 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 |
| 13 | Adaptive evolution of complex innovations through stepwise metabolic niche expansion. <i>Nature Communications</i> , 2016, 7, 11607. | 12.8 | 60 |
| 14 | 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 |
| 15 | Perturbation of Iron Homeostasis Promotes the Evolution of Antibiotic Resistance. <i>Molecular Biology and Evolution</i> , 2014, 31, 2793-2804. | 8.9 | 54 |
| 16 | Conditional DNA repair mutants enable highly precise genome engineering. <i>Nucleic Acids Research</i> , 2014, 42, e62-e62. | 14.5 | 46 |
| 17 | Limited Evolutionary Conservation of the Phenotypic Effects of Antibiotic Resistance Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1601-1611. | 8.9 | 37 |
| 18 | Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159. | 8.9 | 35 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | System-level genome editing in microbes. <i>Current Opinion in Microbiology</i> , 2016, 33, 113-122. | 5.1 | 23 |
| 21 | Scarless Engineering of the Escherichia coli Genome. <i>Methods in Molecular Biology</i> , 2008, 416, 251-259. | 0.9 | 22 |
| 22 | Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182. | 5.6 | 10 |
| 23 | Targeted mutagenesis of multiple chromosomal regions in microbes. <i>Current Opinion in Microbiology</i> , 2020, 57, 22-30. | 5.1 | 10 |
| 24 | Genomewide Screen for Modulators of Evolvability under Toxic Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3453-3456. | 3.2 | 9 |
| 25 | Genetic Manipulation of a CAST of Characters in a Microbial Community. <i>CRISPR Journal</i> , 2022, , . | 2.9 | 1 |