

Pep Charusanti

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

5,552
citations

393982

19
h-index

525886

27
g-index

29
all docs

29
docs citations

29
times ranked

8600
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837. | 9.4 | 2,802 |
| 2 | Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , 2010, 6, 390. | 3.2 | 615 |
| 3 | CRISPR-Cas9 Based Engineering of Actinomycetal Genomes. <i>ACS Synthetic Biology</i> , 2015, 4, 1020-1029. | 1.9 | 365 |
| 4 | Genome-scale metabolic reconstructions of multiple <i>Escherichia coli</i> strains highlight strain-specific adaptations to nutritional environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20338-20343. | 3.3 | 270 |
| 5 | MS/MS networking guided analysis of molecule and gene cluster families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2611-20. | 3.3 | 250 |
| 6 | Systems biology and biotechnology of <i>Streptomyces</i> species for the production of secondary metabolites. <i>Biotechnology Advances</i> , 2014, 32, 255-268. | 6.0 | 199 |
| 7 | Metabolic engineering of antibiotic factories: new tools for antibiotic production in actinomycetes. <i>Trends in Biotechnology</i> , 2015, 33, 15-26. | 4.9 | 159 |
| 8 | An Experimentally Validated Genome-Scale Metabolic Reconstruction of <i>Klebsiella pneumoniae</i> MGH 78578, <i>Yersinia enterocolitica</i> YL1228. <i>Journal of Bacteriology</i> , 2011, 193, 1710-1717. | 1.0 | 132 |
| 9 | A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8. | 3.0 | 128 |
| 10 | Genetic Basis of Growth Adaptation of <i>Escherichia coli</i> after Deletion of <i>pgi</i> , a Major Metabolic Gene. <i>PLoS Genetics</i> , 2010, 6, e1001186. | 1.5 | 121 |
| 11 | Exploiting Adaptive Laboratory Evolution of <i>Streptomyces clavuligerus</i> for Antibiotic Discovery and Overproduction. <i>PLoS ONE</i> , 2012, 7, e33727. | 1.1 | 72 |
| 12 | A Gapless, Unambiguous Genome Sequence of the Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Strain EDL933. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 67 |
| 13 | Capsule deletion via a λ -Red knockout system perturbs biofilm formation and fimbriae expression in <i>Klebsiella pneumoniae</i> MGH 78578. <i>BMC Research Notes</i> , 2014, 7, 13. | 0.6 | 57 |
| 14 | Metabolic engineering with systems biology tools to optimize production of prokaryotic secondary metabolites. <i>Natural Product Reports</i> , 2016, 33, 933-941. | 5.2 | 52 |
| 15 | Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10810-10815. | 3.3 | 42 |
| 16 | An experimentally-supported genome-scale metabolic network reconstruction for <i>Yersinia pestis</i> CO92. <i>BMC Systems Biology</i> , 2011, 5, 163. | 3.0 | 38 |
| 17 | Understanding system dynamics of an adaptive enzyme network from globally profiled kinetic parameters. <i>BMC Systems Biology</i> , 2014, 8, 4. | 3.0 | 38 |
| 18 | Multiple-omic data analysis of <i>Klebsiella pneumoniae</i> MGH 78578 reveals its transcriptional architecture and regulatory features. <i>BMC Genomics</i> , 2012, 13, 679. | 1.2 | 34 |

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|----|--|-----|-----------|
| 19 | Microbial regulatory and metabolic networks. <i>Current Opinion in Biotechnology</i> , 2007, 18, 360-364. | 3.3 | 29 |
| 20 | Systems biology-guided identification of synthetic lethal gene pairs and its potential use to discover antibiotic combinations. <i>Scientific Reports</i> , 2015, 5, 16025. | 1.6 | 19 |
| 21 | Reconciling a <i>Salmonella enterica</i> metabolic model with experimental data confirms that overexpression of the glyoxylate shunt can rescue a lethal <i>ppc</i> deletion mutant. <i>FEMS Microbiology Letters</i> , 2013, 342, 62-69. | 0.7 | 16 |
| 22 | Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. <i>Synthetic and Systems Biotechnology</i> , 2020, 5, 11-18. | 1.8 | 13 |
| 23 | Studying <i>Salmonellae</i> and <i>Yersinia</i> Host-Pathogen Interactions Using Integrated Omics and Modeling. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 21-41. | 0.7 | 10 |
| 24 | Model-driven discovery of synergistic inhibitors against <i>E. coli</i> and <i>S. enterica</i> serovar Typhimurium targeting a novel synthetic lethal pair, <i>aldA</i> and <i>prpC</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 958. | 1.5 | 8 |
| 25 | Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from <i>Kutzneria</i> sp. CA-103260. <i>ACS Chemical Biology</i> , 2021, 16, 1456-1468. | 1.6 | 8 |
| 26 | The aldehyde dehydrogenase, <i>AldA</i> , is essential for L-1,2-propanediol utilization in laboratory-evolved <i>Escherichia coli</i> . <i>Microbiological Research</i> , 2017, 194, 47-52. | 2.5 | 5 |
| 27 | A mathematical model of BCR-ABL autophosphorylation, signaling through the CRKL pathway, and Gleevec dynamics in chronic myeloid leukemia. <i>Discrete and Continuous Dynamical Systems - Series B</i> , 2003, 4, 99-114. | 0.5 | 2 |
| 28 | Exploiting Adaptive Laboratory Evolution of <i>Streptomyces clavuligerus</i> for Antibiotic Discovery and Overproduction. <i>FASEB Journal</i> , 2012, 26, 1b123. | 0.2 | 0 |