

Pep Charusanti

List of Publications by Year in descending order

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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	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
2	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. <i>Synthetic and Systems Biotechnology</i> , 2020, 5, 11-18.	1.8	13
3	The aldehyde dehydrogenase, AldA, 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
4	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
5	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
6	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
7	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
8	CRISPR-Cas9 Based Engineering of Actinomycetal Genomes. <i>ACS Synthetic Biology</i> , 2015, 4, 1020-1029.	1.9	365
9	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
10	Metabolic engineering of antibiotic factories: new tools for antibiotic production in actinomycetes. <i>Trends in Biotechnology</i> , 2015, 33, 15-26.	4.9	159
11	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
12	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
13	Understanding system dynamics of an adaptive enzyme network from globally profiled kinetic parameters. <i>BMC Systems Biology</i> , 2014, 8, 4.	3.0	38
14	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
15	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
16	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
17	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
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	Studying Salmonellae and Yersinia Host-Pathogen Interactions Using Integrated Omics and Modeling. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 21-41.	0.7	10
20	Exploiting Adaptive Laboratory Evolution of <i>Streptomyces clavuligerus</i> for Antibiotic Discovery and Overproduction. <i>PLoS ONE</i> , 2012, 7, e33727.	1.1	72
21	Exploiting Adaptive Laboratory Evolution of <i>Streptomyces clavuligerus</i> for Antibiotic Discovery and Overproduction. <i>FASEB Journal</i> , 2012, 26, lb123.	0.2	0
22	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
23	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
24	An Experimentally Validated Genome-Scale Metabolic Reconstruction of <i>Klebsiella pneumoniae</i> MGH 78578, YL1228. <i>Journal of Bacteriology</i> , 2011, 193, 1710-1717.	1.0	132
25	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
26	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
27	Microbial regulatory and metabolic networks. <i>Current Opinion in Biotechnology</i> , 2007, 18, 360-364.	3.3	29
28	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