Pep Charusanti

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7185711/publications.pdf

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28	5,552	394421	526287
papers	citations	19 h-index	27 g-index

29	29	29	8600
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	17.5	2,802
2	Omic data from evolved E. coli are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
3	CRISPR-Cas9 Based Engineering of Actinomycetal Genomes. ACS Synthetic Biology, 2015, 4, 1020-1029.	3.8	365
4	Genome-scale metabolic reconstructions of multiple Escherichia coli strains highlight strain-specific adaptations to nutritional environments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20338-20343.	7.1	270
5	MS/MS networking guided analysis of molecule and gene cluster families. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2611-20.	7.1	250
6	Systems biology and biotechnology of Streptomyces species for the production of secondary metabolites. Biotechnology Advances, 2014, 32, 255-268.	11.7	199
7	Metabolic engineering of antibiotic factories: new tools for antibiotic production in actinomycetes. Trends in Biotechnology, 2015, 33, 15-26.	9.3	159
8	An Experimentally Validated Genome-Scale Metabolic Reconstruction of Klebsiella pneumoniae MGH 78578, i YL1228. Journal of Bacteriology, 2011, 193, 1710-1717.	2.2	132
9	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128
10	Genetic Basis of Growth Adaptation of Escherichia coli after Deletion of pgi, a Major Metabolic Gene. PLoS Genetics, 2010, 6, e1001186.	3.5	121
11	Exploiting Adaptive Laboratory Evolution of Streptomyces clavuligerus for Antibiotic Discovery and Overproduction. PLoS ONE, 2012, 7, e33727.	2.5	72
12	A Gapless, Unambiguous Genome Sequence of the Enterohemorrhagic Escherichia coli O157:H7 Strain EDL933. Genome Announcements, 2014, 2, .	0.8	67
13	Capsule deletion via a Î»-Red knockout system perturbs biofilm formation and fimbriae expression in Klebsiella pneumoniae MGH 78578. BMC Research Notes, 2014, 7, 13.	1.4	57
14	Metabolic engineering with systems biology tools to optimize production of prokaryotic secondary metabolites. Natural Product Reports, 2016, 33, 933-941.	10.3	52
15	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10810-10815.	7.1	42
16	An experimentally-supported genome-scale metabolic network reconstruction for Yersinia pestis CO92. BMC Systems Biology, 2011, 5, 163.	3.0	38
17	Understanding system dynamics of an adaptive enzyme network from globally profiled kinetic parameters. BMC Systems Biology, 2014, 8, 4.	3.0	38
18	Multiple-omic data analysis of Klebsiella pneumoniae MGH 78578 reveals its transcriptional architecture and regulatory features. BMC Genomics, 2012, 13, 679.	2.8	34

#	Article	IF	Citations
19	Microbial regulatory and metabolic networks. Current Opinion in Biotechnology, 2007, 18, 360-364.	6.6	29
20	Systems biology-guided identification of synthetic lethal gene pairs and its potential use to discover antibiotic combinations. Scientific Reports, 2015, 5, 16025.	3.3	19
21	Reconciling aSalmonella entericametabolic model with experimental data confirms that overexpression of the glyoxylate shunt can rescue a lethalppcdeletion mutant. FEMS Microbiology Letters, 2013, 342, 62-69.	1.8	16
22	Programmable polyketide biosynthesis platform for production of aromatic compounds in yeast. Synthetic and Systems Biotechnology, 2020, 5, 11-18.	3.7	13
23	Studying Salmonellae and Yersiniae Hostâ€“Pathogen Interactions Using Integrated â€˜Omics and Modeling. Current Topics in Microbiology and Immunology, 2012, 363, 21-41.	1.1	10
24	Model-driven discovery of synergistic inhibitors against E. coli and S. enterica serovar Typhimurium targeting a novel synthetic lethal pair, aldA and prpC. Frontiers in Microbiology, 2015, 6, 958.	3.5	8
25	Discovery and Characterization of Epemicins A and B, New 30-Membered Macrolides from Kutzneria sp. CA-103260. ACS Chemical Biology, 2021, 16, 1456-1468.	3.4	8
26	The aldehyde dehydrogenase, AldA, is essential for L-1,2-propanediol utilization in laboratory-evolved Escherichia coli. Microbiological Research, 2017, 194, 47-52.	5.3	5
27	A mathematical model of BCR-ABL autophosphorylation, signaling through the CRKL pathway, and Gleevec dynamics in chronic myeloid leukemia. Discrete and Continuous Dynamical Systems - Series B, 2003, 4, 99-114.	0.9	2
28	Exploiting Adaptive Laboratory Evolution of Streptomyces clavuligerus for Antibiotic Discovery and Overproduction. FASEB Journal, 2012, 26, lb123.	0.5	0