Christopher P Long

List of Publications by Year
in descending order

22 papers	1,563 citations	304368 22 h-index	642321 23 g-index
24 all docs	24 docs citations	24 times ranked	2110 citing authors

#	Article	IF	Citations
1	Hexokinase-2 depletion inhibits glycolysis and induces oxidative phosphorylation in hepatocellular carcinoma and sensitizes to metformin. Nature Communications, 2018, 9, 446.	5.8	311
2	High-resolution 13C metabolic flux analysis. Nature Protocols, 2019, 14, 2856-2877.	5.5	132
3	Comprehensive analysis of glucose and xylose metabolism in Escherichia coli under aerobic and anaerobic conditions by 13C metabolic flux analysis. Metabolic Engineering, 2017, 39, 9-18.	3.6	99
4	Integrated 13 C-metabolic flux analysis of 14 parallel labeling experiments in Escherichia coli. Metabolic Engineering, 2015, 28, 151-158.	3.6	94
5	Genome-Scale Metabolic Model for the Green Alga *Chlorella vulgaris* UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. Plant Physiology, 2016, 172, 589-602.	2.3	86
6	Quantifying Biomass Composition by Gas Chromatography/Mass Spectrometry. Analytical Chemistry, 2014, 86, 9423-9427.	3.2	70
7	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 222-227.	3.3	70
8	Optimal tracers for parallel labeling experiments and 13C metabolic flux analysis: A new precision and synergy scoring system. Metabolic Engineering, 2016, 38, 10-18.	3.6	68
9	Metabolism of the fast-growing bacterium Vibrio natriegens elucidated by 13C metabolic flux analysis. Metabolic Engineering, 2017, 44, 191-197.	3.6	63
10	Fast growth phenotype of E. coli K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. Metabolic Engineering, 2017, 44, 100-107.	3.6	59
11	Evolution of E. coli on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. PLoS ONE, 2016, 11, e0151130.	1.1	54
12	Characterization of physiological responses to 22 gene knockouts in Escherichia coli central carbon metabolism. Metabolic Engineering, 2016, 37, 102-113.	3.6	50
13	Metabolic flux analysis of Escherichia coli knockouts: lessons from the Keio collection and future outlook. Current Opinion in Biotechnology, 2014, 28, 127-133.	3.3	49
14	13C metabolic flux analysis of microbial and mammalian systems is enhanced with GC-MS measurements of glycogen and RNA labeling. Metabolic Engineering, 2016, 38, 65-72.	3.6	49
15	Enzyme I facilitates reverse flux from pyruvate to phosphoenolpyruvate in Escherichia coli. Nature Communications, 2017, 8, 14316.	5.8	41
16	Metabolism in dense microbial colonies: 13C metabolic flux analysis of E. coli grown on agar identifies two distinct cell populations with acetate cross-feeding. Metabolic Engineering, 2018, 49, 242-247.	3.6	40
17	Metabolic flux responses to deletion of 20 core enzymes reveal flexibility and limits of E. coli metabolism. Metabolic Engineering, 2019, 55, 249-257.	3.6	40
18	Complete genome sequence, metabolic model construction and phenotypic characterization of Geobacillus LC300, an extremely thermophilic, fast growing, xylose-utilizing bacterium. Metabolic Engineering, 2015, 32, 74-81.	3.6	38

#	ARTICLE	IF	CITATIONS
19	13C metabolic flux analysis of three divergent extremely thermophilic bacteria: Geobacillus sp. LC300, Thermus thermophilus HB8, and Rhodothermus marinus DSM 4252. Metabolic Engineering, 2017, 44, 182-190.	3.6	37
20	How adaptive evolution reshapes metabolism to improve fitness: recent advances and future outlook. Current Opinion in Chemical Engineering, 2018, 22, 209-215.	3.8	30
21	Heterotrophic bacteria from an extremely phosphate‐poor lake have conditionally reduced phosphorus demand and utilize diverse sources of phosphorus. Environmental Microbiology, 2016, 18, 656-667.	1.8	29
22	Co-utilization of glucose and xylose by evolved Thermus thermophilus LC113 strain elucidated by 13 C metabolic flux analysis and whole genome sequencing. Metabolic Engineering, 2016, 37, 63-71.	3.6	27