

Stephanie Heux

List of Publications by Year in descending order

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32
papers

1,028
citations

623188

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610482

24
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all docs

34
docs citations

34
times ranked

1440
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the Glucose Fluxotype of the E. coli y-ome Using High-Resolution Fluxomics. <i>Metabolites</i> , 2021, 11, 271.	1.3	5
2	Evaluation of Heterologous Biosynthetic Pathways for Methanol-Based 5-Aminovalerate Production by Thermophilic <i>Bacillus methanolicus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 686319.	2.0	10
3	A tripartite carbohydrate-binding module to functionalize cellulose nanocrystal. <i>Biomaterials Science</i> , 2021, 9, 7444-7455.	2.6	1
4	Aerobic Utilization of Methanol for Microbial Growth and Production. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2021, , .	0.6	3
5	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. <i>PLoS Computational Biology</i> , 2020, 16, e1007799.	1.5	12
6	Charting the Metabolic Landscape of the Facultative Methylotroph <i>Bacillus methanolicus</i> . <i>MSystems</i> , 2020, 5, .	1.7	13
7	Flux Enforcement for Fermentative Production of 5-Aminovalerate and Glutarate by <i>Corynebacterium glutamicum</i> . <i>Catalysts</i> , 2020, 10, 1065.	1.6	18
8	Methanol-Essential Growth of <i>Corynebacterium glutamicum</i> : Adaptive Laboratory Evolution Overcomes Limitation due to Methanethiol Assimilation Pathway. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3617.	1.8	38
9	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
10	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
11	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
12	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
13	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
14	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
15	Functional analysis of isoprenoid precursors biosynthesis by quantitative metabolomics and isotopologue profiling. <i>Metabolomics</i> , 2019, 15, 115.	1.4	8
16	Chemical and Metabolic Controls on Dihydroxyacetone Metabolism Lead to Suboptimal Growth of <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	19
17	MetExplore: collaborative edition and exploration of metabolic networks. <i>Nucleic Acids Research</i> , 2018, 46, W495-W502.	6.5	101
18	Synthetic Methylotrophy: Past, Present, and Future. , 2018, , 133-151.		10

#	ARTICLE	IF	CITATIONS
19	Recent advances in high-throughput ¹³ C-fluxomics. <i>Current Opinion in Biotechnology</i> , 2017, 43, 104-109.	3.3	59
20	Quantitative metabolomics of the thermophilic methylotroph <i>Bacillus methanolicus</i> . <i>Microbial Cell Factories</i> , 2016, 15, 92.	1.9	22
21	Functional characterization of a gene locus from an uncultured gut <i>Bacteroides</i> conferring xylooligosaccharides utilization to <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 102, 579-592.	1.2	20
22	Engineering <i>Escherichia coli</i> for methanol conversion. <i>Metabolic Engineering</i> , 2015, 28, 190-201.	3.6	166
23	Production of carbon-13-labeled cadaverine by engineered <i>Corynebacterium glutamicum</i> using carbon-13-labeled methanol as co-substrate. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10163-10176.	1.7	96
24	A novel platform for automated high-throughput fluxome profiling of metabolic variants. <i>Metabolic Engineering</i> , 2014, 25, 8-19.	3.6	33
25	A high-throughput metabolomics method to predict high concentration cytotoxicity of drugs from low concentration profiles. <i>Metabolomics</i> , 2012, 8, 433-443.	1.4	10
26	High-Throughput Workflow for Monitoring and Mining Bioprocess Data and Its Application to Inferring the Physiological Response of <i>Escherichia coli</i> to Perturbations. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7040-7049.	1.4	10
27	High-Throughput Quantitative Metabolomics: Workflow for Cultivation, Quenching, and Analysis of Yeast in a Multiwell Format. <i>Analytical Chemistry</i> , 2009, 81, 3623-3629.	3.2	86
28	Glucose utilization of strains lacking <i>PGI1</i> and expressing a transhydrogenase suggests differences in the pentose phosphate capacity among <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2008, 8, 217-224.	1.1	26
29	Cofactor engineering in <i>Saccharomyces cerevisiae</i> : Expression of a H ₂ O-forming NADH oxidase and impact on redox metabolism. <i>Metabolic Engineering</i> , 2006, 8, 303-314.	3.6	143
30	Engineering a <i>Saccharomyces cerevisiae</i> Wine Yeast That Exhibits Reduced Ethanol Production during Fermentation under Controlled Microoxygenation Conditions. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5822-5828.	1.4	56
31	The Methylentetrahydrofolate Reductase Gene Variant (C677T) as a Risk Factor for Essential Hypertension in Caucasians. <i>Hypertension Research</i> , 2004, 27, 663-667.	1.5	57
32	From a Hetero- to a Methylotrophic Lifestyle: Flash Back on the Engineering Strategies to Create Synthetic Methanol-User Strains. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	4