

# Stephen S Fong

## List of Publications by Year in descending order

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35  
papers

3,357  
citations

394390

19  
h-index

377849

34  
g-index

35  
all docs

35  
docs citations

35  
times ranked

4167  
citing authors

#	ARTICLE	IF	CITATIONS
1	The vaginal microbiome and preterm birth. <i>Nature Medicine</i> , 2019, 25, 1012-1021.	30.7	600
2	Metabolic Burden: Cornerstones in Synthetic Biology and Metabolic Engineering Applications. <i>Trends in Biotechnology</i> , 2016, 34, 652-664.	9.3	463
3	In silico design and adaptive evolution of <i>Escherichia coli</i> for production of lactic acid. <i>Biotechnology and Bioengineering</i> , 2005, 91, 643-648.	3.3	346
4	Metabolic gene deletion strains of <i>Escherichia coli</i> evolve to computationally predicted growth phenotypes. <i>Nature Genetics</i> , 2004, 36, 1056-1058.	21.4	282
5	Systems approach to refining genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17480-17484.	7.1	262
6	Parallel adaptive evolution cultures of <i>Escherichia coli</i> lead to convergent growth phenotypes with different gene expression states. <i>Genome Research</i> , 2005, 15, 1365-1372.	5.5	246
7	Racioethnic diversity in the dynamics of the vaginal microbiome during pregnancy. <i>Nature Medicine</i> , 2019, 25, 1001-1011.	30.7	204
8	Engineering microbial consortia by division of labor. <i>Microbial Cell Factories</i> , 2019, 18, 35.	4.0	175
9	Latent Pathway Activation and Increased Pathway Capacity Enable <i>Escherichia coli</i> Adaptation to Loss of Key Metabolic Enzymes. <i>Journal of Biological Chemistry</i> , 2006, 281, 8024-8033.	3.4	165
10	Description and Interpretation of Adaptive Evolution of <i>Escherichia coli</i> K-12 MG1655 by Using a Genome-Scale In Silico Metabolic Model. <i>Journal of Bacteriology</i> , 2003, 185, 6400-6408.	2.2	114
11	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
12	Challenges and Advances for Genetic Engineering of Non-model Bacteria and Uses in Consolidated Bioprocessing. <i>Frontiers in Microbiology</i> , 2017, 8, 2060.	3.5	68
13	Recent advances on constraint-based models by integrating machine learning. <i>Current Opinion in Biotechnology</i> , 2020, 64, 85-91.	6.6	46
14	Lack of Overt Genome Reduction in the Bryostatin-Producing Bryozoan Symbiont <i>Candidatus Endobugula sertula</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6573-6583.	3.1	41
15	Single sample resolution of rare microbial dark matter in a marine invertebrate metagenome. <i>Scientific Reports</i> , 2016, 6, 34362.	3.3	34
16	Study of in vitro transcriptional binding effects and noise using constitutive promoters combined with UP element sequences in <i>Escherichia coli</i> . <i>Journal of Biological Engineering</i> , 2017, 11, 33.	4.7	25
17	Genome-scale resources for <i>Thermoanaerobacterium saccharolyticum</i> . <i>BMC Systems Biology</i> , 2015, 9, 30.	3.0	24
18	Toward Engineering Synthetic Microbial Metabolism. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 1-10.	3.0	23

#	ARTICLE	IF	CITATIONS
19	Computational approaches to metabolic engineering utilizing systems biology and synthetic biology. Computational and Structural Biotechnology Journal, 2014, 11, 28-34.	4.1	22
20	Computational Modeling of the Human Microbiome. Microorganisms, 2020, 8, 197.	3.6	22
21	Metabolic Profile of the Cellulolytic Industrial Actinomycete Thermobifida fusca. Metabolites, 2017, 7, 57.	2.9	19
22	Proteomics-based metabolic modeling and characterization of the cellulolytic bacterium Thermobifida fusca. BMC Systems Biology, 2014, 8, 86.	3.0	17
23	Cloning and characterization of a chitinase from Thermobifida fusca reveals Tfu_0580 as a thermostable and acidic endochitinase. Biotechnology Reports (Amsterdam, Netherlands), 2018, 19, e00274.	4.4	17
24	Study of ChiR function in Serratia marcescens and its application for improving 2,3-butanediol from crystal chitin. Applied Microbiology and Biotechnology, 2017, 101, 7567-7578.	3.6	15
25	Increasing carbon source uptake rates to improve chemical productivity in metabolic engineering. Current Opinion in Biotechnology, 2018, 53, 254-263.	6.6	14
26	Design and modularized optimization of one-step production of N-acetylneuraminic acid from chitin in Serratia marcescens. Biotechnology and Bioengineering, 2018, 115, 2255-2267.	3.3	11
27	Leveraging genome-scale metabolic models for human health applications. Current Opinion in Biotechnology, 2020, 66, 267-276.	6.6	9
28	Designing novel cellulase systems through agent-based modeling and global sensitivity analysis. Bioengineered, 2014, 5, 243-253.	3.2	6
29	Assessing Inequitable Urban Heat Islands and Air Pollution Disparities with Low-Cost Sensors in Richmond, Virginia. Sustainability, 2020, 12, 10089.	3.2	5
30	Ex vivo DNA Assembly. Frontiers in Bioengineering and Biotechnology, 2013, 1, 12.	4.1	4
31	Synthetic biology. Bioengineered Bugs, 2010, 1, 309-312.	1.7	3
32	Evaluating the efficiency of a photoelectrochemical electrode constructed with photosystem II-enriched thylakoid membrane fragments. Bioelectrochemistry, 2018, 124, 22-27.	4.6	3
33	Enumeration and Cartesian Product Decomposition of Alternate Optimal Fluxes in Cellular Metabolism. INFORMS Journal on Computing, 2017, 29, 197-210.	1.7	2
34	Metabolic characterization of the chitinolytic bacterium Serratia marcescens using a genome-scale metabolic model. BMC Bioinformatics, 2019, 20, 227.	2.6	2
35	Phenomics. , 2014, , 280-287.		0