

Edward J O'brien

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10690837/publications.pdf>

Version: 2024-02-01

20
papers

2,643
citations

394421

19
h-index

752698

20
g-index

20
all docs

20
docs citations

20
times ranked

3261
citing authors

#	ARTICLE	IF	CITATIONS
1	SER-109, an Investigational Microbiome Drug to Reduce Recurrence After <i>Clostridioides difficile</i> Infection: Lessons Learned From a Phase 2 Trial. <i>Clinical Infectious Diseases</i> , 2021, 72, 2132-2140.	5.8	96
2	A Phase 1b Safety Study of SER-287, a Spore-Based Microbiome Therapeutic, for Active Mild to Moderate Ulcerative Colitis. <i>Gastroenterology</i> , 2021, 160, 115-127.e30.	1.3	48
3	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1007066.	3.2	33
4	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	3.2	17
5	COBRAME: A computational framework for genome-scale models of metabolism and gene expression. <i>PLoS Computational Biology</i> , 2018, 14, e1006302.	3.2	123
6	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. <i>Metabolic Engineering</i> , 2017, 39, 220-227.	7.0	34
7	Thermosensitivity of growth is determined by chaperone-mediated proteome reallocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11548-11553.	7.1	79
8	Quantification and Classification of E. coli Proteome Utilization and Unused Protein Costs across Environments. <i>PLoS Computational Biology</i> , 2016, 12, e1004998.	3.2	100
9	Characterizing Strain Variation in Engineered E. coli Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016, 2, 335-346.	6.2	73
10	Multi-omic data integration enables discovery of hidden biological regularities. <i>Nature Communications</i> , 2016, 7, 13091.	12.8	141
11	Systems biology of the structural proteome. <i>BMC Systems Biology</i> , 2016, 10, 26.	3.0	46
12	Global Rebalancing of Cellular Resources by Pleiotropic Point Mutations Illustrates a Multi-scale Mechanism of Adaptive Evolution. <i>Cell Systems</i> , 2016, 2, 260-271.	6.2	107
13	Using Genome-scale Models to Predict Biological Capabilities. <i>Cell</i> , 2015, 161, 971-987.	28.9	590
14	Computing the functional proteome: recent progress and future prospects for genome-scale models. <i>Current Opinion in Biotechnology</i> , 2015, 34, 125-134.	6.6	59
15	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.	7.1	42
16	Decoding genome-wide GadEWX-transcriptional regulatory networks reveals multifaceted cellular responses to acid stress in Escherichia coli. <i>Nature Communications</i> , 2015, 6, 7970.	12.8	87
17	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of Escherichia coli K-12 MG1655 on Glucose Minimal Medium. <i>Applied and Environmental Microbiology</i> , 2015, 81, 17-30.	3.1	235
18	Reconstruction and modeling protein translocation and compartmentalization in Escherichia coli at the genome-scale. <i>BMC Systems Biology</i> , 2014, 8, 110.	3.0	81

#	ARTICLE	IF	CITATIONS
19	Deciphering Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in Escherichia coli. Nature Communications, 2014, 5, 4910.	12.8	241
20	Genome-scale models of metabolism and gene expression extend and refine growth phenotype prediction. Molecular Systems Biology, 2013, 9, 693.	7.2	411