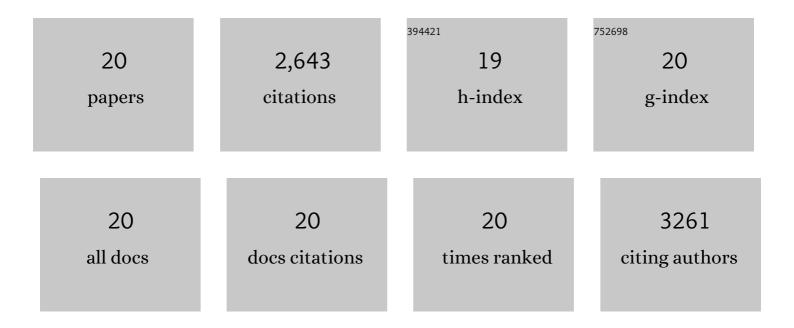
Edward J O'brien

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Using Genome-scale Models to Predict Biological Capabilities. Cell, 2015, 161, 971-987.	28.9	590
2	Genomeâ€scale models of metabolism and gene expression extend and refine growth phenotype prediction. Molecular Systems Biology, 2013, 9, 693.	7.2	411
3	Deciphering Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in Escherichia coli. Nature Communications, 2014, 5, 4910.	12.8	241
4	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of Escherichia coli K-12 MG1655 on Glucose Minimal Medium. Applied and Environmental Microbiology, 2015, 81, 17-30.	3.1	235
5	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	12.8	141
6	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
7	Global Rebalancing of Cellular Resources by Pleiotropic Point Mutations Illustrates a Multi-scale Mechanism of Adaptive Evolution. Cell Systems, 2016, 2, 260-271.	6.2	107
8	Quantification and Classification of E. coli Proteome Utilization and Unused Protein Costs across Environments. PLoS Computational Biology, 2016, 12, e1004998.	3.2	100
9	SER-109, an Investigational Microbiome Drug to Reduce Recurrence After <i>Clostridioides difficile</i> Infection: Lessons Learned From a Phase 2 Trial. Clinical Infectious Diseases, 2021, 72, 2132-2140.	5.8	96
10	Decoding genome-wide GadEWX-transcriptional regulatory networks reveals multifaceted cellular responses to acid stress in Escherichia coli. Nature Communications, 2015, 6, 7970.	12.8	87
11	Reconstruction and modeling protein translocation and compartmentalization in Escherichia coli at the genome-scale. BMC Systems Biology, 2014, 8, 110.	3.0	81
12	Thermosensitivity of growth is determined by chaperone-mediated proteome reallocation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11548-11553.	7.1	79
13	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	6.2	73
14	Computing the functional proteome: recent progress and future prospects for genome-scale models. Current Opinion in Biotechnology, 2015, 34, 125-134.	6.6	59
15	A Phase 1b Safety Study of SER-287, a Spore-Based Microbiome Therapeutic, for Active Mild to Moderate Ulcerative Colitis. Gastroenterology, 2021, 160, 115-127.e30.	1.3	48
16	Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26.	3.0	46
17	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
18	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. Metabolic Engineering, 2017, 39, 220-227.	7.0	34

#	Article	IF	CITATIONS
19	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. PLoS Computational Biology, 2019, 15, e1007066.	3.2	33
20	The genetic basis for adaptation of model-designed syntrophic co-cultures. PLoS Computational Biology, 2019, 15, e1006213.	3.2	17