

# Troy E Sandberg

## List of Publications by Year in descending order

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Version: 2024-02-01

22  
papers

1,540  
citations

516215

16  
h-index

676716

22  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1848  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial fitness landscapes stratify based on proteome allocation associated with discrete aero-types. <i>PLoS Computational Biology</i> , 2021, 17, e1008596.	1.5	14
2	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. <i>Molecular Biology and Evolution</i> , 2020, 37, 660-667.	3.5	52
3	The Bitome: digitized genomic features reveal fundamental genome organization. <i>Nucleic Acids Research</i> , 2020, 48, 10157-10163.	6.5	11
4	Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. <i>Nature Ecology and Evolution</i> , 2020, 4, 1402-1409.	3.4	13
5	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	1.2	23
6	The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. <i>Metabolic Engineering</i> , 2019, 56, 1-16.	3.6	307
7	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14368-14373.	3.3	79
8	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	5.9	21
9	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1007066.	1.5	33
10	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	1.5	17
11	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	3.2	52
12	Evolution of gene knockout strains of <i>E. coli</i> reveal regulatory architectures governed by metabolism. <i>Nature Communications</i> , 2018, 9, 3796.	5.8	59
13	Growth Adaptation of <i>gnd</i> and <i>sdhCB</i> <i>Escherichia coli</i> Deletion Strains Diverges From a Similar Initial Perturbation of the Transcriptome. <i>Frontiers in Microbiology</i> , 2018, 9, 1793.	1.5	23
14	Adaptation to the coupling of glycolysis to toxic methylglyoxal production in <i>tpiA</i> deletion strains of <i>Escherichia coli</i> requires synchronized and counterintuitive genetic changes. <i>Metabolic Engineering</i> , 2018, 48, 82-93.	3.6	38
15	Multiple Optimal Phenotypes Overcome Redox and Glycolytic Intermediate Metabolite Imbalances in <i>Escherichia coli pgi</i> Knockout Evolutions. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	22
16	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in <i>Escherichia coli</i> strains lacking the Phosphotransferase System. <i>Metabolic Engineering</i> , 2018, 48, 233-242.	3.6	43
17	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	76
18	Evolution of <i>E. coli</i> on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. <i>PLoS ONE</i> , 2016, 11, e0151130.	1.1	54

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19	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.	1.4	235
20	Evolution of Escherichia coli to 42 Å°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	3.5	145
21	Fast Metabolic Response to Drug Intervention Through Analysis on a Miniaturized, Highly Integrated Molecular Imaging System. Journal of Nuclear Medicine, 2013, 54, 1820-1824.	2.8	10
22	Human Protein Arginine Methyltransferase 7 (PRMT7) Is a Type III Enzyme Forming I%-N-Monomethylated Arginine Residues. Journal of Biological Chemistry, 2012, 287, 7859-7870.	1.6	208