

Markus J Herrgård

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,272
citations

172457

29
h-index

214800

47
g-index

54
all docs

54
docs citations

54
times ranked

5498
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-scale metabolic modeling of <i>P. thermoglucosidasius</i> NCIMB 11955 reveals metabolic bottlenecks in anaerobic metabolism. <i>Metabolic Engineering</i> , 2021, 65, 123-134.	7.0	14
2	A dual-reporter system for investigating and optimizing protein translation and folding in <i>E. coli</i> . <i>Nature Communications</i> , 2021, 12, 6093.	12.8	12
3	Addressing environmental sustainability of biochemicals. <i>Nature Sustainability</i> , 2020, 3, 167-174.	23.7	112
4	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. <i>Analytical Chemistry</i> , 2020, 92, 15968-15974.	6.5	23
5	Dietary Change Enables Robust Growth-Coupling of Heterologous Methyltransferase Activity in Yeast. <i>ACS Synthetic Biology</i> , 2020, 9, 3408-3415.	3.8	3
6	Combining Environmental and Economic Performance for Bioprocess Optimization. <i>Trends in Biotechnology</i> , 2020, 38, 1203-1214.	9.3	53
7	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
8	Fluctuations in glucose availability prevent global proteome changes and physiological transition during prolonged chemostat cultivations of <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2020, 117, 2074-2088.	3.3	15
9	Integration of enzymatic data in <i>Bacillus subtilis</i> genome-scale metabolic model improves phenotype predictions and enables in silico design of poly- ¹³ C-glutamic acid production strains. <i>Microbial Cell Factories</i> , 2019, 18, 3.	4.0	56
10	OptCouple: Joint simulation of gene knockouts, insertions and medium modifications for prediction of growth-coupled strain designs. <i>Metabolic Engineering Communications</i> , 2019, 8, e00087.	3.6	37
11	MARSI: metabolite analogues for rational strain improvement. <i>Bioinformatics</i> , 2018, 34, 2319-2321.	4.1	7
12	RapidRIP quantifies the intracellular metabolome of 7 industrial strains of <i>E. coli</i> . <i>Metabolic Engineering</i> , 2018, 47, 383-392.	7.0	30
13	Cameo: A Python Library for Computer Aided Metabolic Engineering and Optimization of Cell Factories. <i>ACS Synthetic Biology</i> , 2018, 7, 1163-1166.	3.8	52
14	Selecting the Best: Evolutionary Engineering of Chemical Production in Microbes. <i>Genes</i> , 2018, 9, 249.	2.4	29
15	Microbial Methylophilic Metabolism: Recent Metabolic Modeling Efforts and Their Applications In Industrial Biotechnology. <i>Biotechnology Journal</i> , 2018, 13, e1800011.	3.5	10
16	Computational Methods to Assess the Production Potential of Bio-Based Chemicals. <i>Methods in Molecular Biology</i> , 2018, 1671, 97-116.	0.9	4
17	Increased production of L-serine in <i>Escherichia coli</i> through Adaptive Laboratory Evolution. <i>Metabolic Engineering</i> , 2017, 39, 141-150.	7.0	116
18	Systems biology solutions for biochemical production challenges. <i>Current Opinion in Biotechnology</i> , 2017, 45, 85-91.	6.6	29

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19	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. <i>Microbial Cell Factories</i> , 2017, 16, 204.	4.0	60
20	Stoichiometric Representation of Gene-Protein-Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. <i>PLoS Computational Biology</i> , 2016, 12, e1005140.	3.2	48
21	Seven gene deletions in seven days: Fast generation of <i>Escherichia coli</i> strains tolerant to acetate and osmotic stress. <i>Scientific Reports</i> , 2016, 5, 17874.	3.3	84
22	Engineering and systems-level analysis of <i>Saccharomyces cerevisiae</i> for production of 3-hydroxypropionic acid via malonyl-CoA reductase-dependent pathway. <i>Microbial Cell Factories</i> , 2016, 15, 53.	4.0	98
23	Multi-omics Quantification of Species Variation of <i>Escherichia coli</i> Links Molecular Features with Strain Phenotypes. <i>Cell Systems</i> , 2016, 3, 238-251.e12.	6.2	124
24	Predictable tuning of protein expression in bacteria. <i>Nature Methods</i> , 2016, 13, 233-236.	19.0	116
25	A multi-scale, multi-disciplinary approach for assessing the technological, economic and environmental performance of bio-based chemicals. <i>Biochemical Society Transactions</i> , 2015, 43, 1151-1156.	3.4	3
26	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
27	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 13.	4.1	30
28	Co-evolution of strain design methods based on flux balance and elementary mode analysis. <i>Metabolic Engineering Communications</i> , 2015, 2, 85-92.	3.6	66
29	Multiplex metabolic pathway engineering using CRISPR/Cas9 in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 28, 213-222.	7.0	355
30	Multi-scale exploration of the technical, economic, and environmental dimensions of bio-based chemical production. <i>Metabolic Engineering</i> , 2015, 31, 1-12.	7.0	32
31	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. <i>Nature Communications</i> , 2015, 6, 7101.	12.8	41
32	Establishing a synthetic pathway for high-level production of 3-hydroxypropionic acid in <i>Saccharomyces cerevisiae</i> via β -alanine. <i>Metabolic Engineering</i> , 2015, 27, 57-64.	7.0	185
33	Evolution reveals a glutathione-dependent mechanism of 3-hydroxypropionic acid tolerance. <i>Metabolic Engineering</i> , 2014, 26, 57-66.	7.0	74
34	Combinatorial Strategies for Improving Multiple-Stress Resistance in Industrially Relevant <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6223-6242.	3.1	29
35	Evolution of <i>Escherichia coli</i> to 42 °C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. <i>Molecular Biology and Evolution</i> , 2014, 31, 2647-2662.	8.9	145
36	Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism. <i>PLoS Computational Biology</i> , 2014, 10, e1003580.	3.2	357

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37	Multi-scale modeling for sustainable chemical production. <i>Biotechnology Journal</i> , 2013, 8, 973-984.	3.5	14
38	Model-driven evaluation of the production potential for growth-coupled products of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2010, 12, 173-186.	7.0	221
39	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. <i>BMC Systems Biology</i> , 2009, 3, 37.	3.0	391
40	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	17.5	530
41	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. <i>Nature Protocols</i> , 2007, 2, 727-738.	12.0	757
42	Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2006, 16, 627-635.	5.5	202
43	Untangling the web of functional and physical interactions in yeast. <i>Journal of Biology</i> , 2005, 4, 5.	2.7	4
44	Reconstruction of microbial transcriptional regulatory networks. <i>Current Opinion in Biotechnology</i> , 2004, 15, 70-77.	6.6	149
45	Flagellar Biosynthesis In Silico. <i>Cell</i> , 2004, 117, 689-690.	28.9	4
46	Reconciling Gene Expression Data With Known Genome-Scale Regulatory Network Structures. <i>Genome Research</i> , 2003, 13, 2423-2434.	5.5	96