Markus J HerrgÃ¥rd

List of Publications by Year
in descending order

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	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. Nature Protocols, 2007, 2, 727-738.	12.0	757
2	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
3	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. BMC Systems Biology, 2009, 3, 37.	3.0	391
4	Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism. PLoS Computational Biology, 2014, 10, e1003580.	3.2	357
5	Multiplex metabolic pathway engineering using CRISPR/Cas9 in Saccharomyces cerevisiae. Metabolic Engineering, 2015, 28, 213-222.	7.0	355
6	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
7	Model-driven evaluation of the production potential for growth-coupled products of Escherichia coli. Metabolic Engineering, 2010, 12, 173-186.	7.0	221
8	Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in Saccharomyces cerevisiae. Genome Research, 2006, 16, 627-635.	5.5	202
9	Establishing a synthetic pathway for high-level production of 3-hydroxypropionic acid in Saccharomyces cerevisiae via Î²-alanine. Metabolic Engineering, 2015, 27, 57-64.	7.0	185
10	Reconstruction of microbial transcriptional regulatory networks. Current Opinion in Biotechnology, 2004, 15, 70-77.	6.6	149
11	Evolution of Escherichia coli to 42 Â°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	8.9	145
12	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	6.2	124
13	Predictable tuning of protein expression in bacteria. Nature Methods, 2016, 13, 233-236.	19.0	116
14	Increased production of L-serine in Escherichia coli through Adaptive Laboratory Evolution. Metabolic Engineering, 2017, 39, 141-150.	7.0	116
15	Addressing environmental sustainability of biochemicals. Nature Sustainability, 2020, 3, 167-174.	23.7	112
16	Engineering and systems-level analysis of Saccharomyces cerevisiae for production of 3-hydroxypropionic acid via malonyl-CoA reductase-dependent pathway. Microbial Cell Factories, 2016, 15, 53.	4.0	98
17	Reconciling Gene Expression Data With Known Genome-Scale Regulatory Network Structures. Genome Research, 2003, 13, 2423-2434.	5.5	96
18	Seven gene deletions in seven days: Fast generation of Escherichia coli strains tolerant to acetate and osmotic stress. Scientific Reports, 2016, 5, 17874.	3.3	84

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19	Evolution reveals a glutathione-dependent mechanism of 3-hydroxypropionic acid tolerance. Metabolic Engineering, 2014, 26, 57-66.	7.0	74
20	Do genome‐scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
21	Co-evolution of strain design methods based on flux balance and elementary mode analysis. Metabolic Engineering Communications, 2015, 2, 85-92.	3.6	66
22	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. Microbial Cell Factories, 2017, 16, 204.	4.0	60
23	Integration of enzymatic data in Bacillus subtilis genome-scale metabolic model improves phenotype predictions and enables in silico design of poly-γ-glutamic acid production strains. Microbial Cell Factories, 2019, 18, 3.	4.0	56
24	Combining Environmental and Economic Performance for Bioprocess Optimization. Trends in Biotechnology, 2020, 38, 1203-1214.	9.3	53
25	Cameo: A Python Library for Computer Aided Metabolic Engineering and Optimization of Cell Factories. ACS Synthetic Biology, 2018, 7, 1163-1166.	3.8	52
26	Stoichiometric Representation of Gene–Protein–Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. PLoS Computational Biology, 2016, 12, e1005140.	3.2	48
27	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. Nature Communications, 2015, 6, 7101.	12.8	41
28	OptCouple: Joint simulation of gene knockouts, insertions and medium modifications for prediction of growth-coupled strain designs. Metabolic Engineering Communications, 2019, 8, e00087.	3.6	37
29	Multi-scale exploration of the technical, economic, and environmental dimensions of bio-based chemical production. Metabolic Engineering, 2015, 31, 1-12.	7.0	32
30	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. Frontiers in Bioengineering and Biotechnology, 2015, 3, 13.	4.1	30
31	RapidRIP quantifies the intracellular metabolome of 7 industrial strains of E. coli. Metabolic Engineering, 2018, 47, 383-392.	7.0	30
32	Combinatorial Strategies for Improving Multiple-Stress Resistance in Industrially Relevant Escherichia coli Strains. Applied and Environmental Microbiology, 2014, 80, 6223-6242.	3.1	29
33	Systems biology solutions for biochemical production challenges. Current Opinion in Biotechnology, 2017, 45, 85-91.	6.6	29
34	Selecting the Best: Evolutionary Engineering of Chemical Production in Microbes. Genes, 2018, 9, 249.	2.4	29
35	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. Analytical Chemistry, 2020, 92, 15968-15974.	6.5	23
36	Fluctuations in glucose availability prevent global proteome changes and physiological transition during prolonged chemostat cultivations of Saccharomyces cerevisiae. Biotechnology and Bioengineering, 2020, 117, 2074-2088.	3.3	15

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37	Multi‐scale modeling for sustainable chemical production. Biotechnology Journal, 2013, 8, 973-984.	3.5	14
38	Genome-scale metabolic modeling of P. thermoglucosidasius NCIMB 11955 reveals metabolic bottlenecks in anaerobic metabolism. Metabolic Engineering, 2021, 65, 123-134.	7.0	14
39	A dual-reporter system for investigating and optimizing protein translation and folding in E. coli. Nature Communications, 2021, 12, 6093.	12.8	12
40	Microbial Methylotrophic Metabolism: Recent Metabolic Modeling Efforts and Their Applications In Industrial Biotechnology. Biotechnology Journal, 2018, 13, e1800011.	3.5	10
41	MARSI: metabolite analogues for rational strain improvement. Bioinformatics, 2018, 34, 2319-2321.	4.1	7
42	Flagellar Biosynthesis In Silico. Cell, 2004, 117, 689-690.	28.9	4
43	Untangling the web of functional and physical interactions in yeast. Journal of Biology, 2005, 4, 5.	2.7	4
44	Computational Methods to Assess the Production Potential of Bio-Based Chemicals. Methods in Molecular Biology, 2018, 1671, 97-116.	0.9	4
45	A multi-scale, multi-disciplinary approach for assessing the technological, economic and environmental performance of bio-based chemicals. Biochemical Society Transactions, 2015, 43, 1151-1156.	3.4	3
46	Dietary Change Enables Robust Growth-Coupling of Heterologous Methyltransferase Activity in Yeast. ACS Synthetic Biology, 2020, 9, 3408-3415.	3.8	3