Eduard J Kerkhoven

List of Publications by Year
in descending order

47 papers	2,584 citations	257357 24 h-index	223716 46 g-index
64 all docs	64 docs citations	64 times ranked	2609 citing authors

#	Article	IF	Citations
1	Multiscale models quantifying yeast physiology: towards a whole-cell model. Trends in Biotechnology, 2022, 40, 291-305.	4.9	20
2	Genome-scale metabolic model of oleaginous yeast Papiliotrema laurentii. Biochemical Engineering Journal, 2022, 180, 108353.	1.8	8
3	Improving recombinant protein production by yeast through genome-scale modeling using proteome constraints. Nature Communications, 2022, 13, .	5.8	18
4	Advances in constraint-based models: methods for improved predictive power based on resource allocation constraints. Current Opinion in Microbiology, 2022, 68, 102168.	2.3	9
5	Reconstruction of Genome-Scale Metabolic Model for Hansenula polymorpha Using RAVEN. Methods in Molecular Biology, 2022, , 271-290.	0.4	3
6	Reconstruction of a catalogue of genome-scale metabolic models with enzymatic constraints using GECKO 2.0. Nature Communications, 2022, 13, .	5.8	39
7	Deep learning-based kcat prediction enables improved enzyme-constrained model reconstruction. Nature Catalysis, 2022, 5, 662-672.	16.1	98
8	Evaluating accessibility, usability and interoperability of genome-scale metabolic models for diverse yeasts species. FEMS Yeast Research, 2021, 21, .	1.1	6
9	Reconstruction of a Genome-Scale Metabolic Model of Streptomyces albus J1074: Improved Engineering Strategies in Natural Product Synthesis. Metabolites, 2021, 11, 304.	1.3	12
10	Systems‐level approaches for understanding and engineering of the oleaginous cell factory *Yarrowia lipolytica*. Biotechnology and Bioengineering, 2021, 118, 3640-3654.	1.7	11
11	The yeastGemMap: A process diagram to assist yeast systems‐metabolic studies. Biotechnology and Bioengineering, 2021, 118, 4800-4814.	1.7	1
12	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. Molecular Systems Biology, 2021, 17, e10427.	3.2	17
13	Constraint-based modeling of yeast mitochondria reveals the dynamics of protein import and iron-sulfur cluster biogenesis. IScience, 2021, 24, 103294.	1.9	7
14	Editorial: Multi-Omics Technologies for Optimizing Synthetic Biomanufacturing. Frontiers in Bioengineering and Biotechnology, 2021, 9, 818010.	2.0	1
15	Adaptations in metabolism and protein translation give rise to the Crabtree effect in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	40
16	Nitrogen as the major factor influencing gene expression in Yarrowia lipolytica. Biotechnology Reports (Amsterdam, Netherlands), 2020, 27, e00521.	2.1	18
17	An atlas of human metabolism. Science Signaling, 2020, 13, .	1.6	223
18	Extracting novel hypotheses and findings from RNA-seq data. FEMS Yeast Research, 2020, 20, .	1.1	6

#	Article	IF	Citations
19	C/N ratio and carbon source-dependent lipid production profiling in Rhodotorula toruloides. Applied Microbiology and Biotechnology, 2020, 104, 2639-2649.	1.7	71
20	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	1.9	30
21	A consensus S. cerevisiae metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. Nature Communications, 2019, 10, 3586.	5.8	217
22	Genome-scale model of <i>Rhodotorula toruloides</i> metabolism. Biotechnology and Bioengineering, 2019, 116, 3396-3408.	1.7	55
23	SLIMEr: probing flexibility of lipid metabolism in yeast with an improved constraint-based modeling framework. BMC Systems Biology, 2019, 13, 4.	3.0	43
24	Proteome analysis of xylose metabolism in Rhodotorula toruloides during lipid production. Biotechnology for Biofuels, 2019, 12, 137.	6.2	61
25	Mapping the metabolism of five amino acids in bloodstream form <i>Trypanosoma brucei</i> using U-13C-labelled substrates and LC–MS. Bioscience Reports, 2019, 39, .	1.1	17
26	Investigating the Influence of Glycerol on the Utilization of Glucose in <i>Yarrowia lipolytica</i> Using RNA-Seq-Based Transcriptomics. G3: Genes, Genomes, Genetics, 2019, 9, 4059-4071.	0.8	17
27	Modeling Lipid Metabolism in Yeast. , 2019, , 375-388.		2
28	Regulation of Yeast-to-Hyphae Transition in Yarrowia lipolytica. MSphere, 2018, 3, .	1.3	35
29	Advancing metabolic engineering of Yarrowia lipolytica using the CRISPR/Cas system. Applied Microbiology and Biotechnology, 2018, 102, 9541-9548.	1.7	43
30	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on Streptomyces coelicolor. PLoS Computational Biology, 2018, 14, e1006541.	1.5	228
31	Barriers and opportunities in bio-based production of hydrocarbons. Nature Energy, 2018, 3, 925-935.	19.8	146
32	A molecular genetic toolbox for Yarrowia lipolytica. Biotechnology for Biofuels, 2017, 10, 2.	6.2	62
33	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i>. MBio, 2017, 8, .	1.8	38
34	Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints. Molecular Systems Biology, 2017, 13, 935.	3.2	367
35	Regulation of amino-acid metabolism controls flux to lipid accumulation in Yarrowia lipolytica. Npj Systems Biology and Applications, 2016, 2, 16005.	1.4	141
36	Genome-scale metabolic model of <i>Pichia pastoris</i> with native and humanized glycosylation of recombinant proteins. Biotechnology and Bioengineering, 2016, 113, 961-969.	1.7	43

#	Article	IF	Citations
37	Modeling Lipid Metabolism in Yeast. , 2016, , 1-14.		0
38	Crystal Structure of an Arginase-like Protein from *Trypanosoma brucei* That Evolved without a Binuclear Manganese Cluster. Biochemistry, 2015, 54, 458-471.	1.2	26
39	Probing the Metabolic Network in Bloodstream-Form Trypanosoma brucei Using Untargeted Metabolomics with Stable Isotope Labelled Glucose. PLoS Pathogens, 2015, 11, e1004689.	2.1	128
40	TrypanoCyc: a community-led biochemical pathways database for Trypanosoma brucei. Nucleic Acids Research, 2015, 43, D637-D644.	6.5	35
41	Genome scale metabolic modeling of the riboflavin overproducer *Ashbya gossypii*. Biotechnology and Bioengineering, 2014, 111, 1191-1199.	1.7	35
42	Applications of computational modeling in metabolic engineering of yeast. FEMS Yeast Research, 2014, 15, n/a-n/a.	1.1	28
43	The Silicon Trypanosome. Advances in Microbial Physiology, 2014, 64, 115-143.	1.0	5
44	Trypanosoma brucei: meet the system. Current Opinion in Microbiology, 2014, 20, 162-169.	2.3	10
45	Handling Uncertainty in Dynamic Models: The Pentose Phosphate Pathway in Trypanosoma brucei. PLoS Computational Biology, 2013, 9, e1003371.	1.5	40
46	Dynamic Modelling under Uncertainty: The Case of Trypanosoma brucei Energy Metabolism. PLoS Computational Biology, 2012, 8, e1002352.	1.5	28
47	A domino effect in drug action: from metabolic assault towards parasite differentiation. Molecular Microbiology, 2011, 79, 94-108.	1.2	44