

# Michael Hanscho

## List of Publications by Year in descending order

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1565  
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#	ARTICLE	IF	CITATIONS
1	Inclusion of maintenance energy improves the intracellular flux predictions of CHO. PLoS Computational Biology, 2021, 17, e1009022.	3.2	5
2	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. Metabolic Engineering, 2020, 61, 288-300.	7.0	46
3	Transient manipulation of the expression level of selected growth rate correlating microRNAs does not increase growth rate in CHO-K1 cells. Journal of Biotechnology, 2019, 295, 63-70.	3.8	2
4	Genetic and Epigenetic Variation across Genes Involved in Energy Metabolism and Mitochondria of Chinese Hamster Ovary Cell Lines. Biotechnology Journal, 2019, 14, e1800681.	3.5	13
5	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. Biotechnology and Bioengineering, 2019, 116, 677-692.	3.3	37
6	Designing Optimized Production Hosts by Metabolic Modeling. Methods in Molecular Biology, 2018, 1716, 371-387.	0.9	0
7	What can mathematical modelling say about CHO metabolism and protein glycosylation?. Computational and Structural Biotechnology Journal, 2017, 15, 212-221.	4.1	44
8	On-line clean-up and LC-MS analysis of primary metabolites in cell culture supernatants. Analytical Methods, 2017, 9, 5703-5710.	2.7	2
9	CHOMine: an integrated data warehouse for CHO systems biology and modeling. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	2
10	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. Biotechnology and Bioengineering, 2016, 113, 2241-2253.	3.3	112
11	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
12	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
13	Designing minimal microbial strains of desired functionality using a genetic algorithm. Algorithms for Molecular Biology, 2015, 10, 29.	1.2	6
14	Avoiding the Enumeration of Infeasible Elementary Flux Modes by Including Transcriptional Regulatory Rules in the Enumeration Process Saves Computational Costs. PLoS ONE, 2015, 10, e0129840.	2.5	15
15	Reducing Recon 2 for steady-state flux analysis of HEK cell culture. Journal of Biotechnology, 2014, 184, 172-178.	3.8	54
16	Elementary flux modes in a nutshell: Properties, calculation and applications. Biotechnology Journal, 2013, 8, 1009-1016.	3.5	91
17	Nutritional requirements of the BY series of <i>Saccharomyces cerevisiae</i> strains for optimum growth. FEMS Yeast Research, 2012, 12, 796-808.	2.3	96