

Jürgen Zanghellini

List of Publications by Year in descending order

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63
papers

2,484
citations

218592

26
h-index

214721

47
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79
all docs

79
docs citations

79
times ranked

2712
citing authors

#	ARTICLE	IF	CITATIONS
1	Elementary vectors and autocatalytic sets for resource allocation in next-generation models of cellular growth. <i>PLoS Computational Biology</i> , 2022, 18, e1009843.	1.5	6
2	PeakBot: machine-learning-based chromatographic peak picking. <i>Bioinformatics</i> , 2022, 38, 3422-3428.	1.8	10
3	Error propagation in constraint-based modeling of Chinese hamster ovary cells. <i>Biotechnology Journal</i> , 2021, 16, e2000320.	1.8	4
4	Inclusion of maintenance energy improves the intracellular flux predictions of CHO. <i>PLoS Computational Biology</i> , 2021, 17, e1009022.	1.5	5
5	Thermodynamic Genome-Scale Metabolic Modeling of Metallo-drug Resistance in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 4130.	1.7	5
6	Towards rational glyco-engineering in CHO: from data to predictive models. <i>Current Opinion in Biotechnology</i> , 2021, 71, 9-17.	3.3	9
7	Finger sweat analysis enables short interval metabolic biomonitoring in humans. <i>Nature Communications</i> , 2021, 12, 5993.	5.8	28
8	EFMLrs: a Python package for elementary flux mode enumeration via lexicographic reverse search. <i>BMC Bioinformatics</i> , 2021, 22, 547.	1.2	7
9	The secretome of <i>Pichia pastoris</i> in fed-batch cultivations is largely independent of the carbon source but changes quantitatively over cultivation time. <i>Microbial Biotechnology</i> , 2020, 13, 479-494.	2.0	15
10	The sources and transmission routes of microbial populations throughout a meat processing facility. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 26.	2.9	63
11	Environmental flexibility does not explain metabolic robustness. <i>Npj Systems Biology and Applications</i> , 2020, 6, 39.	1.4	2
12	Key Challenges in Designing CHO Chassis Platforms. <i>Processes</i> , 2020, 8, 643.	1.3	9
13	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. <i>Metabolic Engineering</i> , 2020, 61, 288-300.	3.6	46
14	Robust Analytical Methods for the Accurate Quantification of the Total Biomass Composition of Mammalian Cells. <i>Methods in Molecular Biology</i> , 2020, 2088, 119-160.	0.4	7
15	Genetic and Epigenetic Variation across Genes Involved in Energy Metabolism and Mitochondria of Chinese Hamster Ovary Cell Lines. <i>Biotechnology Journal</i> , 2019, 14, e1800681.	1.8	13
16	Dissecting peak broadening in chromatography columns under non-binding conditions. <i>Journal of Chromatography A</i> , 2019, 1599, 55-65.	1.8	14
17	Flux tope analysis: studying the coordination of reaction directions in metabolic networks. <i>Bioinformatics</i> , 2019, 35, 266-273.	1.8	14
18	Combinatorial in Vitro and in Silico Approach To Describe Shear-Force Dependent Uptake of Nanoparticles in Microfluidic Vascular Models. <i>Analytical Chemistry</i> , 2018, 90, 3651-3655.	3.2	14

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19	Metabolic engineering of <i>Pichia pastoris</i> . <i>Metabolic Engineering</i> , 2018, 50, 2-15.	3.6	163
20	Comprehensive assessment of measurement uncertainty in ¹³ C-based metabolic flux experiments. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 3337-3348.	1.9	18
21	A mathematical framework for yield (vs. rate) optimization in constraint-based modeling and applications in metabolic engineering. <i>Metabolic Engineering</i> , 2018, 47, 153-169.	3.6	37
22	Designing Optimized Production Hosts by Metabolic Modeling. <i>Methods in Molecular Biology</i> , 2018, 1716, 371-387.	0.4	0
23	Microfluidic Migration and Wound Healing Assay Based on Mechanically Induced Injuries of Defined and Highly Reproducible Areas. <i>Analytical Chemistry</i> , 2017, 89, 2326-2333.	3.2	42
24	What can mathematical modelling say about CHO metabolism and protein glycosylation?. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 212-221.	1.9	44
25	Optimal knockout strategies in genome-scale metabolic networks using particle swarm optimization. <i>BMC Bioinformatics</i> , 2017, 18, 78.	1.2	9
26	CHOMine: an integrated data warehouse for CHO systems biology and modeling. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	2
27	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. <i>PLoS Computational Biology</i> , 2017, 13, e1005409.	1.5	60
28	<i>iCT</i> : isotope correction toolbox. <i>Bioinformatics</i> , 2016, 32, 154-156.	1.8	42
29	Which sets of elementary flux modes form thermodynamically feasible flux distributions?. <i>FEBS Journal</i> , 2016, 283, 1782-1794.	2.2	14
30	Exact quantification of cellular robustness in genome-scale metabolic networks. <i>Bioinformatics</i> , 2016, 32, 730-737.	1.8	15
31	Designing minimal microbial strains of desired functionality using a genetic algorithm. <i>Algorithms for Molecular Biology</i> , 2015, 10, 29.	0.3	6
32	Avoiding the Enumeration of Infeasible Elementary Flux Modes by Including Transcriptional Regulatory Rules in the Enumeration Process Saves Computational Costs. <i>PLoS ONE</i> , 2015, 10, e0129840.	1.1	15
33	The 3D pore structure and fluid dynamics simulation of macroporous monoliths: High permeability due to alternating channel width. <i>Journal of Chromatography A</i> , 2015, 1425, 141-149.	1.8	37
34	tEFMA: computing thermodynamically feasible elementary flux modes in metabolic networks. <i>Bioinformatics</i> , 2015, 31, 2232-2234.	1.8	49
35	Predicting genetic engineering targets with Elementary Flux Mode Analysis: a review of four current methods. <i>New Biotechnology</i> , 2015, 32, 534-546.	2.4	9
36	Quantitative Analysis of Proteome and Lipidome Dynamics Reveals Functional Regulation of Global Lipid Metabolism. <i>Chemistry and Biology</i> , 2015, 22, 412-425.	6.2	77

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37	Metabolomics integrated elementary flux mode analysis in large metabolic networks. Scientific Reports, 2015, 5, 8930.	1.6	49
38	Design of Optimally Constructed Metabolic Networks of Minimal Functionality. PLoS ONE, 2014, 9, e92583.	1.1	15
39	The response of the maize nitrate transport system to nitrogen demand and supply across the lifecycle. New Phytologist, 2013, 198, 82-94.	3.5	108
40	Elementary flux modes in a nutshell: Properties, calculation and applications. Biotechnology Journal, 2013, 8, 1009-1016.	1.8	91
41	regEfmtool: Speeding up elementary flux mode calculation using transcriptional regulatory rules in the form of three-state logic. BioSystems, 2013, 113, 37-39.	0.9	47
42	Fast Computation of Minimal Cut Sets in Metabolic Networks with a Berge Algorithm that Utilizes Binary Bit Pattern Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1-1.	1.9	8
43	Comparison and improvement of algorithms for computing minimal cut sets. BMC Bioinformatics, 2013, 14, 318.	1.2	22
44	Nutritional requirements of the BY series of <i>Saccharomyces cerevisiae</i> strains for optimum growth. FEMS Yeast Research, 2012, 12, 796-808.	1.1	96
45	Designing optimal cell factories: integer programming couples elementary mode analysis with regulation. BMC Systems Biology, 2012, 6, 103.	3.0	26
46	Improving the measurement sensitivity of interdigital dielectric capacitors (IDC) by optimizing the dielectric property of the homogeneous passivation layer. Sensors and Actuators B: Chemical, 2012, 162, 418-424.	4.0	7
47	3D numerical simulation of a lab-on-a-chipâ€”increasing measurement sensitivity of interdigitated capacitors by passivation optimization. Lab on A Chip, 2011, 11, 1318.	3.1	20
48	Phospholipid demixing and the birth of a lipid droplet. Journal of Theoretical Biology, 2010, 264, 952-961.	0.8	61
49	Phospholipid Demixing. Behavior Research Methods, 2010, , 1-28.	2.3	2
50	A Comparative Study of Shear Stresses in Collagen-Glycosaminoglycan and Calcium Phosphate Scaffolds in Bone Tissue-Engineering Bioreactors. Tissue Engineering - Part A, 2009, 15, 1141-1149.	1.6	77
51	Deformation simulation of cells seeded on a collagen-GAG scaffold in a flow perfusion bioreactor using a sequential 3D CFD-elastostatics model. Medical Engineering and Physics, 2009, 31, 420-427.	0.8	84
52	Quantitative modeling of triacylglycerol homeostasis in yeast â€” metabolic requirement for lipolysis to promote membrane lipid synthesis and cellular growth. FEBS Journal, 2008, 275, 5552-5563.	2.2	54
53	Ion charge state distribution in the laser-induced Coulomb explosion of argon clusters. Journal of Physics B: Atomic, Molecular and Optical Physics, 2006, 39, 625-632.	0.6	19
54	Plasmon signatures in high harmonic generation. Journal of Physics B: Atomic, Molecular and Optical Physics, 2006, 39, 709-718.	0.6	24

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55	FEW/MANY BODY DYNAMICS IN STRONG LASER FIELDS. , 2006, , .		0
56	Multi-electron dynamics in strong laser fields. Journal of Modern Optics, 2005, 52, 479-488.	0.6	9
57	The softening of two-dimensional colloidal crystals. Journal of Physics Condensed Matter, 2005, 17, S3579-S3586.	0.7	24
58	Intense VUV laser cluster interaction in the strong coupling regime. Journal of Physics B: Atomic, Molecular and Optical Physics, 2005, 38, 3029-3036.	0.6	87
59	Shakeup Excitation during Optical Tunnel Ionization. Physical Review Letters, 2005, 94, 033003.	2.9	58
60	Correlated multielectron systems in strong laser fields: A multiconfiguration time-dependent Hartree-Fock approach. Physical Review A, 2005, 71, .	1.0	279
61	Microscopic Analysis of Large-Cluster Explosion in Intense Laser Fields. Physical Review Letters, 2004, 92, 133401.	2.9	139
62	Ionization dynamics of extended multielectron systems. Physical Review A, 2004, 70, .	1.0	51
63	Testing the multi-configuration time-dependent Hartree-Fock method. Journal of Physics B: Atomic, Molecular and Optical Physics, 2004, 37, 763-773.	0.6	105