

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	Correlated multielectron systems in strong laser fields: A multiconfiguration time-dependent Hartree-Fock approach. <i>Physical Review A</i> , 2005, 71, .	1.0	279
2	Metabolic engineering of <i>Pichia pastoris</i> . <i>Metabolic Engineering</i> , 2018, 50, 2-15.	3.6	163
3	Microscopic Analysis of Large-Cluster Explosion in Intense Laser Fields. <i>Physical Review Letters</i> , 2004, 92, 133401.	2.9	139
4	The response of the maize nitrate transport system to nitrogen demand and supply across the lifecycle. <i>New Phytologist</i> , 2013, 198, 82-94.	3.5	108
5	Testing the multi-configuration time-dependent Hartree-Fock method. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2004, 37, 763-773.	0.6	105
6	Nutritional requirements of the BY series of <i>Saccharomyces cerevisiae</i> strains for optimum growth. <i>FEMS Yeast Research</i> , 2012, 12, 796-808.	1.1	96
7	Elementary flux modes in a nutshell: Properties, calculation and applications. <i>Biotechnology Journal</i> , 2013, 8, 1009-1016.	1.8	91
8	Intense VUV laser cluster interaction in the strong coupling regime. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2005, 38, 3029-3036.	0.6	87
9	Deformation simulation of cells seeded on a collagen-GAG scaffold in a flow perfusion bioreactor using a sequential 3D CFD-elastostatics model. <i>Medical Engineering and Physics</i> , 2009, 31, 420-427.	0.8	84
10	A Comparative Study of Shear Stresses in Collagen-Glycosaminoglycan and Calcium Phosphate Scaffolds in Bone Tissue-Engineering Bioreactors. <i>Tissue Engineering - Part A</i> , 2009, 15, 1141-1149.	1.6	77
11	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
12	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
13	Phospholipid demixing and the birth of a lipid droplet. <i>Journal of Theoretical Biology</i> , 2010, 264, 952-961.	0.8	61
14	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
15	Shakeup Excitation during Optical Tunnel Ionization. <i>Physical Review Letters</i> , 2005, 94, 033003.	2.9	58
16	Quantitative modeling of triacylglycerol homeostasis in yeast - metabolic requirement for lipolysis to promote membrane lipid synthesis and cellular growth. <i>FEBS Journal</i> , 2008, 275, 5552-5563.	2.2	54
17	Ionization dynamics of extended multielectron systems. <i>Physical Review A</i> , 2004, 70, .	1.0	51
18	tEFMA: computing thermodynamically feasible elementary flux modes in metabolic networks. <i>Bioinformatics</i> , 2015, 31, 2232-2234.	1.8	49

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19	Metabolomics integrated elementary flux mode analysis in large metabolic networks. Scientific Reports, 2015, 5, 8930.	1.6	49
20	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
21	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. Metabolic Engineering, 2020, 61, 288-300.	3.6	46
22	What can mathematical modelling say about CHO metabolism and protein glycosylation?. Computational and Structural Biotechnology Journal, 2017, 15, 212-221.	1.9	44
23	<i>ICT</i>: isotope correction toolbox. Bioinformatics, 2016, 32, 154-156.	1.8	42
24	Microfluidic Migration and Wound Healing Assay Based on Mechanically Induced Injuries of Defined and Highly Reproducible Areas. Analytical Chemistry, 2017, 89, 2326-2333.	3.2	42
25	The 3D pore structure and fluid dynamics simulation of macroporous monoliths: High permeability due to alternating channel width. Journal of Chromatography A, 2015, 1425, 141-149.	1.8	37
26	A mathematical framework for yield (vs. rate) optimization in constraint-based modeling and applications in metabolic engineering. Metabolic Engineering, 2018, 47, 153-169.	3.6	37
27	Finger sweat analysis enables short interval metabolic biomonitoring in humans. Nature Communications, 2021, 12, 5993.	5.8	28
28	Designing optimal cell factories: integer programming couples elementary mode analysis with regulation. BMC Systems Biology, 2012, 6, 103.	3.0	26
29	The softening of two-dimensional colloidal crystals. Journal of Physics Condensed Matter, 2005, 17, S3579-S3586.	0.7	24
30	Plasmon signatures in high harmonic generation. Journal of Physics B: Atomic, Molecular and Optical Physics, 2006, 39, 709-718.	0.6	24
31	Comparison and improvement of algorithms for computing minimal cut sets. BMC Bioinformatics, 2013, 14, 318.	1.2	22
32	3D numerical simulation of a lab-on-a-chipâ€™s increasing measurement sensitivity of interdigitated capacitors by passivation optimization. Lab on A Chip, 2011, 11, 1318.	3.1	20
33	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
34	Comprehensive assessment of measurement uncertainty in ¹³ C-based metabolic flux experiments. Analytical and Bioanalytical Chemistry, 2018, 410, 3337-3348.	1.9	18
35	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.	1.1	15
36	Exact quantification of cellular robustness in genome-scale metabolic networks. Bioinformatics, 2016, 32, 730-737.	1.8	15

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37	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
38	Design of Optimally Constructed Metabolic Networks of Minimal Functionality. <i>PLoS ONE</i> , 2014, 9, e92583.	1.1	15
39	Which sets of elementary flux modes form thermodynamically feasible flux distributions?. <i>FEBS Journal</i> , 2016, 283, 1782-1794.	2.2	14
40	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
41	Dissecting peak broadening in chromatography columns under non-binding conditions. <i>Journal of Chromatography A</i> , 2019, 1599, 55-65.	1.8	14
42	Flux tope analysis: studying the coordination of reaction directions in metabolic networks. <i>Bioinformatics</i> , 2019, 35, 266-273.	1.8	14
43	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
44	PeakBot: machine-learning-based chromatographic peak picking. <i>Bioinformatics</i> , 2022, 38, 3422-3428.	1.8	10
45	Multi-electron dynamics in strong laser fields. <i>Journal of Modern Optics</i> , 2005, 52, 479-488.	0.6	9
46	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
47	Optimal knockout strategies in genome-scale metabolic networks using particle swarm optimization. <i>BMC Bioinformatics</i> , 2017, 18, 78.	1.2	9
48	Key Challenges in Designing CHO Chassis Platforms. <i>Processes</i> , 2020, 8, 643.	1.3	9
49	Towards rational glyco-engineering in CHO: from data to predictive models. <i>Current Opinion in Biotechnology</i> , 2021, 71, 9-17.	3.3	9
50	Fast Computation of Minimal Cut Sets in Metabolic Networks with a Berge Algorithm that Utilizes Binary Bit Pattern Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1-1.	1.9	8
51	Improving the measurement sensitivity of interdigital dielectric capacitors (IDC) by optimizing the dielectric property of the homogeneous passivation layer. <i>Sensors and Actuators B: Chemical</i> , 2012, 162, 418-424.	4.0	7
52	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
53	EFMLrs: a Python package for elementary flux mode enumeration via lexicographic reverse search. <i>BMC Bioinformatics</i> , 2021, 22, 547.	1.2	7
54	Designing minimal microbial strains of desired functionality using a genetic algorithm. <i>Algorithms for Molecular Biology</i> , 2015, 10, 29.	0.3	6

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55	Elementary vectors and autocatalytic sets for resource allocation in next-generation models of cellular growth. PLoS Computational Biology, 2022, 18, e1009843.	1.5	6
56	Inclusion of maintenance energy improves the intracellular flux predictions of CHO. PLoS Computational Biology, 2021, 17, e1009022.	1.5	5
57	Thermodynamic Genome-Scale Metabolic Modeling of Metallo drug Resistance in Colorectal Cancer. Cancers, 2021, 13, 4130.	1.7	5
58	Error propagation in constraint-based modeling of Chinese hamster ovary cells. Biotechnology Journal, 2021, 16, e2000320.	1.8	4
59	CHOMine: an integrated data warehouse for CHO systems biology and modeling. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	2
60	Environmental flexibility does not explain metabolic robustness. Npj Systems Biology and Applications, 2020, 6, 39.	1.4	2
61	Phospholipid Demixing. Behavior Research Methods, 2010, , 1-28.	2.3	2
62	Designing Optimized Production Hosts by Metabolic Modeling. Methods in Molecular Biology, 2018, 1716, 371-387.	0.4	0
63	FEW/MANY BODY DYNAMICS IN STRONG LASER FIELDS. , 2006, , .		0