

# Daniel Weindl

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2377107/publications.pdf>

Version: 2024-02-01

26  
papers

1,421  
citations

516710

16  
h-index

580821

25  
g-index

33  
all docs

33  
docs citations

33  
times ranked

2571  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mini-batch optimization enables training of ODE models on large-scale datasets. Nature Communications, 2022, 13, 34.	12.8	8
2	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
3	PEtab – Interoperable specification of parameter estimation problems in systems biology. PLoS Computational Biology, 2021, 17, e1008646.	3.2	55
4	AMICI: high-performance sensitivity analysis for large ordinary differential equation models. Bioinformatics, 2021, 37, 3676-3677.	4.1	45
5	Efficient gradient-based parameter estimation for dynamic models using qualitative data. Bioinformatics, 2021, 37, 4493-4500.	4.1	6
6	Dynamic models for metabolomics data integration. Current Opinion in Systems Biology, 2021, 28, 100358.	2.6	3
7	Efficient parameterization of large-scale dynamic models based on relative measurements. Bioinformatics, 2020, 36, 594-602.	4.1	32
8	Parameterization of mechanistic models from qualitative data using an efficient optimal scaling approach. Journal of Mathematical Biology, 2020, 81, 603-623.	1.9	8
9	Benchmarking optimization methods for parameter estimation in large kinetic models. Bioinformatics, 2019, 35, 830-838.	4.1	90
10	Efficient computation of steady states in large-scale ODE models of biochemical reaction networks. IFAC-PapersOnLine, 2019, 52, 32-37.	0.9	4
11	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	6.5	48
12	PESTO: Parameter ESTimation TOolbox. Bioinformatics, 2018, 34, 705-707.	4.1	83
13	Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. Cell Systems, 2018, 7, 567-579.e6.	6.2	99
14	LNA++: Linear Noise Approximation with First and Second Order Sensitivities. Lecture Notes in Computer Science, 2018, , 300-306.	1.3	0
15	MIA: non-targeted mass isotopologue analysis. Bioinformatics, 2016, 32, 2875-2876.	4.1	21
16	Bridging the gap between non-targeted stable isotope labeling and metabolic flux analysis. Cancer & Metabolism, 2016, 4, 10.	5.0	28
17	Loss of DJ-1 impairs antioxidant response by altered glutamine and serine metabolism. Neurobiology of Disease, 2016, 89, 112-125.	4.4	47
18	Non-targeted Tracer Fate Detection. Methods in Enzymology, 2015, 561, 277-302.	1.0	13

#	ARTICLE	IF	CITATIONS
19	Metabolome-Wide Analysis of Stable Isotope Labelingâ€”Is It Worth the Effort?. <i>Frontiers in Physiology</i> , 2015, 6, 344.	2.8	15
20	Isotopologue ratio normalization for non-targeted metabolomics. <i>Journal of Chromatography A</i> , 2015, 1389, 112-119.	3.7	20
21	How metabolites modulate metabolic flux. <i>Current Opinion in Biotechnology</i> , 2015, 34, 16-22.	6.6	88
22	Fragment Formula Calculator (FFC): Determination of Chemical Formulas for Fragment Ions in Mass Spectrometric Data. <i>Analytical Chemistry</i> , 2014, 86, 2221-2228.	6.5	26
23	Simultaneous extraction of proteins and metabolites from cells in culture. <i>MethodsX</i> , 2014, 1, 74-80.	1.6	125
24	Complexity of dopamine metabolism. <i>Cell Communication and Signaling</i> , 2013, 11, 34.	6.5	468
25	Isotope Cluster-Based Compound Matching in Gas Chromatography/Mass Spectrometry for Non-Targeted Metabolomics. <i>Analytical Chemistry</i> , 2013, 85, 4030-4037.	6.5	15
26	NTFDâ€”a stand-alone application for the non-targeted detection of stable isotope-labeled compounds in GC/MS data. <i>Bioinformatics</i> , 2013, 29, 1226-1228.	4.1	37