

# 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	Complexity of dopamine metabolism. <i>Cell Communication and Signaling</i> , 2013, 11, 34.	6.5	468
2	Simultaneous extraction of proteins and metabolites from cells in culture. <i>MethodsX</i> , 2014, 1, 74-80.	1.6	125
3	Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. <i>Cell Systems</i> , 2018, 7, 567-579.e6.	6.2	99
4	Benchmarking optimization methods for parameter estimation in large kinetic models. <i>Bioinformatics</i> , 2019, 35, 830-838.	4.1	90
5	How metabolites modulate metabolic flux. <i>Current Opinion in Biotechnology</i> , 2015, 34, 16-22.	6.6	88
6	PESTO: Parameter ESTimation TOolbox. <i>Bioinformatics</i> , 2018, 34, 705-707.	4.1	83
7	PEtabâ€”Interoperable specification of parameter estimation problems in systems biology. <i>PLoS Computational Biology</i> , 2021, 17, e1008646.	3.2	55
8	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019, 20, 659-670.	6.5	48
9	Loss of DJ-1 impairs antioxidant response by altered glutamine and serine metabolism. <i>Neurobiology of Disease</i> , 2016, 89, 112-125.	4.4	47
10	AMICI: high-performance sensitivity analysis for large ordinary differential equation models. <i>Bioinformatics</i> , 2021, 37, 3676-3677.	4.1	45
11	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
12	Efficient parameterization of large-scale dynamic models based on relative measurements. <i>Bioinformatics</i> , 2020, 36, 594-602.	4.1	32
13	Bridging the gap between non-targeted stable isotope labeling and metabolic flux analysis. <i>Cancer &amp; Metabolism</i> , 2016, 4, 10.	5.0	28
14	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
15	MIA: non-targeted mass isotopologue analysis. <i>Bioinformatics</i> , 2016, 32, 2875-2876.	4.1	21
16	Isotopologue ratio normalization for non-targeted metabolomics. <i>Journal of Chromatography A</i> , 2015, 1389, 112-119.	3.7	20
17	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
18	Metabolome-Wide Analysis of Stable Isotope Labelingâ€”Is It Worth the Effort?. <i>Frontiers in Physiology</i> , 2015, 6, 344.	2.8	15

#	ARTICLE	IF	CITATIONS
19	Non-targeted Tracer Fate Detection. <i>Methods in Enzymology</i> , 2015, 561, 277-302.	1.0	13
20	BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> , 2022, 50, W108-W114.	14.5	11
21	Parameterization of mechanistic models from qualitative data using an efficient optimal scaling approach. <i>Journal of Mathematical Biology</i> , 2020, 81, 603-623.	1.9	8
22	Mini-batch optimization enables training of ODE models on large-scale datasets. <i>Nature Communications</i> , 2022, 13, 34.	12.8	8
23	Efficient gradient-based parameter estimation for dynamic models using qualitative data. <i>Bioinformatics</i> , 2021, 37, 4493-4500.	4.1	6
24	Efficient computation of steady states in large-scale ODE models of biochemical reaction networks. <i>IFAC-PapersOnLine</i> , 2019, 52, 32-37.	0.9	4
25	Dynamic models for metabolomics data integration. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100358.	2.6	3
26	LNA++: Linear Noise Approximation with First and Second Order Sensitivities. <i>Lecture Notes in Computer Science</i> , 2018, , 300-306.	1.3	0