

# Dagmar Waltemath

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

1,818  
citations

430874

18  
h-index

330143

37  
g-index

86  
all docs

86  
docs citations

86  
times ranked

2277  
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the evolution of biochemical models at the network level. PLoS ONE, 2022, 17, e0265735.	2.5	0
2	Opportunities of Digital Infrastructures for Disease Management—Exemplified on COVID-19-Related Change in Diagnosis Counts for Diabetes-Related Eye Diseases. Nutrients, 2022, 14, 2016.	4.1	4
3	Addressing barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology. Briefings in Bioinformatics, 2022, 23, .	6.5	10
4	Overview: Standards for Modeling in Systems Medicine. , 2021, , 345-353.		4
5	Initiatives, Concepts, and Implementation Practices of FAIR (Findable, Accessible, Interoperable, and) Research Protocols, 2021, 10, e22505.	1.0	25
6	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. Briefings in Bioinformatics, 2021, 22, .	6.5	4
7	Facilitating Study and Item Level Browsing for Clinical and Epidemiological COVID-19 Studies. Studies in Health Technology and Informatics, 2021, 281, 794-798.	0.3	3
8	Approaches and Criteria for Provenance in Biomedical Data Sets and Workflows: Protocol for a Scoping Review. JMIR Research Protocols, 2021, 10, e31750.	1.0	15
9	OMEX metadata specification (version 1.2). Journal of Integrative Bioinformatics, 2021, 18, .	1.5	8
10	Specifications of standards in systems and synthetic biology: status and developments in 2021. Journal of Integrative Bioinformatics, 2021, 18, .	1.5	2
11	The simulation experiment description markup language (SED-ML): language specification for level 1 version 4. Journal of Integrative Bioinformatics, 2021, 18, 20210021.	1.5	8
12	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). Journal of Integrative Bioinformatics, 2020, 17, .	1.5	18
13	Towards standardization guidelines for <i>in silico</i> approaches in personalized medicine. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	9
14	Specifications of standards in systems and synthetic biology: status and developments in 2020. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	10
15	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
16	Open modeling and exchange (OMEX) metadata specification version 1.0. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	9
17	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2019. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	7
18	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	78

#	ARTICLE	IF	CITATIONS
19	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	6.5	52
20	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. <i>Methods in Molecular Biology</i> , 2019, 2049, 285-314.	0.9	3
21	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw090.	6.5	17
22	Evolution of computational models in BioModels Database and the Physiome Model Repository. <i>BMC Systems Biology</i> , 2018, 12, 53.	3.0	3
23	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2017. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	7
24	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 3 (L1V3). <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	27
25	Identifying frequent patterns in biochemical reaction networks: a workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	8
26	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	13
27	The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	57
28	Quick tips for creating effective and impactful biological pathways using the Systems Biology Graphical Notation. <i>PLoS Computational Biology</i> , 2018, 14, e1005740.	3.2	6
29	The JWS online simulation database. <i>Bioinformatics</i> , 2017, 33, 1589-1590.	4.1	28
30	SED-ML web tools: generate, modify and export standard-compliant simulation studies. <i>Bioinformatics</i> , 2017, 33, 1253-1254.	4.1	7
31	A brief history of COMBINE. , 2017, , .		6
32	How Modeling Standards, Software, and Initiatives Support Reproducibility in Systems Biology and Systems Medicine. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 1999-2006.	4.2	43
33	Toward Community Standards and Software for Whole-Cell Modeling. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 2007-2014.	4.2	51
34	STON: exploring biological pathways using the SBGN standard and graph databases. <i>BMC Bioinformatics</i> , 2016, 17, 494.	2.6	19
35	Specifications of Standards in Systems and Synthetic Biology: Status and Developments in 2016. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 1-7.	1.5	12
36	COMODI: an ontology to characterise differences in versions of computational models in biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 46.	1.6	15

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37	An algorithm to detect and communicate the differences in computational models describing biological systems. <i>Bioinformatics</i> , 2016, 32, 563-570.	4.1	23
38	A fully featured COMBINE archive of a simulation study on syncytial mitotic cycles in <i>Drosophila</i> embryos. <i>F1000Research</i> , 2016, 5, 2421.	1.6	10
39	Combining computational models, semantic annotations and simulation experiments in a graph database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	42
40	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 1-3.	1.5	11
41	Simulation Experiment Description Markup Language (SED-ML) Level 1 Version 2. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 119-212.	1.5	10
42	Systems Biology Markup Language (SBML) Level 2 Version 5: Structures and Facilities for Model Definitions. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 731-901.	1.5	7
43	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19.	4.1	72
44	Annotation-based feature extraction from sets of SBML models. <i>Journal of Biomedical Semantics</i> , 2015, 6, 20.	1.6	13
45	A call for virtual experiments: Accelerating the scientific process. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 99-106.	2.9	31
46	Specifications of Standards in Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 258.	1.5	14
47	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. <i>BMC Bioinformatics</i> , 2014, 15, 369.	2.6	114
48	Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). <i>Standards in Genomic Sciences</i> , 2014, 9, 1285-1301.	1.5	21
49	Information Retrieval in Life Sciences: A Programmatic Survey. , 2014, , 73-109.		6
50	Annotation-Based Feature Extraction from Sets of SBML Models. <i>Lecture Notes in Computer Science</i> , 2014, , 81-95.	1.3	1
51	Improving the reuse of computational models through version control. <i>Bioinformatics</i> , 2013, 29, 742-748.	4.1	21
52	Reproducibility of Model-Based Results in Systems Biology. , 2013, , 301-320.		7
53	SBML Level 3 Package Proposal: Annotation. <i>Nature Precedings</i> , 2011, , .	0.1	1
54	Simulation Experiment Description Markup Language (SED-ML) : Level 1 Version 1. <i>Nature Precedings</i> , 2011, , .	0.1	6

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55	Reproducible computational biology experiments with SED-ML - The Simulation Experiment Description Markup Language. BMC Systems Biology, 2011, 5, 198.	3.0	211
56	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
57	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
58	Ranked retrieval of Computational Biology models. BMC Bioinformatics, 2010, 11, 423.	2.6	24
59	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 0, , .	0.1	1