Nicolas Rodriguez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6841019/publications.pdf

Version: 2024-02-01

23 papers 2,342 citations

394421 19 h-index 24 g-index

29 all docs 29 docs citations

29 times ranked 3384 citing authors

#	Article	IF	CITATIONS
1	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467
2	BioModels: ten-year anniversary. Nucleic Acids Research, 2015, 43, D542-D548.	14.5	334
3	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
4	$\langle \text{scp} \rangle \text{SBML} \langle \text{scp} \rangle$ Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
5	BioModels—15 years of sharing computational models in life science. Nucleic Acids Research, 2020, 48, D407-D415.	14.5	175
6	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135.	3.0	145
7	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
8	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. BMC Bioinformatics, 2014, 15, 369.	2.6	114
9	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	4.1	81
10	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	14.5	80
11	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. Nucleic Acids Research, 2006, 34, D327-D331.	14.5	59
12	Designing and encoding models for synthetic biology. Journal of the Royal Society Interface, 2009, 6, S405-17.	3.4	51
13	Modeling Meets Metabolomics—The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism Caenorhabditis elegans. Frontiers in Molecular Biosciences, 2018, 5, 96.	3.5	40
14	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	4.1	37
15	MELTING, a flexible platform to predict the melting temperatures of nucleic acids. BMC Bioinformatics, 2012, 13, 101.	2.6	36
16	The systems biology format converter. BMC Bioinformatics, 2016, 17, 154.	2.6	30
17	SBMLeditor: effective creation of models in the Systems Biology Markup Language (SBML). BMC Bioinformatics, 2007, 8, 79.	2.6	29
18	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27

#	Article	IF	CITATIONS
19	Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2014, 9, 1285-1301.	1.5	21
20	Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653.	4.1	20
21	Systems biology markup language (SBML) level 3 package: multistate, multicomponent and multicompartment species, version 1, release 2. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	8
22	Data Integration and Semantic Enrichment of Systems Biology Models and Simulations. Lecture Notes in Computer Science, 2009, , 5-15.	1.3	1
23	JSBML. Nature Precedings, 2010, , .	0.1	0