Nicolas Rodriguez

List of Publications by Year
in descending order

23 papers	2,342 citations	394421 19 h-index	610901 24 g-index
29 all docs	29 docs citations	29 times ranked	3384 citing authors

#	Article	IF	Citations
1	BioModels—15 years of sharing computational models in life science. Nucleic Acids Research, 2020, 48, D407-D415.	14.5	175
2	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
3	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
4	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	14.5	80
5	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
6	The systems biology format converter. BMC Bioinformatics, 2016, 17, 154.	2.6	30
7	BioModels: ten-year anniversary. Nucleic Acids Research, 2015, 43, D542-D548.	14.5	334
8	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	4.1	37
9	COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. BMC Bioinformatics, 2014, 15, 369.	2.6	114
10	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
11	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27
12	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
13	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
14	Qualitative translation of relations from BioPAX to SBML qual. Bioinformatics, 2012, 28, 2648-2653.	4.1	20
15	MELTING, a flexible platform to predict the melting temperatures of nucleic acids. BMC Bioinformatics, 2012, 13, 101.	2.6	36
16	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
17	JSBML: a flexible Java library for working with SBML. Bioinformatics, 2011, 27, 2167-2168.	4.1	81
18	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467

#	Article	IF	Citations
19	JSBML. Nature Precedings, 2010, , .	0.1	0
20	Designing and encoding models for synthetic biology. Journal of the Royal Society Interface, 2009, 6, S405-17.	3.4	51
21	Data Integration and Semantic Enrichment of Systems Biology Models and Simulations. Lecture Notes in Computer Science, 2009, , 5-15.	1.3	1
22	SBMLeditor: effective creation of models in the Systems Biology Markup Language (SBML). BMC Bioinformatics, 2007, 8, 79.	2.6	29
23	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. Nucleic Acids Research, 2006, 34, D327-D331.	14.5	59