

# Bruce E Shapiro

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12189805/publications.pdf>

Version: 2024-02-01

16  
papers

1,418  
citations

759233

12  
h-index

1058476

14  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1678  
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
2	A Pycellerator Tutorial. <i>Methods in Molecular Biology</i> , 2019, 1945, 1-32.	0.9	0
3	Pycellerator: an arrow-based reaction-like modelling language for biological simulations. <i>Bioinformatics</i> , 2016, 32, 629-631.	4.1	8
4	Analysis of cell division patterns in the <i>Arabidopsis</i> shoot apical meristem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4815-4820.	7.1	78
5	Using cellzilla for plant growth simulations at the cellular level. <i>Frontiers in Plant Science</i> , 2013, 4, 408.	3.6	17
6	An auxin-driven polarized transport model for phyllotaxis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1633-1638.	7.1	558
7	APPLICATION OF A GENERALIZED MWC MODEL FOR THE MATHEMATICAL SIMULATION OF METABOLIC PATHWAYS REGULATED BY ALLOSTERIC ENZYMES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 335-355.	0.8	23
8	A Mathematical Model for the Branched Chain Amino Acid Biosynthetic Pathways of <i>Escherichia coli</i> K12. <i>Journal of Biological Chemistry</i> , 2005, 280, 11224-11232.	3.4	36
9	An enzyme mechanism language for the mathematical modeling of metabolic pathways. <i>Bioinformatics</i> , 2005, 21, 774-780.	4.1	44
10	Modeling the organization of the WUSCHEL expression domain in the shoot apical meristem. <i>Bioinformatics</i> , 2005, 21, i232-i240.	4.1	145
11	MathSBML: a package for manipulating SBML-based biological models. <i>Bioinformatics</i> , 2004, 20, 2829-2831.	4.1	55
12	Cellerator: extending a computer algebra system to include biochemical arrows for signal transduction simulations. <i>Bioinformatics</i> , 2003, 19, 677-678.	4.1	116
13	Osmotic forces and gap junctions in spreading depression: a computational model. <i>Journal of Computational Neuroscience</i> , 2001, 10, 99-120.	1.0	95
14	Graphical method for force analysis: Macromolecular mechanics with atomic force microscopy. , 1999, 37, 576-581.		18
15	Hysteresis in Force Probe Measurements: a Dynamical Systems Perspective. <i>Journal of Theoretical Biology</i> , 1998, 194, 551-559.	1.7	13
16	A quantitative analysis of single protein-ligand complex separation with the atomic force microscope. <i>Biophysical Chemistry</i> , 1997, 67, 211-219.	2.8	34