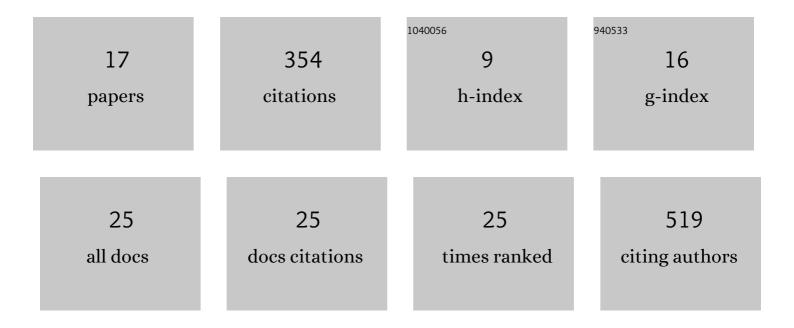
## Vincent Noel

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8831586/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling. Frontiers in Molecular Biosciences, 2022, 9, 800152.	3.5	6
2	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i> . Briefings in Bioinformatics, 2022, 23, .	6.5	10
3	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25
4	Personalized logical models to investigate cancer response to BRAF treatments in melanomas and colorectal cancers. PLoS Computational Biology, 2021, 17, e1007900.	3.2	30
5	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
6	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. Frontiers in Molecular Biosciences, 2021, 8, 754444.	3.5	3
7	Dynamical Boolean Modeling of Immunogenic Cell Death. Frontiers in Physiology, 2020, 11, 590479.	2.8	13
8	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. BMC Bioinformatics, 2020, 21, 241.	2.6	1
9	Synthesis and Simulation of Ensembles of Boolean Networks for Cell Fate Decision. Lecture Notes in Computer Science, 2020, , 193-209.	1.3	12
10	Fibroblast Growth Factor 2 lethally sensitizes cancer cells to stressâ€ŧargeted therapeutic inhibitors. Molecular Oncology, 2019, 13, 290-306.	4.6	18
11	An Interdisciplinary Approach for Designing Kinetic Models of the Ras/MAPK Signaling Pathway. Methods in Molecular Biology, 2017, 1636, 455-474.	0.9	2
12	Glyceraldehyde 3-Phosphate Dehydrogenase-Telomere Association Correlates with Redox Status in Trypanosoma cruzi. PLoS ONE, 2015, 10, e0120896.	2.5	20
13	Tropical Geometries and Dynamics of Biochemical Networks Application to Hybrid Cell Cycle Models. Electronic Notes in Theoretical Computer Science, 2012, 284, 75-91.	0.9	28
14	Reduction of dynamical biochemical reactions networks in computational biology. Frontiers in Genetics, 2012, 3, 131.	2.3	78
15	Algorithm for Identification of Piecewise Smooth Hybrid Systems: Application to Eukaryotic Cell Cycle Regulation. Lecture Notes in Computer Science, 2011, , 225-236.	1.3	5
16	A hybrid mammalian cell cycle model. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 125, 68-83.	0.8	3
17	Hybrid models of the cell cycle molecular machinery. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 92, 88-105.	0.8	3