Carlos F Lopez

List of Publications by Year
in descending order

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Version: 2024-02-01

41	2,735	236612	301761
papers	citations	25 h-index	39 g-index

57	57	57	3851
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Thunor: visualization and analysis of high-throughput doseâ€“response datasets. Nucleic Acids Research, 2021, 49, W633-W640.	6.5	4
2	Unsupervised logic-based mechanism inference for network-driven biological processes. PLoS Computational Biology, 2021, 17, e1009035.	1.5	4
3	Selective Inhibition of JAK1 Primes STAT5-Driven Human Leukemia Cells for ATRA-Induced Differentiation. Targeted Oncology, 2021, 16, 663-674.	1.7	2
4	MuSyC is a consensus framework that unifies multi-drug synergy metrics for combinatorial drug discovery. Nature Communications, 2021, 12, 4607.	5.8	50
5	Programmatic modeling for biological systems. Current Opinion in Systems Biology, 2021, 27, 100343.	1.3	3
6	Interactive Multiresolution Visualization of Cellular Network Processes. IScience, 2020, 23, 100748.	1.9	8
7	ACDC: Automated Cell Detection and Counting for Time-Lapse Fluorescence Microscopy. Applied Sciences (Switzerland), 2020, 10, 6187.	1.3	9
8	A Probabilistic Approach to Explore Signal Execution Mechanisms With Limited Experimental Data. Frontiers in Genetics, 2020, 11, 686.	1.1	9
9	Charting the Fragmented Landscape of Drug Synergy. Trends in Pharmacological Sciences, 2020, 41, 266-280.	4.0	56
10	Signal integration and information transfer in an allosterically regulated network. Npj Systems Biology and Applications, 2019, 5, 23.	1.4	11
11	Cardiolipin-Dependent Properties of Model Mitochondrial Membranes from Molecular Simulations. Biophysical Journal, 2019, 117, 429-444.	0.2	36
12	Systems-level network modeling of Small Cell Lung Cancer subtypes identifies master regulators and destabilizers. PLoS Computational Biology, 2019, 15, e1007343.	1.5	77
13	Arrestin-3 scaffolding of the JNK3 cascade suggests a mechanism for signal amplification. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 810-815.	3.3	34
14	PyDREAM: high-dimensional parameter inference for biological models in python. Bioinformatics, 2018, 34, 695-697.	1.8	60
15	Integrated, High-Throughput, Multiomics Platform Enables Data-Driven Construction of Cellular Responses and Reveals Global Drug Mechanisms of Action. Journal of Proteome Research, 2017, 16, 1364-1375.	1.8	34
16	GPU-powered model analysis with PySB/cupSODA. Bioinformatics, 2017, 33, 3492-3494.	1.8	17
17	Activated Oncogenic Pathway Modifies Iron Network in Breast Epithelial Cells: A Dynamic Modeling Perspective. PLoS Computational Biology, 2017, 13, e1005352.	1.5	22
18	An unbiased metric of antiproliferative drug effect in vitro. Nature Methods, 2016, 13, 497-500.	9.0	92

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19	CASP11 â€“ An Evaluation of a Modular BCL::Fold-Based Protein Structure Prediction Pipeline. PLoS ONE, 2016, 11, e0152517.	1.1	13
20	Competition and allostery govern substrate selectivity of cyclooxygenase-2. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12366-12371.	3.3	24
21	Ruleâ€based modeling: a computational approach for studying biomolecular site dynamics in cell signaling systems. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 13-36.	6.6	97
22	Programming biological models in Python using PySB. Molecular Systems Biology, 2013, 9, 646.	3.2	216
23	A Programmatic Modeling Approach to Explore Alternative Hypothesis of Mitochondrial Regulation in Extrinsic Apoptosis Signaling. Biophysical Journal, 2013, 104, 493a-494a.	0.2	0
24	Understanding and Tracking Pro- and Anti-Apoptotic BCL-2 protein Interactions and their Relation to Cancer in Extrinsic Apoptosis. Biophysical Journal, 2011, 100, 164a-165a.	0.2	1
25	Modeling Extrinsic Apoptosis Regulatory Network Pathways Using A Rules-based Framework. Biophysical Journal, 2009, 96, 304a.	0.2	0
26	Mechanistic Elements of Protein Cold Denaturation. Journal of Physical Chemistry B, 2008, 112, 5961-5967.	1.2	104
27	Hydrophobicity of protein surfaces: Separating geometry from chemistry. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2274-2279.	3.3	242
28	Probing Membrane Insertion Activity of Antimicrobial Polymers via Coarse-Grain Molecular Dynamics. Journal of Chemical Theory and Computation, 2006, 2, 649-655.	2.3	52
29	Modeling Surfactant Adsorption on Hydrophobic Surfaces. Physical Review Letters, 2005, 94, 228301.	2.9	33
30	Structure and Dynamics of Model Pore Insertion into a Membrane. Biophysical Journal, 2005, 88, 3083-3094.	0.2	60
31	Understanding nature's design for a nanosyringe. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4431-4434.	3.3	280
32	Membrane Bound Hydraphiles Facilitate Cation Translocation. Journal of Physical Chemistry B, 2004, 108, 4231-4235.	1.2	17
33	Hydrogen Bonding Structure and Dynamics of Water at the Dimyristoylphosphatidylcholine Lipid Bilayer Surface from a Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2004, 108, 6603-6610.	1.2	157
34	Coarse grain models and the computer simulation of soft materials. Journal of Physics Condensed Matter, 2004, 16, R481-R512.	0.7	359
35	Transmembrane Peptide-Induced Lipid Sorting and Mechanism of LÎ±-to-Inverted Phase Transition Using Coarse-Grain Molecular Dynamics. Biophysical Journal, 2004, 87, 2107-2115.	0.2	53
36	A coarse grain model for n-alkanes parameterized from surface tension data. Journal of Chemical Physics, 2003, 119, 7043-7049.	1.2	121

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37	Molecular Dynamics Investigations of Lipid Langmuir Monolayers Using a Coarse-Grain Model. Journal of Physical Chemistry B, 2003, 107, 13911-13917.	1.2	56
38	Self-assembly of a phospholipid Langmuir monolayer using coarse-grained molecular dynamics simulations. Journal of Physics Condensed Matter, 2002, 14, 9431-9444.	0.7	31
39	Molecular Dynamics Investigation of Membrane-Bound Bundles of the Channel-Forming Transmembrane Domain of Viral Protein U from the Human Immunodeficiency Virus HIV-1. Biophysical Journal, 2002, 83, 1259-1267.	0.2	52
40	Computer simulation studies of biomembranes using a coarse grain model. Computer Physics Communications, 2002, 147, 1-6.	3.0	94
41	Dynamical Properties of a Hydrated Lipid Bilayer from a Multinanosecond Molecular Dynamics Simulation. Biophysical Journal, 2001, 81, 2484-2494.	0.2	134