Laura Orellana

List of Publications by Year
in descending order

29 papers	897 citations	687363 13 h-index	794594 19 g-index
32 all docs	32 docs citations	32 times ranked	1506 citing authors

#	Article	IF	Citations
1	Epidermal Growth Factor Receptor Extracellular Domain Mutations in Glioblastoma Present Opportunities for Clinical Imaging and Therapeutic Development. Cancer Cell, 2018, 34, 163-177.e7.	16.8	145
2	Inhibition of Nuclear PTEN Tyrosine Phosphorylation Enhances Glioma Radiation Sensitivity through Attenuated DNA Repair. Cancer Cell, 2019, 35, 504-518.e7.	16.8	102
3	Correlated motions are a fundamental property of Î²-sheets. Nature Communications, 2014, 5, 4070.	12.8	82
4	Large-Scale Conformational Changes and Protein Function: Breaking the in silico Barrier. Frontiers in Molecular Biosciences, 2019, 6, 117.	3.5	81
5	FlexServ: an integrated tool for the analysis of protein flexibility. Bioinformatics, 2009, 25, 1709-1710.	4.1	72
6	The molecular basis for sugar import in malaria parasites. Nature, 2020, 578, 321-325.	27.8	65
7	Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations. Nature Communications, 2016, 7, 12575.	12.8	62
8	Approaching Elastic Network Models to Molecular Dynamics Flexibility. Journal of Chemical Theory and Computation, 2010, 6, 2910-2923.	5.3	60
9	Oncogenic mutations at the EGFR ectodomain structurally converge to remove a steric hindrance on a kinase-coupled cryptic epitope. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10009-10018.	7.1	46
10	Coarse-grained Representation of Protein Flexibility. Foundations, Successes, and Shortcomings. Advances in Protein Chemistry and Structural Biology, 2011, 85, 183-215.	2.3	33
11	Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. EMBO Journal, 2020, 39, 4541-4559.	7.8	31
12	Finding Conformational Transition Pathways from Discrete Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2012, 8, 4707-4718.	5.3	29
13	Structure, mechanism and lipid-mediated remodeling of the mammalian Na+/H+ exchanger NHA2. Nature Structural and Molecular Biology, 2022, 29, 108-120.	8.2	27
14	eBDIMS server: protein transition pathways with ensemble analysis in 2D-motion spaces. Bioinformatics, 2019, 35, 3505-3507.	4.1	19
15	Crystal structures of human MGST2 reveal synchronized conformational changes regulating catalysis. Nature Communications, 2021, 12, 1728.	12.8	15
16	Convergence of EGFR glioblastoma mutations: evolution and allostery rationalizing targeted therapy. Molecular and Cellular Oncology, 2019, 6, e1630798.	0.7	6
17	Exploring the Conformational Impact of Glycine Receptor TM1-2 Mutations Through Coarse-Grained Analysis and Atomistic Simulations. Frontiers in Molecular Biosciences, 0, 9, .	3.5	2
18	NextGenVOICES. Science, 2012, 336, 32-34.	12.6	1

#	Article	IF	Citations
19	CSIG-22. MUTATIONAL HETEROGENEITY OF THE EGFR EXTRACELLULAR DOMAIN PROMOTES AN ONCOGENIC UNTETHERED TRANSITIONAL CONFORMATION AND THE POTENTIAL FOR GREATER THERAPEUTIC TARGETING IN GBM PATIENTS. Neuro-Oncology, 2016, 18, vi45-vi45.	1.2	1
20	Gating Ritual: Simulations of Gating in Glutamate-Gated Chloride Channel. Biophysical Journal, 2015, 108, 431a.	0.5	0
21	ATPS-86MUTATIONS IN THE EGF RECEPTOR EXTRACELLULAR DOMAIN REVEAL AN UNTETHERED TRANSITIONAL STATE WHICH MEDIATES mAb806 BINDING. Neuro-Oncology, 2015, 17, v37.3-v37.	1.2	0
22	Revealing the Mechanism for Conformational Changes from Structurally Rich Ensembles. Biophysical Journal, 2016, 110, 54a.	0.5	0
23	Principal Components from Ligand-Gated Ion Channel Structures Enable Ensemble Studies of Microsecond-Scale Transitions. Biophysical Journal, 2016, 110, 454a.	0.5	0
24	Trapping On-Pathway Intermediates for Large Scale Conformational Changes with Coarse-Grained Simulations. Biophysical Journal, 2017, 112, 485a.	0.5	0
25	Allosteric Modulation via Transmembrane Interfaces in a Pentameric Ligand-Gated Ion Channel. Biophysical Journal, 2019, 116, 245a-246a.	0.5	0
26	Understanding the Conformational Dynamics of a Pentameric Ligand-Gated Ion Channel through Markov State Modeling. Biophysical Journal, 2019, 116, 395a-396a.	0.5	0
27	Mapping pH-Dependent State Transitions of a Pentameric Ligand-gated Ion Channel through Markov State Modeling. Biophysical Journal, 2020, 118, 191a.	0.5	0
28	Allosteric Gating Determinants in the Transmembrane Domain of Pentameric Ligand-Gated Ion Channels. Biophysical Journal, 2020, 118, 584a.	0.5	0
29	Computational techniques to study protein dynamics and conformations. , 2022, , 199-212.		0