Laura Orellana

List of Publications by Year
in descending order

29 papers	897 citations	686830 13 h-index	794141 19 g-index
32 all docs	32 docs citations	32 times ranked	1506 citing authors

#	Article	IF	Citations
1	Computational techniques to study protein dynamics and conformations. , 2022, , 199-212.		0
2	Structure, mechanism and lipid-mediated remodeling of the mammalian Na+/H+ exchanger NHA2. Nature Structural and Molecular Biology, 2022, 29, 108-120.	3.6	27
3	Crystal structures of human MGST2 reveal synchronized conformational changes regulating catalysis. Nature Communications, 2021, 12, 1728.	5.8	15
4	Mapping pH-Dependent State Transitions of a Pentameric Ligand-gated Ion Channel through Markov State Modeling. Biophysical Journal, 2020, 118, 191a.	0.2	0
5	Allosteric Gating Determinants in the Transmembrane Domain of Pentameric Ligand-Gated Ion Channels. Biophysical Journal, 2020, 118, 584a.	0.2	0
6	The molecular basis for sugar import in malaria parasites. Nature, 2020, 578, 321-325.	13.7	65
7	Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. EMBO Journal, 2020, 39, 4541-4559.	3.5	31
8	Convergence of EGFR glioblastoma mutations: evolution and allostery rationalizing targeted therapy. Molecular and Cellular Oncology, 2019, 6, e1630798.	0.3	6
9	Large-Scale Conformational Changes and Protein Function: Breaking the in silico Barrier. Frontiers in Molecular Biosciences, 2019, 6, 117.	1.6	81
10	Allosteric Modulation via Transmembrane Interfaces in a Pentameric Ligand-Gated Ion Channel. Biophysical Journal, 2019, 116, 245a-246a.	0.2	0
11	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.	3.3	46
12	Understanding the Conformational Dynamics of a Pentameric Ligand-Gated Ion Channel through Markov State Modeling. Biophysical Journal, 2019, 116, 395a-396a.	0.2	0
13	eBDIMS server: protein transition pathways with ensemble analysis in 2D-motion spaces. Bioinformatics, 2019, 35, 3505-3507.	1.8	19
14	Inhibition of Nuclear PTEN Tyrosine Phosphorylation Enhances Glioma Radiation Sensitivity through Attenuated DNA Repair. Cancer Cell, 2019, 35, 504-518.e7.	7.7	102
15	Epidermal Growth Factor Receptor Extracellular Domain Mutations in Glioblastoma Present Opportunities for Clinical Imaging and Therapeutic Development. Cancer Cell, 2018, 34, 163-177.e7.	7.7	145
16	Trapping On-Pathway Intermediates for Large Scale Conformational Changes with Coarse-Grained Simulations. Biophysical Journal, 2017, 112, 485a.	0.2	0
17	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.	0.6	1
18	Revealing the Mechanism for Conformational Changes from Structurally Rich Ensembles. Biophysical Journal, 2016, 110, 54a.	0.2	0

#	Article	IF	Citations
19	Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations. Nature Communications, 2016, 7, 12575.	5.8	62
20	Principal Components from Ligand-Gated Ion Channel Structures Enable Ensemble Studies of Microsecond-Scale Transitions. Biophysical Journal, 2016, 110, 454a.	0.2	0
21	Gating Ritual: Simulations of Gating in Glutamate-Gated Chloride Channel. Biophysical Journal, 2015, 108, 431a.	0.2	0
22	ATPS-86MUTATIONS IN THE EGF RECEPTOR EXTRACELLULAR DOMAIN REVEAL AN UNTETHERED TRANSITIONAL STATE WHICH MEDIATES mAb806 BINDING. Neuro-Oncology, 2015, 17, v37.3-v37.	0.6	0
23	Correlated motions are a fundamental property of Î²-sheets. Nature Communications, 2014, 5, 4070.	5.8	82
24	NextGenVOICES. Science, 2012, 336, 32-34.	6.0	1
25	Finding Conformational Transition Pathways from Discrete Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2012, 8, 4707-4718.	2.3	29
26	Coarse-grained Representation of Protein Flexibility. Foundations, Successes, and Shortcomings. Advances in Protein Chemistry and Structural Biology, 2011, 85, 183-215.	1.0	33
27	Approaching Elastic Network Models to Molecular Dynamics Flexibility. Journal of Chemical Theory and Computation, 2010, 6, 2910-2923.	2.3	60
28	FlexServ: an integrated tool for the analysis of protein flexibility. Bioinformatics, 2009, 25, 1709-1710.	1.8	72
29	Exploring the Conformational Impact of Glycine Receptor TM1-2 Mutations Through Coarse-Grained Analysis and Atomistic Simulations. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2