

Laura Orellana

List of Publications by Year in descending order

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papers

897
citations

687363

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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.	8.2	27
3	Crystal structures of human MGST2 reveal synchronized conformational changes regulating catalysis. Nature Communications, 2021, 12, 1728.	12.8	15
4	Mapping pH-Dependent State Transitions of a Pentameric Ligand-gated Ion Channel through Markov State Modeling. Biophysical Journal, 2020, 118, 191a.	0.5	0
5	Allosteric Gating Determinants in the Transmembrane Domain of Pentameric Ligand-Gated Ion Channels. Biophysical Journal, 2020, 118, 584a.	0.5	0
6	The molecular basis for sugar import in malaria parasites. Nature, 2020, 578, 321-325.	27.8	65
7	Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. EMBO Journal, 2020, 39, 4541-4559.	7.8	31
8	Convergence of <i>EGFR</i> glioblastoma mutations: evolution and allostery rationalizing targeted therapy. Molecular and Cellular Oncology, 2019, 6, e1630798.	0.7	6
9	Large-Scale Conformational Changes and Protein Function: Breaking the in silico Barrier. Frontiers in Molecular Biosciences, 2019, 6, 117.	3.5	81
10	Allosteric Modulation via Transmembrane Interfaces in a Pentameric Ligand-Gated Ion Channel. Biophysical Journal, 2019, 116, 245a-246a.	0.5	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.	7.1	46
12	Understanding the Conformational Dynamics of a Pentameric Ligand-Gated Ion Channel through Markov State Modeling. Biophysical Journal, 2019, 116, 395a-396a.	0.5	0
13	eBDIMS server: protein transition pathways with ensemble analysis in 2D-motion spaces. Bioinformatics, 2019, 35, 3505-3507.	4.1	19
14	Inhibition of Nuclear PTEN Tyrosine Phosphorylation Enhances Glioma Radiation Sensitivity through Attenuated DNA Repair. Cancer Cell, 2019, 35, 504-518.e7.	16.8	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.	16.8	145
16	Trapping On-Pathway Intermediates for Large Scale Conformational Changes with Coarse-Grained Simulations. Biophysical Journal, 2017, 112, 485a.	0.5	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.	1.2	1
18	Revealing the Mechanism for Conformational Changes from Structurally Rich Ensembles. Biophysical Journal, 2016, 110, 54a.	0.5	0

#	ARTICLE	IF	CITATIONS
19	Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations. <i>Nature Communications</i> , 2016, 7, 12575.	12.8	62
20	Principal Components from Ligand-Gated Ion Channel Structures Enable Ensemble Studies of Microsecond-Scale Transitions. <i>Biophysical Journal</i> , 2016, 110, 454a.	0.5	0
21	Gating Ritual: Simulations of Gating in Glutamate-Gated Chloride Channel. <i>Biophysical Journal</i> , 2015, 108, 431a.	0.5	0
22	ATPS-86MUTATIONS IN THE EGF RECEPTOR EXTRACELLULAR DOMAIN REVEAL AN UNTETHERED TRANSITIONAL STATE WHICH MEDIATES mAb806 BINDING. <i>Neuro-Oncology</i> , 2015, 17, v37.3-v37.	1.2	0
23	Correlated motions are a fundamental property of β^2 -sheets. <i>Nature Communications</i> , 2014, 5, 4070.	12.8	82
24	NextGenVOICES. <i>Science</i> , 2012, 336, 32-34.	12.6	1
25	Finding Conformational Transition Pathways from Discrete Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 4707-4718.	5.3	29
26	Coarse-grained Representation of Protein Flexibility. Foundations, Successes, and Shortcomings. <i>Advances in Protein Chemistry and Structural Biology</i> , 2011, 85, 183-215.	2.3	33
27	Approaching Elastic Network Models to Molecular Dynamics Flexibility. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 2910-2923.	5.3	60
28	FlexServ: an integrated tool for the analysis of protein flexibility. <i>Bioinformatics</i> , 2009, 25, 1709-1710.	4.1	72
29	Exploring the Conformational Impact of Glycine Receptor TM1-2 Mutations Through Coarse-Grained Analysis and Atomistic Simulations. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	2