Ben Hall

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7350700/publications.pdf

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60	1,677	304743	315739
papers	citations	22 h-index	38 g-index

76	76	76	2588
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Tumor-induced stromal reprogramming drives lymph node transformation. Nature Immunology, 2016, 17, 1118-1127.	14.5	126
2	Computing Clinically Relevant Binding Free Energies of HIV-1 Protease Inhibitors. Journal of Chemical Theory and Computation, 2014, 10, 1228-1241.	5.3	123
3	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. Nature Genetics, 2020, 52, 604-614.	21.4	107
4	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. Nature, 2021, 598, 510-514.	27.8	95
5	Dynamite: a simple way to gain insight into protein motions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2280-2287.	2.5	81
6	Changes in Transmembrane Helix Alignment by Arginine Residues Revealed by Solid-State NMR Experiments and Coarse-Grained MD Simulations. Journal of the American Chemical Society, 2010, 132, 5803-5811.	13.7	78
7	Epidermal Tissue Adapts to Restrain Progenitors Carrying Clonal p53 Mutations. Cell Stem Cell, 2018, 23, 687-699.e8.	11.1	72
8	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. Nature Communications, 2013, 4, 2465.	12.8	71
9	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. Cancer Discovery, 2021, 11, 340-361.	9.4	66
10	Lung tumors with distinct p53 mutations respond similarly to p53 targeted therapy but exhibit genotype-specific statin sensitivity. Genes and Development, 2017, 31, 1339-1353.	5.9	58
11	A single-progenitor model as the unifying paradigm of epidermal and esophageal epithelial maintenance in mice. Nature Communications, 2020, 11, 1429.	12.8	57
12	Structural Flexibility of the Macrophage Dengue Virus Receptor CLEC5A. Journal of Biological Chemistry, 2011, 286, 24208-24218.	3.4	48
13	Exploring Peptide-Membrane Interactions with Coarse-Grained MD Simulations. Biophysical Journal, 2011, 100, 1940-1948.	0.5	46
14	Conformational Dynamics of the Ligand-Binding Domain of Inward Rectifier K Channels as Revealed by Molecular Dynamics Simulations: Toward an Understanding of Kir Channel Gating. Biophysical Journal, 2005, 88, 3310-3320.	0.5	42
15	Coarse-Grain Simulations Reveal Movement of the Synaptobrevin C-Terminus in Response to Piconewton Forces. Biophysical Journal, 2012, 103, 959-969.	0.5	42
16	A Helix Heterodimer in a Lipid Bilayer: Prediction of the Structure of an Integrin Transmembrane Domain via Multiscale Simulations. Structure, 2011, 19, 1477-1484.	3.3	39
17	Transmembrane Helix Dynamics of Bacterial Chemoreceptors Supports a Piston Model of Signalling. PLoS Computational Biology, 2011, 7, e1002204.	3.2	39
18	Mechanism of Bacterial Signal Transduction Revealed by Molecular Dynamics of Tsr Dimers and Trimers of Dimers in Lipid Vesicles. PLoS Computational Biology, 2012, 8, e1002685.	3.2	37

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19	Simulations of a Protein Translocation Pore:Â SecYâ€. Biochemistry, 2006, 45, 13018-13024.	2.5	30
20	Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. Journal of Chemical Theory and Computation, 2014, 10, 2165-2175.	5.3	27
21	Coarse-Grained MD Simulations and Proteinâ^'Protein Interactions: The Cohesinâ^'Dockerin System. Journal of Chemical Theory and Computation, 2009, 5, 2465-2471.	5.3	25
22	The Energetics of Transmembrane Helix Insertion into a Lipid Bilayer. Biophysical Journal, 2010, 99, 2534-2540.	0.5	25
23	Primary and Secondary Dimer Interfaces of the Fibroblast Growth Factor Receptor 3 Transmembrane Domain: Characterization via Multiscale Molecular Dynamics Simulations. Biochemistry, 2014, 53, 323-332.	2.5	24
24	Accommodation of a Central Arginine in a Transmembrane Peptide by Changing the Placement of Anchor Residues. Journal of Physical Chemistry B, 2012, 116, 12980-12990.	2.6	22
25	Characterization of Protein Conformational States by Normal-Mode Frequencies. Journal of the American Chemical Society, 2007, 129, 11394-11401.	13.7	21
26	Cancer-causingBRCA2missense mutations disrupt an intracellular protein assembly mechanism to disable genome maintenance. Nucleic Acids Research, 2021, 49, 5588-5604.	14.5	20
27	How Lipid Headgroups Sense the Membrane Environment: An Application of 14N NMR. Biophysical Journal, 2012, 103, 1245-1253.	0.5	19
28	Probing the Solution Structure of IÎºB Kinase (IKK) Subunit Î³ and Its Interaction with Kaposi Sarcoma-associated Herpes Virus Flice-interacting Protein and IKK Subunit Î² by EPR Spectroscopy. Journal of Biological Chemistry, 2015, 290, 16539-16549.	3.4	17
29	Exploring the role of stromal osmoregulation in cancer and disease using executable modelling. Nature Communications, 2018, 9, 3011.	12.8	17
30	Relating evolutionary selection and mutant clonal dynamics in normal epithelia. Journal of the Royal Society Interface, 2019, 16, 20190230.	3.4	16
31	SARS-CoV-2 Variants Are Selecting for Spike Protein Mutations That Increase Protein Stability. Journal of Chemical Information and Modeling, 2021, 61, 4152-4155.	5.4	14
32	Reproducibility in Research: Systems, Infrastructure, Culture. Journal of Open Research Software, 2017, 5, 32.	5.9	14
33	Drug Target Optimization in Chronic Myeloid Leukemia Using Innovative Computational Platform. Scientific Reports, 2015, 5, 8190.	3.3	13
34	Emergent Stem Cell Homeostasis in the C.Âelegans Germline Is Revealed by Hybrid Modeling. Biophysical Journal, 2015, 109, 428-438.	0.5	12
35	Cellular survival over genomic perfection. Science, 2019, 366, 802-803.	12.6	12
36	Computational Saturation Screen Reveals the Landscape of Mutations in Human Fumarate Hydratase. Journal of Chemical Information and Modeling, 2021, 61, 1970-1980.	5.4	12

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37	Multi-Scale Simulation of the Simian Immunodeficiency Virus Fusion Peptide. Journal of Physical Chemistry B, 2012, 116, 13713-13721.	2.6	11
38	Data integration in logic-based models of biological mechanisms. Current Opinion in Systems Biology, 2021, 28, 100386.	2.6	9
39	Tumor-Derived Lactic Acid Modulates Activation and Metabolic Status of Draining Lymph Node Stroma. Cancer Immunology Research, 2022, 10, 482-497.	3.4	9
40	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. Computational Biology, 2019, , 133-153.	0.2	7
41	Bookshelf: a simple curation system for the storage of biomolecular simulation data. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq033-baq033.	3.0	6
42	Global Conformational Dynamics of HIV-1 Reverse Transcriptase Bound to Non-Nucleoside Inhibitors. Biology, 2012, 1, 222-244.	2.8	6
43	A toolbox for discrete modelling of cell signalling dynamics. Integrative Biology (United Kingdom), 2018, 10, 370-382.	1.3	6
44	Simulations reveal that different responses to cell crowding determine the expansion of p53 and Notch mutant clones in squamous epithelia. Journal of the Royal Society Interface, 2021, 18, 20210607.	3.4	6
45	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. Current Protocols in Bioinformatics, 2020, 69, e95.	25.8	5
46	Bringing LTL Model Checking to Biologists. Lecture Notes in Computer Science, 2017, , 1-13.	1.3	5
47	Quantized Water Access to the HIV-1 Protease Active Site as a Proposed Mechanism for Cooperative Mutations in Drug Affinity. Biochemistry, 2012, 51, 6487-6489.	2.5	3
48	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. Journal of the Royal Society Interface, 2014, 11, 20140245.	3.4	3
49	How Transmembrane Model Peptides Affect Lipid Head Group Orientation: An Application of 14N NMR. Biophysical Journal, 2011, 100, 638a-639a.	0.5	1
50	""""Share and Enjoy"""": Publishing Useful and Usable Scientific Models. , 2014, , .		1
51	Methods for analysing lineage tracing datasets. Royal Society Open Science, 2021, 8, 202231.	2.4	1
52	High Throughput Coarse-Grained Simulations of the Insertion of Transmembrane Helices. Biophysical Journal, 2009, 96, 194a.	0.5	0
53	Sensitivity of Coarse Grain Models of Peptides to the Introduction of Charged Residues in Model Peptides and Bacterial Chemoreceptors. Biophysical Journal, 2010, 98, 644a.	0.5	0
54	Insertion Properties of Cftr Explored with High Throughput, Coarse Grain Molecular Dynamics. Biophysical Journal, 2011, 100, 203a-204a.	0.5	0

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55	Coarse Grain Simulations Reveal Movement of Synaptobrevin C Terminus in Response to Piconewton Forces Suggesting a Novel Fusion Pore Mechanism. Biophysical Journal, 2012, 102, 318a.	0.5	0
56	Structure of NEMO through EPR Spectroscopy and Multiscale Modelling. Biophysical Journal, 2013, 104, 567a.	0.5	0
57	Predicting and Retrodicting Fate Patterns in C. elegans Vulval Development using Logic Programming. Biophysical Journal, 2014, 106, 376a.	0.5	0
58	Emergent Behaviours of Stem Cells in Organogenesis Demonstrated by Hybrid Modelling. Biophysical Journal, 2015, 108, 365a.	0.5	0
59	Carbon Nanoparticles and Their Differential Association with the Membranes of E. coli: A Coarse-Grained Molecular Dynamics Simulation Study. Biophysical Journal, 2016, 110, 326a.	0.5	0
60	Cancer-associated Mutations Co-locate with TRPA1 Hinge Formation in the Ankyrin Repeat Region. Biophysical Journal, 2020, 118, 11a-12a.	0.5	0