

Ben Hall

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

1,677
citations

304368

22
h-index

315357

38
g-index

76
all docs

76
docs citations

76
times ranked

2588
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumor-induced stromal reprogramming drives lymph node transformation. <i>Nature Immunology</i> , 2016, 17, 1118-1127.	7.0	126
2	Computing Clinically Relevant Binding Free Energies of HIV-1 Protease Inhibitors. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 1228-1241.	2.3	123
3	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. <i>Nature Genetics</i> , 2020, 52, 604-614.	9.4	107
4	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. <i>Nature</i> , 2021, 598, 510-514.	13.7	95
5	Dynamite: a simple way to gain insight into protein motions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Journal of the American Chemical Society</i> , 2010, 132, 5803-5811.	6.6	78
7	Epidermal Tissue Adapts to Restrain Progenitors Carrying Clonal p53 Mutations. <i>Cell Stem Cell</i> , 2018, 23, 687-699.e8.	5.2	72
8	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. <i>Nature Communications</i> , 2013, 4, 2465.	5.8	71
9	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. <i>Cancer Discovery</i> , 2021, 11, 340-361.	7.7	66
10	Lung tumors with distinct p53 mutations respond similarly to p53 targeted therapy but exhibit genotype-specific statin sensitivity. <i>Genes and Development</i> , 2017, 31, 1339-1353.	2.7	58
11	A single-progenitor model as the unifying paradigm of epidermal and esophageal epithelial maintenance in mice. <i>Nature Communications</i> , 2020, 11, 1429.	5.8	57
12	Structural Flexibility of the Macrophage Dengue Virus Receptor CLEC5A. <i>Journal of Biological Chemistry</i> , 2011, 286, 24208-24218.	1.6	48
13	Exploring Peptide-Membrane Interactions with Coarse-Grained MD Simulations. <i>Biophysical Journal</i> , 2011, 100, 1940-1948.	0.2	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. <i>Biophysical Journal</i> , 2005, 88, 3310-3320.	0.2	42
15	Coarse-Grain Simulations Reveal Movement of the Synaptobrevin C-Terminus in Response to Piconewton Forces. <i>Biophysical Journal</i> , 2012, 103, 959-969.	0.2	42
16	A Helix Heterodimer in a Lipid Bilayer: Prediction of the Structure of an Integrin Transmembrane Domain via Multiscale Simulations. <i>Structure</i> , 2011, 19, 1477-1484.	1.6	39
17	Transmembrane Helix Dynamics of Bacterial Chemoreceptors Supports a Piston Model of Signalling. <i>PLoS Computational Biology</i> , 2011, 7, e1002204.	1.5	39
18	Mechanism of Bacterial Signal Transduction Revealed by Molecular Dynamics of Tsr Dimers and Trimers of Dimers in Lipid Vesicles. <i>PLoS Computational Biology</i> , 2012, 8, e1002685.	1.5	37

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19	Simulations of a Protein Translocation Pore: SecY ϵ . <i>Biochemistry</i> , 2006, 45, 13018-13024.	1.2	30
20	Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 2165-2175.	2.3	27
21	Coarse-Grained MD Simulations and Protein-Protein Interactions: The Cohesin-Dockerin System. <i>Journal of Chemical Theory and Computation</i> , 2009, 5, 2465-2471.	2.3	25
22	The Energetics of Transmembrane Helix Insertion into a Lipid Bilayer. <i>Biophysical Journal</i> , 2010, 99, 2534-2540.	0.2	25
23	Primary and Secondary Dimer Interfaces of the Fibroblast Growth Factor Receptor 3 Transmembrane Domain: Characterization via Multiscale Molecular Dynamics Simulations. <i>Biochemistry</i> , 2014, 53, 323-332.	1.2	24
24	Accommodation of a Central Arginine in a Transmembrane Peptide by Changing the Placement of Anchor Residues. <i>Journal of Physical Chemistry B</i> , 2012, 116, 12980-12990.	1.2	22
25	Characterization of Protein Conformational States by Normal-Mode Frequencies. <i>Journal of the American Chemical Society</i> , 2007, 129, 11394-11401.	6.6	21
26	Cancer-causing BRCA2 missense mutations disrupt an intracellular protein assembly mechanism to disable genome maintenance. <i>Nucleic Acids Research</i> , 2021, 49, 5588-5604.	6.5	20
27	How Lipid Headgroups Sense the Membrane Environment: An Application of 14N NMR. <i>Biophysical Journal</i> , 2012, 103, 1245-1253.	0.2	19
28	Probing the Solution Structure of β Kinase (IKK) Subunit β^3 and Its Interaction with Kaposi Sarcoma-associated Herpes Virus Flice-interacting Protein and IKK Subunit β^2 by EPR Spectroscopy. <i>Journal of Biological Chemistry</i> , 2015, 290, 16539-16549.	1.6	17
29	Exploring the role of stromal osmoregulation in cancer and disease using executable modelling. <i>Nature Communications</i> , 2018, 9, 3011.	5.8	17
30	Relating evolutionary selection and mutant clonal dynamics in normal epithelia. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190230.	1.5	16
31	SARS-CoV-2 Variants Are Selecting for Spike Protein Mutations That Increase Protein Stability. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 4152-4155.	2.5	14
32	Reproducibility in Research: Systems, Infrastructure, Culture. <i>Journal of Open Research Software</i> , 2017, 5, 32.	2.7	14
33	Drug Target Optimization in Chronic Myeloid Leukemia Using Innovative Computational Platform. <i>Scientific Reports</i> , 2015, 5, 8190.	1.6	13
34	Emergent Stem Cell Homeostasis in the <i>C. elegans</i> Germline Is Revealed by Hybrid Modeling. <i>Biophysical Journal</i> , 2015, 109, 428-438.	0.2	12
35	Cellular survival over genomic perfection. <i>Science</i> , 2019, 366, 802-803.	6.0	12
36	Computational Saturation Screen Reveals the Landscape of Mutations in Human Fumarate Hydratase. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1970-1980.	2.5	12

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37	Multi-Scale Simulation of the Simian Immunodeficiency Virus Fusion Peptide. <i>Journal of Physical Chemistry B</i> , 2012, 116, 13713-13721.	1.2	11
38	Data integration in logic-based models of biological mechanisms. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100386.	1.3	9
39	Tumor-Derived Lactic Acid Modulates Activation and Metabolic Status of Draining Lymph Node Stroma. <i>Cancer Immunology Research</i> , 2022, 10, 482-497.	1.6	9
40	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. <i>Computational Biology</i> , 2019, , 133-153.	0.1	7
41	Bookshelf: a simple curation system for the storage of biomolecular simulation data. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq033-baq033.	1.4	6
42	Global Conformational Dynamics of HIV-1 Reverse Transcriptase Bound to Non-Nucleoside Inhibitors. <i>Biology</i> , 2012, 1, 222-244.	1.3	6
43	A toolbox for discrete modelling of cell signalling dynamics. <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 370-382.	0.6	6
44	Simulations reveal that different responses to cell crowding determine the expansion of <i>p53</i> and <i>Notch</i> mutant clones in squamous epithelia. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210607.	1.5	6
45	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e95.	25.8	5
46	Bringing LTL Model Checking to Biologists. <i>Lecture Notes in Computer Science</i> , 2017, , 1-13.	1.0	5
47	Quantized Water Access to the HIV-1 Protease Active Site as a Proposed Mechanism for Cooperative Mutations in Drug Affinity. <i>Biochemistry</i> , 2012, 51, 6487-6489.	1.2	3
48	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140245.	1.5	3
49	How Transmembrane Model Peptides Affect Lipid Head Group Orientation: An Application of ¹⁴ N NMR. <i>Biophysical Journal</i> , 2011, 100, 638a-639a.	0.2	1
50	Share and Enjoy: Publishing Useful and Usable Scientific Models. , 2014, , .		1
51	Methods for analysing lineage tracing datasets. <i>Royal Society Open Science</i> , 2021, 8, 202231.	1.1	1
52	High Throughput Coarse-Grained Simulations of the Insertion of Transmembrane Helices. <i>Biophysical Journal</i> , 2009, 96, 194a.	0.2	0
53	Sensitivity of Coarse Grain Models of Peptides to the Introduction of Charged Residues in Model Peptides and Bacterial Chemoreceptors. <i>Biophysical Journal</i> , 2010, 98, 644a.	0.2	0
54	Insertion Properties of C _{tr} Explored with High Throughput, Coarse Grain Molecular Dynamics. <i>Biophysical Journal</i> , 2011, 100, 203a-204a.	0.2	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. <i>Biophysical Journal</i> , 2012, 102, 318a.	0.2	0
56	Structure of NEMO through EPR Spectroscopy and Multiscale Modelling. <i>Biophysical Journal</i> , 2013, 104, 567a.	0.2	0
57	Predicting and Retrodicting Fate Patterns in <i>C. elegans</i> Vulval Development using Logic Programming. <i>Biophysical Journal</i> , 2014, 106, 376a.	0.2	0
58	Emergent Behaviours of Stem Cells in Organogenesis Demonstrated by Hybrid Modelling. <i>Biophysical Journal</i> , 2015, 108, 365a.	0.2	0
59	Carbon Nanoparticles and Their Differential Association with the Membranes of <i>E. coli</i> : A Coarse-Grained Molecular Dynamics Simulation Study. <i>Biophysical Journal</i> , 2016, 110, 326a.	0.2	0
60	Cancer-associated Mutations Co-locate with TRPA1 Hinge Formation in the Ankyrin Repeat Region. <i>Biophysical Journal</i> , 2020, 118, 11a-12a.	0.2	0