Ben Hall

List of Publications by Year
in descending order

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60 papers	1,677 citations	304602 22 h-index	315616 38 g-index
76 all docs	76 docs citations	76 times ranked	2588 citing authors

#	Article	IF	Citations
1	Tumor-Derived Lactic Acid Modulates Activation and Metabolic Status of Draining Lymph Node Stroma. Cancer Immunology Research, 2022, 10, 482-497.	1.6	9
2	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. Cancer Discovery, 2021, 11, 340-361.	7.7	66
3	Computational Saturation Screen Reveals the Landscape of Mutations in Human Fumarate Hydratase. Journal of Chemical Information and Modeling, 2021, 61, 1970-1980.	2.5	12
4	Methods for analysing lineage tracing datasets. Royal Society Open Science, 2021, 8, 202231.	1.1	1
5	Cancer-causingBRCA2missense mutations disrupt an intracellular protein assembly mechanism to disable genome maintenance. Nucleic Acids Research, 2021, 49, 5588-5604.	6.5	20
6	SARS-CoV-2 Variants Are Selecting for Spike Protein Mutations That Increase Protein Stability. Journal of Chemical Information and Modeling, 2021, 61, 4152-4155.	2.5	14
7	Data integration in logic-based models of biological mechanisms. Current Opinion in Systems Biology, 2021, 28, 100386.	1.3	9
8	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. Nature, 2021, 598, 510-514.	13.7	95
9	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.	1.5	6
10	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. Nature Genetics, 2020, 52, 604-614.	9.4	107
11	A single-progenitor model as the unifying paradigm of epidermal and esophageal epithelial maintenance in mice. Nature Communications, 2020, 11, 1429.	5.8	57
12	Constructing and Analyzing Computational Models of Cell Signaling with BioModelAnalyzer. Current Protocols in Bioinformatics, 2020, 69, e95.	25.8	5
13	Cancer-associated Mutations Co-locate with TRPA1 Hinge Formation in the Ankyrin Repeat Region. Biophysical Journal, 2020, 118, 11a-12a.	0.2	0
14	Using State Space Exploration to Determine How Gene Regulatory Networks Constrain Mutation Order in Cancer Evolution. Computational Biology, 2019, , 133-153.	0.1	7
15	Cellular survival over genomic perfection. Science, 2019, 366, 802-803.	6.0	12
16	Relating evolutionary selection and mutant clonal dynamics in normal epithelia. Journal of the Royal Society Interface, 2019, 16, 20190230.	1.5	16
17	Epidermal Tissue Adapts to Restrain Progenitors Carrying Clonal p53 Mutations. Cell Stem Cell, 2018, 23, 687-699.e8.	5.2	72
18	Exploring the role of stromal osmoregulation in cancer and disease using executable modelling. Nature Communications, 2018, 9, 3011.	5.8	17

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19	A toolbox for discrete modelling of cell signalling dynamics. Integrative Biology (United Kingdom), 2018, 10, 370-382.	0.6	6
20	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.	2.7	58
21	Bringing LTL Model Checking to Biologists. Lecture Notes in Computer Science, 2017, , 1-13.	1.0	5
22	Reproducibility in Research: Systems, Infrastructure, Culture. Journal of Open Research Software, 2017, 5, 32.	2.7	14
23	Tumor-induced stromal reprogramming drives lymph node transformation. Nature Immunology, 2016, 17, 1118-1127.	7.0	126
24	Carbon Nanoparticles and Their Differential Association with the Membranes of E. coli: A Coarse-Grained Molecular Dynamics Simulation Study. Biophysical Journal, 2016, 110, 326a.	0.2	0
25	Emergent Stem Cell Homeostasis in the C.Âelegans Germline Is Revealed by Hybrid Modeling. Biophysical Journal, 2015, 109, 428-438.	0.2	12
26	Probing the Solution Structure of Iî°B 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.	1.6	17
27	Drug Target Optimization in Chronic Myeloid Leukemia Using Innovative Computational Platform. Scientific Reports, 2015, 5, 8190.	1.6	13
28	Emergent Behaviours of Stem Cells in Organogenesis Demonstrated by Hybrid Modelling. Biophysical Journal, 2015, 108, 365a.	0.2	0
29	""""Share and Enjoy"""": Publishing Useful and Usable Scientific Models. , 2014, , .		1
30	Computing Clinically Relevant Binding Free Energies of HIV-1 Protease Inhibitors. Journal of Chemical Theory and Computation, 2014, 10, 1228-1241.	2.3	123
31	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.	1.2	24
32	Logic programming to predict cell fate patterns and retrodict genotypes in organogenesis. Journal of the Royal Society Interface, 2014, 11, 20140245.	1.5	3
33	Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. Journal of Chemical Theory and Computation, 2014, 10, 2165-2175.	2.3	27
34	Predicting and Retrodicting Fate Patterns in C. elegans Vulval Development using Logic Programming. Biophysical Journal, 2014, 106, 376a.	0.2	0
35	Structure of NEMO through EPR Spectroscopy and Multiscale Modelling. Biophysical Journal, 2013, 104, 567a.	0.2	0
36	Role of the C-terminal domain in the structure and function of tetrameric sodium channels. Nature Communications, 2013, 4, 2465.	5.8	71

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37	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.	1.5	37
38	Coarse-Grain Simulations Reveal Movement of the Synaptobrevin C-Terminus in Response to Piconewton Forces. Biophysical Journal, 2012, 103, 959-969.	0.2	42
39	Multi-Scale Simulation of the Simian Immunodeficiency Virus Fusion Peptide. Journal of Physical Chemistry B, 2012, 116, 13713-13721.	1.2	11
40	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.	1.2	22
41	How Lipid Headgroups Sense the Membrane Environment: An Application of 14N NMR. Biophysical Journal, 2012, 103, 1245-1253.	0.2	19
42	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.	0.2	0
43	Global Conformational Dynamics of HIV-1 Reverse Transcriptase Bound to Non-Nucleoside Inhibitors. Biology, 2012, 1, 222-244.	1.3	6
44	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.	1.2	3
45	Insertion Properties of Cftr Explored with High Throughput, Coarse Grain Molecular Dynamics. Biophysical Journal, 2011, 100, 203a-204a.	0.2	0
46	Exploring Peptide-Membrane Interactions with Coarse-Grained MD Simulations. Biophysical Journal, 2011, 100, 1940-1948.	0.2	46
47	How Transmembrane Model Peptides Affect Lipid Head Group Orientation: An Application of 14N NMR. Biophysical Journal, 2011, 100, 638a-639a.	0.2	1
48	A Helix Heterodimer in a Lipid Bilayer: Prediction of the Structure of an Integrin Transmembrane Domain via Multiscale Simulations. Structure, 2011, 19, 1477-1484.	1.6	39
49	Structural Flexibility of the Macrophage Dengue Virus Receptor CLEC5A. Journal of Biological Chemistry, 2011, 286, 24208-24218.	1.6	48
50	Transmembrane Helix Dynamics of Bacterial Chemoreceptors Supports a Piston Model of Signalling. PLoS Computational Biology, 2011, 7, e1002204.	1.5	39
51	Bookshelf: a simple curation system for the storage of biomolecular simulation data. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq033-baq033.	1.4	6
52	Sensitivity of Coarse Grain Models of Peptides to the Introduction of Charged Residues in Model Peptides and Bacterial Chemoreceptors. Biophysical Journal, 2010, 98, 644a.	0.2	0
53	The Energetics of Transmembrane Helix Insertion into a Lipid Bilayer. Biophysical Journal, 2010, 99, 2534-2540.	0.2	25
54	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.	6.6	78

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55	High Throughput Coarse-Grained Simulations of the Insertion of Transmembrane Helices. Biophysical Journal, 2009, 96, 194a.	0.2	0
56	Coarse-Grained MD Simulations and Proteinâ˜'Protein Interactions: The Cohesinâ˜'Dockerin System. Journal of Chemical Theory and Computation, 2009, 5, 2465-2471.	2.3	25
57	Characterization of Protein Conformational States by Normal-Mode Frequencies. Journal of the American Chemical Society, 2007, 129, 11394-11401.	6.6	21
58	Simulations of a Protein Translocation Pore:Â SecYâ€. Biochemistry, 2006, 45, 13018-13024.	1.2	30
59	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.	0.2	42
60	Dynamite: a simple way to gain insight into protein motions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2280-2287.	2.5	81