

Nigel J Burroughs

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,115
citations

516710

16
h-index

434195

31
g-index

45
all docs

45
docs citations

45
times ranked

1575
citing authors

#	ARTICLE	IF	CITATIONS
1	A Virulent Strain of Deformed Wing Virus (DWW) of Honeybees (<i>Apis mellifera</i>) Prevails after <i>Varroa destructor</i> -Mediated, or In Vitro, Transmission. <i>PLoS Pathogens</i> , 2014, 10, e1004230.	4.7	294
2	Actomyosin Ring Formation and Tension Generation in Eukaryotic Cytokinesis. <i>Current Biology</i> , 2016, 26, R719-R737.	3.9	95
3	Kinesin expands and stabilizes the GDP-microtubule lattice. <i>Nature Nanotechnology</i> , 2018, 13, 386-391.	31.5	81
4	Regulation of Gene Expression in <i>Shewanella oneidensis</i> MR-1 during Electron Acceptor Limitation and Bacterial Nanowire Formation. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5428-5443.	3.1	59
5	Ligand Detection and Discrimination by Spatial Relocalization: A Kinase-Phosphatase Segregation Model of TCR Activation. <i>Biophysical Journal</i> , 2006, 91, 1619-1629.	0.5	51
6	Changes in Gene Expression in Space and Time Orchestrate Environmentally Mediated Shaping of Root Architecture. <i>Plant Cell</i> , 2017, 29, 2393-2412.	6.6	49
7	Matched Sizes of Activating and Inhibitory Receptor/Ligand Pairs Are Required for Optimal Signal Integration by Human Natural Killer Cells. <i>PLoS ONE</i> , 2010, 5, e15374.	2.5	45
8	Ensemble-Level Organization of Human Kinetochores and Evidence for Distinct Tension and Attachment Sensors. <i>Cell Reports</i> , 2020, 31, 107535.	6.4	40
9	Discriminating self from nonself with short peptides from large proteomes. <i>Immunogenetics</i> , 2004, 56, 311-320.	2.4	39
10	Detection of Diffusion Heterogeneity in Single Particle Tracking Trajectories Using a Hidden Markov Model with Measurement Noise Propagation. <i>PLoS ONE</i> , 2015, 10, e0140759.	2.5	38
11	Human kinetochores are swivel joints that mediate microtubule attachments. <i>ELife</i> , 2016, 5, .	6.0	30
12	Inferring the Forces Controlling Metaphase Kinetochose Oscillations by Reverse Engineering System Dynamics. <i>PLoS Computational Biology</i> , 2015, 11, e1004607.	3.2	29
13	Stochasticity and spatial heterogeneity in T cell activation. <i>Immunological Reviews</i> , 2007, 216, 69-80.	6.0	25
14	Boltzmann Energy-based Image Analysis Demonstrates that Extracellular Domain Size Differences Explain Protein Segregation at Immune Synapses. <i>PLoS Computational Biology</i> , 2011, 7, e1002076.	3.2	24
15	Kinetochose life histories reveal an Aurora-B-dependent error correction mechanism in anaphase. <i>Developmental Cell</i> , 2021, 56, 3082-3099.e5.	7.0	24
16	Probing microtubule polymerisation state at single kinetochores during metaphase chromosome motion. <i>Journal of Cell Science</i> , 2015, 128, 1991-2001.	2.0	23
17	A Hidden Markov Model for Detecting Confinement in Single-Particle Tracking Trajectories. <i>Biophysical Journal</i> , 2018, 115, 1741-1754.	0.5	23
18	Super-resolution kinetochose tracking reveals the mechanisms of human sister kinetochose directional switching. <i>ELife</i> , 2015, 4, .	6.0	20

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19	Close contact fluctuations: The seeding of signalling domains in the immunological synapse. <i>Europhysics Letters</i> , 2007, 77, 48003.	2.0	15
20	Actin turnover ensures uniform tension distribution during cytokinetic actomyosin ring contraction. <i>Molecular Biology of the Cell</i> , 2019, 30, 933-941.	2.1	14
21	Solar powered biohydrogen production requires specific localization of the hydrogenase. <i>Energy and Environmental Science</i> , 2014, 7, 3791-3800.	30.8	12
22	Size matters for single-cell C ₄ photosynthesis in <i>Bienertia</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 255-267.	4.8	12
23	KiT: a MATLAB package for kinetochore tracking. <i>Bioinformatics</i> , 2016, 32, 1917-1919.	4.1	11
24	Mitotic live-cell imaging at different timescales. <i>Methods in Cell Biology</i> , 2018, 145, 1-27.	1.1	8
25	MosaicSolver: a tool for determining recombinants of viral genomes from pileup data. <i>Nucleic Acids Research</i> , 2014, 42, e123-e123.	14.5	6
26	Modelling the suppression of autoimmunity after pathogen infection. <i>Mathematical Methods in the Applied Sciences</i> , 2018, 41, 8565-8570.	2.3	6
27	Computational modelling predicts substantial carbon assimilation gains for C3 plants with a single-celled C4 biochemical pump. <i>PLoS Computational Biology</i> , 2019, 15, e1007373.	3.2	6
28	The Effect of a Linear Tuning between the Antigenic Stimulations of CD4+ T Cells and CD4+ Tregs. <i>Mathematics</i> , 2020, 8, 293.	2.2	6
29	Bayesian inference of origin firing time distributions, origin interference and licencing probabilities from Next Generation Sequencing data. <i>Nucleic Acids Research</i> , 2019, 47, 2229-2243.	14.5	4
30	Error correction and diversity analysis of population mixtures determined by NGS. <i>PeerJ</i> , 2014, 2, e645.	2.0	4
31	Correcting for link loss in causal network inference caused by regulator interference. <i>Bioinformatics</i> , 2014, 30, 2779-2786.	4.1	2
32	Subcellular Euclidean distance measurements with multicolor fluorescence localization imaging in cultured cells. <i>STAR Protocols</i> , 2021, 2, 100774.	1.2	2
33	Kinetochore tracking in 3D from lattice light-sheet imaging data with KiT. <i>Bioinformatics</i> , 2022, 38, 3315-3317.	4.1	1