Anton Arkhipov

List of Publications by Year
in descending order

#	Article	IF	Citations
1	Measuring Stimulus-Evoked Neurophysiological Differentiation in Distinct Populations of Neurons in Mouse Visual Cortex. ENeuro, 2022, 9, ENEURO.0280-21.2021.	1.9	5
2	Local connectivity and synaptic dynamics in mouse and human neocortex. Science, 2022, 375, eabj5861.	12.6	124
3	Consistent cross-modal identification of cortical neurons with coupled autoencoders. Nature Computational Science, 2021, 1, 120-127.	8.0	29
4	Survey of spiking in the mouse visual system reveals functional hierarchy. Nature, 2021, 592, 86-92.	27.8	284
5	Human neocortical expansion involves glutamatergic neuron diversification. Nature, 2021, 598, 151-158.	27.8	160
6	Integrated Morphoelectric and Transcriptomic Classification of Cortical GABAergic Cells. Cell, 2020, 183, 935-953.e19.	28.9	290
7	Systematic Integration of Structural and Functional Data into Multi-scale Models of Mouse Primary Visual Cortex. Neuron, 2020, 106, 388-403.e18.	8.1	163
8	The SONATA data format for efficient description of large-scale network models. PLoS Computational Biology, 2020, 16, e1007696.	3.2	32
9	Brain Modeling ToolKit: An open source software suite for multiscale modeling of brain circuits. PLoS Computational Biology, 2020, 16, e1008386.	3.2	34
10	Classification of electrophysiological and morphological neuron types in the mouse visual cortex. Nature Neuroscience, 2019, 22, 1182-1195.	14.8	333
11	Systematic generation of biophysically detailed models for diverse cortical neuron types. Nature Communications, 2018, 9, 710.	12.8	123
12	Visual physiology of the layer 4 cortical circuit in silico. PLoS Computational Biology, 2018, 14, e1006535.	3.2	75
13	BioNet: A Python interface to NEURON for modeling large-scale networks. PLoS ONE, 2018, 13, e0201630.	2.5	58
14	Oligomerization of the Epidermal Growth Factor Receptor Organizes Kinase-Active Dimers into Competent Signaling Platforms. Biophysical Journal, 2017, 112, 26a-27a.	0.5	0
15	Inferring cortical function in the mouse visual system through large-scale systems neuroscience. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7337-7344.	7.1	82
16	EGFR oligomerization organizes kinase-active dimers into competent signalling platforms. Nature Communications, 2016, 7, 13307.	12.8	146
17	How Synaptotagmin I, N-BAR and F-BAR Domains Generate Membrane Curvature. Biophysical Journal, 2015, 108, 555a.	0.5	0
18	Membrane Interaction of Bound Ligands Contributes to the Negative Binding Cooperativity of the EGF Receptor. PLoS Computational Biology, 2014, 10, e1003742.	3.2	39

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19	Architecture and Membrane Interactions of the EGF Receptor. Cell, 2013, 152, 557-569.	28.9	417
20	Conformational Coupling across the Plasma Membrane in Activation of the EGF Receptor. Cell, 2013, 152, 543-556.	28.9	423
21	Transitions to catalytically inactive conformations in EGFR kinase. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7270-7275.	7.1	186
22	Her2 activation mechanism reflects evolutionary preservation of asymmetric ectodomain dimers in the human EGFR family. ELife, 2013, 2, e00708.	6.0	62
23	Computer Simulation of Membrane Tubulation by EFC F-BAR Domain Lattices. Biophysical Journal, 2012, 102, 237a.	0.5	0
24	Oncogenic Mutations Counteract Intrinsic Disorder in the EGFR Kinase and Promote Receptor Dimerization. Cell, 2012, 149, 860-870.	28.9	304
25	Mobility Analysis in Living Yeast using 4Pi CFM. Biophysical Journal, 2010, 98, 580a.	0.5	0
26	Simulation of Membrane Sculpting by EFC F-BAR Domain Lattices. Biophysical Journal, 2010, 98, 632a.	0.5	0
27	Multi-scale Simulations of Membrane Sculpting by N-BAR Domains. RSC Biomolecular Sciences, 2010, , 146-176.	0.4	1
28	Simulations of Membrane Tubulation by Lattices of Amphiphysin N-BAR Domains. Structure, 2009, 17, 882-892.	3.3	131
29	Limits for reduction of effective focal volume in multiple-beam light microscopy. Optics Express, 2009, 17, 2861.	3.4	8
30	Elucidating the Mechanism behind Irreversible Deformation of Viral Capsids. Biophysical Journal, 2009, 97, 2061-2069.	0.5	94
31	Membrane-Bending Mechanism of Amphiphysin N-BAR Domains. Biophysical Journal, 2009, 97, 2727-2735.	0.5	101
32	Four-Scale Description of Membrane Sculpting by BAR Domains. Biophysical Journal, 2008, 95, 2806-2821.	0.5	251
33	Chapter 11 Molecular Modeling of the Structural Properties and Formation of High-Density Lipoprotein Particles. Current Topics in Membranes, 2008, 60, 313-342.	0.9	8
34	Application of Residue-Based and Shape-Based Coarse-Graining to Biomolecular Simulations. , 2008, , 299-315.		5
35	Assembly of lipoprotein particles revealed by coarse-grained molecular dynamics simulations. Journal of Structural Biology, 2007, 157, 579-592.	2.8	115
36	Assembly of Lipids and Proteins into Lipoprotein Particles. Journal of Physical Chemistry B, 2007, 111, 11095-11104.	2.6	60

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37	Continuous Fluorescence Microphotolysis and Correlation Spectroscopy Using 4Pi Microscopy. Biophysical Journal, 2007, 93, 4006-4017.	0.5	20
38	Imaging the Migration Pathways for O2, CO, NO, and Xe Inside Myoglobin. Biophysical Journal, 2006, 91, 1844-1857.	0.5	258
39	Coarse-Grained Molecular Dynamics Simulations of a Rotating Bacterial Flagellum. Biophysical Journal, 2006, 91, 4589-4597.	0.5	93
40	Coarse Grained Proteinâ˘'Lipid Model with Application to Lipoprotein Particlesâ€. Journal of Physical Chemistry B, 2006, 110, 3674-3684.	2.6	244
41	Stability and Dynamics of Virus Capsids Described by Coarse-Grained Modeling. Structure, 2006, 14, 1767-1777.	3.3	245
42	The role of molecular modeling in bionanotechnology. Physical Biology, 2006, 3, S40-S53.	1.8	68
43	The SONATA Data Format for Efficient Description of Large-Scale Network Models. SSRN Electronic Journal, 0, , .	0.4	6
44	Systematic Integration of Structural and Functional Data into Multi-Scale Models of Mouse Primary Visual Cortex. SSRN Electronic Journal, 0, , .	0.4	6