Antreas C Kalli

List of Publications by Year
in descending order

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40	1,603	293460	371746
papers	citations	24 h-index	37 g-index

50	50	50	2123
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pocket delipidation induced by membrane tension or modification leads to a structurally analogous mechanosensitive channel state. Structure, 2022, 30, 608-622.e5.	1.6	16
2	Organization and Dynamics of the Red Blood Cell Band 3 Anion Exchanger SLC4A1: Insights From Molecular Dynamics Simulations. Frontiers in Physiology, 2022, 13, 817945.	1.3	6
3	Characterization of the membrane interactions of phospholipase CÎ³ reveals key features of the active enzyme. Science Advances, 2022, 8, .	4.7	7
4	The guidance and adhesion protein FLRT2 dimerizes in cis via dual small-X3-small transmembrane motifs. Structure, 2022, 30, 1354-1365.e5.	1.6	4
5	Modeling of full-length Piezo1 suggests importance of the proximal N-terminus for dome structure. Biophysical Journal, 2021, 120, 1343-1356.	0.2	23
6	Molecular dynamics simulations of Piezo1 channel opening by increases in membrane tension. Biophysical Journal, 2021, 120, 1510-1521.	0.2	33
7	Allosteric activation of TÂcell antigen receptor signaling by quaternary structure relaxation. Cell Reports, 2021, 36, 109375.	2.9	23
8	Multi-scale simulations of the T cell receptor reveal its lipid interactions, dynamics and the arrangement of its cytoplasmic region. PLoS Computational Biology, 2021, 17, e1009232.	1.5	13
9	Sphingomyelinase Disables Inactivation in Endogenous PIEZO1 Channels. Cell Reports, 2020, 33, 108225.	2.9	47
10	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. Communications Biology, 2020, 3, 766.	2.0	32
11	RBCs prevent rapid PIEZO1 inactivation and expose slow deactivation as a mechanism of dehydrated hereditary stomatocytosis. Blood, 2020, 136, 140-144.	0.6	23
12	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. Science Advances, 2020, 6, eaay5736.	4.7	44
13	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. Nature Communications, 2020, 11, 2155.	5.8	48
14	Membrane Recognition and Binding by the Phosphatidylinositol Phosphate Kinase PIP5K1A: A Multiscale Simulation Study. Structure, 2019, 27, 1336-1346.e2.	1.6	22
15	Force Sensing by Piezo Channels in Cardiovascular Health and Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2228-2239.	1.1	147
16	Molecular Simulations of Intact Anion Exchanger 1 Reveal Specific Domain and Lipid Interactions. Biophysical Journal, 2019, 117, 1364-1379.	0.2	16
17	Î²1 integrin is a sensor of blood flow direction. Journal of Cell Science, 2019, 132, .	1.2	41
18	Modes of Interaction of Pleckstrin Homology Domains with Membranes: Toward a Computational Biochemistry of Membrane Recognition. Journal of Molecular Biology, 2018, 430, 372-388.	2.0	42

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19	Distinctive phosphoinositide- and Ca2+-binding properties of normal and cognitive performanceâ€“linked variant forms of KIBRA C2 domain. Journal of Biological Chemistry, 2018, 293, 9335-9344.	1.6	8
20	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. Cell Chemical Biology, 2018, 25, 840-848.e4.	2.5	64
21	Interaction of the human erythrocyte Band 3 anion exchanger 1 (AE1, SLC4A1) with lipids and glycophorin A: Molecular organization of the Wright (Wr) blood group antigen. PLoS Computational Biology, 2018, 14, e1006284.	1.5	37
22	Interactions of the EphA2 Kinase Domain with PIPs in Membranes: Implications for Receptor Function. Structure, 2018, 26, 1025-1034.e2.	1.6	33
23	Dynamic interactions between a membrane binding protein and lipids induce fluctuating diffusivity. Science Advances, 2017, 3, e1601871.	4.7	59
24	Structure and lipid-binding properties of the kindlin-3 pleckstrin homology domain. Biochemical Journal, 2017, 474, 539-556.	1.7	40
25	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. Journal of Molecular Biology, 2017, 429, 3776-3792.	2.0	63
26	The Integrin Receptor in Biologically Relevant Bilayers: Insights from Molecular Dynamics Simulations. Journal of Membrane Biology, 2017, 250, 337-351.	1.0	29
27	Multiscale Simulations Suggest a Mechanism for the Association of the Dok7 PH Domain with PIP-Containing Membranes. PLoS Computational Biology, 2016, 12, e1005028.	1.5	24
28	On the interpretation of reflectivity data from lipid bilayers in terms of molecular-dynamics models. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1227-1240.	1.1	10
29	Band 3, the human red cell chloride/bicarbonate anion exchanger (AE1, SLC4A1), in a structural context. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1507-1532.	1.4	154
30	Interactions of Pleckstrin Homology Domains with Membranes: Adding Back the Bilayer via High-Throughput Molecular Dynamics. Structure, 2016, 24, 1421-1431.	1.6	68
31	Anomalous Dynamics of a Lipid Recognition Protein on a Membrane Surface. Scientific Reports, 2016, 5, 18245.	1.6	38
32	Association of Peripheral Membrane Proteins with Membranes: Free Energy of Binding of GRP1 PH Domain with Phosphatidylinositol Phosphate-Containing Model Bilayers. Journal of Physical Chemistry Letters, 2016, 7, 1219-1224.	2.1	47
33	Molecular Dynamics Simulations of the Bacterial UraA H+-Uracil Symporter in Lipid Bilayers Reveal a Closed State and a Selective Interaction with Cardiolipin. PLoS Computational Biology, 2015, 11, e1004123.	1.5	40
34	Interactions of peripheral proteins with model membranes as viewed by molecular dynamics simulations. Biochemical Society Transactions, 2014, 42, 1418-1424.	1.6	31
35	Interactions of Phosphatase and Tensin Homologue (PTEN) Proteins with Phosphatidylinositol Phosphates: Insights from Molecular Dynamics Simulations of PTEN and Voltage Sensitive Phosphatase. Biochemistry, 2014, 53, 1724-1732.	1.2	42
36	Interactions of the Auxilin-1 PTEN-like Domain with Model Membranes Result in Nanoclustering of Phosphatidyl Inositol Phosphates. Biophysical Journal, 2013, 105, 137-145.	0.2	24

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37	Conformational Changes in Talin on Binding to Anionic Phospholipid Membranes Facilitate Signaling by Integrin Transmembrane Helices. PLoS Computational Biology, 2013, 9, e1003316.	1.5	30
38	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
39	Multiscale simulations suggest a mechanism for integrin inside-out activation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11890-11895.	3.3	62
40	The Structure of the Talin/Integrin Complex at a Lipid Bilayer: An NMR and MD Simulation Study. Structure, 2010, 18, 1280-1288.	1.6	57