Antreas C Kalli

List of Publications by Year in Descending Order

42 papers	1,009 citations	20 h-index	31 g-index
50 ext. papers	1,363 ext. citations	5.9 avg, IF	4.87 L-index

#	Paper	IF	Citations
42	Organization and Dynamics of the Red Blood Cell Band 3 Anion Exchanger SLC4A1: Insights From Molecular Dynamics Simulations.. *Frontiers in Physiology*, **2022**, 13, 817945	4.6	0
41	Pocket delipidation induced by membrane tension or modification leads to a structurally analogous mechanosensitive channel state.. *Structure*, **2021**,	5.2	3
40	Modeling of full-length Piezo1 suggests importance of the proximal N-terminus for dome structure. *Biophysical Journal*, **2021**, 120, 1343-1356	2.9	6
39	Molecular dynamics simulations of Piezo1 channel opening by increases in membrane tension. *Biophysical Journal*, **2021**, 120, 1510-1521	2.9	5
38	Allosteric activation of T□cell antigen receptor signaling by quaternary structure relaxation. *Cell Reports*, **2021**, 36, 109375	10.6	3
37	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	5	1
36	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. *Communications Biology*, **2020**, 3, 766	6.7	13
35	RBCs prevent rapid PIEZO1 inactivation and expose slow deactivation as a mechanism of dehydrated hereditary stomatocytosis. *Blood*, **2020**, 136, 140-144	2.2	12
34	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. *Science Advances*, **2020**, 6, eaay5736	14.3	17
33	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. *Nature Communications*, **2020**, 11, 2155	17.4	28
32	Sphingomyelinase Disables Inactivation in Endogenous PIEZO1 Channels. *Cell Reports*, **2020**, 33, 108225	10.6	16
31	Force Sensing by Piezo Channels in Cardiovascular Health and Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2019**, 39, 2228-2239	9.4	70
30	Molecular Simulations of Intact Anion Exchanger 1 Reveal Specific Domain and Lipid Interactions. *Biophysical Journal*, **2019**, 117, 1364-1379	2.9	7
29	□1 integrin is a sensor of blood flow direction. *Journal of Cell Science*, **2019**, 132,	5.3	23
28	Membrane Recognition and Binding by the Phosphatidylinositol Phosphate Kinase PIP5K1A: A Multiscale Simulation Study. *Structure*, **2019**, 27, 1336-1346.e2	5.2	8
27	Modes of Interaction of Pleckstrin Homology Domains with Membranes: Toward a Computational Biochemistry of Membrane Recognition. *Journal of Molecular Biology*, **2018**, 430, 372-388	6.5	28
26	Distinctive phosphoinositide- and Ca-binding properties of normal and cognitive performance-linked variant forms of KIBRA C2 domain. *Journal of Biological Chemistry*, **2018**, 293, 9335-9344	5.4	5

25	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	5	18
24	Interactions of the EphA2 Kinase Domain with PIPs in Membranes: Implications for Receptor Function. *Structure*, **2018**, 26, 1025-1034.e2	5.2	20
23	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. *Cell Chemical Biology*, **2018**, 25, 840-848.e4	8.2	46
22	Dynamic interactions between a membrane binding protein and lipids induce fluctuating diffusivity. *Science Advances*, **2017**, 3, e1601871	14.3	40
21	Structure and lipid-binding properties of the kindlin-3 pleckstrin homology domain. *Biochemical Journal*, **2017**, 474, 539-556	3.8	30
20	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. *Journal of Molecular Biology*, **2017**, 429, 3776-3792	6.5	49
19	The Integrin Receptor in Biologically Relevant Bilayers: Insights from Molecular Dynamics Simulations. *Journal of Membrane Biology*, **2017**, 250, 337-351	2.3	17
18	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, 1219-24	6.4	34
17	Multiscale Simulations Suggest a Mechanism for the Association of the Dok7 PH Domain with PIP-Containing Membranes. *PLoS Computational Biology*, **2016**, 12, e1005028	5	20
16	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	5.5	8
15	Band 3, the human red cell chloride/bicarbonate anion exchanger (AE1, SLC4A1), in a structural context. *Biochimica Et Biophysica Acta - Biomembranes*, **2016**, 1858, 1507-32	3.8	103
14	Interactions of Pleckstrin Homology Domains with Membranes: Adding Back the Bilayer via High-Throughput Molecular Dynamics. *Structure*, **2016**, 24, 1421-1431	5.2	51
13	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	5	30
12	Anomalous Dynamics of a Lipid Recognition Protein on a Membrane Surface. *Scientific Reports*, **2015**, 5, 18245	4.9	34
11	Interactions of peripheral proteins with model membranes as viewed by molecular dynamics simulations. *Biochemical Society Transactions*, **2014**, 42, 1418-24	5.1	29
10	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, 1724-32	3.2	35
9	Interactions of the auxilin-1 PTEN-like domain with model membranes result in nanoclustering of phosphatidyl inositol phosphates. *Biophysical Journal*, **2013**, 105, 137-45	2.9	22
8	Conformational changes in talin on binding to anionic phospholipid membranes facilitate signaling by integrin transmembrane helices. *PLoS Computational Biology*, **2013**, 9, e1003316	5	23

7	A helix heterodimer in a lipid bilayer: prediction of the structure of an integrin transmembrane domain via multiscale simulations. *Structure*, **2011**, 19, 1477-84	5.2	35
6	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, 11890-5	11.5	56
5	The structure of the talin/integrin complex at a lipid bilayer: an NMR and MD simulation study. *Structure*, **2010**, 18, 1280-8	5.2	53
4	Sphingomyelinase disables Piezo1 channel inactivation to enable sustained response to mechanical force		2
3	Genetic variants of PIEZO1 associate with COVID-19 fatality		3
2	Computational reconstruction of the complete Piezo1 structure reveals a unique footprint and specific lipid interactions		3
1	Molecular principles of Piezo1 activation by increased membrane tension		2