

Phillip James Stansfeld

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

125
papers

4,560
citations

37
h-index

64
g-index

165
ext. papers

5,798
ext. citations

9
avg, IF

5.88
L-index

#	Paper	IF	Citations
125	PyLipID: A Python Package for Analysis of Protein-Lipid Interactions from Molecular Dynamics Simulations.. <i>Journal of Chemical Theory and Computation</i> , 2022 ,	6.4	10
124	Structure, substrate recognition and initiation of hyaluronan synthase.. <i>Nature</i> , 2022 ,	50.4	5
123	Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients.. <i>Nature Communications</i> , 2022 , 13, 2278	17.4	1
122	Structural, Functional and Computational Studies of Membrane Recognition by Plasmodium Perforin-Like Proteins 1 and 2. <i>Journal of Molecular Biology</i> , 2022 , 434, 167642	6.5	
121	High-resolution mapping of metal ions reveals principles of surface layer assembly in <i>Caulobacter crescentus</i> cells. <i>Structure</i> , 2021 ,	5.2	2
120	Mechanism of lipid droplet formation by the yeast Sei1/Ldb16 Seipin complex. <i>Nature Communications</i> , 2021 , 12, 5892	17.4	5
119	Alternative Architecture of the Chemosensory Array. <i>Biomolecules</i> , 2021 , 11,	5.9	2
118	Switching Cytolytic Nanopores into Antimicrobial Fractal Ruptures by a Single Side Chain Mutation. <i>ACS Nano</i> , 2021 , 15, 9679-9689	16.7	9
117	Cryo-EM Structures of CusA Reveal a Mechanism of Metal-Ion Export. <i>MBio</i> , 2021 , 12,	7.8	4
116	NaViA: A Program for the Visual Analysis of Complex Mass Spectra. <i>Bioinformatics</i> , 2021 ,	7.2	3
115	A Bacterial Inflammation Sensor Regulates c-di-GMP Signaling, Adhesion, and Biofilm Formation. <i>MBio</i> , 2021 , 12, e0017321	7.8	1
114	Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021 , 17, 187-195	11.7	18
113	Membrane Binding of Antimicrobial Peptides Is Modulated by Lipid Charge Modification. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 1218-1228	6.4	2
112	Identification and assessment of cardiolipin interactions with inner membrane proteins. <i>Science Advances</i> , 2021 , 7,	14.3	7
111	From Bench to Biomolecular Simulation: Phospholipid Modulation of Potassium Channels. <i>Journal of Molecular Biology</i> , 2021 , 433, 167105	6.5	1
110	An outer-pore gate modulates the pharmacology of the TMEM16A channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
109	Deciphering ion transport and ATPase coupling in the intersubunit tunnel of KdpFABC. <i>Nature Communications</i> , 2021 , 12, 5098	17.4	2

108	Relative Affinities of Protein-Cholesterol Interactions from Equilibrium Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 6548-6558	6.4	3
107	CG2AT2: an Enhanced Fragment-Based Approach for Serial Multi-scale Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 6472-6482	6.4	14
106	Structural basis of trehalose recognition by the mycobacterial LpqY-SugABC transporter. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100307	5.4	3
105	Identification and Characterization of Specific Protein-Lipid Interactions Using Molecular Simulation. <i>Methods in Molecular Biology</i> , 2021 , 2315, 121-139	1.4	2
104	New insights into K channel gene mutations and neonatal diabetes mellitus. <i>Nature Reviews Endocrinology</i> , 2020 , 16, 378-393	15.2	41
103	Atomistic mechanism of transmembrane helix association. <i>PLoS Computational Biology</i> , 2020 , 16, e1007919	5.1	4
102	Characterizing Membrane Association and Periplasmic Transfer of Bacterial Lipoproteins through Molecular Dynamics Simulations. <i>Structure</i> , 2020 , 28, 475-487.e3	5.2	11
101	Structure and mechanism of bactericidal mammalian perforin-2, an ancient agent of innate immunity. <i>Science Advances</i> , 2020 , 6, eaax8286	14.3	32
100	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. <i>Science Advances</i> , 2020 , 6, eaay5736	14.3	17
99	Complete structure of the chemosensory array core signalling unit in an E. coli minicell strain. <i>Nature Communications</i> , 2020 , 11, 743	17.4	19
98	Targeting of proteins to the twin-arginine translocation pathway. <i>Molecular Microbiology</i> , 2020 , 113, 861-871	4.1	22
97	Structural basis of proton-coupled potassium transport in the KUP family. <i>Nature Communications</i> , 2020 , 11, 626	17.4	35
96	The Unconventional Cytoplasmic Sensing Mechanism for Ethanol Chemotaxis in <i>Bacillus subtilis</i> . <i>MBio</i> , 2020 , 11,	7.8	10
95	The energetics of protein-lipid interactions as viewed by molecular simulations. <i>Biochemical Society Transactions</i> , 2020 , 48, 25-37	5.1	22
94	Insights into bacterial cell division from a structure of EnvC bound to the FtsX periplasmic domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28355-28365	11.5	9
93	Structure and dynamics of the E. coli chemotaxis core signaling complex by cryo-electron tomography and molecular simulations. <i>Communications Biology</i> , 2020 , 3, 24	6.7	16
92	In Situ Structure of an Intact Lipopolysaccharide-Bound Bacterial Surface Layer. <i>Cell</i> , 2020 , 180, 348-358.e15	11.5	37
91	A Mass-Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 3523-3528	16.4	18

90	A bipartite structural organization defines the SERINC family of HIV-1 restriction factors. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 78-83	17.6	34
89	A Mass-Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie</i> , 2020 , 132, 3551-3556	3.6	1
88	Conformational dynamics of a G protein-coupled receptor helix 8 in lipid membranes. <i>Science Advances</i> , 2020 , 6, eaav8207	14.3	10
87	Greasing the Gears of Mechanosensitive Piezo Channels with Phosphoinositides and Cholesterol. <i>Biophysical Journal</i> , 2020 , 119, 1467-1469	2.9	
86	The SARS-COV-2 Spike Protein Binds Sialic Acids and Enables Rapid Detection in a Lateral Flow Point of Care Diagnostic Device. <i>ACS Central Science</i> , 2020 , 6, 2046-2052	16.8	116
85	Structures of the stator complex that drives rotation of the bacterial flagellum. <i>Nature Microbiology</i> , 2020 , 5, 1553-1564	26.6	61
84	Evaluating inositol phospholipid interactions with inward rectifier potassium channels and characterising their role in disease. <i>Communications Chemistry</i> , 2020 , 3,	6.3	8
83	The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K. <i>Nature Communications</i> , 2019 , 10, 3956	17.4	55
82	Insights into Membrane Protein-Lipid Interactions from Free Energy Calculations. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 5727-5736	6.4	33
81	Sharing Data from Molecular Simulations. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 4093-4099	6.0	11
80	A heuristic derived from analysis of the ion channel structural proteome permits the rapid identification of hydrophobic gates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 13989-13995	11.5	23
79	Structural basis for substrate specificity and regulation of nucleotide sugar transporters in the lipid bilayer. <i>Nature Communications</i> , 2019 , 10, 4657	17.4	10
78	The molecular basis for an allosteric inhibition of K-flux gating in K channels. <i>ELife</i> , 2019 , 8,	8.9	16
77	A lipid gating mechanism for the channel-forming O antigen ABC transporter. <i>Nature Communications</i> , 2019 , 10, 824	17.4	34
76	The MemProtMD database: a resource for membrane-embedded protein structures and their lipid interactions. <i>Nucleic Acids Research</i> , 2019 , 47, D390-D397	20.1	70
75	Water and hydrophobic gates in ion channels and nanopores. <i>Faraday Discussions</i> , 2018 , 209, 231-247	3.6	28
74	Balancing Force Field Protein-Lipid Interactions To Capture Transmembrane Helix-Helix Association. <i>Journal of Chemical Theory and Computation</i> , 2018 , 14, 1706-1715	6.4	24
73	Crystal structure of undecaprenyl-pyrophosphate phosphatase and its role in peptidoglycan biosynthesis. <i>Nature Communications</i> , 2018 , 9, 1078	17.4	31

72	Structures of monomeric and oligomeric forms of the perforin-like protein 1. <i>Science Advances</i> , 2018 , 4, eaaq0762	14.3	20
71	Interactions of the EphA2 Kinase Domain with PIPs in Membranes: Implications for Receptor Function. <i>Structure</i> , 2018 , 26, 1025-1034.e2	5.2	20
70	Interactions of a Bacterial Cu(I)-ATPase with a Complex Lipid Environment. <i>Biochemistry</i> , 2018 , 57, 4063-4073	3.7	3
69	Lipid binding attenuates channel closure of the outer membrane protein OmpF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 6691-6696	11.5	21
68	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017 , 541, 421-424	50.4	238
67	Computational studies of membrane proteins: from sequence to structure to simulation. <i>Current Opinion in Structural Biology</i> , 2017 , 45, 133-141	8.1	15
66	A BEST example of channel structure annotation by molecular simulation. <i>Channels</i> , 2017 , 11, 347-353	3	19
65	Substrate-triggered position switching of TatA and TatB during Tat transport in. <i>Open Biology</i> , 2017 , 7,	7	16
64	Structural insights into the mechanism of the membrane integral N-acyltransferase step in bacterial lipoprotein synthesis. <i>Nature Communications</i> , 2017 , 8, 15952	17.4	40
63	Convergence and Sampling in Determining Free Energy Landscapes for Membrane Protein Association. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3364-3375	3.4	69
62	Coupling Form and Function: How the Oligomerisation Symmetry of the SAS-6 Protein Contributes to the Architecture of Centriole Organelles. <i>Symmetry</i> , 2017 , 9, 74	2.7	
61	Structural analysis of P. falciparum KAHRP and PfEMP1 complexes with host erythrocyte spectrin suggests a model for cytoadherent knob protrusions. <i>PLoS Pathogens</i> , 2017 , 13, e1006552	7.6	18
60	Interaction of lipids with the neurotensin receptor 1. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 1278-87	3.8	12
59	Structural basis of lipoprotein signal peptidase II action and inhibition by the antibiotic globomycin. <i>Science</i> , 2016 , 351, 876-80	33.3	77
58	Structural basis of outer membrane protein insertion by the BAM complex. <i>Nature</i> , 2016 , 531, 64-9	50.4	182
57	Assembling the Tat protein translocase. <i>ELife</i> , 2016 , 5,	8.9	39
56	Calmodulin Regulates Human Ether γ -Go-Go 1 (hEAG1) Potassium Channels through Interactions of the Eag Domain with the Cyclic Nucleotide Binding Homology Domain. <i>Journal of Biological Chemistry</i> , 2016 , 291, 17907-18	5.4	11
55	MemProtMD: Automated Insertion of Membrane Protein Structures into Explicit Lipid Membranes. <i>Structure</i> , 2015 , 23, 1350-61	5.2	204

54	Lipopolysaccharide is inserted into the outer membrane through an intramembrane hole, a lumen gate, and the lateral opening of LptD. <i>Structure</i> , 2015 , 23, 496-504	5.2	53
53	Structure and function of the Escherichia coli Tol-Pal stator protein TolR. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26675-87	5.4	16
52	The centriolar protein CPAP G-box: an amyloid fibril in a single domain. <i>Biochemical Society Transactions</i> , 2015 , 43, 838-43	5.1	6
51	A Coarse Grained Model for a Lipid Membrane with Physiological Composition and Leaflet Asymmetry. <i>PLoS ONE</i> , 2015 , 10, e0144814	3.7	38
50	The TatC component of the twin-arginine protein translocase functions as an obligate oligomer. <i>Molecular Microbiology</i> , 2015 , 98, 111-29	4.1	20
49	Ternary structure reveals mechanism of a membrane diacylglycerol kinase. <i>Nature Communications</i> , 2015 , 6, 10140	17.4	27
48	Dimerization of the EphA1 receptor tyrosine kinase transmembrane domain: Insights into the mechanism of receptor activation. <i>Biochemistry</i> , 2014 , 53, 6641-52	3.2	32
47	Structural basis for outer membrane lipopolysaccharide insertion. <i>Nature</i> , 2014 , 511, 52-6	50.4	181
46	Direct gating of ATP-activated ion channels (P2X2 receptors) by lipophilic attachment at the outer end of the second transmembrane domain. <i>Journal of Biological Chemistry</i> , 2014 , 289, 618-26	5.4	14
45	Structural biology of Tat protein transport. <i>Current Opinion in Structural Biology</i> , 2014 , 27, 32-7	8.1	19
44	The structural basis of ZMPSTE24-dependent laminopathies. <i>Science</i> , 2013 , 339, 1604-7	33.3	75
43	Simulation-based prediction of phosphatidylinositol 4,5-bisphosphate binding to an ion channel. <i>Biochemistry</i> , 2013 , 52, 279-81	3.2	54
42	Structural analysis of the G-box domain of the microcephaly protein CPAP suggests a role in centriole architecture. <i>Structure</i> , 2013 , 21, 2069-77	5.2	59
41	Multiscale simulations reveal conserved patterns of lipid interactions with aquaporins. <i>Structure</i> , 2013 , 21, 810-9	5.2	64
40	Side pockets provide the basis for a new mechanism of Kv channel-specific inhibition. <i>Nature Chemical Biology</i> , 2013 , 9, 507-13	11.7	43
39	Structures of ABCB10, a human ATP-binding cassette transporter in apo- and nucleotide-bound states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 9710-5 ^{11.5}		193
38	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012 , 492, 210-4	50.4	126
37	Functional analysis of missense variants in the TRESK (KCNK18) K channel. <i>Scientific Reports</i> , 2012 , 2, 237	4.9	70

36	Memprotmd: Adding the Grease to Membrane Protein Structures. <i>Biophysical Journal</i> , 2012 , 102, 469a	2.9	
35	State-independent intracellular access of quaternary ammonium blockers to the pore of TREK-1. <i>Channels</i> , 2012 , 6, 473-8	3	34
34	A leucine zipper motif essential for gating of hyperpolarization-activated channels. <i>Journal of Biological Chemistry</i> , 2012 , 287, 40150-60	5.4	6
33	From Coarse Grained to Atomistic: A Serial Multiscale Approach to Membrane Protein Simulations. <i>Journal of Chemical Theory and Computation</i> , 2011 , 7, 1157-66	6.4	200
32	The pore structure and gating mechanism of K2P channels. <i>EMBO Journal</i> , 2011 , 30, 3607-19	13	129
31	A conserved tryptophan at the membrane-water interface acts as a gatekeeper for Kir6.2/SUR1 channels and causes neonatal diabetes when mutated. <i>Journal of Physiology</i> , 2011 , 589, 3071-83	3.9	13
30	Biophysical and computational studies of membrane penetration by the GRP1 pleckstrin homology domain. <i>Structure</i> , 2011 , 19, 1338-46	5.2	50
29	Molecular simulation approaches to membrane proteins. <i>Structure</i> , 2011 , 19, 1562-72	5.2	136
28	A specific two-pore domain potassium channel blocker defines the structure of the TASK-1 open pore. <i>Journal of Biological Chemistry</i> , 2011 , 286, 13977-84	5.4	62
27	Mechanistic insight into human ether-à-go-go-related gene (hERG) K ⁺ channel deactivation gating from the solution structure of the EAG domain. <i>Journal of Biological Chemistry</i> , 2011 , 286, 6184-91	5.4	78
26	The pore structure and gating mechanism of K2P channels. <i>EMBO Journal</i> , 2011 , 30, 4515-4515	13	2
25	Lipidbook: a public repository for force-field parameters used in membrane simulations. <i>Journal of Membrane Biology</i> , 2010 , 236, 255-8	2.3	131
24	The response of the tandem pore potassium channel TASK-3 (K(2P)9.1) to voltage: gating at the cytoplasmic mouth. <i>Journal of Physiology</i> , 2009 , 587, 4769-83	3.9	22
23	Ion-blocking sites of the Kir2.1 channel revealed by multiscale modeling. <i>Biochemistry</i> , 2009 , 48, 8758-63	3.2	14
22	PIP(2)-binding site in Kir channels: definition by multiscale biomolecular simulations. <i>Biochemistry</i> , 2009 , 48, 10926-33	3.2	108
21	Simulations of the BM2 proton channel transmembrane domain from influenza virus B. <i>Biochemistry</i> , 2009 , 48, 9949-51	3.2	12
20	Molecular modeling and simulation studies of ion channel structures, dynamics and mechanisms. <i>Methods in Cell Biology</i> , 2008 , 90, 233-65	1.8	22
19	Insight into the mechanism of inactivation and pH sensitivity in potassium channels from molecular dynamics simulations. <i>Biochemistry</i> , 2008 , 47, 7414-22	3.2	46

18	Structural Determinants for High-Affinity Block of hERG Potassium Channels. <i>Novartis Foundation Symposium</i> , 2008 , 136-154		24
17	Drug block of the hERG potassium channel: insight from modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 568-80	4.2	87
16	The selectivity, voltage-dependence and acid sensitivity of the tandem pore potassium channel TASK-1: contributions of the pore domains. <i>Pflugers Archiv European Journal of Physiology</i> , 2007 , 455, 333-48	4.6	25
15	Activation gating of hERG potassium channels: S6 glycines are not required as gating hinges. <i>Journal of Biological Chemistry</i> , 2007 , 282, 31972-81	5.4	34
14	Drug binding interactions in the inner cavity of HERG channels: molecular insights from structure-activity relationships of clofilium and ibutilide analogs. <i>Molecular Pharmacology</i> , 2006 , 69, 509-19	4.3	72
13	Molecular mechanisms for drug interactions with hERG that cause long QT syndrome. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2006 , 2, 81-94	5.5	38
12	Structural features of the glutamate binding site in recombinant NR1/NR2A N-methyl-D-aspartate receptors determined by site-directed mutagenesis and molecular modeling. <i>Molecular Pharmacology</i> , 2005 , 67, 1470-84	4.3	124
11	Homology Models Applied to Toxicology	433-468	
10	A Heuristic Derived from Analysis of the Ion Channel Structural Proteome Permits the Rapid Identification of Hydrophobic Gates		1
9	Substrate-triggered position-switching of TatA and TatB is an essential step in the Escherichia coli Tat protein export pathway		3
8	Structures of the stator complex that drives rotation of the bacterial flagellum		4
7	Evaluating Inositol phospholipid interactions with Inward Rectifier Potassium Channels and characterising their role in Disease		1
6	The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K		9
5	Insights into Membrane Protein-Lipid Interactions from Free Energy Calculations		1
4	Identification and assessment of cardiolipin interactions with E. coli inner membrane proteins		3
3	CG2AT2: An Enhanced Fragment-based approach for Serial Multi-scale Molecular Dynamics simulations		4
2	The dynamic interplay of PIP2 and ATP in the regulation of the KATP channel		1
1	PyLipID: A Python package for analysis of protein-lipid interactions from MD simulations		3

