

Lucy Rachel Forrest

List of Publications by Citations

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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.

80
papers

4,188
citations

34
h-index

64
g-index

94
ext. papers

4,819
ext. citations

6.5
avg, IF

5.7
L-index

#	Paper	IF	Citations
80	The structural basis of secondary active transport mechanisms. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2011 , 1807, 167-88	4.6	312
79	Mechanism for alternating access in neurotransmitter transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 10338-43	11.5	299
78	The rocking bundle: a mechanism for ion-coupled solute flux by symmetrical transporters. <i>Physiology</i> , 2009 , 24, 377-86	9.8	212
77	On the accuracy of homology modeling and sequence alignment methods applied to membrane proteins. <i>Biophysical Journal</i> , 2006 , 91, 508-17	2.9	202
76	Identification of a chloride ion binding site in Na ⁺ /Cl ⁻ -dependent transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12761-6	11.5	171
75	Membrane simulations: bigger and better?. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 174-81	8.1	160
74	Lipid properties and the orientation of aromatic residues in OmpF, influenza M2, and alamethicin systems: molecular dynamics simulations. <i>Biochemistry</i> , 1998 , 37, 17554-61	3.2	151
73	The alternating-access mechanism of MFS transporters arises from inverted-topology repeats. <i>Journal of Molecular Biology</i> , 2011 , 407, 698-715	6.5	143
72	Inward-facing conformation of glutamate transporters as revealed by their inverted-topology structural repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20752-7	11.5	125
71	Homology modeling and molecular dynamics simulation studies of an inward rectifier potassium channel. <i>Biophysical Journal</i> , 2000 , 78, 2929-42	2.9	120
70	Intestinal serotonin and fluoxetine exposure modulate bacterial colonization in the gut. <i>Nature Microbiology</i> , 2019 , 4, 2064-2073	26.6	109
69	Membrane protein prediction methods. <i>Methods</i> , 2007 , 41, 460-74	4.6	97
68	Exploring models of the influenza A M2 channel: MD simulations in a phospholipid bilayer. <i>Biophysical Journal</i> , 2000 , 78, 55-69	2.9	96
67	Molecular dynamics simulation of dark-adapted rhodopsin in an explicit membrane bilayer: coupling between local retinal and larger scale conformational change. <i>Journal of Molecular Biology</i> , 2003 , 333, 493-514	6.5	88
66	Structural Symmetry in Membrane Proteins. <i>Annual Review of Biophysics</i> , 2015 , 44, 311-37	21.1	87
65	A study of the evolution of inverted-topology repeats from LeuT-fold transporters using AlignMe. <i>Biochemistry</i> , 2010 , 49, 10702-13	3.2	87
64	Conformational sampling and dynamics of membrane proteins from 10-nanosecond computer simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 783-91	4.2	86

63	Helical packing patterns in membrane and soluble proteins. <i>Biophysical Journal</i> , 2004 , 87, 4075-86	2.9	84
62	Fluoxetine (Prozac) binding to serotonin transporter is modulated by chloride and conformational changes. <i>Journal of Neuroscience</i> , 2009 , 29, 9635-43	6.6	72
61	Structure and dynamics of K channel pore-lining helices: a comparative simulation study. <i>Biophysical Journal</i> , 2000 , 78, 79-92	2.9	69
60	Gating topology of the proton-coupled oligopeptide symporters. <i>Structure</i> , 2015 , 23, 290-301	5.2	67
59	Defining the transmembrane helix of M2 protein from influenza A by molecular dynamics simulations in a lipid bilayer. <i>Biophysical Journal</i> , 1999 , 76, 1886-96	2.9	61
58	Investigation of the sodium-binding sites in the sodium-coupled betaine transporter BetP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E3035-44	11.5	59
57	AlignMe--a membrane protein sequence alignment web server. <i>Nucleic Acids Research</i> , 2014 , 42, W246-51	0.1	58
56	Conformational dynamics of a neurotransmitter:sodium symporter in a lipid bilayer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E1786-E1795	11.5	55
55	The bacterial dicarboxylate transporter VcINDY uses a two-domain elevator-type mechanism. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 256-63	17.6	55
54	Two Na ⁺ Sites Control Conformational Change in a Neurotransmitter Transporter Homolog. <i>Journal of Biological Chemistry</i> , 2016 , 291, 1456-71	5.4	51
53	Structural biology. (Pseudo-)symmetrical transport. <i>Science</i> , 2013 , 339, 399-401	33.3	49
52	Molecular dynamics of synthetic leucine-serine ion channels in a phospholipid membrane. <i>Biophysical Journal</i> , 1999 , 77, 2400-10	2.9	48
51	GRIFFIN: A versatile methodology for optimization of protein-lipid interfaces for membrane protein simulations. <i>Journal of Chemical Theory and Computation</i> , 2011 , 7, 1167-1176	6.4	47
50	Structure and dynamics of the pore-lining helix of the nicotinic receptor: MD simulations in water, lipid bilayers, and transbilayer bundles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 39, 47-55	4.2	46
49	Alignment of helical membrane protein sequences using AlignMe. <i>PLoS ONE</i> , 2013 , 8, e57731	3.7	44
48	Substrate-bound outward-open state of the betaine transporter BetP provides insights into Na ⁺ coupling. <i>Nature Communications</i> , 2014 , 5, 4231	17.4	38
47	Structure and regulatory interactions of the cytoplasmic terminal domains of serotonin transporter. <i>Biochemistry</i> , 2014 , 53, 5444-60	3.2	37
46	The ins and outs of vesicular monoamine transporters. <i>Journal of General Physiology</i> , 2018 , 150, 671-682	3.4	33

45	Mechanism of Paroxetine (Paxil) Inhibition of the Serotonin Transporter. <i>Scientific Reports</i> , 2016 , 6, 23789	4.9	33
44	Repeat-swap homology modeling of secondary active transporters: updated protocol and prediction of elevator-type mechanisms. <i>Frontiers in Pharmacology</i> , 2015 , 6, 183	5.6	33
43	Two models of the influenza A M2 channel domain: verification by comparison. <i>Folding & Design</i> , 1998 , 3, 443-8		32
42	An assessment of the accuracy of methods for predicting hydrogen positions in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 296-309	4.2	32
41	Structural fold and binding sites of the human Na ⁺ -phosphate cotransporter NaPi-II. <i>Biophysical Journal</i> , 2014 , 106, 1268-79	2.9	31
40	The role of trimerization in the osmoregulated betaine transporter BetP. <i>EMBO Reports</i> , 2011 , 12, 804-10	5.5	31
39	Transmembrane domains of viral ion channel proteins: a molecular dynamics simulation study. <i>Biopolymers</i> , 2000 , 53, 529-38	2.2	29
38	Structural asymmetry in a trimeric Na ⁺ /betaine symporter, BetP, from <i>Corynebacterium glutamicum</i> . <i>Journal of Molecular Biology</i> , 2011 , 407, 368-81	6.5	27
37	Identification of molecular hinge points mediating alternating access in the vesicular monoamine transporter VMAT2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E1332-41	11.5	26
36	Reconstructing a chloride-binding site in a bacterial neurotransmitter transporter homologue. <i>Journal of Biological Chemistry</i> , 2011 , 286, 2834-42	5.4	26
35	A model-structure of a periplasm-facing state of the NhaA antiporter suggests the molecular underpinnings of pH-induced conformational changes. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18249-54	5.4	26
34	Discrimination of native loop conformations in membrane proteins: decoy library design and evaluation of effective energy scoring functions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 492-509	4.2	24
33	Large-scale state-dependent membrane remodeling by a transporter protein. <i>ELife</i> , 2019 , 8,	8.9	24
32	Asymmetry of inverted-topology repeats in the AE1 anion exchanger suggests an elevator-like mechanism. <i>Journal of General Physiology</i> , 2017 , 149, 1149-1164	3.4	22
31	Dissecting a regulatory calcium-binding site of CLC-K kidney chloride channels. <i>Journal of General Physiology</i> , 2012 , 140, 681-96	3.4	21
30	Viral ion channels: molecular modeling and simulation. <i>BioEssays</i> , 1998 , 20, 992-1000	4.1	21
29	Methionine uptake in <i>Corynebacterium glutamicum</i> by MetQNI and by MetPS, a novel methionine and alanine importer of the NSS neurotransmitter transporter family. <i>Biochemistry</i> , 2008 , 47, 12698-709	3.2	20
28	Modeling and simulation of ion-coupled and ATP-driven membrane proteins. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 173-9	8.1	18

27	Identification of the first sodium binding site of the phosphate cotransporter NaPi-IIa (SLC34A1). <i>Biophysical Journal</i> , 2015 , 108, 2465-2480	2.9	17
26	Global alignment and assessment of TRP channel transmembrane domain structures to explore functional mechanisms. <i>ELife</i> , 2020 , 9,	8.9	16
25	Family resemblances: A common fold for some dimeric ion-coupled secondary transporters. <i>Journal of General Physiology</i> , 2015 , 146, 423-34	3.4	14
24	Cation Interactions and Membrane Potential Induce Conformational Changes in NaPi-IIb. <i>Biophysical Journal</i> , 2016 , 111, 973-88	2.9	12
23	Structural elements required for coupling ion and substrate transport in the neurotransmitter transporter homolog LeuT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8854-E8862	11.5	12
22	An Extra Amino Acid Residue in Transmembrane Domain 10 of the γ -Aminobutyric Acid (GABA) Transporter GAT-1 Is Required for Efficient Ion-coupled Transport. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5418-5428	5.4	11
21	Interpretation of HDX Data by Maximum-Entropy Reweighting of Simulated Structural Ensembles. <i>Biophysical Journal</i> , 2020 , 118, 1649-1664	2.9	11
20	A structural model of the human serotonin transporter in an outward-occluded state. <i>PLoS ONE</i> , 2019 , 14, e0217377	3.7	10
19	Structural models of the NaPi-II sodium-phosphate cotransporters. <i>Pflugers Archiv European Journal of Physiology</i> , 2019 , 471, 43-52	4.6	10
18	Molecular Determinants of Substrate Specificity in Sodium-coupled Glutamate Transporters. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28988-96	5.4	9
17	Cysteine scanning mutagenesis of transmembrane helix 3 of a brain glutamate transporter reveals two conformationally sensitive positions. <i>Journal of Biological Chemistry</i> , 2013 , 288, 964-73	5.4	9
16	Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 1720-32	4.2	8
15	EncoMPASS: an online database for analyzing structure and symmetry in membrane proteins. <i>Nucleic Acids Research</i> , 2019 , 47, D315-D321	20.1	7
14	Emulating proton-induced conformational changes in the vesicular monoamine transporter VMAT2 by mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7390-E7398	11.5	6
13	Chloride-dependent conformational changes in the GlyT1 glycine transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
12	Functionally important carboxyls in a bacterial homologue of the vesicular monoamine transporter (VMAT). <i>Journal of Biological Chemistry</i> , 2014 , 289, 34229-40	5.4	5
11	Simulations of the M2 channel for influenza A virus. <i>Biochemical Society Transactions</i> , 1998 , 26, S303	5.1	5
10	MemSTATS: A Benchmark Set of Membrane Protein Symmetries and Pseudosymmetries. <i>Journal of Molecular Biology</i> , 2020 , 432, 597-604	6.5	5

9	Role of N-glycosylation in renal betaine transport. <i>Biochemical Journal</i> , 2015 , 470, 169-79	3.8	4
8	Molecular contacts in the transmembrane c-subunit oligomer of F-ATPases identified by tryptophan substitution mutagenesis. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000 , 1459, 49-60	4.6	4
7	Interpretation of spectroscopic data using molecular simulations for the secondary active transporter BetP. <i>Journal of General Physiology</i> , 2019 , 151, 381-394	3.4	3
6	Modeling the native ensemble of PhuS using enhanced sampling MD and HDX-ensemble reweighting. <i>Biophysical Journal</i> , 2021 , 120, 5141-5157	2.9	3
5	Global alignment and assessment of TRP channel transmembrane domain structures to explore functional mechanisms		1
4	Chloride-dependent conformational changes in the GlyT1 glycine transporter		1
3	Refining pairwise sequence alignments of membrane proteins by the incorporation of anchors. <i>PLoS ONE</i> , 2021 , 16, e0239881	3.7	1
2	On the Role of a Conserved Methionine in the Na-Coupling Mechanism of a Neurotransmitter Transporter Homolog. <i>Neurochemical Research</i> , 2021 , 1	4.6	1
1	Membrane Protein Simulations: Modelling a Complex Environment 2006 , 3-20		