Lucy Rachel Forrest

List of Publications by Year in Descending Order

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	Modeling the native ensemble of PhuS using enhanced sampling MD and HDX-ensemble reweighting. *Biophysical Journal*, **2021**, 120, 5141-5157	2.9	3
79	Chloride-dependent conformational changes in the GlyT1 glycine transporter. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	6
78	Refining pairwise sequence alignments of membrane proteins by the incorporation of anchors. *PLoS ONE*, **2021**, 16, e0239881	3.7	1
77	On the Role of a Conserved Methionine in the Na-Coupling Mechanism of a Neurotransmitter Transporter Homolog. *Neurochemical Research*, **2021**, 1	4.6	1
76	Interpretation of HDX Data by Maximum-Entropy Reweighting of Simulated Structural Ensembles. *Biophysical Journal*, **2020**, 118, 1649-1664	2.9	11
75	Global alignment and assessment of TRP channel transmembrane domain structures to explore functional mechanisms. *ELife*, **2020**, 9,	8.9	16
74	MemSTATS: A Benchmark Set of Membrane Protein Symmetries and Pseudosymmetries. *Journal of Molecular Biology*, **2020**, 432, 597-604	6.5	5
73	Intestinal serotonin and fluoxetine exposure modulate bacterial colonization in the gut. *Nature Microbiology*, **2019**, 4, 2064-2073	26.6	109
72	Interpretation of spectroscopic data using molecular simulations for the secondary active transporter BetP. *Journal of General Physiology*, **2019**, 151, 381-394	3.4	3
71	A structural model of the human serotonin transporter in an outward-occluded state. *PLoS ONE*, **2019**, 14, e0217377	3.7	10
70	Large-scale state-dependent membrane remodeling by a transporter protein. *ELife*, **2019**, 8,	8.9	24
69	Structural models of the NaPi-II sodium-phosphate cotransporters. *Pflugers Archiv European Journal of Physiology*, **2019**, 471, 43-52	4.6	10
68	EncoMPASS: an online database for analyzing structure and symmetry in membrane proteins. *Nucleic Acids Research*, **2019**, 47, D315-D321	20.1	7
67	The ins and outs of vesicular monoamine transporters. *Journal of General Physiology*, **2018**, 150, 671-682	3.4	33
66	Structural elements required for coupling ion and substrate transport in the neurotransmitter transporter homolog LeuT. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E8854-E8862	11.5	12
65	Conformational dynamics of a neurotransmitter:sodium symporter in a lipid bilayer. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E1786-E1795	11.5	55
64	An Extra Amino Acid Residue in Transmembrane Domain 10 of the Aminobutyric Acid (GABA) Transporter GAT-1 Is Required for Efficient Ion-coupled Transport. *Journal of Biological Chemistry*, **2017**, 292, 5418-5428	5.4	11

63	Asymmetry of inverted-topology repeats in the AE1 anion exchanger suggests an elevator-like mechanism. *Journal of General Physiology*, **2017**, 149, 1149-1164	3.4	22
62	Mechanism of Paroxetine (Paxil) Inhibition of the Serotonin Transporter. *Scientific Reports*, **2016**, 6, 23789	4.9	33
61	Emulating proton-induced conformational changes in the vesicular monoamine transporter VMAT2 by mutagenesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E7390-E7398	11.5	6
60	Two Na+ Sites Control Conformational Change in a Neurotransmitter Transporter Homolog. *Journal of Biological Chemistry*, **2016**, 291, 1456-71	5.4	51
59	The bacterial dicarboxylate transporter VcINDY uses a two-domain elevator-type mechanism. *Nature Structural and Molecular Biology*, **2016**, 23, 256-63	17.6	55
58	Cation Interactions and Membrane Potential Induce Conformational Changes in NaPi-IIb. *Biophysical Journal*, **2016**, 111, 973-88	2.9	12
57	Structural Symmetry in Membrane Proteins. *Annual Review of Biophysics*, **2015**, 44, 311-37	21.1	87
56	Family resemblances: A common fold for some dimeric ion-coupled secondary transporters. *Journal of General Physiology*, **2015**, 146, 423-34	3.4	14
55	Molecular Determinants of Substrate Specificity in Sodium-coupled Glutamate Transporters. *Journal of Biological Chemistry*, **2015**, 290, 28988-96	5.4	9
54	Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1720-32	4.2	8
53	Repeat-swap homology modeling of secondary active transporters: updated protocol and prediction of elevator-type mechanisms. *Frontiers in Pharmacology*, **2015**, 6, 183	5.6	33
52	Identification of the first sodium binding site of the phosphate cotransporter NaPi-IIa (SLC34A1). *Biophysical Journal*, **2015**, 108, 2465-2480	2.9	17
51	Role of N-glycosylation in renal betaine transport. *Biochemical Journal*, **2015**, 470, 169-79	3.8	4
50	Gating topology of the proton-coupled oligopeptide symporters. *Structure*, **2015**, 23, 290-301	5.2	67
49	Structure and regulatory interactions of the cytoplasmic terminal domains of serotonin transporter. *Biochemistry*, **2014**, 53, 5444-60	3.2	37
48	Functionally important carboxyls in a bacterial homologue of the vesicular monoamine transporter (VMAT). *Journal of Biological Chemistry*, **2014**, 289, 34229-40	5.4	5
47	Substrate-bound outward-open state of the betaine transporter BetP provides insights into Na+ coupling. *Nature Communications*, **2014**, 5, 4231	17.4	38
46	AlignMe--a membrane protein sequence alignment web server. *Nucleic Acids Research*, **2014**, 42, W246-51	10.1	58

45	Structural fold and binding sites of the human Na+-phosphate cotransporter NaPi-II. *Biophysical Journal*, **2014**, 106, 1268-79	2.9	31
44	Structural biology. (Pseudo-)symmetrical transport. *Science*, **2013**, 339, 399-401	33.3	49
43	Cysteine scanning mutagenesis of transmembrane helix 3 of a brain glutamate transporter reveals two conformationally sensitive positions. *Journal of Biological Chemistry*, **2013**, 288, 964-73	5.4	9
42	Identification of molecular hinge points mediating alternating access in the vesicular monoamine transporter VMAT2. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, E1332-41	11.5	26
41	Alignment of helical membrane protein sequences using AlignMe. *PLoS ONE*, **2013**, 8, e57731	3.7	44
40	Investigation of the sodium-binding sites in the sodium-coupled betaine transporter BetP. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E3035-44	11.5	59
39	Dissecting a regulatory calcium-binding site of CLC-K kidney chloride channels. *Journal of General Physiology*, **2012**, 140, 681-96	3.4	21
38	A model-structure of a periplasm-facing state of the NhaA antiporter suggests the molecular underpinnings of pH-induced conformational changes. *Journal of Biological Chemistry*, **2012**, 287, 18249-61	5.4	26
37	GRIFFIN: A versatile methodology for optimization of protein-lipid interfaces for membrane protein simulations. *Journal of Chemical Theory and Computation*, **2011**, 7, 1167-1176	6.4	47
36	Structural asymmetry in a trimeric Na+/betaine symporter, BetP, from Corynebacterium glutamicum. *Journal of Molecular Biology*, **2011**, 407, 368-81	6.5	27
35	The alternating-access mechanism of MFS transporters arises from inverted-topology repeats. *Journal of Molecular Biology*, **2011**, 407, 698-715	6.5	143
34	The role of trimerization in the osmoregulated betaine transporter BetP. *EMBO Reports*, **2011**, 12, 804-10	8.5	31
33	Modeling and simulation of ion-coupled and ATP-driven membrane proteins. *Current Opinion in Structural Biology*, **2011**, 21, 173-9	8.1	18
32	The structural basis of secondary active transport mechanisms. *Biochimica Et Biophysica Acta - Bioenergetics*, **2011**, 1807, 167-88	4.6	312
31	Reconstructing a chloride-binding site in a bacterial neurotransmitter transporter homologue. *Journal of Biological Chemistry*, **2011**, 286, 2834-42	5.4	26
30	A study of the evolution of inverted-topology repeats from LeuT-fold transporters using AlignMe. *Biochemistry*, **2010**, 49, 10702-13	3.2	87
29	The rocking bundle: a mechanism for ion-coupled solute flux by symmetrical transporters. *Physiology*, **2009**, 24, 377-86	9.8	212
28	Fluoxetine (Prozac) binding to serotonin transporter is modulated by chloride and conformational changes. *Journal of Neuroscience*, **2009**, 29, 9635-43	6.6	72

27	Inward-facing conformation of glutamate transporters as revealed by their inverted-topology structural repeats. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 20752-7	11.5	125
26	Methionine uptake in Corynebacterium glutamicum by MetQNI and by MetPS, a novel methionine and alanine importer of the NSS neurotransmitter transporter family. *Biochemistry*, **2008**, 47, 12698-709	3.2	20
25	Mechanism for alternating access in neurotransmitter transporters. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 10338-43	11.5	299
24	Identification of a chloride ion binding site in Na+/Cl -dependent transporters. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12761-6	11.5	171
23	Membrane protein prediction methods. *Methods*, **2007**, 41, 460-74	4.6	97
22	On the accuracy of homology modeling and sequence alignment methods applied to membrane proteins. *Biophysical Journal*, **2006**, 91, 508-17	2.9	202
21	Membrane Protein Simulations: Modelling a Complex Environment **2006**, 3-20		
20	An assessment of the accuracy of methods for predicting hydrogen positions in protein structures. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61, 296-309	4.2	32
19	Conformational sampling and dynamics of membrane proteins from 10-nanosecond computer simulations. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 783-91	4.2	86
18	Helical packing patterns in membrane and soluble proteins. *Biophysical Journal*, **2004**, 87, 4075-86	2.9	84
17	Discrimination of native loop conformations in membrane proteins: decoy library design and evaluation of effective energy scoring functions. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 492-509	4.2	24
16	Molecular dynamics simulation of dark-adapted rhodopsin in an explicit membrane bilayer: coupling between local retinal and larger scale conformational change. *Journal of Molecular Biology* , **2003**, 333, 493-514	6.5	88
15	Transmembrane domains of viral ion channel proteins: a molecular dynamics simulation study. *Biopolymers*, **2000**, 53, 529-38	2.2	29
14	Structure and dynamics of the pore-lining helix of the nicotinic receptor: MD simulations in water, lipid bilayers, and transbilayer bundles. *Proteins: Structure, Function and Bioinformatics*, **2000**, 39, 47-55	4.2	46
13	Membrane simulations: bigger and better?. *Current Opinion in Structural Biology*, **2000**, 10, 174-81	8.1	160
12	Exploring models of the influenza A M2 channel: MD simulations in a phospholipid bilayer. *Biophysical Journal*, **2000**, 78, 55-69	2.9	96
11	Structure and dynamics of K channel pore-lining helices: a comparative simulation study. *Biophysical Journal*, **2000**, 78, 79-92	2.9	69
10	Homology modeling and molecular dynamics simulation studies of an inward rectifier potassium channel. *Biophysical Journal*, **2000**, 78, 2929-42	2.9	120

9	Molecular contacts in the transmembrane c-subunit oligomer of F-ATPases identified by tryptophan substitution mutagenesis. *Biochimica Et Biophysica Acta - Bioenergetics*, **2000**, 1459, 49-60	4.6	4
8	Molecular dynamics of synthetic leucine-serine ion channels in a phospholipid membrane. *Biophysical Journal*, **1999**, 77, 2400-10	2.9	48
7	Defining the transmembrane helix of M2 protein from influenza A by molecular dynamics simulations in a lipid bilayer. *Biophysical Journal*, **1999**, 76, 1886-96	2.9	61
6	Two models of the influenza A M2 channel domain: verification by comparison. *Folding & Design*, **1998**, 3, 443-8		32
5	Lipid properties and the orientation of aromatic residues in OmpF, influenza M2, and alamethicin systems: molecular dynamics simulations. *Biochemistry*, **1998**, 37, 17554-61	3.2	151
4	Simulations of the M2 channel for influenza A virus. *Biochemical Society Transactions*, **1998**, 26, S303	5.1	5
3	Viral ion channels: molecular modeling and simulation. *BioEssays*, **1998**, 20, 992-1000	4.1	21
2	Global alignment and assessment of TRP channel transmembrane domain structures to explore functional mechanisms		1
1	Chloride-dependent conformational changes in the GlyT1 glycine transporter		1