

# Robin A Corey

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

1,344  
citations

394286

19  
h-index

414303

32  
g-index

68  
all docs

68  
docs citations

68  
times ranked

1407  
citing authors

#	ARTICLE	IF	CITATIONS
1	PyLipID: A Python Package for Analysis of Protein–Lipid Interactions from Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 1188-1201.	2.3	69
2	Specific interactions of peripheral membrane proteins with lipids: what can molecular simulations show us?. <i>Bioscience Reports</i> , 2022, 42, .	1.1	25
3	Structure, substrate recognition and initiation of hyaluronan synthase. <i>Nature</i> , 2022, 604, 195-201.	13.7	53
4	Rate-limiting transport of positively charged arginine residues through the Sec-machinery is integral to the mechanism of protein secretion. <i>ELife</i> , 2022, 11, .	2.8	13
5	Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients. <i>Nature Communications</i> , 2022, 13, 2278.	5.8	20
6	The guidance and adhesion protein FLRT2 dimerizes in cis via dual small-X3-small transmembrane motifs. <i>Structure</i> , 2022, 30, 1354-1365.e5.	1.6	4
7	Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021, 17, 187-195.	3.9	41
8	Jostling for Position: Defining How Multiple Lipid Species Interact with Inward Rectifier Potassium (Kir) Channels. <i>Biophysical Journal</i> , 2021, 120, 1a.	0.2	0
9	Molecular Simulations of Biogenesis Processes within the Bacterial Cell Envelope. <i>Biophysical Journal</i> , 2021, 120, 49a.	0.2	0
10	PyLipid: A Python Toolkit for Analysis of Lipid-Protein Interactions from MD Simulations. <i>Biophysical Journal</i> , 2021, 120, 48a.	0.2	11
11	Assessment and Correction of Small-Angle Scattering Data for Combination with other Experimental Data and with Molecular Simulations. <i>Biophysical Journal</i> , 2021, 120, 264a-265a.	0.2	0
12	The Energetics of Cholesterol Transport through Patched1: MD Simulations and Free Energy Calculations. <i>Biophysical Journal</i> , 2021, 120, 72a.	0.2	0
13	Maintenance of complex I and its supercomplexes by NDUF-11 is essential for mitochondrial structure, function and health. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	17
14	Identification and assessment of cardiolipin interactions with <i>E. coli</i> inner membrane proteins. <i>Science Advances</i> , 2021, 7, .	4.7	49
15	Deciphering ion transport and ATPase coupling in the intersubunit tunnel of KdpFABC. <i>Nature Communications</i> , 2021, 12, 5098.	5.8	10
16	Relative Affinities of Protein–Cholesterol Interactions from Equilibrium Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 6548-6558.	2.3	21
17	Identification and Characterization of Specific Protein–Lipid Interactions Using Molecular Simulation. <i>Methods in Molecular Biology</i> , 2021, 2315, 121-139.	0.4	2
18	Membrane protein biogenesis by the EMC. <i>EMBO Journal</i> , 2021, 40, e107407.	3.5	10

#	ARTICLE	IF	CITATIONS
19	Mechanism of lipid droplet formation by the yeast Sei1/Ldb16 Seipin complex. <i>Nature Communications</i> , 2021, 12, 5892.	5.8	40
20	Structure of the hexameric fungal plasma membrane proton pump in its autoinhibited state. <i>Science Advances</i> , 2021, 7, eabj5255.	4.7	20
21	Lipid Interactions of a Ciliary Membrane TRP Channel: Simulation and Structural Studies of Polycystin-2. <i>Structure</i> , 2020, 28, 169-184.e5.	1.6	37
22	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.	7.2	33
23	A bipartite structural organization defines the SERINC family of HIV-1 restriction factors. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 78-83.	3.6	50
24	A Mass Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie</i> , 2020, 132, 3551-3556.	1.6	2
25	The SERCA residue Glu340 mediates interdomain communication that guides Ca <sup>2+</sup> transport. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31114-31122.	3.3	12
26	Evaluating inositol phospholipid interactions with inward rectifier potassium channels and characterising their role in disease. <i>Communications Chemistry</i> , 2020, 3, .	2.0	23
27	Insights Into Membrane Protein-Lipid Interactions from Free Energy Calculations. <i>Biophysical Journal</i> , 2020, 118, 18a.	0.2	1
28	Structural basis of proton-coupled potassium transport in the KUP family. <i>Nature Communications</i> , 2020, 11, 626.	5.8	60
29	Defining how multiple lipid species interact with inward rectifier potassium (Kir2) channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7803-7813.	3.3	83
30	The energetics of protein-lipid interactions as viewed by molecular simulations. <i>Biochemical Society Transactions</i> , 2020, 48, 25-37.	1.6	48
31	Structural basis for substrate specificity and regulation of nucleotide sugar transporters in the lipid bilayer. <i>Nature Communications</i> , 2019, 10, 4657.	5.8	23
32	The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K. <i>Nature Communications</i> , 2019, 10, 3956.	5.8	101
33	Insights into Membrane Protein-Lipid Interactions from Free Energy Calculations. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 5727-5736.	2.3	70
34	Structure and Dynamics of the Central Lipid Pool and Proteins of the Bacterial Holo-Translocon. <i>Biophysical Journal</i> , 2019, 116, 1931-1940.	0.2	22
35	A lipid gating mechanism for the channel-forming O antigen ABC transporter. <i>Nature Communications</i> , 2019, 10, 824.	5.8	44
36	ATP-induced asymmetric pre-protein folding as a driver of protein translocation through the Sec machinery. <i>ELife</i> , 2019, 8, .	2.8	32

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37	HDX-MS reveals nucleotide-dependent, anti-correlated opening and closure of SecA and SecY channels of the bacterial translocon. <i>ELife</i> , 2019, 8, .	2.8	20
38	Specific cardiolipin-secY interactions are required for proton-motive force stimulation of protein secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7967-7972.	3.3	65
39	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018, 7, .	2.8	52
40	Composition and Activity of the Non-canonical Gram-positive SecY2 Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 21474-21484.	1.6	10
41	Protein translocation: what's the problem?. <i>Biochemical Society Transactions</i> , 2016, 44, 753-759.	1.6	14
42	Unlocking the Bacterial SecY Translocon. <i>Structure</i> , 2016, 24, 518-527.	1.6	37
43	Channel crossing: how are proteins shipped across the bacterial plasma membrane?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20150025.	1.8	53
44	Interaction With the Lipid Membrane Influences Fentanyl Pharmacology. <i>Advances in Drug and Alcohol Research</i> , 0, 2, .	2.5	8