

# Daniel P Farrell

## List of Publications by Year in Descending Order

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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.

20  
papers

229  
citations

9  
h-index

15  
g-index

24  
ext. papers

453  
ext. citations

16.7  
avg, IF

3.18  
L-index

#	Paper	IF	Citations
20	Structural and functional insight into regulation of kinesin-1 by microtubule-associated protein MAP7.. <i>Science</i> , <b>2022</b> , 375, 326-331	33.3	8
19	Cryo-EM structures of CTP synthase filaments reveal mechanism of pH-sensitive assembly during budding yeast starvation. <i>ELife</i> , <b>2021</b> , 10,	8.9	5
18	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , <b>2021</b> , 12, 6947	17.4	0
17	Structure and lipid dynamics in the maintenance of lipid asymmetry inner membrane complex of <i>A. baumannii</i> . <i>Communications Biology</i> , <b>2021</b> , 4, 817	6.7	4
16	Cryo-electron Microscopy Imaging of Alzheimer's Amyloid-beta 42 Oligomer Displayed on a Functionally and Structurally Relevant Scaffold. <i>Angewandte Chemie</i> , <b>2021</b> , 133, 18828-18835	3.6	1
15	Cryo-electron Microscopy Imaging of Alzheimer's Amyloid-beta 42 Oligomer Displayed on a Functionally and Structurally Relevant Scaffold. <i>Angewandte Chemie - International Edition</i> , <b>2021</b> , 60, 18680-18687	16.4	9
14	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , <b>2021</b> , 18, 156-164	21.6	22
13	BRCA1/BARD1 site-specific ubiquitylation of nucleosomal H2A is directed by BARD1. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 268-277	17.6	21
12	The cryo-EM structure of the bacterial flagellum cap complex suggests a molecular mechanism for filament elongation. <i>Nature Communications</i> , <b>2020</b> , 11, 3210	17.4	9
11	Polymerization in the actin ATPase clan regulates hexokinase activity in yeast. <i>Science</i> , <b>2020</b> , 367, 1039-1042	35.3	13
10	Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM. <i>IUCrJ</i> , <b>2020</b> , 7, 881-892	4.7	5
9	A Structural Model of the Endogenous Human BAF Complex Informs Disease Mechanisms. <i>Cell</i> , <b>2020</b> , 183, 802-817.e24	56.2	31
8	Structural basis for autophagy inhibition by the human Rubicon-Rab7 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 17003-17010	11.5	9
7	The Molecular Architecture of Native BBSome Obtained by an Integrated Structural Approach. <i>Structure</i> , <b>2019</b> , 27, 1384-1394.e4	5.2	33
6	DNA binding drives the association of BRG1/hBRM bromodomains with nucleosomes. <i>Nature Communications</i> , <b>2017</b> , 8, 16080	17.4	39
5	Bronsted acid catalyzed intramolecular benzylic cyclizations of alkylpyridines. <i>Organic and Biomolecular Chemistry</i> , <b>2014</b> , 12, 1090-9	3.9	16
4	Structural basis for autophagy inhibition by the human Rubicon-Rab7 complex		1

- 3 Independent evolution of polymerization in the Actin ATPase clan regulates hexokinase activity 1
- 2 Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM 1
- 1 Cryo-EM Structures of CTP Synthase Filaments Reveal Mechanism of pH-Sensitive Assembly During Budding Yeast Starvation 1