

# Firas Khatib

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5658648/publications.pdf>

Version: 2024-02-01

16  
papers

3,117  
citations

759233

12  
h-index

996975

15  
g-index

16  
all docs

16  
docs citations

16  
times ranked

3889  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting protein structures with a multiplayer online game. <i>Nature</i> , 2010, 466, 756-760.	27.8	1,062
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
3	Crystal structure of a monomeric retroviral protease solved by protein folding game players. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1175-1177.	8.2	463
4	Algorithm discovery by protein folding game players. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18949-18953.	7.1	450
5	Increased Diels-Alderase activity through backbone remodeling guided by Foldit players. <i>Nature Biotechnology</i> , 2012, 30, 190-192.	17.5	259
6	De novo protein design by citizen scientists. <i>Nature</i> , 2019, 570, 390-394.	27.8	105
7	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. <i>Bioinformatics</i> , 2017, 33, 2765-2767.	4.1	77
8	WeFold: A coepetition for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1850-1868.	2.6	48
9	Determining crystal structures through crowdsourcing and coursework. <i>Nature Communications</i> , 2016, 7, 12549.	12.8	47
10	High-resolution structure of a retroviral protease folded as a monomer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 907-914.	2.5	22
11	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
12	Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction. <i>Computational Biology and Chemistry</i> , 2016, 61, 162-177.	2.3	15
13	Introducing Foldit Education Mode. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 769-770.	8.2	15
14	Increasing Public Involvement in Structural Biology. <i>Structure</i> , 2013, 21, 1482-1484.	3.3	12
15	Building de novo cryo-electron microscopy structures collaboratively with citizen scientists. <i>PLoS Biology</i> , 2019, 17, e3000472.	5.6	10
16	An initial examination of computer programs as creative works.. <i>Psychology of Aesthetics, Creativity, and the Arts</i> , 0, , .	1.3	0