Firas Khatib

List of Publications by Year
in descending order

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

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