Seth Cooper

List of Publications by Citations

34 papers	3,493 citations	15 h-index	38 g-index
38 ext. papers	4,480 ext. citations	15.2 avg, IF	4.33 L-index

#	Paper	IF	Citations
34	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
33	Predicting protein structures with a multiplayer online game. *Nature*, **2010**, 466, 756-60	50.4	821
32	Crystal structure of a monomeric retroviral protease solved by protein folding game players. *Nature Structural and Molecular Biology*, **2011**, 18, 1175-7	17.6	316
31	Algorithm discovery by protein folding game players. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 18949-53	11.5	289
30	Increased Diels-Alderase activity through backbone remodeling guided by Foldit players. *Nature Biotechnology*, **2012**, 30, 190-2	44.5	206
29	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
28	The challenge of designing scientific discovery games **2010**,		67
27	De novo protein design by citizen scientists. *Nature*, **2019**, 570, 390-394	50.4	63
26	The impact of tutorials on games of varying complexity **2012**,		60
25	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. *Bioinformatics*, **2017**, 33, 2765-2767	7.2	44
24	WeFold: a coopetition for protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 1850-68	4.2	39
23	Determining crystal structures through crowdsourcing and coursework. *Nature Communications*, **2016**, 7, 12549	17.4	35
22	Verification games **2012**,		27
21	Analysis of social gameplay macros in the Foldit cookbook **2011**,		19
20	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. *Scientific Reports*, **2018**, 8, 9939	4.9	16
19	High-resolution structure of a retroviral protease folded as a monomer. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 907-14		15
18	Engagement effects of player rating system-based matchmaking for level ordering in human computation games **2017**,		13

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17	Feature-based projections for effective playtrace analysis **2011**,		12
16	Increasing public involvement in structural biology. *Structure*, **2013**, 21, 1482-4	5.2	10
15	Creating custom Foldit puzzles for teaching biochemistry. *Biochemistry and Molecular Biology Education*, **2019**, 47, 133-139	1.3	10
14	To Three or not to Three: Improving Human Computation Game Onboarding with a Three-Star System **2017**, 2017, 5034-5039		9
13	Building de novo cryo-electron microscopy structures collaboratively with citizen scientists. *PLoS Biology*, **2019**, 17, e3000472	9.7	9
12	Proactive Sensing for Improving Hand Pose Estimation **2016**,		5
11	Repurposing Citizen Science Games as Software Tools for Professional Scientists **2018**, 2018,		5
10	Comparing paid and volunteer recruitment in human computation games **2018**,		5
9	Introducing Foldit Education Mode. *Nature Structural and Molecular Biology*, **2020**, 27, 769-770	17.6	4
8	Predicting Human Computation Game Scores with Player Rating Systems. *Lecture Notes in Computer Science*, **2017**, 284-289	0.9	2
7	Expertise and Engagement: Re-Designing Citizen Science Games With PlayersbMinds in Mind **2019**, 2019,		2
6	Meet your match rating **2018**,		2
5	How do Players and Developers of Citizen Science Games Conceptualize Skill Chains?. *Proceedings of the ACM on Human-Computer Interaction*, **2021**, 5, 1-29	3.4	1
4	Large-Scale Analysis of Visualization Options in a Citizen Science Game **2019**, 2019, 535-542		1
3	Using Q-Learning for Sequencing Level Difficulties in a Citizen Science Matching Game **2019**,		1
2	Designing Videogames to Crowdsource Accelerometer Data Annotation for Activity Recognition Research **2019**, 2019, 135-147		0
1	A Monte Carlo Approach to Skill-Based Automated Playtesting **2018**, 2018, 166-172		