

James Thompson

List of Publications by Citations

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Version: 2024-04-25

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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.

11
papers

3,018
citations

11
h-index

12
g-index

12
ext. papers

3,696
ext. citations

6.2
avg, IF

4.06
L-index

#	Paper	IF	Citations
11	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. <i>Methods in Enzymology</i> , 2011 , 487, 545-74	1.7	1216
10	High-resolution comparative modeling with RosettaCM. <i>Structure</i> , 2013 , 21, 1735-42	5.2	649
9	Structure prediction for CASP8 with all-atom refinement using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 89-99	4.2	342
8	Crystal structure of a monomeric retroviral protease solved by protein folding game players. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1175-7	17.6	316
7	Scientific benchmarks for guiding macromolecular energy function improvement. <i>Methods in Enzymology</i> , 2013 , 523, 109-43	1.7	164
6	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 118-28	4.2	158
5	Integrative genomic mining for enzyme function to enable engineering of a non-natural biosynthetic pathway. <i>Nature Communications</i> , 2015 , 6, 10005	17.4	56
4	Structure-guided forcefield optimization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 1898-909	4.2	42
3	Incorporation of evolutionary information into Rosetta comparative modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2380-8	4.2	39
2	Rosetta in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3212-8	4.2	17
1	High-resolution structure of a retroviral protease folded as a monomer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 907-14		15