

# Robert Oeffner

## 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.

8

papers

17,659

citations

6

h-index

8

g-index

8

ext. papers

21,634

ext. citations

5.3

avg, IF

5.56

L-index

#	Paper	IF	Citations
8	Phasertng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 1-10	5.5	6
7	Factors influencing estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 19-27	5.5	4
6	Measuring and using information gained by observing diffraction data. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 238-247	5.5	1
5	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 861-877	5.5	1527
4	Gyre and gimble: a maximum-likelihood replacement for Patterson correlation refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 279-289	5.5	13
3	On the application of the expected log-likelihood gain to decision making in molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 245-255	5.5	22
2	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 290-304	5.5	19
1	PHENIX: a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 213-21		16067