

Robert Oeffner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8668527/publications.pdf>

Version: 2024-02-01

8

papers

24,727

citations

1651377

6

h-index

1762888

8

g-index

8

all docs

8

docs citations

8

times ranked

40192

citing authors

#	ARTICLE	IF	CITATIONS
1	Phasertrng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1-10.	1.1	10
2	Factors influencing estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 19-27.	1.1	6
3	Measuring and using information gained by observing diffraction data. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 238-247.	1.1	3
4	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>< i>Phenix</i></i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	1.1	4,060
5	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> , 2018, 74, 290-304.	1.1	30
6	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 279-289.	1.1	14
7	On the application of the expected log-likelihood gain to decision making in molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 245-255.	1.1	40
8	<i>< i>PHENIX</i></i> : a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 213-221.	2.5	20,564