

# Massimo Sammito

## 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.

28  
papers

1,985  
citations

14  
h-index

44  
g-index

52  
ext. papers

3,454  
ext. citations

3.4  
avg, IF

4.6  
L-index

#	Paper	IF	Citations
28	Implications of AlphaFold2 for crystallographic phasing by molecular replacement.. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2022</b> , 78, 1-13	5.5	11
27	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 522-533	5.5	
26	Phasertng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 1-10	5.5	6
25	Detection of translational noncrystallographic symmetry in Patterson functions. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 131-141	5.5	2
24	Assessing the utility of CASP14 models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2021</b> , 89, 1752-1769	4.2	18
23	The amphibian antimicrobial peptide uperin 3.5 is a cross- $\alpha$ -chameleon functional amyloid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	11
22	SEQUENCE SLIDER: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 221-237	5.5	5
21	ALEPH: a network-oriented approach for the generation of fragment-based libraries and for structure interpretation. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 193-208	5.5	9
20	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
19	Evaluation of template-based modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1113-1127	4.2	38
18	Evaluation of model refinement in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 1249-1262	4.2	25
17	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
16	ARCIMBOLDO on coiled coils. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 194-204	5.5	20
15	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
14	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
13	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
12	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1006079	7.6	17

11	ARCIMBOLDO_LITE: single-workstation implementation and use. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1921-30		37
10	Combining phase information in reciprocal space for molecular replacement with partial models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1931-45		10
9	Macromolecular ab initio phasing enforcing secondary and tertiary structure. <i>IUCrJ</i> , <b>2015</b> , 2, 95-105	4-7	35
8	Structure of a 13-fold superhelix (almost) determined from first principles. <i>IUCrJ</i> , <b>2015</b> , 2, 177-87	4-7	2
7	Structure solution with ARCIMBOLDO using fragments derived from distant homology models. <i>FEBS Journal</i> , <b>2014</b> , 281, 4029-45	5-7	33
6	Structure solution of DNA-binding proteins and complexes with ARCIMBOLDO libraries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 1743-57		15
5	Exploiting tertiary structure through local folds for crystallographic phasing. <i>Nature Methods</i> , <b>2013</b> , 10, 1099-101	21.6	51
4	Phasing Through Location of Small Fragments and Density Modification with ARCIMBOLDO. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , <b>2013</b> , 123-133	0.1	0
3	Practical structure solution with ARCIMBOLDO. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 336-43		43
2	Possible Implications of AlphaFold2 for Crystallographic Phasing by Molecular Replacement		5
1	Assessing the utility of CASP14 models for molecular replacement		1