

Massimo Sammito

List of Publications by Year in descending order

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47
papers

4,794
citations

516215

16
h-index

454577

30
g-index

52
all docs

52
docs citations

52
times ranked

7957
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Implications of <i><i>AlphaFold</i>2</i> for crystallographic phasing by molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1-13.	1.1	65
3	Exploiting tertiary structure through local folds for crystallographic phasing. <i>Nature Methods</i> , 2013, 10, 1099-1101.	9.0	63
4	Evaluation of template-based modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1113-1127.	1.5	56
5	<i><i>ARCIMBOLDO_LITE</i></i> : single-workstation implementation and use. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1921-1930.	2.5	51
6	Practical structure solution with <i><i>ARCIMBOLDO</i></i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 336-343.	2.5	50
7	Macromolecular <i><i>ab initio</i></i> phasing enforcing secondary and tertiary structure. <i>IUCr</i> , 2015, 2, 95-105.	1.0	47
8	Assessing the utility of <i><sc>CASP14</sc></i> models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	1.5	47
9	Structure solution with <i><sc>ARCIMBOLDO</sc></i> using fragments derived from distant homology models. <i>FEBS Journal</i> , 2014, 281, 4029-4045.	2.2	41
10	<i><i>ARCIMBOLDO</i></i> on coiled coils. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 194-204.	1.1	41
11	The amphibian antimicrobial peptide uperin 3.5 is a cross- $\hat{\pm}$ /cross- $\hat{\pm}^2$ chameleon functional amyloid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	41
12	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
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> , 2018, 74, 290-304.	1.1	30
14	Evaluation of model refinement in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1249-1262.	1.5	28
15	Structure solution of DNA-binding proteins and complexes with <i><i>ARCIMBOLDO</i></i> libraries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1743-1757.	2.5	19
16	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. <i>PLoS Pathogens</i> , 2016, 12, e1006079.	2.1	19
17	<i><i>ALEPH</i></i> : a network-oriented approach for the generation of fragment-based libraries and for structure interpretation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 193-208.	1.1	16
18	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 279-289.	1.1	14

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19	Combining phase information in reciprocal space for molecular replacement with partial models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1931-1945.	2.5	12
20	Phasertng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1-10.	1.1	10
21	<i>SEQUENCE SLIDER</i> : expanding polyalanine fragments for phasing with multiple side-chain hypotheses. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 221-237.	1.1	10
22	Factors influencing estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 19-27.	1.1	6
23	Detection of translational noncrystallographic symmetry in Patterson functions. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 131-141.	1.1	5
24	Structure of a 13-fold superhelix (almost) determined from first principles. <i>IUCr</i> , 2015, 2, 177-187.	1.0	3
25	Using <i>PHASER</i> for phasing in conjunction with wide-convergence refinement and model building techniques. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s40-s40.	0.3	2
26	SEQUENCE SLIDER: a multi sequence evaluator and its application in venomics. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s167-s167.	0.0	1
27	BORGES-ARCIMBOLDO exploiting tertiary folds as fragments libraries for phasing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s670-s670.	0.3	1
28	PLA2s-like membrane perturbation mechanism: extracting the most of crystallography data. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s226-s226.	0.0	1
29	Phasing Through Location of Small Fragments and Density Modification with ARCIMBOLDO. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 123-133.	0.5	1
30	BORGES_MATRIX: a tool to generate models for ab initio phasing and for structure interpretation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s23-s23.	0.0	1
31	<i>Phaser.Voyager</i> : data-guided model generation and visualization. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, e182-e182.	0.0	1
32	BORGESlibraries: from phasing to structural bioinformatics. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s271-s272.	0.0	0
33	ARCIMBOLDO, an ab initio approach to MR phasing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s20-s21.	0.0	0
34	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 522-533.	1.1	0
35	BORGES-ARCIMBOLDO exploiting tertiary folds as fragments libraries for phasing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s271-s271.	0.3	0
36	Reciprocal space clustering of BORGES-ARCIMBOLDO partial solutions: practical cases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s294-s294.	0.3	0

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37	Use of clustering algorithms to combine partial solutions in reciprocal space. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s165-s165.	0.0	0
38	ARCIMBOLDO_SHREDDER's contribution to MR: phasing with fragments from distant homologs. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s198-s199.	0.0	0
39	New in the <i>ARCIMBOLDO</i> toolbox for phasing with small fragments. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C881-C881.	0.0	0
40	Overcoming phasing difficulties in coiled coils with ARCIMBOLDO_LITE: verifying solutions. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e229-e229.	0.0	0
41	The expected log-likelihood gain for decision making in molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e411-e411.	0.0	0
42	Expanding partial structures by assembling most probable side-chain composition. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e410-e410.	0.0	0
43	Revealing the properties of small local folds with ALEPH: from structure annotation to ab initio phasing. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e228-e229.	0.0	0
44	Dealing with modulated macromolecular structures with translational non-crystallographic symmetry. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e197-e197.	0.0	0
45	ALEPH: a new software for structural analysis and generation of fragment libraries for molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e184-e184.	0.0	0
46	A new 3D reflection data viewer based on NGL. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e165-e165.	0.0	0
47	Combining the use of libraries from several distant homologs in ARCIMBOLDO_SHREDDER spheres. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e178-e178.	0.0	0