Massimo Sammito

List of Publications by Year
in descending order

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47	4,794	516215 16	454577 30
papers	citations	h-index	g-index

52	52	52	7957
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Implications of AlphaFold2 for crystallographic phasing by molecular replacement. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1-13.	1.1	65
2	Phasertng: directed acyclic graphs for crystallographic phasing. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1-10.	1.1	10
3	Detection of translational noncrystallographic symmetry in Patterson functions. Acta Crystallographica Section D: Structural Biology, 2021, 77, 131-141.	1.1	5
4	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. Acta Crystallographica Section D: Structural Biology, 2021, 77, 522-533.	1.1	0
5	Assessing the utility of <scp>CASP14</scp> models for molecular replacement. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1752-1769.	1.5	47
6	The amphibian antimicrobial peptide uperin 3.5 is a cross-Î±/cross-Î² chameleon functional amyloid. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	41
7	SEQUENCE SLIDER: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. Acta Crystallographica Section D: Structural Biology, 2020, 76, 221-237.	1.1	10
8	ALEPH: a network-oriented approach for the generation of fragment-based libraries and for structure interpretation. Acta Crystallographica Section D: Structural Biology, 2020, 76, 193-208.	1.1	16
9	Factors influencing estimates of coordinate error for molecular replacement. Acta Crystallographica Section D: Structural Biology, 2020, 76, 19-27.	1.1	6
10	Evaluation of templateâ€based modeling in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1113-1127.	1.5	56
11	Evaluation of model refinement in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1249-1262.	1.5	28
12	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. Acta Crystallographica Section D: Structural Biology, 2019, 75, 861-877.	1.1	4,060
13	Dealing with modulated macromolecular structures with translational non-crystallographic symmetry. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e197-e197.	0.0	0
14	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
15	A new 3D reflection data viewer based on NGL. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e165-e165.	0.0	0
16	Phaser.Voyager: data-guided model generation and visualization. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e182-e182.	0.0	1
17	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
18	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. Acta Crystallographica Section D: Structural Biology, 2018, 74, 290-304.	1.1	30

#	Article	IF	Citations
19	ARCIMBOLDOon coiled coils. Acta Crystallographica Section D: Structural Biology, 2018, 74, 194-204.	1.1	41
20	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 279-289.	1.1	14
21	On the application of the expected log-likelihood gain to decision making in molecular replacement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 245-255.	1.1	40
22	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
23	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
24	Expanding partial structures by assembling most probable side-chain composition. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e410-e410.	0.0	0
25	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
26	New in the ARCIMBOLDO toolbox for phasing with small fragments. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C881-C881.	0.0	0
27	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. PLoS Pathogens, 2016, 12, e1006079.	2.1	19
28	PLA2s-like membrane perturbation mechanism: extracting the most of crystallography data. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s226-s226.	0.0	1
29	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
30	BORGES_MATRIX: a tool to generate models for ab initio phasing and for structure interpretation. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s23-s23.	0.0	1
31	Macromolecularab initiophasing enforcing secondary and tertiary structure. IUCrJ, 2015, 2, 95-105.	1.0	47
32	SEQUENCE SLIDER: a multi sequence evaluator and its application in venomics. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s167-s167.	0.0	1
33	BORGESlibraries: from phasing to structural bioinformatics. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s271-s272.	0.0	0
34	ARCIMBOLDO, anab initioapproach to MR phasing. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s20-s21.	0.0	0
35	ARCIMBOLDO_LITE: single-workstation implementation and use. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1921-1930.	2.5	51
36	Combining phase information in reciprocal space for molecular replacement with partial models. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1931-1945.	2.5	12

#	Article	IF	Citations
37	Structure of a 13-fold superhelix (almost) determined from first principles. IUCrJ, 2015, 2, 177-187.	1.0	3
38	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
39	Structure solution with <scp>ARCIMBOLDO</scp> using fragments derived from distant homology models. FEBS Journal, 2014, 281, 4029-4045.	2.2	41
40	Structure solution of DNA-binding proteins and complexes withARCIMBOLDOlibraries. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1743-1757.	2.5	19
41	Exploiting tertiary structure through local folds for crystallographic phasing. Nature Methods, 2013, 10, 1099-1101.	9.0	63
42	BORGES-ARCIMBOLDOexploiting tertiary folds as fragments libraries for phasing. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s670-s670.	0.3	1
43	UsingPHASERfor phasing in conjunction with wide-convergence refinement and model building techniques. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s40-s40.	0.3	2
44	Phasing Through Location of Small Fragments and Density Modification with ARCIMBOLDO. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 123-133.	0.5	1
45	BORGES-ARCIMBOLDOexploiting tertiary folds as fragments libraries for phasing. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s271-s271.	0.3	0
46	Reciprocal space clustering ofBORGES-ARCIMBOLDOpartial solutions: practical cases. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s294-s294.	0.3	0
47	Practical structure solution with ARCIMBOLDO . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 336-343.	2.5	50