Giovanni Luca Cascarano

List of Publications by Year
in descending order

54 papers	10,718 citations	430874 18 h-index	197818 49 g-index
54 all docs	54 docs citations	54 times ranked	8719 citing authors

#	Article	IF	Citations
1	Towards the automatic crystal structure solution of nucleic acids: automated model building using the new CAB program. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1602-1613.	2.3	3
2	Properties of Fourier Syntheses and New Syntheses. Crystals, 2020, 10, 538.	2.2	1
3	Cyclic Automated Model Building (CAB) Applied to Nucleic Acids. Crystals, 2020, 10, 280.	2.2	3
4	How far are we from automatic crystal structure solution via molecular-replacement techniques?. Acta Crystallographica Section D: Structural Biology, 2020, 76, 9-18.	2.3	3
5	Phasingviapure crystallographic least squares: an unexpected feature. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, 123-130.	0.1	0
6	CAB: a cyclic automatic model-building procedure. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1096-1104.	2.3	5
7	Probabilistic Estimate of |Foa| from FEL Data. Crystals, 2018, 8, 175.	2.2	0
8	About difference electron densities and their properties. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, 460-473.	0.1	3
9	Synergy among phase-refinement techniques in macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 877-888.	2.3	6
10	Solving proteins at non-atomic resolution by direct methods: update. Journal of Applied Crystallography, 2017, 50, 1048-1055.	4.5	6
11	MPF, a multipurpose figure of merit for phasing procedures. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, 69-76.	0.1	1
12	The phantom derivative method when a structure model is available: about its theoretical basis. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, 218-226.	0.1	1
13	Phase improvementviathePhantom Derivativetechnique: ancils that are related to the target structure. Acta Crystallographica Section D: Structural Biology, 2016, 72, 551-557.	2.3	9
14	Crystal structure determination and refinementviaSIR2014. Journal of Applied Crystallography, 2015, 48, 306-309.	4.5	729
15	Refining a model electron-density mapviathePhantom Derivativemethod. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1864-1871.	2.5	5
16	Advances in molecular-replacement procedures: theREVANpipeline. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1856-1863.	2.5	8
17	Protein phasing at non-atomic resolution by combining Patterson andVLDtechniques. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1994-2006.	2.5	9
18	Determination of the crystal structure of U6Fe5Al8Si9 by electron crystallography. Journal of Physics and Chemistry of Solids, 2013, 74, 1868-1874.	4.0	0

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19	On the use of theCmap in Patterson deconvolution procedures. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 98-107.	0.3	6
20	The use ofVLD(vive la difference) in the molecular-replacement approach: a pipeline. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1038-1044.	2.5	8
21	VLD algorithm and hybrid Fourier syntheses. Journal of Applied Crystallography, 2012, 45, 1287-1294.	4.5	19
22	Automatic Î±-helix identification in Patterson maps. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1-12.	2.5	5
23	SIR2011: a new package for crystal structure determination and refinement. Journal of Applied Crystallography, 2012, 45, 357-361.	4.5	538
24	Automated determination of the extinction symbolviaelectron diffraction data. Journal of Applied Crystallography, 2012, 45, 351-356.	4.5	48
25	Estimates of triplet invariants given a model structure. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, 513-520.	0.3	7
26	Advances in the VLD algorithm. Journal of Applied Crystallography, 2011, 44, 1143-1151.	4.5	23
27	About the hybrid Fourier syntheses: a probabilistic approach. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, 447-455.	0.3	3
28	Crystal structure solution via precession electron diffraction data: The BEA algorithm. Ultramicroscopy, 2010, 111, 56-61.	1.9	11
29	The cross-correlation function: main properties and first applications. Journal of Applied Crystallography, 2010, 43, 221-226.	4.5	5
30	New computational tools for H/D determination in macromolecular structures from neutron data. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1164-1171.	2.5	0
31	Molecular replacement: the probabilistic approach of the programREMO09and its applications. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, 512-527.	0.3	26
32	Advances in the EDMâ€“DEDM procedure. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 249-256.	2.5	7
33	EDMâ€“DEDM and protein crystal structure solution. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 477-484.	2.5	9
34	Crystal structure solution of small-to-medium-sized molecules at non-atomic resolution. Journal of Applied Crystallography, 2009, 42, 302-307.	4.5	9
35	The (F_oâ^’F_c) Fourier synthesis: a probabilistic study. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, 519-528.	0.3	10
36	Ab initiophasing of proteins with heavy atoms at non-atomic resolution: pushing the size limit of solvable structures up to 7890 non-H atoms in the asymmetric unit. Journal of Applied Crystallography, 2008, 41, 548-553.	4.5	28

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37	The revenge of the Patterson methods. II. Substructure applications. Journal of Applied Crystallography, 2007, 40, 211-217.	4.5	10
38	The revenge of the Patterson methods. III.Ab initiophasing from powder diffraction data. Journal of Applied Crystallography, 2007, 40, 834-840.	4.5	8
39	Advances in thefree lunchmethod. Journal of Applied Crystallography, 2007, 40, 931-937.	4.5	24
40	Advances inab initioprotein phasing by Patterson deconvolution techniques. Journal of Applied Crystallography, 2007, 40, 883-890.	4.5	22
41	Molecular replacement: the approach of the programREMO. Journal of Applied Crystallography, 2006, 39, 185-193.	4.5	21
42	The revenge of the Patterson methods. I. Proteinab initiophasing. Journal of Applied Crystallography, 2006, 39, 527-535.	4.5	25
43	Use of Patterson-based methods automatically to determine the structures of heavy-atom-containing proteins with up to 6000 non-hydrogen atoms in the asymmetric unit. Journal of Applied Crystallography, 2006, 39, 728-734.	4.5	17
44	Direct methods in powder diffractionâ€"applications. , 2006, , 190-201.		0
45	The partial structure with errors: a probabilistic treatment. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, 343-349.	0.3	26
46	MAD phasing: choosing the most informative wavelength combination. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1683-1686.	2.5	1
47	Benzophenone Photophore Flexibility and Proximity: Molecular and Crystal-State Structure of a Bpa-Containing Trichogin Dodecapeptide Analogue. ChemBioChem, 2004, 5, 541-544.	2.6	18
48	SAD or MAD phasing: location of the anomalous scatterers. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 662-669.	2.5	8
49	MAD phasing: probabilistic estimate of |Foa|. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 928-935.	2.5	6
50	SIR2000-N, a program for large and small crystal structures. Journal of Applied Crystallography, 2001, 34, 523-526.	4.5	19
51	Solving crystal structures inP1: an automated procedure for finding an allowed origin in the correct space group. Journal of Applied Crystallography, 2000, 33, 307-311.	4.5	27
52	SIR2000, a program for the automaticab initiocrystal structure solution of proteins. Acta Crystallographica Section A: Foundations and Advances, 2000, 56, 451-457.	0.3	38
53	Structures of nanometre-size crystals determined from selected-area electron diffraction data. Acta Crystallographica Section A: Foundations and Advances, 2000, 56, 29-35.	0.3	72
54	SIR97: a new tool for crystal structure determination and refinement. Journal of Applied Crystallography, 1999, 32, 115-119.	4.5	8,822