Garib N Murshudov

List of Publications by Year
in descending order

92 papers	36,483 citations	44069 48 h-index	43889 91 g-index
104 all docs	104 docs citations	104 times ranked	39222 citing authors

#	Article	IF	Citations
1	Overview of theCCP4 suite and current developments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 235-242.	2.5	11,098
2	REFMAC5 for the refinement of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 355-367.	2.5	7,247
3	How good are my data and what is the resolution?. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1204-1214.	2.5	3,739
4	Cryo-EM structures of tau filaments from Alzheimerâ€™s disease. Nature, 2017, 547, 185-190.	27.8	1,502
5	REFMAC5 dictionary: organization of prior chemical knowledge and guidelines for its use. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2184-2195.	2.5	1,207
6	Efficient anisotropic refinement of macromolecular structures using FFT. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 247-255.	2.5	867
7	High-resolution noise substitution to measure overfitting and validate resolution in 3D structure determination by single particle electron cryomicroscopy. Ultramicroscopy, 2013, 135, 24-35.	1.9	843
8	Macromolecular TLS Refinement in REFMAC at Moderate Resolutions. Methods in Enzymology, 2003, 374, 300-321.	1.0	725
9	ThePDB_REDOserver for macromolecular structure model optimization. IUCrJ, 2014, 1, 213-220.	2.2	709
10	BALBES: a molecular-replacement pipeline. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 125-132.	2.5	663
11	Structures of filaments from Pickâ€™s disease reveal a novel tau protein fold. Nature, 2018, 561, 137-140.	27.8	625
12	Single-particle cryo-EM at atomic resolution. Nature, 2020, 587, 152-156.	27.8	572
13	Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 136-153.	2.5	537
14	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. Science, 2014, 343, 1485-1489.	12.6	521
15	Developments in theCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2288-2294.	2.5	516
16	JLigand: a graphical tool for the CCP4 template-restraint library. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 431-440.	2.5	373
17	Structure of the large ribosomal subunit from human mitochondria. Science, 2014, 346, 718-722.	12.6	260
18	AceDRG: a stereochemical description generator for ligands. Acta Crystallographica Section D: Structural Biology, 2017, 73, 112-122.	2.3	254

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19	Initiation of Translation by Cricket Paralysis Virus IRES Requires Its Translocation in the Ribosome. Cell, 2014, 157, 823-831.	28.9	211
20	Low-resolution refinement tools in REFMAC5. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 404-417.	2.5	209
21	PDB_REDO: constructive validation, more than just looking for errors. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 484-496.	2.5	195
22	Overview of refinement procedures withinREFMAC5: utilizing data from different sources. Acta Crystallographica Section D: Structural Biology, 2018, 74, 215-227.	2.3	194
23	Crystal structure of dodecameric vanadium-dependent bromoperoxidase from the red algae Corallina officinalis 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 299, 1035-1049.	4.2	185
24	Incorporation of Prior Phase Information Strengthens Maximum-Likelihood Structure Refinement. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1285-1294.	2.5	172
25	Conformation-independent structural comparison of macromolecules withProSMART. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2487-2499.	2.5	161
26	ARP/wARPand molecular replacement: the next generation. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 49-60.	2.5	142
27	Substrate Distortion by a -Mannanase: Snapshots of the Michaelis and Covalent-Intermediate Complexes Suggest a B2,5 Conformation for the Transition State. Angewandte Chemie - International Edition, 2002, 41, 2824-2827.	13.8	127
28	Direct incorporation of experimental phase information in model refinement. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2196-2201.	2.5	121
29	Model preparation inMOLREPand examples of model improvement using X-ray data. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 33-39.	2.5	121
30	Cryo-EM single-particle structure refinement and map calculation usingServalcat. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1282-1291.	2.3	117
31	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. Structure, 1997, 5, 1017-1032.	3.3	111
32	The structure of the exo-Î²-(1,3)-glucanase from Candida albicans in native and bound forms: relationship between a pocket and groove in family 5 glycosyl hydrolases 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 294, 771-783.	4.2	98
33	Current approaches for the fitting and refinement of atomic models into cryo-EM maps usingCCP-EM. Acta Crystallographica Section D: Structural Biology, 2018, 74, 492-505.	2.3	93
34	The crystal structures of the oligopeptide-binding protein OppA complexed with tripeptide and tetrapeptide ligands. Structure, 1995, 3, 1395-1406.	3.3	91
35	MutS/MutL crystal structure reveals that the MutS sliding clamp loads MutL onto DNA. ELife, 2015, 4, e06744.	6.0	91
36	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in Bacillus subtilis. Journal of Molecular Biology, 2001, 306, 759-771.	4.2	90

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37	The three-dimensional structure of a Trichoderma reesei Î²-mannanase from glycoside hydrolase familyÂ5. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 3-13.	2.5	87
38	Surprises and pitfalls arising from (pseudo)symmetry. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 99-107.	2.5	81
39	DNA Topoisomerase Inhibitors: Trapping a DNA-Cleaving Machine in Motion. Journal of Molecular Biology, 2019, 431, 3427-3449.	4.2	79
40	Structures of actin-like ParM filaments show architecture of plasmid-segregating spindles. Nature, 2015, 523, 106-110.	27.8	73
41	The three-dimensional structure of human S100A12. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 20-29.	2.5	71
42	Structure of the Heme d of Penicillium vitale and Escherichia coli Catalases. Journal of Biological Chemistry, 1996, 271, 8863-8868.	3.4	64
43	Intensity statistics in twinned crystals with examples from the PDB. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 83-95.	2.5	58
44	The Structures and Electronic Configuration of Compound I Intermediates ofHelicobacterpyloriandPenicillium vitaleCatalases Determined by X-ray Crystallography and QM/MM Density Functional Theory Calculations. Journal of the American Chemical Society, 2007, 129, 4193-4205.	13.7	58
45	Automated refinement of macromolecular structures at low resolution using prior information. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1149-1161.	2.3	58
46	Fisher's information in maximum-likelihood macromolecular crystallographic refinement. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2114-2124.	2.5	57
47	The structures ofMicrococcus lysodeikticuscatalase, its ferryl intermediate (compound II) and NADPH complex. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1972-1982.	2.5	55
48	The Structure of NADH in the Enzyme dTDP-d-glucose Dehydratase (RmlB). Journal of the American Chemical Society, 2003, 125, 11872-11878.	13.7	51
49	Structural Flexibility of the Macrophage Dengue Virus Receptor CLEC5A. Journal of Biological Chemistry, 2011, 286, 24208-24218.	3.4	48
50	Binding of non-catalytic ATP to human hexokinase I highlights the structural components for enzymeâ€“membrane association control. Structure, 1999, 7, 1427-1437.	3.3	47
51	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). Acta Crystallographica Section D: Structural Biology, 2019, 75, 451-454.	2.3	46
52	Simultaneous use of solution NMR and X-ray data inREFMAC5 for joint refinement/detection of structural differences. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 958-967.	2.5	45
53	Robust background modelling in DIALS. Journal of Applied Crystallography, 2016, 49, 1912-1921.	4.5	44
54	Refinement of Atomic Structures Against cryo-EM Maps. Methods in Enzymology, 2016, 579, 277-305.	1.0	39

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55	Structure of the Bacillus Cell Fate Determinant SpoIIAA in Phosphorylated and Unphosphorylated Forms. Structure, 2001, 9, 605-614.	3.3	36
56	Data mining of iron(II) and iron(III) bond-valence parameters, and their relevance for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 316-325.	2.3	33
57	NMR trial models: experiences with the colicin immunity protein Im7 and the p85Î± C-terminal SH2â€“peptide complex. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1397-1404.	2.5	31
58	Crystal structure of an extracellular fragment of the rat CD4 receptor containing domains 3 and 4. Structure, 1994, 2, 469-481.	3.3	30
59	Structures ofPlasmodium falciparumpurine nucleoside phosphorylase complexed with sulfate and its natural substrate inosine. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1245-1254.	2.5	29
60	How to tackle protein structural data from solution and solid state: An integrated approach. Progress in Nuclear Magnetic Resonance Spectroscopy, 2016, 92-93, 54-70.	7.5	27
61	X-ray structure of bovine pancreatic phospholipase A2at atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 516-526.	2.5	26
62	Evaluating the solution fromMrBUMPandBALBES. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 313-323.	2.5	23
63	EMDA: A Python package for Electron Microscopy Data Analysis. Journal of Structural Biology, 2022, 214, 107826.	2.8	22
64	â€œConditional Restraintsâ€• Restraining the Free Atoms in ARP/wARP. Structure, 2009, 17, 183-189.	3.3	20
65	Validation and extraction of molecular-geometry information from small-molecule databases. Acta Crystallographica Section D: Structural Biology, 2017, 73, 103-111.	2.3	19
66	The polypeptide chain fold in tyrosine phenol-lyase, a pyridoxal-5â€²-phosphate-dependent enzyme. FEBS Letters, 1992, 302, 256-260.	2.8	17
67	AUSPEX: a graphical tool for X-ray diffraction data analysis. Acta Crystallographica Section D: Structural Biology, 2017, 73, 729-737.	2.3	16
68	Joint X-ray/NMR structure refinement of multidomain/multisubunit systems. Journal of Biomolecular NMR, 2019, 73, 265-278.	2.8	16
69	Structural characterization of Helicobacterâ€ƒpylori dethiobiotin synthetase reveals differences between family members. FEBS Journal, 2012, 279, 1093-1105.	4.7	15
70	DNA variability in five crystal structures of d(CGCAATTGCG). Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 680-685.	2.5	14
71	Background modelling of diffraction data in the presence of ice rings. IUCrJ, 2017, 4, 626-638.	2.2	14
72	Analysis and validation of macromolecular B values. Acta Crystallographica Section D: Structural Biology, 2019, 75, 505-518.	2.3	14

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73	Data to knowledge: how to get meaning from your result. IUCrJ, 2015, 2, 45-58.	2.2	12
74	Pathological macromolecular crystallographic data affected by twinning, partial-disorder and exhibiting multiple lattices for testing of data processing and refinement tools. Scientific Reports, 2018, 8, 14876.	3.3	11
75	Variable role of ions in two drug intercalation complexes of DNA. Journal of Biological Inorganic Chemistry, 2005, 10, 476-482.	2.6	10
76	Modelling covalent linkages in CCP4. Acta Crystallographica Section D: Structural Biology, 2021, 77, 712-726.	2.3	10
77	The missing link: covalent linkages in structural models. Acta Crystallographica Section D: Structural Biology, 2021, 77, 727-745.	2.3	10
78	Low Resolution Refinement of Atomic Models Against Crystallographic Data. Methods in Molecular Biology, 2017, 1607, 565-593.	0.9	10
79	Crystallization and preliminary X-ray diffraction studies of a fungal hydrolase fromOphiostoma novo-ulmi. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1879-1882.	2.5	9
80	Local and global analysis of macromolecular atomic displacement parameters. Acta Crystallographica Section D: Structural Biology, 2020, 76, 926-937.	2.3	9
81	A multivariate likelihood SIRAS function for phasing and model refinement. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1051-1061.	2.5	8
82	Solution of the structure of the cofactor-binding fragment of CysB: a struggle against non-isomorphism. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 369-378.	2.5	7
83	On the complementarity of X-ray and NMR data. Journal of Structural Biology: X, 2020, 4, 100019.	1.3	7
84	The predictive power of data-processing statistics. IUCrJ, 2020, 7, 342-354.	2.2	7
85	Recent Advances in Low Resolution Refinement Tools in REFMAC5. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 231-258.	0.5	6
86	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. ELife, 2021, 10, .	6.0	5
87	[ECâ€03â€“02]: CRYOâ€EM STRUCTURES OF TAU FILAMENTS FROM ALZHEIMER'S DISEASE BRAIN. Alzheimer's and Dementia, 2017, 13, P892.	0.8	3
88	Supercell refinement: a cautionary tale. Acta Crystallographica Section D: Structural Biology, 2019, 75, 852-860.	2.3	3
89	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. Microscopy and Microanalysis, 2014, 20, 1252-1253.	0.4	1
90	Validation of B-factor distributions in protein crystal structures. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s315-s315.	0.3	1

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91	Tools for Refinement against Low Resolution X-ray Data and Fit to EM Reconstructions. Nihon Kessho Gakkaishi, 2014, 56, s26-s26.	0.0	0
92	Application of (3+1)D based motion restraints to improve the refinement of a superspace approximation of an incommensurately modulated protein crystal. , 0, , .		0