

Garib N Murshudov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/709718/publications.pdf>

Version: 2024-02-01

92
papers

36,483
citations

50566

48
h-index

49824

91
g-index

104
all docs

104
docs citations

104
times ranked

43108
citing authors

#	ARTICLE	IF	CITATIONS
1	EMDA: A Python package for Electron Microscopy Data Analysis. <i>Journal of Structural Biology</i> , 2022, 214, 107826.	1.3	22
2	Modelling covalent linkages in <i>CCP4</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 712-726.	1.1	10
3	The missing link: covalent linkages in structural models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 727-745.	1.1	10
4	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , 2021, 10, .	2.8	5
5	Cryo-EM single-particle structure refinement and map calculation using <i>Servalcat</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1282-1291.	1.1	117
6	On the complementarity of X-ray and NMR data. <i>Journal of Structural Biology: X</i> , 2020, 4, 100019.	0.7	7
7	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	13.7	572
8	The predictive power of data-processing statistics. <i>IUCr</i> , 2020, 7, 342-354.	1.0	7
9	Local and global analysis of macromolecular atomic displacement parameters. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 926-937.	1.1	9
10	DNA Topoisomerase Inhibitors: Trapping a DNA-Cleaving Machine in Motion. <i>Journal of Molecular Biology</i> , 2019, 431, 3427-3449.	2.0	79
11	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	1.1	46
12	Joint X-ray/NMR structure refinement of multidomain/multisubunit systems. <i>Journal of Biomolecular NMR</i> , 2019, 73, 265-278.	1.6	16
13	Analysis and validation of macromolecular <i>B</i> values. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 505-518.	1.1	14
14	Supercell refinement: a cautionary tale. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 852-860.	1.1	3
15	Pathological macromolecular crystallographic data affected by twinning, partial-disorder and exhibiting multiple lattices for testing of data processing and refinement tools. <i>Scientific Reports</i> , 2018, 8, 14876.	1.6	11
16	Structures of filaments from Pickâ€™s disease reveal a novel tau protein fold. <i>Nature</i> , 2018, 561, 137-140.	13.7	625
17	Overview of refinement procedures within <i>REFMAC5</i> : utilizing data from different sources. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 215-227.	1.1	194
18	Current approaches for the fitting and refinement of atomic models into cryo-EM maps using <i>CCP-EM</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 492-505.	1.1	93

#	ARTICLE	IF	CITATIONS
19	Data mining of iron(II) and iron(III) bond-valence parameters, and their relevance for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 316-325.	1.1	33
20	[ECâ€“03â€“02]: CRYOâ€“EM STRUCTURES OF TAU FILAMENTS FROM ALZHEIMER'S DISEASE BRAIN. <i>Alzheimer's and Dementia</i> , 2017, 13, P892.	0.4	3
21	Cryo-EM structures of tau filaments from Alzheimerâ€™s disease. <i>Nature</i> , 2017, 547, 185-190.	13.7	1,502
22	<i>AUSPEX</i>: a graphical tool for X-ray diffraction data analysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 729-737.	1.1	16
23	<i>AceDRG</i>: a stereochemical description generator for ligands. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 112-122.	1.1	254
24	Low Resolution Refinement of Atomic Models Against Crystallographic Data. <i>Methods in Molecular Biology</i> , 2017, 1607, 565-593.	0.4	10
25	Background modelling of diffraction data in the presence of ice rings. <i>IUCr</i> , 2017, 4, 626-638.	1.0	14
26	Validation and extraction of molecular-geometry information from small-molecule databases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 103-111.	1.1	19
27	Refinement of Atomic Structures Against cryo-EM Maps. <i>Methods in Enzymology</i> , 2016, 579, 277-305.	0.4	39
28	Automated refinement of macromolecular structures at low resolution using prior information. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1149-1161.	1.1	58
29	How to tackle protein structural data from solution and solid state: An integrated approach. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2016, 92-93, 54-70.	3.9	27
30	Robust background modelling in <i>DIALS</i>. <i>Journal of Applied Crystallography</i> , 2016, 49, 1912-1921.	1.9	44
31	Data to knowledge: how to get meaning from your result. <i>IUCr</i> , 2015, 2, 45-58.	1.0	12
32	Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 136-153.	2.5	537
33	Structures of actin-like ParM filaments show architecture of plasmid-segregating spindles. <i>Nature</i> , 2015, 523, 106-110.	13.7	73
34	MutS/MutL crystal structure reveals that the MutS sliding clamp loads MutL onto DNA. <i>ELife</i> , 2015, 4, e06744.	2.8	91
35	The<i>PDB_REDO</i>server for macromolecular structure model optimization. <i>IUCr</i> , 2014, 1, 213-220.	1.0	709
36	Conformation-independent structural comparison of macromolecules with<i>ProSMART</i>. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2487-2499.	2.5	161

#	ARTICLE	IF	CITATIONS
37	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
38	Initiation of Translation by Cricket Paralysis Virus IRES Requires Its Translocation in the Ribosome. <i>Cell</i> , 2014, 157, 823-831.	13.5	211
39	Simultaneous use of solution NMR and X-ray data in <i>REFMAC5</i> for joint refinement/detection of structural differences. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 958-967.	2.5	45
40	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260
41	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Microscopy and Microanalysis</i> , 2014, 20, 1252-1253.	0.2	1
42	Tools for Refinement against Low Resolution X-ray Data and Fit to EM Reconstructions. <i>Nihon Kessho Gakkaishi</i> , 2014, 56, s26-s26.	0.0	0
43	High-resolution noise substitution to measure overfitting and validate resolution in 3D structure determination by single particle electron cryomicroscopy. <i>Ultramicroscopy</i> , 2013, 135, 24-35.	0.8	843
44	How good are my data and what is the resolution?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1204-1214.	2.5	3,739
45	Recent Advances in Low Resolution Refinement Tools in <i>REFMAC5</i> . <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 231-258.	0.5	6
46	Structural characterization of <i>Helicobacter pylori</i> dethiobiotin synthetase reveals differences between family members. <i>FEBS Journal</i> , 2012, 279, 1093-1105.	2.2	15
47	<i>PDB_REDO</i> : constructive validation, more than just looking for errors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 484-496.	2.5	195
48	Low-resolution refinement tools in <i>REFMAC5</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 404-417.	2.5	209
49	<i>JLigand</i> : a graphical tool for the <i>CCP4</i> template-restraint library. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 431-440.	2.5	373
50	Overview of the <i>CCP4</i> suite and current developments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 235-242.	2.5	11,098
51	<i>REFMAC5</i> for the refinement of macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 355-367.	2.5	7,247
52	Evaluating the solution from <i>MrBUMP</i> and <i>BALBES</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 313-323.	2.5	23
53	Structural Flexibility of the Macrophage Dengue Virus Receptor CLEC5A. <i>Journal of Biological Chemistry</i> , 2011, 286, 24208-24218.	1.6	48
54	Validation of B-factor distributions in protein crystal structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s315-s315.	0.3	1

#	ARTICLE	IF	CITATIONS
55	â€œConditional Restraintsâ€ Restraining the Free Atoms in ARP/wARP. <i>Structure</i> , 2009, 17, 183-189.	1.6	20
56	A multivariate likelihood SIRAS function for phasing and model refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1051-1061.	2.5	8
57	<i>ARP</i>/<i>wARP</i> and molecular replacement: the next generation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 49-60.	2.5	142
58	Model preparation in <i>MOLREP</i> and examples of model improvement using X-ray data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 33-39.	2.5	121
59	<i>BALBES</i>: a molecular-replacement pipeline. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 125-132.	2.5	663
60	Surprises and pitfalls arising from (pseudo)symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 99-107.	2.5	81
61	The Structures and Electronic Configuration of Compound I Intermediates of <i>Helicobacter pylori</i> and <i>Penicillium vitale</i> Catalases Determined by X-ray Crystallography and QM/MM Density Functional Theory Calculations. <i>Journal of the American Chemical Society</i> , 2007, 129, 4193-4205.	6.6	58
62	Intensity statistics in twinned crystals with examples from the PDB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 83-95.	2.5	58
63	Variable role of ions in two drug intercalation complexes of DNA. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 476-482.	1.1	10
64	Structures of <i>Plasmodium falciparum</i> purine nucleoside phosphorylase complexed with sulfate and its natural substrate inosine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1245-1254.	2.5	29
65	DNA variability in five crystal structures of d(CGCAATTGCG). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 680-685.	2.5	14
66	Crystallization and preliminary X-ray diffraction studies of a fungal hydrolase from <i>Ophiostoma novo-ulmi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1879-1882.	2.5	9
67	Direct incorporation of experimental phase information in model refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2196-2201.	2.5	121
68	REFMAC5 dictionary: organization of prior chemical knowledge and guidelines for its use. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2184-2195.	2.5	1,207
69	Developments in the CCP4 molecular-graphics project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2288-2294.	2.5	516
70	Fisher's information in maximum-likelihood macromolecular crystallographic refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2114-2124.	2.5	57
71	The Structure of NADH in the Enzyme dTDP-d-glucose Dehydratase (RmlB). <i>Journal of the American Chemical Society</i> , 2003, 125, 11872-11878.	6.6	51
72	Macromolecular TLS Refinement in REFMAC at Moderate Resolutions. <i>Methods in Enzymology</i> , 2003, 374, 300-321.	0.4	725

#	ARTICLE	IF	CITATIONS
73	Substrate Distortion by a -Mannanase: Snapshots of the Michaelis and Covalent-Intermediate Complexes Suggest a B _{2,5} Conformation for the Transition State. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 2824-2827.	7.2	127
74	The structures of <i>Micrococcus lysodeikticus</i> catalase, its ferryl intermediate (compound II) and NADPH complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1972-1982.	2.5	55
75	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2001, 306, 759-771.	2.0	90
76	The three-dimensional structure of human S100A12. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 20-29.	2.5	71
77	X-ray structure of bovine pancreatic phospholipase A ₂ at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 516-526.	2.5	26
78	NMR trial models: experiences with the colicin immunity protein Im7 and the p85± C-terminal SH2â€“peptide complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1397-1404.	2.5	31
79	Structure of the <i>Bacillus</i> Cell Fate Determinant SpoIIAA in Phosphorylated and Unphosphorylated Forms. <i>Structure</i> , 2001, 9, 605-614.	1.6	36
80	The three-dimensional structure of a <i>Trichoderma reesei</i> Î²-mannanase from glycoside hydrolase family A5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 3-13.	2.5	87
81	Crystal structure of dodecameric vanadium-dependent bromoperoxidase from the red algae <i>Corallina officinalis</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 1035-1049.	2.0	185
82	Solution of the structure of the cofactor-binding fragment of CysB: a struggle against non-isomorphism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 369-378.	2.5	7
83	Efficient anisotropic refinement of macromolecular structures using FFT. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 247-255.	2.5	867
84	Binding of non-catalytic ATP to human hexokinase I highlights the structural components for enzymeâ€“membrane association control. <i>Structure</i> , 1999, 7, 1427-1437.	1.6	47
85	The structure of the exo-Î²-(1,3)-glucanase from <i>Candida albicans</i> in native and bound forms: relationship between a pocket and groove in family 5 glycosyl hydrolases 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 294, 771-783.	2.0	98
86	Incorporation of Prior Phase Information Strengthens Maximum-Likelihood Structure Refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1285-1294.	2.5	172
87	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. <i>Structure</i> , 1997, 5, 1017-1032.	1.6	111
88	Structure of the Heme d of <i>Penicillium vitale</i> and <i>Escherichia coli</i> Catalases. <i>Journal of Biological Chemistry</i> , 1996, 271, 8863-8868.	1.6	64
89	The crystal structures of the oligopeptide-binding protein OppA complexed with tripeptide and tetrapeptide ligands. <i>Structure</i> , 1995, 3, 1395-1406.	1.6	91
90	Crystal structure of an extracellular fragment of the rat CD4 receptor containing domains 3 and 4. <i>Structure</i> , 1994, 2, 469-481.	1.6	30

#	ARTICLE	IF	CITATIONS
91	The polypeptide chain fold in tyrosine phenol-lyase, a pyridoxal-5â€²-phosphate-dependent enzyme. FEBS Letters, 1992, 302, 256-260.	1.3	17
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