

Zbigniew Dauter

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,170
citations

361413

20
h-index

395702

33
g-index

48
all docs

48
docs citations

48
times ranked

1524
citing authors

#	ARTICLE	IF	CITATIONS
1	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. <i>Protein Science</i> , 2022, 31, 784-786.	7.6	6
2	The Euler characteristic as a basis for teaching topology concepts to crystallographers. <i>Journal of Applied Crystallography</i> , 2022, 55, 154-167.	4.5	0
3	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	7.6	15
4	Crystallographic models of SARS-CoV-2 3CL ^{pro} : in-depth assessment of structure quality and validation. <i>IUCr</i> , 2021, 8, 238-256.	2.2	21
5	Arithmetic proof of the multiplicity-weighted Euler characteristic for symmetrically arranged space-filling polyhedra. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, 126-129.	0.1	2
6	Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407.	2.2	5
7	A topological proof of the modified Euler characteristic based on the orbifold concept. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2021, 77, 317-326.	0.1	2
8	Dr. Alexander Wlodawer celebrating five decades of service to the structural biology community. <i>FEBS Journal</i> , 2021, 288, 4160-4164.	4.7	0
9	Celebrating the 75th birthday of Professor Wladek Minor, one of the most accomplished Polish-American structural biologists. <i>Acta Biochimica Polonica</i> , 2021, 68, 1-4.	0.5	0
10	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. <i>FEBS Journal</i> , 2020, 287, 3703-3718.	4.7	35
11	Molecular structure of a U ₄ A-U-rich RNA triple helix with 11 consecutive base triples. <i>Nucleic Acids Research</i> , 2020, 48, 3304-3314.	14.5	16
12	On the evolution of the quality of macromolecular models in the PDB. <i>FEBS Journal</i> , 2020, 287, 2685-2698.	4.7	15
13	Multiplicity-weighted Euler's formula for symmetrically arranged space-filling polyhedra. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2020, 76, 580-583.	0.1	3
14	Unexpected Specificity of a Trypsin-like Enzyme. <i>Structure</i> , 2018, 26, 530-531.	3.3	0
15	The crystal structure of Z-DNA with untypically coordinated Ca ²⁺ ions. <i>Journal of Biological Inorganic Chemistry</i> , 2018, 23, 253-259.	2.6	0
16	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	4.7	49
17	Crystallographically correct but confusing presentation of structural models deposited in the Protein Data Bank. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 939-945.	2.3	2
18	'Atomic resolution': a badly abused term in structural biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 379-380.	2.3	25

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19	High-Resolution Cryo-EM Maps and Models: A Crystallographer's Perspective. <i>Structure</i> , 2017, 25, 1589-1597.e1.	3.3	47
20	Embarras de richesses – It is not good to be too anomalous: Accurate structure of selenourea, a chiral crystal of planar molecules. <i>PLoS ONE</i> , 2017, 12, e0171740.	2.5	5
21	Many Ways to Derivatize Macromolecules and Their Crystals for Phasing. <i>Methods in Molecular Biology</i> , 2017, 1607, 349-356.	0.9	11
22	Collection of X-Ray Diffraction Data from Macromolecular Crystals. <i>Methods in Molecular Biology</i> , 2017, 1607, 165-184.	0.9	17
23	Geometry of guanidinium groups in arginines. <i>Protein Science</i> , 2016, 25, 1753-1756.	7.6	5
24	Detection of twinning in macromolecular crystallography. <i>Zeitschrift Fur Kristallographie - Crystalline Materials</i> , 2016, 231, 561-571.	0.8	1
25	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	3.3	34
26	Progress in protein crystallography. <i>Protein and Peptide Letters</i> , 2016, 23, 201-210.	0.9	23
27	Protonation and geometry of histidine rings. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1444-1454.	2.5	20
28	On the accuracy of unit-cell parameters in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2217-2226.	2.5	6
29	Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1965-1979.	2.5	52
30	<i>ACHESYM</i> : an algorithm and server for standardized placement of macromolecular models in the unit cell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3290-3298.	2.5	57
31	Weak data do not make a free lunch, only a cheap meal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 253-260.	2.5	17
32	The Quality and Validation of Structures from Structural Genomics. <i>Methods in Molecular Biology</i> , 2014, 1091, 297-314.	0.9	23
33	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	2.2	58
34	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. <i>FEBS Journal</i> , 2013, 280, 5705-5736.	4.7	95
35	Placement of molecules in (not out of) the cell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2-4.	2.5	4
36	On optimal placement of molecules in the unit cell. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 872-878.	2.5	4

#	ARTICLE	IF	CITATIONS
37	Deprotonated imidodiphosphate in AMPPNP-containing protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 1073-1075.	2.5	5
38	Carrying out an optimal experiment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 389-392.	2.5	23
39	Impact of synchrotron radiation on macromolecular crystallography: a personal view. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 433-444.	2.4	34
40	Protein crystallography for non-crystallographers, or how to get the best (but not more) from published macromolecular structures. <i>FEBS Journal</i> , 2008, 275, 1-21.	4.7	231
41	Stereochemical restraints revisited: how accurate are refinement targets and how much should protein structures be allowed to deviate from them?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 611-620.	2.5	61
42	What happens when the signs of anomalous differences or the handedness of substructure are inverted?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 751-758.	2.5	5
43	Numerology versus reality: a voice in a recent dispute. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1282-1283.	2.5	10
44	Current state and prospects of macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1-11.	2.5	29
45	Estimation of anomalous signal in diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 867-876.	2.5	34
46	Use of polynuclear metal clusters in protein crystallography. <i>Comptes Rendus Chimie</i> , 2005, 8, 1808-1814.	0.5	22
47	Efficient use of synchrotron radiation for macromolecular diffraction data collection. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 153-172.	2.9	17
48	Pathological crystallography: case studies of several unusual macromolecular crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 967-975.	2.5	24