

Wladek Minor

List of Publications by Year in descending order

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Version: 2024-02-01

246
papers

42,693
citations

31902

53
h-index

2071

204
g-index

283
all docs

283
docs citations

283
times ranked

39472
citing authors

#	ARTICLE	IF	CITATIONS
1	[20] Processing of X-ray diffraction data collected in oscillation mode. <i>Methods in Enzymology</i> , 1997, 276, 307-326.	0.4	30,205
2	HKL-3000: the integration of data reduction and structure solution “ from diffraction images to an initial model in minutes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 859-866.	2.5	1,822
3	Structural and immunologic characterization of bovine, horse, and rabbit serum albumins. <i>Molecular Immunology</i> , 2012, 52, 174-182.	1.0	756
4	Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003, 59, 228-234.	0.3	623
5	Double chromodomains cooperate to recognize the methylated histone H3 tail. <i>Nature</i> , 2005, 438, 1181-1185.	13.7	484
6	Crystal Structure of Soybean Lipoxygenase L-1 at 1.4 Å... Resolution“„. <i>Biochemistry</i> , 1996, 35, 10687-10701.	1.2	416
7	Structure of Sindbis virus core protein reveals a chymotrypsin-like serine proteinase and the organization of the virion. <i>Nature</i> , 1991, 354, 37-43.	13.7	329
8	Data mining of metal ion environments present in protein structures. <i>Journal of Inorganic Biochemistry</i> , 2008, 102, 1765-1776.	1.5	273
9	<i>CheckMyMetal</i> : a macromolecular metal-binding validation tool. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 223-233.	1.1	268
10	Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. <i>Nature Protocols</i> , 2014, 9, 156-170.	5.5	254
11	Phosphorylation Regulates SIRT1 Function. <i>PLoS ONE</i> , 2008, 3, e4020.	1.1	244
12	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.	2.2	231
13	In situ proteolysis for protein crystallization and structure determination. <i>Nature Methods</i> , 2007, 4, 1019-1021.	9.0	197
14	Asymmetric Synthesis of 2,3-Dihydro-2-arylquinazolin-4-ones: Methodology and Application to a Potent Fluorescent Tubulin Inhibitor with Anticancer Activity. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 4620-4631.	2.9	184
15	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. <i>Journal of Biological Chemistry</i> , 2008, 283, 20361-20371.	1.6	177
16	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011, 50, 9950-9962.	1.2	169
17	Crystallographic determination of the active site iron and its ligands in soybean lipoxygenase L-1. <i>Biochemistry</i> , 1993, 32, 6320-6323.	1.2	162
18	Crystal structure of RhoA-GDP and its functional implications. <i>Nature Structural Biology</i> , 1997, 4, 699-703.	9.7	158

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19	Determination of Protein Structures—A Series of Fortunate Events. <i>Biophysical Journal</i> , 2008, 95, 1-9.	0.2	128
20	The tetramer structure of the Neryv homology two domain, NHR2, is critical for AML1/ETO's activity. <i>Cancer Cell</i> , 2006, 9, 249-260.	7.7	121
21	Structural and Functional Characterization of Second-Coordination Sphere Mutants of Soybean Lipoxygenase-1. <i>Biochemistry</i> , 2001, 40, 7509-7517.	1.2	120
22	Mechanism of Enolase: The Crystal Structure of Asymmetric Dimer Enolase ² -Phospho-d-glycerate/Enolase ² -Phosphoenolpyruvate at 2.0 Å... Resolution. <i>Biochemistry</i> , 1997, 36, 12526-12534.	1.2	115
23	NRMT is an N-methyltransferase that methylates RCC1 and retinoblastoma protein. <i>Nature</i> , 2010, 466, 1125-1128.	13.7	109
24	Structure of a microbial homologue of mammalian platelet-activating factor acetylhydrolases: <i>Streptomyces exfoliatus</i> lipase at 1.9 Å resolution. <i>Structure</i> , 1998, 6, 511-519.	1.6	107
25	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193.	1.1	103
26	Human Thymidylate Synthase Is in the Closed Conformation When Complexed with dUMP and Raltitrexed, an Antifolate Drug. <i>Biochemistry</i> , 2001, 40, 1897-1902.	1.2	100
27	<i>Alternaria alternata</i> allergen Alt a 1: A unique β -barrel protein dimer found exclusively in fungi. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 241-247.e9.	1.5	99
28	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. <i>FEBS Journal</i> , 2013, 280, 5705-5736.	2.2	95
29	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009, 37, D365-D368.	6.5	94
30	Structural and functional insight into the universal stress protein family. <i>Evolutionary Applications</i> , 2013, 6, 434-449.	1.5	94
31	Structural and Immunologic Characterization of Ara h 1, a Major Peanut Allergen. <i>Journal of Biological Chemistry</i> , 2011, 286, 39318-39327.	1.6	89
32	Serum albumins—Unusual allergens. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 5375-5381.	1.1	89
33	Magnesium-binding architectures in RNA crystal structures: validation, binding preferences, classification and motif detection. <i>Nucleic Acids Research</i> , 2015, 43, 3789-3801.	6.5	89
34	Crystal Structure of <i>Pseudomonas aeruginosa</i> SPM-1 Provides Insights into Variable Zinc Affinity of Metallo- β -lactamases. <i>Journal of Molecular Biology</i> , 2006, 357, 890-903.	2.0	88
35	Characterizing metal-binding sites in proteins with X-ray crystallography. <i>Nature Protocols</i> , 2018, 13, 1062-1090.	5.5	86
36	Double trouble—Buffer selection and His-tag presence may be responsible for nonreproducibility of biomedical experiments. <i>Protein Science</i> , 2014, 23, 1359-1368.	3.1	83

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37	Single Enantiomer of YK-4-279 Demonstrates Specificity in Targeting the Oncogene EWS-FLI1. <i>Oncotarget</i> , 2012, 3, 172-182.	0.8	83
38	Crystal Structures of Mite Allergens Der f 1 and Der p 1 Reveal Differences in Surface-Exposed Residues that May Influence Antibody Binding. <i>Journal of Molecular Biology</i> , 2009, 386, 520-530.	2.0	79
39	Molecular Determinants for Antibody Binding on Group 1 House Dust Mite Allergens. <i>Journal of Biological Chemistry</i> , 2012, 287, 7388-7398.	1.6	75
40	Strategies for macromolecular synchrotron crystallography. <i>Structure</i> , 2000, 8, R105-R110.	1.6	73
41	Continua of Interactions between Pairs of Atoms in Molecular Crystals. <i>Chemistry - A European Journal</i> , 2006, 12, 1941-1949.	1.7	73
42	Crystal Structure of the MACPF Domain of Human Complement Protein C8Î± in Complex with the C8Î³ Subunit. <i>Journal of Molecular Biology</i> , 2008, 379, 331-342.	2.0	70
43	The future of crystallography in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2014, 9, 125-137.	2.5	70
44	Structure of Human Thymidylate Synthase Suggests Advantages of Chemotherapy with Noncompetitive Inhibitors. <i>Journal of Biological Chemistry</i> , 2001, 276, 14170-14177.	1.6	67
45	Circulatory zinc transport is controlled by distinct interdomain sites on mammalian albumins. <i>Chemical Science</i> , 2016, 7, 6635-6648.	3.7	67
46	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65
47	Structural Insight into the Mechanism of Substrate Specificity and Catalytic Activity of an HD-Domain Phosphohydrolase: The 5'-Deoxyribonucleotidase YfbR from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2008, 378, 215-226.	2.0	62
48	The impact of structural genomics: the first quinquennial. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 1-16.	1.2	60
49	Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2031-2038.	2.5	59
50	X-ray crystallography over the past decade for novel drug discovery – where are we heading next?. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 975-989.	2.5	59
51	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	1.0	58
52	Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 426-436.	2.5	57
53	Analysis of solvent content and oligomeric states in protein crystals – does symmetry matter?. <i>Protein Science</i> , 2008, 17, 623-632.	3.1	54
54	Uncovering a Calcium-Regulated Membrane-Binding Mechanism for Soybean Lipoxygenase-1. <i>Biochemistry</i> , 1998, 37, 15481-15490.	1.2	53

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55	Expression, Purification and the 1.8Å... Resolution Crystal Structure of Human Neuron Specific Enolase. <i>Journal of Molecular Biology</i> , 2004, 341, 1015-1021.	2.0	53
56	X-ray crystallography: assessment and validation of proteinâ€“small molecule complexes for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 771-782.	2.5	53
57	Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. <i>Molecular Biology of the Cell</i> , 2012, 23, 1457-1466.	0.9	53
58	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
59	Substrate Specificity of Mammalian N-Terminal Î±-Amino Methyltransferase NRMT. <i>Biochemistry</i> , 2012, 51, 5942-5950.	1.2	51
60	Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 587-597.	2.6	49
61	The HP1a Disordered C Terminus and Chromo Shadow Domain Cooperate to Select Target Peptide Partners. <i>ChemBioChem</i> , 2011, 12, 1084-1096.	1.3	49
62	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	2.2	49
63	The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 24-33.	1.0	48
64	A close look onto structural models and primary ligands of metallo-Î²-lactamases. <i>Drug Resistance Updates</i> , 2018, 40, 1-12.	6.5	47
65	Protein purification and crystallization artifacts: The tale usually not told. <i>Protein Science</i> , 2016, 25, 720-733.	3.1	46
66	Identification of Unknown Protein Function Using Metabolite Cocktail Screening. <i>Structure</i> , 2012, 20, 1715-1725.	1.6	45
67	Broadâ€“substrate screen as a tool to identify substrates for bacterial Gcn5â€“related acetyltransferases with unknown substrate specificity. <i>Protein Science</i> , 2013, 22, 222-230.	3.1	45
68	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. <i>Molecular Immunology</i> , 2013, 56, 794-803.	1.0	43
69	Refining the macromolecular model â€“ achieving the best agreement with the data from X-ray diffraction experiment. <i>Crystallography Reviews</i> , 2018, 24, 236-262.	0.4	43
70	Structural genomics: keeping up with expanding knowledge of the protein universe. <i>Current Opinion in Structural Biology</i> , 2007, 17, 347-353.	2.6	42
71	Biochemical and Structural Characterization of Apolipoprotein A-I Binding Protein, a Novel Phosphoprotein with a Potential Role in Sperm Capacitation. <i>Endocrinology</i> , 2008, 149, 2108-2120.	1.4	42
72	Crystal Structure of Human Complement Protein C8Î² at 1.2 Å... Resolution Reveals a Lipocalin Fold and a Distinct Ligand Binding Siteâ€“â€“. <i>Biochemistry</i> , 2002, 41, 7030-7037.	1.2	41

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73	Neutron scattering studies of Cd _{1-x} MnxTe (invited). <i>Journal of Applied Physics</i> , 1984, 55, 2305-2309.	1.1	39
74	Targeting a Uniquely Nonspecific Prenyl Synthase with Bisphosphonates to Combat Cryptosporidiosis. <i>Chemistry and Biology</i> , 2008, 15, 1296-1306.	6.2	39
75	Testosterone meets albumin – the molecular mechanism of sex hormone transport by serum albumins. <i>Chemical Science</i> , 2019, 10, 1607-1618.	3.7	38
76	Crystal Structure of RNase T, an Exoribonuclease Involved in tRNA Maturation and End Turnover. <i>Structure</i> , 2007, 15, 417-428.	1.6	37
77	Structural, Functional, and Inhibition Studies of a Gcn5-related N-Acetyltransferase (GNAT) Superfamily Protein PA4794. <i>Journal of Biological Chemistry</i> , 2013, 288, 30223-30235.	1.6	37
78	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 6847-6862.	2.9	37
79	The structural genomics experimental pipeline: Insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 201-210.	1.5	36
80	New surface contacts formed upon reductive lysine methylation: Improving the probability of protein crystallization. <i>Protein Science</i> , 2010, 19, 1395-1404.	3.1	35
81	Ligand-centered assessment of SARS-CoV-2 drug target models in the Protein Data Bank. <i>FEBS Journal</i> , 2020, 287, 3703-3718.	2.2	35
82	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	1.6	34
83	Data Management in the Modern Structural Biology and Biomedical Research Environment. <i>Methods in Molecular Biology</i> , 2014, 1140, 1-25.	0.4	34
84	100 Years later: Celebrating the contributions of x-ray crystallography to allergy and clinical immunology. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 29-37.e10.	1.5	33
85	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
86	Correcting the record of structural publications requires joint effort of the community and journal editors. <i>FEBS Journal</i> , 2016, 283, 4452-4457.	2.2	31
87	Molstack – Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. <i>Protein Science</i> , 2018, 27, 86-94.	3.1	31
88	DENZO and SCALEPACK. , 2006, , 226-235.		29
89	The Crystal Structure of N10-Formyltetrahydrofolate Synthetase from <i>Moorella thermoacetica</i> . <i>Biochemistry</i> , 2000, 39, 3920-3926.	1.2	27
90	Benefits of Structural Genomics for Drug Discovery Research. <i>Infectious Disorders - Drug Targets</i> , 2009, 9, 459-474.	0.4	26

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91	Structure of human thymidylate synthase under low-salt conditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 622-627.	2.5	25
92	<i>Fitmunk</i> : improving protein structures by accurate, automatic modeling of side-chain conformations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 266-280.	1.1	25
93	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019, 6, 064301.	0.9	25
94	Harvesting the high-hanging fruit: the structure of the YdeN gene product from <i>Bacillus subtilis</i> at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1101-1107.	2.5	23
95	An extremely SAD case: structure of a putative redox-enzyme maturation protein from <i>Archaeoglobus fulgidus</i> at 3.4 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 348-354.	2.5	23
96	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. <i>Journal of Biological Chemistry</i> , 2009, 284, 25268-25279.	1.6	23
97	To automate or not to automate: this is the question. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 211-221.	1.2	23
98	Structural Analysis of Der p 1 Antibody Complexes and Comparison with Complexes of Proteins or Peptides with Monoclonal Antibodies. <i>Journal of Immunology</i> , 2015, 195, 307-316.	0.4	23
99	The Quality and Validation of Structures from Structural Genomics. <i>Methods in Molecular Biology</i> , 2014, 1091, 297-314.	0.4	23
100	Crystallization and preliminary structure analysis of an insect virus with T=4 quasi-symmetry: <i>Nudaurelia capensis</i> virus. <i>Acta Crystallographica Section B: Structural Science</i> , 1991, 47, 23-29.	1.8	22
101	Crystal structure of a putative isochorismatase hydrolase from <i>Oleispira antarctica</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 27-36.	1.2	22
102	The major cockroach allergen Bla g 4 binds tyramine and octopamine. <i>Molecular Immunology</i> , 2014, 60, 86-94.	1.0	22
103	Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019, 35, 452-461.	1.8	22
104	Mechanism of N ¹⁰ -formyltetrahydrofolate synthetase derived from complexes with intermediates and inhibitors. <i>Protein Science</i> , 2012, 21, 219-228.	3.1	21
105	Classification, substrate specificity and structural features of D-2-hydroxyacid dehydrogenases: 2HADH knowledgebase. <i>BMC Evolutionary Biology</i> , 2018, 18, 199.	3.2	21
106	Catalytic Cysteine of Thymidylate Synthase Is Activated upon Substrate Binding. <i>Biochemistry</i> , 2000, 39, 6969-6978.	1.2	20
107	Asymmetric synthesis and evaluation of a hydroxyphenylamide voltage-gated sodium channel blocker in human prostate cancer xenografts. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 2180-2188.	1.4	20
108	Antigenic Determinants of Der p 1: Specificity and Cross-Reactivity Associated with IgE Antibody Recognition. <i>Journal of Immunology</i> , 2017, 198, 1334-1344.	0.4	20

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109	Removal of salt from a salt-induced protein crystal without cross-linking. Preliminary examination of "desalted" crystals of phosphoglucomutase by x-ray crystallography at low temperature. <i>Biochemistry</i> , 1991, 30, 6866-6875.	1.2	19
110	Structure of <i>Bacillus subtilis</i> YXKO A member of the UPF0031 family and a putative kinase. <i>Journal of Structural Biology</i> , 2002, 139, 161-170.	1.3	19
111	Crystal structure of equine serum albumin in complex with cetirizine reveals a novel drug binding site. <i>Molecular Immunology</i> , 2016, 71, 143-151.	1.0	19
112	The structure determination of Sindbis virus core protein using isomorphous replacement and molecular replacement averaging between two crystal forms. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1992, 48, 430-442.	0.3	17
113	Kinetic, Spectroscopic, and Structural Investigations of the Soybean Lipoxygenase-1 First-Coordination Sphere Mutant, Asn694Gly. <i>Biochemistry</i> , 2006, 45, 10233-10242.	1.2	17
114	Crystal structures of TM0549 and NE1324-two orthologs of <i>E. coli</i> HAS isozyme III small regulatory subunit. <i>Protein Science</i> , 2007, 16, 1360-1367.	3.1	17
115	An experimental charge density of HEPES. <i>Acta Crystallographica Section B: Structural Science</i> , 2010, 66, 482-492.	1.8	17
116	Structural Analysis of a Putative Aminoglycoside N-Acetyltransferase from <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2011, 410, 411-423.	2.0	17
117	Pyrimidine biosynthesis in pathogens Structures and analysis of dihydroorotases from <i>Yersinia pestis</i> and <i>Vibrio cholerae</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 136, 1176-1187.	3.6	17
118	Crystallization of Fe-Si-B metallic glasses studied by X-ray synchrotron radiation. <i>Journal of Materials Science</i> , 1987, 22, 4144-4152.	1.7	16
119	Cation Binding and Thermostability of FTHFS Monovalent Cation Binding Sites and Thermostability of N10-Formyltetrahydrofolate Synthetase from <i>Moorella thermoacetica</i> . <i>Biochemistry</i> , 2000, 39, 14481-14486.	1.2	16
120	Structure of <i>Escherichia coli</i> RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the <i>rut</i> operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1294-1299.	0.7	15
121	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
122	Regioselectivity of hyoscyamine 6 β -hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. <i>Dalton Transactions</i> , 2020, 49, 4454-4469.	1.6	15
123	On the evolution of the quality of macromolecular models in the PDB. <i>FEBS Journal</i> , 2020, 287, 2685-2698.	2.2	15
124	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	3.1	15
125	Dissecting the Structural Elements for the Activation of β -Ketoacyl-(Acyl Carrier Protein) Reductase from <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2016, 198, 463-476.	1.0	14
126	Dexamethasone at 119 K. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2007, 63, o2791-o2793.	0.2	13

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127	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from <i>Thermoplasma acidophilum</i> . <i>Journal of Structural Biology</i> , 2010, 169, 304-311.	1.3	13
128	Factors correlating with significant differences between X-ray structures of myoglobin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 481-491.	2.5	13
129	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 55-64.	1.1	13
130	Explanation of neutron diffraction phenomena observed in vibrating piezoelectric crystals. <i>Physica Status Solidi A</i> , 1972, 9, 423-433.	1.7	12
131	STUDIES OF FCC HEISENBERG ANTIFERROMAGNETS BY MONTE CARLO SIMULATION ON LARGE SPIN ARRAYS. <i>Journal De Physique Colloque</i> , 1988, 49, C8-1551-C8-1552.	0.2	12
132	Data to knowledge: how to get meaning from your result. <i>IUCr</i> , 2015, 2, 45-58.	1.0	12
133	Recombinant production of enzymatically active male contraceptive drug target hTSSK2 - Localization of the TSKS domain phosphorylated by TSSK2. <i>Protein Expression and Purification</i> , 2016, 121, 88-96.	0.6	12
134	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. <i>Biochemistry</i> , 2018, 57, 963-977.	1.2	12
135	A transient post-translational modification of active site cysteine alters binding properties of the parkinsonism protein DJ-1. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 328-333.	1.0	12
136	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. <i>IUCr</i> , 2020, 7, 1048-1058.	1.0	12
137	A phenomenological description of the paramagnet-antiferromagnet transition in Cd ₁ -Mn Te. <i>Journal of Magnetism and Magnetic Materials</i> , 1982, 30, 215-222.	1.0	11
138	Synthesis and Solid-State Study of Supramolecular Host-Guest Assemblies: Bis[6-O,6-O- ϵ^2 -(1,2:3,4-diisopropylidene- β -D-galactopyranosyl)thiophosphoryl] Dichalcogenides. <i>Journal of Organic Chemistry</i> , 2008, 73, 4388-4397.	1.7	11
139	The crystal structure of the AF2331 protein from <i>Archaeoglobus fulgidus</i> DSM 4304 forms an unusual interdigitated dimer with a new type of $\beta\alpha + \beta^2$ fold. <i>Protein Science</i> , 2009, 18, 2410-2419.	3.1	11
140	A Gcn5-Related N-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibiotics in Vitro. <i>Biochemistry</i> , 2018, 57, 7011-7020.	1.2	11
141	Energetics of interactions in the solid state of 2-hydroxy-8-quinoline derivatives (β) <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i> <i>2019, 6, 868-883.</i>	1.0	11
142	Spin waves in Fe-Al-Si system. <i>Solid State Communications</i> , 1983, 46, 217-219.	0.9	10
143	X-Ray Diffraction Experiment. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 77, 23-40.	1.0	10
144	Assessing the accuracy of template-based structure prediction metaservers by comparison with structural genomics structures. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 213-225.	1.2	10

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145	Edc3 Function in Yeast and Mammals Is Modulated by Interaction with NAD-Related Compounds. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 613-622.	0.8	10
146	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 455-457.	1.1	10
147	Crystallization and preliminary X-ray analysis of the cytoplasmic domain of human erythrocyte band 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 293-297.	1.5	9
148	Using surface-bound rubidium ions for protein phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1008-1012.	2.5	9
149	Crystal structure of a transcriptional regulator TM1030 from <i>Thermotoga maritima</i> solved by an unusual MAD experiment. <i>Journal of Structural Biology</i> , 2007, 159, 424-432.	1.3	9
150	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 97-108.	1.2	9
151	Ultratight crystal packing of a 10â€¦kDa protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 464-470.	2.5	9
152	Sperm Lysozyme-Like Protein 1 (SLLP1), an intra-acrosomal oolemmal-binding sperm protein, reveals filamentous organization in protein crystal form. <i>Andrology</i> , 2015, 3, 756-771.	1.9	9
153	Molstack: A platform for interactive presentations of electron density and cryoâ€¦EM maps and their interpretations. <i>Protein Science</i> , 2020, 29, 120-127.	3.1	9
154	Recognizing and validating ligands with CheckMyBlob. <i>Nucleic Acids Research</i> , 2021, 49, W86-W92.	6.5	9
155	Detecting anomalies in X-ray diffraction images using convolutional neural networks. <i>Expert Systems With Applications</i> , 2021, 174, 114740.	4.4	9
156	â€œHotâ€•Macromolecular Crystals. <i>Crystal Growth and Design</i> , 2010, 10, 580-586.	1.4	8
157	Gcn5-Related N-Acetyltransferases (GNATs) With a Catalytic Serine Residue Can Play Ping-Pong Too. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 646046.	1.6	8
158	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>IUCr</i> , 2019, 6, 341-343.	1.0	8
159	Phason velocities in TaS ₂ by x-ray diffuse scattering. <i>Physical Review B</i> , 1989, 39, 1360-1362.	1.1	7
160	A multiâ€¦faceted analysis of RutD reveals a novel family of $\hat{1}\pm/\hat{1}^2$ hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2359-2368.	1.5	7
161	Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 15-26.	1.2	7
162	Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. <i>Molecular Pharmacology</i> , 2020, 98, 648-657.	1.0	7

#	ARTICLE	IF	CITATIONS
163	Spinning single crystal tof method for structure analysis. <i>Nuclear Instruments & Methods</i> , 1970, 77, 13-20.	1.2	6
164	Neutron Scattering Studies of the "Antiferromagnetic Phase" of Cd ₁ -XMnXTe. <i>Physica Scripta</i> , 1982, 25, 731-734.	1.2	6
165	Stacks of DMANH+â€“ scaffolding for ribbon shaped Clâˆ“bridged oxonium ions. <i>CrystEngComm</i> , 2007, 9, 152-157.	1.3	6
166	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from <i>Streptococcus pyogenes</i> . <i>BMC Structural Biology</i> , 2009, 9, 75.	2.3	6
167	Crystal structure of a putative transcriptional regulator SCO0520 from <i>Streptomyces coelicolor</i> A3(2) reveals an unusual dimer among TetR family proteins. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 149-157.	1.2	6
168	Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665.	0.4	6
169	Optimal structure determination from subâ€“optimal diffraction data. <i>Protein Science</i> , 2022, 31, 259-268.	3.1	6
170	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. <i>Protein Science</i> , 2022, 31, 784-786.	3.1	6
171	Organism-specific differences in the binding of ketoprofen to serum albumin. <i>IUCr</i> , 2022, 9, 551-561.	1.0	6
172	High temperature behaviour of spin waves in Fe ₃ -xMnxSi. <i>Solid State Communications</i> , 1986, 57, 47-51.	0.9	5
173	Function-Biased Choice of Additives for Optimization of Protein Crystallization: The Case of the Putative Thioesterase PA5185 from <i>Pseudomonas aeruginosa</i> PAO1. <i>Crystal Growth and Design</i> , 2008, 8, 4054-4061.	1.4	5
174	Optimization of overexpression of a chaperone protein of steroid C25 dehydrogenase for biochemical and biophysical characterization. <i>Protein Expression and Purification</i> , 2017, 134, 47-62.	0.6	5
175	Generating enzyme and radicalâ€“mediated bisubstrates as tools for investigating Gcn5â€“related acetyltransferases. <i>FEBS Letters</i> , 2017, 591, 2348-2361.	1.3	5
176	A study on the structure, mechanism, and biochemistry of kanamycin B dioxygenase (KanJ)â€“an enzyme with a broad range of substrates. <i>FEBS Journal</i> , 2021, 288, 1366-1386.	2.2	5
177	Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407.	1.0	5
178	virusMED: an atlas of hotspots of viral proteins. <i>IUCr</i> , 2021, 8, 931-942.	1.0	5
179	State-of-the-Art Data Management: Improving the Reproducibility, Consistency, and Traceability of Structural Biology and in Vitro Biochemical Experiments. <i>Methods in Molecular Biology</i> , 2021, 2199, 209-236.	0.4	5
180	Map2modâ€“a server for evaluation of crystallographic models and their agreement with electron density maps. <i>Bioinformatics</i> , 2006, 22, 1660-1661.	1.8	4

#	ARTICLE	IF	CITATIONS
181	Structure of anabolic ornithine carbamoyltransferase from <i>Campylobacter jejuni</i> at 2.7 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1018-1024.	0.7	4
182	Spin waves in Fe ₃ xMnxSi ordered alloys. <i>Solid State Communications</i> , 1981, 38, 773-775.	0.9	3
183	L-Methioninium chloride and L-selenomethioninium chloride at 103 K. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2004, 60, o868-o871.	0.4	3
184	3-(1-Pyridinio)propanesulfonate and 3-(benzyltrimethylammonio)propanesulfonate monohydrate. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2007, 63, o114-o116.	0.4	3
185	Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 632-637.	0.7	3
186	Differences in substrate specificity of <i>V. cholerae</i> FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. <i>FEBS Journal</i> , 2018, 285, 2900-2921.	2.2	3
187	Structural and biochemical analysis of <i>Bacillus Anthracis</i> prephenate dehydrogenase reveals an unusual mode of inhibition by tyrosine via the ACT domain. <i>FEBS Journal</i> , 2020, 287, 2235-2255.	2.2	3
188	Comparison of metal-bound and unbound structures of aminopeptidase B proteins from <i>Escherichia coli</i> and <i>Yersinia pestis</i> . <i>Protein Science</i> , 2020, 29, 1618-1628.	3.1	3
189	Synchrotron radiation as a tool for macromolecular X-Ray Crystallography: A XXI century perspective. <i>Nuclear Instruments & Methods in Physics Research B</i> , 2021, 489, 30-40.	0.6	3
190	2,3-Difluorobenzoic acid. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2008, 64, o466-o466.	0.2	3
191	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 321-323.	0.4	3
192	New ligand-binding sites identified in the crystal structures of β -lactoglobulin complexes with desipramine. <i>IUCr</i> , 2022, 9, 386-398.	1.0	3
193	Crystallization and preliminary X-ray investigation of lipoxygenase-3 from soybeans. <i>Protein Science</i> , 1995, 4, 1233-1235.	3.1	2
194	3-(Morpholinium-1-yl)propanesulfonate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2005, 61, o3190-o3191.	0.2	2
195	3-(Ethyltrimethylammonio)propanesulfonate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2006, 62, o5757-o5759.	0.2	2
196	Is too 'creative' language acceptable in crystallography?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1041-1042.	2.5	2
197	Structure of isochorismate synthase Dhbc from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 956-961.	0.7	2
198	Sharing Big Data. <i>IUCr</i> , 2017, 4, 3-4.	1.0	2

#	ARTICLE	IF	CITATIONS
199	The young person's guide to the PDB. Postepy Biochemii, 2016, 62, 242-249.	0.5	2
200	Crystallization at low salt concentration and alkaline pH and preliminary crystallographic data for a monoclinic form of yeast enolase. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 335-336.	2.5	1
201	3-(1-Methylpiperidinio)-1-propanesulfonate. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o282-o283.	0.2	1
202	N,N,Nâ€²,Nâ€²-Tetrakis(carboxymethyl)-2,2â€²-(ethylenedioxy)dianilinium dichloride dihydrate. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o754-o756.	0.2	1
203	Structural and immunologic characterization of Ara h 1, a major peanut allergen.. Journal of Biological Chemistry, 2011, 286, 44294.	1.6	1
204	Structural Analysis Reveals Molecular Basis for Interactions of Group 1 Allergens with Species Specific and Cross-Reactive Antibodies. Journal of Allergy and Clinical Immunology, 2013, 131, AB15.	1.5	1
205	Structural characterization of the putative ABC-type 2 transporter from Thermotoga maritima MSB8. Journal of Structural and Functional Genomics, 2014, 15, 215-222.	1.2	1
206	Antigenic Determinants On Der p 1 Identified By Mutagenesis Analysis Based On The Structure Of Allergen-Antibody Complexes. Journal of Allergy and Clinical Immunology, 2014, 133, AB164.	1.5	1
207	2,4-Dichlorobenzaldehyde. Acta Crystallographica Section E: Structure Reports Online, 2010, 66, o243-o243.	0.2	1
208	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	1.9	1
209	Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO.. Blood, 2004, 104, 482-482.	0.6	1
210	A public database of macromolecular diffraction experiments. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C627-C627.	0.0	1
211	A simple method of orientating single crystals on time-of-flight neutron spectrometers. Nuclear Instruments & Methods, 1974, 119, 141-144.	1.2	0
212	Secondary extinction in rotating single-crystal slabs. The Acta Crystallographica Section A, Crystal Physics, Diffractionoretical and General Crystallography, 1979, 35, 861-870.	0.6	0
213	Antiferromagnetic states in CopMg1âˆŒpO (abstract). Journal of Applied Physics, 1990, 67, 5990-5990.	1.1	0
214	Crystal structure of 6-(4-difluoromethoxy-3-methoxyphenyl)-3(2H)- pyridazinone, C12H10F2N2O3. Zeitschrift Fur Kristallographie - New Crystal Structures, 2006, 221, 359-360.	0.1	0
215	Crystal structure of 2,6-dichlorobenzaldehyde, C7H4Cl2O. Zeitschrift Fur Kristallographie - New Crystal Structures, 2006, 221, 545-546.	0.1	0
216	Disodium 4-nitrophenylphosphate hexahydrate. Acta Crystallographica Section E: Structure Reports Online, 2006, 62, m884-m886.	0.2	0

#	ARTICLE	IF	CITATIONS
217	2-(Biphenyl-4-yl)-2,3-dihydroquinazolin-4(1H)-one. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o891-o893.	0.2	0
218	3-Iodo-L-tyrosine hemihydrate. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o1557-o1559.	0.2	0
219	2-Amino-4-(4-chloro-3-methylphenyl)-5-propyl-1,3-thiazolium iodide. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o1598-o1600.	0.2	0
220	trans-1-Hydroxycyclopentan-2-aminium chloride. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o2697-o2698.	0.2	0
221	Absolute configuration from a redetermination of (+)-5-bromo-1-[(2R,4S,5R)-4-hydroxy-5-(hydroxymethyl)oxolan-2-yl]pyrimidine-2,4-dione at 118 K. Acta Crystallographica Section E: Structure Reports Online, 2007, 63, o4159-o4160.	0.2	0
222	How to use the PSI Structural Genomics Knowledgebase to Enable Research. Biophysical Journal, 2010, 98, 250a.	0.2	0
223	The Structural Biology Knowledgebase - search Online for Protein Sequences, Structures, Functions, Methods and More. Biophysical Journal, 2011, 100, 319a.	0.2	0
224	Structure and Function of the Peanut Panallergen Ara h 8. Journal of Allergy and Clinical Immunology, 2013, 131, AB19.	1.5	0
225	De Novo Creation of an Antibody Binding Epitope On Group 1 Mite Allergens. Journal of Allergy and Clinical Immunology, 2013, 131, AB16.	1.5	0
226	The crystal structure of pyrimidine/thiamin biosynthesis precursor-like domain-containing protein CAE31940 from proteobacterium Bordetella bronchiseptica RB50, and evolutionary insight into the NMT1/THI5 family. Journal of Structural and Functional Genomics, 2014, 15, 73-81.	1.2	0
227	Check your metal - not every density blob is a water molecule. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1483-C1483.	0.0	0
228	Transforming biomedical and structural data into information and knowledge. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C492-C492.	0.0	0
229	Structural Basis of Non-Steroidal Anti-Inflammatory Drug (NSAID) Transport by Serum Albumin. Biophysical Journal, 2020, 118, 323a-324a.	0.2	0
230	Dr. Alexander Wlodawer "celebrating five decades of service to the structural biology community. FEBS Journal, 2021, 288, 4160-4164.	2.2	0
231	The Integrated Resource for Reproducibility in Molecular Crystallography: experiences of the first five years. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, a187-a187.	0.0	0
232	Rapid response to biomedical challenges and threats. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, a268-a268.	0.0	0
233	The Protein Structure Initiative Structural Genomics Knowledgebase. FASEB Journal, 2009, 23, 858.10.	0.2	0
234	HOW TO USE THE PSI STRUCTURAL GENOMICS KNOWLEDGEBASE TO ENABLE RESEARCH. FASEB Journal, 2010, 24, 902.2.	0.2	0

#	ARTICLE	IF	CITATIONS
235	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. FASEB Journal, 2012, 26, lb194.	0.2	0
236	Abstract 2747: EWS-FLI1 reduces RNA Helicase A activity.. , 2013, , .		0
237	Structural analysis of GNAT acetyltransferases and protein acetylation. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C299-C299.	0.0	0
238	Structural Biology Knowledgebase: An Integrated Resource for Modern Biologists. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C493-C493.	0.0	0
239	The Integrated Resource for Reproducibility in Macromolecular Crystallography (IRRM). Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a218-a218.	0.0	0
240	What's hiding in the PDB? Reinvestigation of structural data for the biomedically important enzymes metallo- β -lactamases. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a281-a281.	0.0	0
241	Crystallographic tools towards understanding of macromolecular structureâ€“function relationships. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C35-C35.	0.0	0
242	Credible measures of resolution limits. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a326-a326.	0.0	0
243	The Integrated Resource for Reproducibility in Macromolecular Crystallography (IRRM). Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a259-a259.	0.0	0
244	ACT domain of Bacillus anthracis prephenate dehydrogenase acts as tyrosine sensor and inhibits the enzyme via a mechanical switch. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a341-a341.	0.0	0
245	Decomposition methods for analysis of specific radiation damage. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a330-a330.	0.0	0
246	Comparison of X-ray wavefunction refinement and multipole refinement based on the energetic analysis of the crystal structures of 2-hydroxy-8-X-quinoline derivatives (X = Cl, Br, I, S-Ph). Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e454-e454.	0.0	0