

Mariusz Jaskolski

List of Publications by Year in descending order

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265
papers

9,540
citations

57631

44
h-index

49773

87
g-index

270
all docs

270
docs citations

270
times ranked

8056
citing authors

#	ARTICLE	IF	CITATIONS
1	Conserved folding in retroviral proteases: crystal structure of a synthetic HIV-1 protease. <i>Science</i> , 1989, 245, 616-621.	6.0	1,201
2	Crystal structure of a monomeric retroviral protease solved by protein folding game players. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1175-1177.	3.6	463
3	Crystal structure of a retroviral protease proves relationship to aspartic protease family. <i>Nature</i> , 1989, 337, 576-579.	13.7	378
4	Human cystatin C, an amyloidogenic protein, dimerizes through three-dimensional domain swapping. <i>Nature Structural Biology</i> , 2001, 8, 316-320.	9.7	353
5	EARLY FLOWERING4 Recruitment of EARLY FLOWERING3 in the Nucleus Sustains the <i>Arabidopsis</i> Circadian Clock. <i>Plant Cell</i> , 2012, 24, 428-443.	3.1	275
6	Crystal structure of <i>Escherichia coli</i> L-asparaginase, an enzyme used in cancer therapy.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 1474-1478.	3.3	252
7	Structure at 2.5-Å resolution of chemically synthesized Human Immunodeficiency Virus Type 1 protease complexed with a hydroxyethylene-based inhibitor. <i>Biochemistry</i> , 1991, 30, 1600-1609.	1.2	242
8	High-resolution Structure of the Catalytic Domain of Avian Sarcoma Virus Integrase. <i>Journal of Molecular Biology</i> , 1995, 253, 333-346.	2.0	241
9	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
10	Structural and functional aspects of α 10 proteins. <i>FEBS Journal</i> , 2013, 280, 1169-1199.	2.2	191
11	Molecular modeling of the HIV-1 protease and its substrate binding site. <i>Science</i> , 1989, 243, 928-931.	6.0	179
12	Crystal engineering with hydrogen bonds and halogen bonds. <i>CrystEngComm</i> , 2005, 7, 355.	1.3	177
13	The catalytic domain of avian sarcoma virus integrase: conformation of the active-site residues in the presence of divalent cations. <i>Structure</i> , 1996, 4, 89-96.	1.6	171
14	Fibrillogenic Oligomers of Human Cystatin C Are Formed by Propagated Domain Swapping. <i>Journal of Biological Chemistry</i> , 2007, 282, 18318-18326.	1.6	112
15	Structural aspects of L-asparaginases, their friends and relations.. <i>Acta Biochimica Polonica</i> , 2006, 53, 627-640.	0.3	104
16	Prevention of Domain Swapping Inhibits Dimerization and Amyloid Fibril Formation of Cystatin C. <i>Journal of Biological Chemistry</i> , 2004, 279, 24236-24245.	1.6	102
17	Structure of the aspartic protease from Rous sarcoma retrovirus refined at 2-Å resolution. <i>Biochemistry</i> , 1990, 29, 5889-5898.	1.2	100
18	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

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19	3D domain-swapped human cystatin C with amyloidlike intermolecular β -sheets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 570-578.	1.5	93
20	The Role of Cystatin C in Cerebral Amyloid Angiopathy and Stroke: Cell Biology and Animal Models. <i>Brain Pathology</i> , 2006, 16, 60-70.	2.1	92
21	Crystal Structure of <i>Vigna radiata</i> Cytokinin-Specific Binding Protein in Complex with Zeatin. <i>Plant Cell</i> , 2006, 18, 2622-2634.	3.1	90
22	Crystal Structures of Two Homologous Pathogenesis-related Proteins from Yellow Lupine. <i>Journal of Molecular Biology</i> , 2002, 319, 1223-1234.	2.0	85
23	A brief history of macromolecular crystallography, illustrated by a family tree and its <sc>obel fruits. <i>FEBS Journal</i> , 2014, 281, 3985-4009.	2.2	83
24	Piecing together the structure of retroviral integrase, an important target in AIDS therapy. <i>FEBS Journal</i> , 2009, 276, 2926-2946.	2.2	80
25	Crystal structure of human cystatin ϵ C stabilized against amyloid formation. <i>FEBS Journal</i> , 2010, 277, 1726-1737.	2.2	73
26	Domain Swapping in N-truncated Human Cystatin C. <i>Journal of Molecular Biology</i> , 2004, 341, 151-160.	2.0	71
27	On the Aromatic Character of the Heterocyclic Bases of DNA and RNA#. <i>Journal of Organic Chemistry</i> , 2003, 68, 8607-8613.	1.7	70
28	Crystal Structure of Plant Asparaginase. <i>Journal of Molecular Biology</i> , 2006, 360, 105-116.	2.0	67
29	<i>Lupinus luteus</i> Pathogenesis-Related Protein as a Reservoir for Cytokinin. <i>Journal of Molecular Biology</i> , 2008, 378, 1040-1051.	2.0	66
30	Topological Equivalences between Organic and Coordination Polymer Crystal Structures: An Organic Ladder Formed with Three-Connected Molecular and Supramolecular Synthons. <i>Organic Letters</i> , 2002, 4, 921-924.	2.4	61
31	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
32	Expression, purification and catalytic activity of <i>Lupinus luteus</i> asparagine β -amidohydrolase and its <i>Escherichia coli</i> homolog. <i>FEBS Journal</i> , 2004, 271, 3215-3226.	0.2	59
33	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	1.0	58
34	Crystal Structure of the Parasite Protease Inhibitor Chagasin in Complex with a Host Target Cysteine Protease. <i>Journal of Molecular Biology</i> , 2007, 371, 137-153.	2.0	57
35	<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
36	High regularity of Z-DNA revealed by ultra high-resolution crystal structure at 0.55Å. <i>Nucleic Acids Research</i> , 2011, 39, 6238-6248.	6.5	56

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37	Hinge-loop mutation can be used to control 3D domain swapping and amyloidogenesis of human cystatin C. <i>Journal of Structural Biology</i> , 2011, 173, 406-413.	1.3	55
38	Insect Juvenile Hormone Binding Protein Shows Ancestral Fold Present in Human Lipid-Binding Proteins. <i>Journal of Molecular Biology</i> , 2008, 377, 870-881.	2.0	53
39	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
40	Circadian oscillator proteins across the kingdoms of life: structural aspects. <i>BMC Biology</i> , 2019, 17, 13.	1.7	50
41	Cytokinin-induced structural adaptability of a <i>Lupinus fluteus</i> PR10 protein. <i>FEBS Journal</i> , 2009, 276, 1596-1609.	2.2	49
42	Crystal structure of Hyp-1, a St. John's wort protein implicated in the biosynthesis of hypericin. <i>Journal of Structural Biology</i> , 2010, 169, 161-171.	1.3	49
43	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	2.2	49
44	Ultrahigh-resolution structure of a BPTI mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 649-663.	2.5	48
45	Crystal Structure of Isoaspartyl Aminopeptidase in Complex with L-Aspartate. <i>Journal of Biological Chemistry</i> , 2005, 280, 28484-28491.	1.6	48
46	Crystal structure of human T cell leukemia virus protease, a novel target for anticancer drug design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18332-18337.	3.3	48
47	The Mechanism of Autocatalytic Activation of Plant-type L-Asparaginases. <i>Journal of Biological Chemistry</i> , 2008, 283, 13388-13397.	1.6	48
48	A close look onto structural models and primary ligands of metallo- β -lactamases. <i>Drug Resistance Updates</i> , 2018, 40, 1-12.	6.5	47
49	Multiple molecules in the crystallographic asymmetric unit. Self-host-guest and doubly interpenetrated hydrogen bond networks in a pair of keto-bisphenols. <i>CrystEngComm</i> , 2003, 5, 447.	1.3	44
50	X-ray, Fourier-transform infrared, ^1H and ^{13}C nuclear magnetic resonance, and PM3 studies of (N^+H^-) and $(\text{O}^-\text{H}^+)\text{H}^+$ intramolecular hydrogen bonds in a complex of 1,8-bis(dimethylamino)naphthalene with maleic acid. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1993, 89, 2085-2094.	1.7	42
51	High-resolution structure of bovine pancreatic trypsin inhibitor with altered binding loop sequence. <i>Journal of Molecular Biology</i> , 2000, 295, 1237-1249.	2.0	40
52	Supramolecular synthons based on N^+H^- and $\text{C}^=\text{H}^+\text{O}^-$ hydrogen bonds. Crystal engineering of a helical structure with 5,5-diethylbarbituric acid. <i>Chemical Communications</i> , 2002, , 1830-1831.	2.2	39
53	Structure of a yellow lupin pathogenesis-related PR-10 protein belonging to a novel subclass. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 99-107.	2.5	39
54	Displacement of the Occluding Loop by the Parasite Protein, Chagasin, Results in Efficient Inhibition of Human Cathepsin B. <i>Journal of Biological Chemistry</i> , 2008, 283, 22815-22825.	1.6	37

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55	Novel DNA-binding element within the C-terminal extension of the nuclear receptor DNA-binding domain. <i>Nucleic Acids Research</i> , 2007, 35, 2705-2718.	6.5	36
56	An Optically Active Nickel(II) Schiff Base Coordination Compound N,N'-(1R,2R)-(-)-1,2-Cyclohexylenebis(salicylideneiminato)nickel(II).. <i>Acta Chemica Scandinavica</i> , 1997, 51, 274-278.	0.7	36
57	Stabilizing Bound O ₂ in Myoglobin by Valine68(E11) to Asparagine Substitution. <i>Biochemistry</i> , 1998, 37, 15896-15907.	1.2	35
58	Crystal Structure of Hyp-1, a <i>Hypericum perforatum</i> PR-10 Protein, in Complex with Melatonin. <i>Frontiers in Plant Science</i> , 2016, 7, 668.	1.7	35
59	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
60	Crystal structure of the parasite inhibitor chagasin in complex with papain allows identification of structural requirements for broad reactivity and specificity determinants for target proteases. <i>FEBS Journal</i> , 2009, 276, 793-806.	2.2	34
61	Impact of synchrotron radiation on macromolecular crystallography: a personal view. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 433-444.	1.0	34
62	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	1.6	34
63	Mechanochemical Encapsulation of Fullerenes in Peptidic Containers Prepared by Dynamic Chiral Self-Sorting and Self-Assembly. <i>Chemistry - A European Journal</i> , 2016, 22, 3148-3155.	1.7	33
64	3D domain swapping, protein oligomerization, and amyloid formation. <i>Acta Biochimica Polonica</i> , 2001, 48, 807-27.	0.3	33
65	<sc>PR</sc>-10 proteins as potential mediators of melatonin-cytokinin cross-talk in plants: crystallographic studies of LI<sc>PR</sc>-10.2B isoform from yellow lupine. <i>FEBS Journal</i> , 2018, 285, 1907-1922.	2.2	32
66	Structure of Î³-conglutin: insight into the quaternary structure of 7S basic globulins from legumes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 224-238.	2.5	31
67	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
68	Structural aspects of L-asparaginases, their friends and relations. <i>Acta Biochimica Polonica</i> , 2006, 53, 627-40.	0.3	31
69	Crystallization and preliminary crystallographic studies of juvenile hormone-binding protein from <i>Galleria mellonella</i> haemolymph. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 519-521.	2.5	30
70	Structure-based analysis of thermodynamic and mechanical properties of cavity-containing proteins. A case study of plant pathogenesis-related proteins of class 10. <i>FEBS Journal</i> , 2014, 281, 416-429.	2.2	30
71	Structural Studies of Glutamate Dehydrogenase (Isoform 1) From <i>Arabidopsis thaliana</i> , an Important Enzyme at the Branch-Point Between Carbon and Nitrogen Metabolism. <i>Frontiers in Plant Science</i> , 2020, 11, 754.	1.7	30
72	Crystal structure and molecular motion in pyridine N-oxide semiperchlorate. <i>Journal of Molecular Structure</i> , 1999, 476, 81-95.	1.8	29

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73	Molecular structure, hydrogen bonding, basicity and spectroscopic properties of N,N-dimethylpiperazine betaines and their hydrohalides. <i>Journal of Molecular Structure</i> , 2002, 614, 23-32.	1.8	29
74	Structure of thiocanate salt of 1,8-bis(dimethylamino)naphthalene (dmanH ⁺ .SCN ⁻) at 188 and 290 K. <i>Acta Crystallographica Section B: Structural Science</i> , 1994, 50, 358-363.	1.8	28
75	Expression of a selenomethionyl derivative and preliminary crystallographic studies of human cystatin C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1939-1942.	2.5	28
76	Bayesian phylogenetic analysis reveals two-domain topology of S-adenosylhomocysteine hydrolase protein sequences. <i>Molecular Phylogenetics and Evolution</i> , 2005, 34, 15-28.	1.2	27
77	Specific binding of gibberellic acid by Cytokinin-Specific Binding Proteins: a new aspect of plant hormone-binding proteins with the PR-10 fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2032-2041.	2.5	27
78	Crystal structure of active site mutant of antileukemic L-asparaginase reveals conserved zinc-binding site. <i>FEBS Journal</i> , 2014, 281, 4097-4111.	2.2	27
79	Structures of two highly homologous bacterial L-asparaginases: a case of enantiomorphic space groups. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 369-377.	2.5	26
80	Checking the conformational stability of cystatin C and its L68Q variant by molecular dynamics studies: Why is the L68Q variant amyloidogenic?. <i>Journal of Structural Biology</i> , 2006, 154, 68-78.	1.3	26
81	Isostructurality in crystalline oxa-androgens: a case of C=O...H...O and C=H...O interaction mimicry and solid solution formation. <i>Chemical Communications</i> , 1998, , 2537-2538.	2.2	25
82	T-to-R switch of muscle fructose-1,6-bisphosphatase involves fundamental changes of secondary and quaternary structure. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 536-550.	1.1	25
83	High-resolution structure of NodZ fucosyltransferase involved in the biosynthesis of the nodulation factor.. <i>Acta Biochimica Polonica</i> , 2007, 54, 537-549.	0.3	25
84	X-ray, phase transition, IR and Raman studies of the solid complex of bis(pyridine betaine)-sulphuric acid. <i>Journal of Molecular Structure</i> , 1997, 406, 127-135.	1.8	24
85	Crystal structure and vibrational spectrum of N-methylpiperidine betaine hexafluorosilicate. <i>Journal of Molecular Structure</i> , 2001, 598, 267-276.	1.8	24
86	Likelihood-based molecular-replacement solution for a highly pathological crystal with tetartohedral twinning and sevenfold translational noncrystallographic symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 471-480.	2.5	24
87	Comparative structural analysis of cytidine, ethenocytidine, and their protonated salts. I. Crystal and molecular structure of ethenocytidine. <i>Nucleic Acids Research</i> , 1981, 9, 5423-5442.	6.5	23
88	Na ⁺ /K ⁺ exchange switches the catalytic apparatus of potassium-dependent plant L-asparaginase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1854-1872.	2.5	23
89	High-resolution structure of a retroviral protease folded as a monomer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 907-914.	2.5	22
90	The volume of cavities in proteins and virus capsids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1275-1286.	1.5	22

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91	Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019, 35, 452-461.	1.8	22
92	Structural and biophysical aspects of <i>L</i> -asparaginases: a growing family with amazing diversity. <i>IUCr</i> , 2021, 8, 514-531.	1.0	22
93	Crystallization and preliminary crystallographic studies of five crystal forms of <i>Escherichia coli</i> L-asparaginase II (Asp90Glu mutant). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 130-132.	2.5	21
94	Structures of an active-site mutant of a plant 1,3- β -glucanase in complex with oligosaccharide products of hydrolysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 52-62.	2.5	21
95	Crystallographic models of SARS-CoV-2 3CL ^{pro} : in-depth assessment of structure quality and validation. <i>IUCr</i> , 2021, 8, 238-256.	1.0	21
96	Crystallization and preliminary crystallographic studies of a new L-asparaginase encoded by the <i>Escherichia coli</i> genome. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1505-1507.	2.5	20
97	Bis(N-methylpiperidine betaine) hydrobromide: crystal structure and hydrogen bonding. <i>Journal of Molecular Structure</i> , 2002, 615, 33-43.	1.8	20
98	Crystal and molecular structure of N-methylpiperidine betaine hydrochloride. <i>Journal of Molecular Structure</i> , 2003, 654, 71-80.	1.8	20
99	Structures of NodZ \pm 1,6-fucosyltransferase in complex with GDP and GDP-fucose. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 160-168.	2.5	20
100	Protonation and geometry of histidine rings. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1444-1454.	2.5	20
101	Interaction of polyamines, their protonated salts and metal complexes with nucleic acid fragments. <i>Pure and Applied Chemistry</i> , 1987, 59, 407-414.	0.9	19
102	Crystal and molecular structure of N-methylpiperidine betaine hydrofluoride. <i>Journal of Molecular Structure</i> , 2004, 706, 49-55.	1.8	19
103	Purification, crystallization and preliminary crystallographic studies of plant <i>S</i> -adenosyl- <i>L</i> -homocysteine hydrolase (<i>Lupinus luteus</i>). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 671-673.	0.7	19
104	High-resolution structures of complexes of plant <i>S</i> -adenosyl- <i>L</i> -homocysteine hydrolase (<i>Lupinus luteus</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 218-231.	2.5	19
105	Ultrahigh-resolution crystal structures of Z-DNA in complex with Mn ²⁺ and Zn ²⁺ ions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1180-1190.	2.5	19
106	Crystallographic and CD probing of ligand-induced conformational changes in a plant PR-10 protein. <i>Journal of Structural Biology</i> , 2016, 193, 55-66.	1.3	19
107	The crystal and molecular structures of dichlorobis(5,7-diphenyl-1,2,4-triazolo[1,5- λ]pyrimidine)zinc(II) (1) and dichlorobis(5,7-diphenyl-1,2,4-triazolo[1,5- λ]pyrimidine)cobalt(II) (2). <i>Inorganica Chimica Acta</i> , 1997, 260, 145-150.	1.2	18
108	Structure, conformation and hydrogen bonding of 4-(N-methylpiperidinium)-butyric acid bromide. <i>Journal of Molecular Structure</i> , 2007, 828, 19-24.	1.8	18

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109	Stress-induced expression and structure of the putative gene hyp-1 for hypericin biosynthesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 114, 207-216.	1.2	18
110	Self-Assembly and Ordering of Peptide-Based Cavitations in Water and DMSO: The Power of Hydrophobic Effects Combined with Neutral Hydrogen Bonds. <i>Chemistry - A European Journal</i> , 2019, 25, 3091-3097.	1.7	18
111	Crystal chemistry of some synthetic 2-oxa-steroids: conformation, packing motifs and isostructurality. <i>Acta Crystallographica Section B: Structural Science</i> , 2000, 56, 512-525.	1.8	17
112	Atomic resolution structure of squash trypsin inhibitor: unexpected metal coordination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1448-1461.	2.5	17
113	Crystal and molecular structure of bis(N-methylpiperidine betaine) hydroiodide. <i>Journal of Molecular Structure</i> , 2004, 691, 217-225.	1.8	17
114	Crystal packing of plant-type asparaginase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 309-320.	2.5	17
115	Comparative structural analysis of cytidine, ethenocytidine and their protonated salts. II. IR spectral studies. <i>Nucleic Acids Research</i> , 1982, 10, 2741-2753.	6.5	16
116	X-ray, FTIR, 1H and 13C NMR, PM3 and AM1 studies of (N ⁺ H ⁻ N) ⁺ and (O ⁺ H ⁻ O) ⁻ hydrogen bonds in a complex of 1,8-diaminonaphthalene with maleic acid: proton cavity and basicity of proton sponges. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1995, 91, 87-92.	1.7	16
117	Binding modes of a new epoxysuccinyl peptide inhibitor of cysteine proteases. Where and how do cysteine proteases express their selectivity?. <i>BBA - Proteins and Proteomics</i> , 1999, 1431, 290-305.	2.1	16
118	Two high-resolution structures of potato endo-1,3-β-glucanase reveal subdomain flexibility with implications for substrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 713-723.	2.5	16
119	The landscape of cytokinin binding by a plant nodulin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2365-2380.	2.5	16
120	Conformation-dependent restraints for polynucleotides: I. Clustering of the geometry of the phosphodiester group. <i>Nucleic Acids Research</i> , 2016, 44, 8479-8489.	6.5	16
121	Conformation-dependent restraints for polynucleotides: the sugar moiety. <i>Nucleic Acids Research</i> , 2020, 48, 962-973.	6.5	16
122	Synthesis and crystal and molecular structure of 1,2-Di(N-piperidyl)ethane-bis-N-oxide tetrahydrate. <i>Journal of Molecular Structure</i> , 1979, 52, 77-94.	1.8	15
123	Comparative Analysis of the Performance of the Computer Programs SCOGS, MINIQUAD, and SUPERQUAD in Studies of Complex-Formation Equilibria. <i>Journal of Chemical Education</i> , 1995, 72, 27.	1.1	15
124	<i>Medicago truncatula</i> histidine-containing phosphotransfer protein. <i>FEBS Journal</i> , 2013, 280, 3709-3720.	2.2	15
125	On the propagation of errors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1865-1866.	2.5	15
126	ANS complex of St John's wort PR-10 protein with 28 copies in the asymmetric unit: a fiendish combination of pseudosymmetry with tetartohedral twinning. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 829-843.	2.5	15

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127	On the evolution of the quality of macromolecular models in the PDB. FEBS Journal, 2020, 287, 2685-2698.	2.2	15
128	Covid-19.bioreproducibility.org: A web resource for <scp>SARS-CoV-2</scp>-related structural models. Protein Science, 2021, 30, 115-124.	3.1	15
129	Complex formation studies on copper(II) and zinc(II) with asparagine and aspartic acid in aqueous solution. Monatshefte für Chemie, 1983, 114, 1185-1188.	0.9	14
130	Hydrogen bonds in 1:1 complex of piperidine-3-carboxylic acid with salicylic acid. Journal of Molecular Structure, 2009, 920, 68-74.	1.8	14
131	Structure of 1H-2-oxo-2,3-dihydroimidazo[1,2-a]pyridinium perchlorate studied by X-ray diffraction, DFT calculations and by FTIR and NMR spectroscopy. Journal of Molecular Structure, 2010, 976, 119-128.	1.8	14
132	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1140-1151.	2.5	14
133	Structural basis of potassium activation in plant asparaginases. FEBS Journal, 2018, 285, 1528-1539.	2.2	14
134	Metal-cation regulation of enzyme dynamics is a key factor influencing the activity of S-adenosyl-l-homocysteine hydrolase from <i>Pseudomonas aeruginosa</i> . Scientific Reports, 2018, 8, 11334.	1.6	14
135	Accurate geometrical restraints for Watson-Crick base pairs. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2019, 75, 235-245.	0.5	14
136	OHO hydrogen bond and electrostatic interactions in a complex of pyridine betaine with phenylacetic acid studied by X-ray diffraction, FTIR spectroscopy and PM3, DFT calculations. Journal of Molecular Structure, 2000, 555, 191-201.	1.8	13
137	Crystal Structures of NodS N-Methyltransferase from <i>Bradyrhizobium japonicum</i> in Ligand-Free Form and as SAH Complex. Journal of Molecular Biology, 2010, 404, 874-889.	2.0	13
138	Crystallographic identification of an unexpected protein complex in silkworm haemolymph. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2353-2364.	2.5	13
139	High-resolution crystal structure of Z-DNA in complex with Cr ³⁺ cations. Journal of Biological Inorganic Chemistry, 2015, 20, 595-602.	1.1	13
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