

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	Inhibitors of HIV Protease and Their Role as Drugs Against AIDS. , 2023, , 960-969.		1
2	Group depositions to the Protein Data Bank need adequate presentation and different archiving protocol. Protein Science, 2022, 31, 784-786.	3.1	6
3	The Euler characteristic as a basis for teaching topology concepts to crystallographers. Journal of Applied Crystallography, 2022, 55, 154-167.	1.9	0
4	New ligand-binding sites identified in the crystal structures of \hat{I}^2 -lactoglobulin complexes with desipramine. IUCr, 2022, 9, 386-398.	1.0	3
5	Identification of a Steric Zipper Motif in the Amyloidogenic Core of Human Cystatin C and Its Use for the Design of Self-Assembling Peptides. International Journal of Molecular Sciences, 2022, 23, 5800.	1.8	1
6	New aspects of DNA recognition by group II WRKY transcription factor revealed by structural and functional study of AtWRKY18 DNA binding domain. International Journal of Biological Macromolecules, 2022, 213, 589-601.	3.6	9
7	Biochemical and structural insights into an unusual, alkali-metal-independent <i>S</i> -adenosyl-L-homocysteine hydrolase from <i>Synechocystis</i> sp. PCC 6803. Acta Crystallographica Section D: Structural Biology, 2022, 78, 865-882.	1.1	1
8	Structural and biophysical studies of new L-asparaginase variants: lessons from random mutagenesis of the prototypic <i>Escherichia coli</i> Ntn-amidohydrolase. Acta Crystallographica Section D: Structural Biology, 2022, 78, 911-926.	1.1	3
9	Synthesis, structure and evaluation of anticancer activity of 4-amino-1,3-thiazolinone/pyrazoline hybrids. Journal of Molecular Structure, 2021, 1224, 129059.	1.8	11
10	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. Protein Science, 2021, 30, 115-124.	3.1	15
11	Strong interactions between Salp15 homologues from the tick <i>I. ricinus</i> and distinct types of the outer surface OspC protein from <i>Borrelia</i> . Ticks and Tick-borne Diseases, 2021, 12, 101630.	1.1	5
12	In-vitro anti-fungal assay and association analysis reveal a role for the <i>Pinus monticola</i> PR10 gene (PmPR10-3.1) in quantitative disease resistance to white pine blister rust. Genome, 2021, 64, 693-704.	0.9	7
13	Structural studies of human muscle FBPase. Acta Biochimica Polonica, 2021, 68, 5-14.	0.3	2
14	Serendipitous crystallization of <i>E. coli</i> HPII catalase, a sequel to "the tale usually not told". Acta Biochimica Polonica, 2021, 68, 29-31.	0.3	1
15	Crystallographic models of SARS-CoV-2 3CL ^{pro} : in-depth assessment of structure quality and validation. IUCr, 2021, 8, 238-256.	1.0	21
16	Arithmetic proof of the multiplicity-weighted Euler characteristic for symmetrically arranged space-filling polyhedra. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, 126-129.	0.0	2
17	Rapid response to emerging biomedical challenges and threats. IUCr, 2021, 8, 395-407.	1.0	5
18	Sensitized photo-oxidation of plant cytokinin-specific binding protein - Does the environment of the thioether group influence the oxidation reaction? From primary intermediates to stable products. Free Radical Biology and Medicine, 2021, 165, 411-420.	1.3	2

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19	Crystal structures of inhibitor complexes of M ^o PMV protease with visible flap loops. <i>Protein Science</i> , 2021, 30, 1258-1263.	3.1	2
20	Crystal structure of Z-DNA in complex with the polyamine putrescine and potassium cations at ultra-high resolution. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2021, 77, 331-338.	0.5	3
21	Structural and biophysical aspects of L-asparaginases: a growing family with amazing diversity. <i>IUCr</i> , 2021, 8, 514-531.	1.0	22
22	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.	0.0	2
23	Dr. Alexander Wlodawer – celebrating five decades of service to the structural biology community. <i>FEBS Journal</i> , 2021, 288, 4160-4164.	2.2	0
24	3D Domain Swapping Dimerization of the Receiver Domain of Cytokinin Receptor CRE1 From <i>Arabidopsis thaliana</i> and <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 756341.	1.7	3
25	Celebrating the 75th birthday of Professor Wlodek Minor, one of the most accomplished Polish-American structural biologists. <i>Acta Biochimica Polonica</i> , 2021, 68, 1-4.	0.3	0
26	Crystal structures of the elusive <i>Rhizobium etli</i> l-asparaginase reveal a peculiar active site. <i>Nature Communications</i> , 2021, 12, 6717.	5.8	5
27	Conformation-dependent restraints for polynucleotides: the sugar moiety. <i>Nucleic Acids Research</i> , 2020, 48, 962-973.	6.5	16
28	Properties of Cavities in Biological Structures – A Survey of the Protein Data Bank. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 591381.	1.6	11
29	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
30	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
31	Flexible loops of New Delhi metallo-β-lactamase modulate its activity towards different substrates. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 104-115.	3.6	11
32	On the evolution of the quality of macromolecular models in the PDB. <i>FEBS Journal</i> , 2020, 287, 2685-2698.	2.2	15
33	Multiplicity-weighted Euler's formula for symmetrically arranged space-filling polyhedra. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2020, 76, 580-583.	0.0	3
34	3D domain swapping in the TIM barrel of the β subunit of <i>Streptococcus pneumoniae</i> tryptophan synthase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 166-175.	1.1	4
35	A new modulated crystal structure of the ANS complex of the St John's wort Hyp-1 protein with 36 protein molecules in the asymmetric unit of the supercell. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 653-667.	1.1	2
36	C ₆₀ in a peptidic cage: a case of symmetry mismatch studied by crystallography and solid-state NMR. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2020, 76, 815-824.	0.5	1

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37	Self-Assembly and Ordering of Peptide-Based Cavities 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
38	Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019, 35, 452-461.	1.8	22
39	Borrelia outer surface protein C is capable of human fibrinogen binding. <i>FEBS Journal</i> , 2019, 286, 2415-2428.	2.2	13
40	Circadian oscillator proteins across the kingdoms of life: structural aspects. <i>BMC Biology</i> , 2019, 17, 13.	1.7	50
41	Comparison of a retroviral protease in monomeric and dimeric states. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 904-917.	1.1	2
42	Crystal structures of plant inorganic pyrophosphatase, an enzyme with a moonlighting autoproteolytic activity. <i>Biochemical Journal</i> , 2019, 476, 2297-2319.	1.7	10
43	Accurate geometrical restraints for Watson-Crick base pairs. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2019, 75, 235-245.	0.5	14
44	Structural basis of potassium activation in plant asparaginases. <i>FEBS Journal</i> , 2018, 285, 1528-1539.	2.2	14
45	10 proteins as potential mediators of melatonin-cytokinin crosstalk in plants: crystallographic studies of L10.2B isoform from yellow lupine. <i>FEBS Journal</i> , 2018, 285, 1907-1922.	2.2	32
46	On the helical arrangements of protein molecules. <i>Protein Science</i> , 2018, 27, 643-652.	3.1	4
47	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	2.2	49
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	Metal-cation regulation of enzyme dynamics is a key factor influencing the activity of S-adenosyl-L-homocysteine hydrolase from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2018, 8, 11334.	1.6	14
50	S-Adenosyl-L-Homocysteine Hydrolase Inhibition by a Synthetic Nicotinamide Cofactor Biomimetic. <i>Frontiers in Microbiology</i> , 2018, 9, 505.	1.5	7
51	Crystal Structure of S-adenosyl-L-homocysteine Hydrolase from <i>Cytophaga hutchinsonii</i> , a Case of Combination of Crystallographic and Non-crystallographic Symmetry. <i>Croatica Chemica Acta</i> , 2018, 91, .	0.1	4
52	S-adenosyl-L-homocysteine hydrolase from a hyperthermophile (<i>Thermotoga maritima</i>) is expressed in <i>Escherichia coli</i> in inactive form " Biochemical and structural studies. <i>International Journal of Biological Macromolecules</i> , 2017, 104, 584-596.	3.6	8
53	Crystallographic and SAXS studies of S-adenosyl-L-homocysteine hydrolase from <i>Bradyrhizobium elkanii</i> . <i>IUCr</i> , 2017, 4, 271-282.	1.0	11
54	Structure Refinement at Atomic Resolution. <i>Methods in Molecular Biology</i> , 2017, 1607, 549-563.	0.4	3

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55	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
56	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
57	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
58	The volume of cavities in proteins and virus capsids. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1275-1286.	1.5	22
59	Prior knowledge or freedom of interpretation? A critical look at a recently published classification of "novel" Zn binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 770-776.	1.5	12
60	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
61	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
62	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
63	Ultrahigh-resolution centrosymmetric crystal structure of Z-DNA reveals the massive presence of alternate conformations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1203-1211.	1.1	7
64	Atomic resolution structure of a chimeric DNA-RNA Z-type duplex in complex with Ba ²⁺ ions: a case of complicated multi-domain twinning. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 211-223.	1.1	8
65	Safeguarding Structural Data Repositories against Bad Apples. <i>Structure</i> , 2016, 24, 216-220.	1.6	34
66	The young person's guide to the PDB. <i>Postepy Biochemii</i> , 2016, 62, 242-249.	0.5	2
67	Crystal pathologies in macromolecular crystallography. <i>Postepy Biochemii</i> , 2016, 62, 401-407.	0.5	5
68	The young person's guide to the PDB. <i>Postepy Biochemii</i> , 2016, 62, 242-249.	0.5	3
69	Crystal pathologies in macromolecular crystallography. <i>Postepy Biochemii</i> , 2016, 62, 401-407.	0.5	3
70	Elucidation of the structure of retroviral proteases: a reminiscence. <i>FEBS Journal</i> , 2015, 282, 4059-4066.	2.2	8
71	An enzyme captured in two conformational states: crystal structure of <i>S</i> -adenosyl-L-homocysteine hydrolase from <i>Bradyrhizobium elkanii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2422-2432.	2.5	9
72	High-resolution crystal structure of Z-DNA in complex with Cr ³⁺ cations. <i>Journal of Biological Inorganic Chemistry</i> , 2015, 20, 595-602.	1.1	13

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73	Protonation and geometry of histidine rings. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1444-1454.	2.5	20
74	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
75	Structure of \hat{I}^3 -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
76	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
77	Atomic Resolution Structure of a Protein Prepared by Non-Enzymatic His-Tag Removal. Crystallographic and NMR Study of GmSPI-2 Inhibitor. <i>PLoS ONE</i> , 2014, 9, e106936.	1.1	8
78	Crystal Structure of Bombyx mori Lipoprotein 6: Comparative Structural Analysis of the 30-kDa Lipoprotein Family. <i>PLoS ONE</i> , 2014, 9, e108761.	1.1	11
79	Doing the right things. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1-1.	2.5	2
80	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
81	<i>Introduction:</i> Celebrating the International Year of Crystallography. <i>FEBS Journal</i> , 2014, 281, 3983-3984.	2.2	2
82	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
83	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
84	Insights into the relationship between the haem-binding pocket and the redox potential of <i>Cy6</i> cytochromes: four atomic resolution structures of <i>Cy6</i> and <i>Cy6</i> -like proteins from <i>Synechococcus</i> sp. PCC 7002. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2823-2832.	2.5	5
85	<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
86	A brief history of macromolecular crystallography, illustrated by a family tree and its <i>Nobel</i> fruits. <i>FEBS Journal</i> , 2014, 281, 3985-4009.	2.2	83
87	Missed opportunities in crystallography. <i>FEBS Journal</i> , 2014, 281, 4010-4020.	2.2	1
88	Experiences with applications of macromolecular tools in supramolecular crystallography. <i>CrystEngComm</i> , 2014, 16, 3773-3780.	1.3	4
89	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
90	Cytochrome c6B of <i>Synechococcus</i> sp. WH 8102—Crystal structure and basic properties of novel c6-like family representative. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 1131-1135.	1.0	5

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91	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
92	Structure of a proteolytically resistant analogue of (<i>N</i>Lys) ⁵ SFTI-1 in complex with trypsin: evidence for the direct participation of the Ser214 carbonyl group in serine protease-mediated proteolysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 668-675.	2.5	10
93	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. <i>IUCr</i> , 2014, 1, 179-193.	1.0	58
94	<i>M</i>edicagoÂtruncatula</i> histidineâ€containing phosphotransfer protein. <i>FEBS Journal</i> , 2013, 280, 3709-3720.	2.2	15
95	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
96	Structures of an active-site mutant of a plant 1,3-Î²-glucanase in complex with oligosaccharide products of hydrolysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 52-62.	2.5	21
97	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
98	3D Domain Swapping. , 2013, , 1-7.		2
99	The landscape of cytokinin binding by a plant nodulin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2365-2380.	2.5	16
100	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
101	On the propagation of errors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1865-1866.	2.5	15
102	Crystallographic identification of an unexpected protein complex in silkworm haemolymph. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2353-2364.	2.5	13
103	Structural and functional aspects of <sc>PR</sc>â€10 proteins. <i>FEBS Journal</i> , 2013, 280, 1169-1199.	2.2	191
104	Isoaspartyl Aminopeptidase (Threonine Type). , 2013, , 3705-3712.		0
105	Two Crystal Structures of Bombyx mori Lipoprotein 3 - Structural Characterization of a New 30-kDa Lipoprotein Family Member. <i>PLoS ONE</i> , 2013, 8, e61303.	1.1	6
106	High Resolution Macromolecular Crystallography. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 259-275.	0.5	4
107	Identification of amino acid sequences via X-ray crystallography: a mini review of case studies. <i>Biotechnologia</i> , 2013, 1, 9-14.	0.3	1
108	Hyp-1 protein from St Johnâ€™s wort as a PR-10 protein. <i>Biotechnologia</i> , 2013, 1, 47-50.	0.3	5

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109	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
110	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1140-1151.	2.5	14
111	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
112	Structure of an RNA/DNA dodecamer corresponding to the HIV-1 polypurine tract at 1.6 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 169-175.	2.5	2
113	High-resolution structures of complexes of plant <i>S</i> -adenosyl-L-homocysteine hydrolase (<i>Lupinus luteus</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 218-231.	2.5	19
114	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
115	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
116	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
117	A New Piece in the 3D Jigsaw of Malaria Parasite. <i>Structure</i> , 2011, 19, 901-902.	1.6	0
118	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
119	Structure of E69Q mutant of human muscle fructose-1,6-bisphosphatase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 1028-1034.	2.5	11
120	Isolation, purification, crystallization and preliminary X-ray studies of two 30 kDa proteins from silkworm haemolymph. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 372-376.	0.7	10
121	Structure of the RuBisCO chaperone RbcX from the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 851-857.	0.7	9
122	Diastereomeric complex of (R/S)-piperidine-3-carboxylic acid with (2R,3R)-tartaric acid: Structural, spectroscopic and computational studies. <i>Journal of Molecular Structure</i> , 2011, 999, 98-105.	1.8	6
123	High regularity of Z-DNA revealed by ultra high-resolution crystal structure at 0.55 Å. <i>Nucleic Acids Research</i> , 2011, 39, 6238-6248.	6.5	56
124	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. <i>Journal of Molecular Structure</i> , 2010, 976, 119-128.	1.8	14
125	How to read (and understand) Volume A of <i>International Tables for Crystallography</i> : an introduction for nonspecialists. <i>Journal of Applied Crystallography</i> , 2010, 43, 1150-1171.	1.9	12
126	Is too 'creative' language acceptable in crystallography?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1041-1042.	2.5	2

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127	Impact of synchrotron radiation on macromolecular crystallography: a personal view. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 433-444.	1.0	34
128	Crystal structure of human cystatinâ€fC stabilized against amyloid formation. <i>FEBS Journal</i> , 2010, 277, 1726-1737.	2.2	73
129	Crystal structure of Hyp-1, a St. Johnâ€™s wort protein implicated in the biosynthesis of hypericin. <i>Journal of Structural Biology</i> , 2010, 169, 161-171.	1.3	49
130	Crystal Structures of NodS N-Methyltransferase from <i>Bradyrhizobium japonicum</i> in Ligand-Free Form and as SAH Complex. <i>Journal of Molecular Biology</i> , 2010, 404, 874-889.	2.0	13
131	Personal remarks on the future of protein crystallography and structural biology. <i>Acta Biochimica Polonica</i> , 2010, 57, 261-4.	0.3	0
132	Structural, spectroscopic, and theoretical studies of a very short OHO hydrogen bond in bis(4â€methylpiperidinium)â€butyrate) hydrobromide. <i>Journal of Physical Organic Chemistry</i> , 2009, 22, 356-361.	0.9	9
133	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
134	Cytokininâ€induced structural adaptability of a <i>Lupinusâ€fluteus</i> PRâ€10 protein. <i>FEBS Journal</i> , 2009, 276, 1596-1609.	2.2	49
135	Piecing together the structure of retroviral integrase, an important target in AIDS therapy. <i>FEBS Journal</i> , 2009, 276, 2926-2946.	2.2	80
136	Atomicâ€resolution structure of reduced cyanobacterial cytochrome <i>c</i> ₆ with an unusual sequence insertion. <i>FEBS Journal</i> , 2009, 276, 4426-4436.	2.2	12
137	Hydrogen bonds in 1:1 complex of piperidine-3-carboxylic acid with salicylic acid. <i>Journal of Molecular Structure</i> , 2009, 920, 68-74.	1.8	14
138	Conformational richness and multiple <i>Z</i> â€ in salt co-crystal of <i>N</i> -methylpiperidine betaine with <i>N</i> -methylpiperidine betaine hexafluorosilicate. <i>Acta Crystallographica Section B: Structural Science</i> , 2008, 64, 483-490.	1.8	11
139	Crystal packing of plant-type <i>L</i> -asparaginase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 309-320.	2.5	17
140	MAD phasing using the (Ta6Br12) ₂ -cluster: a retrospective study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 595-606.	2.5	11
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