List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	β-Methyltryptamine Provoking the Crucial Role of Strictosidine Synthase Tyr151-OH for Its Stereoselective Pictetâ^'Spengler Reactions to Tryptoline-type Alkaloids. ACS Chemical Biology, 2022, 17, 187-197.	3.4	3
2	Crystal structure of the putative cell-wall lipoglycan biosynthesis protein LmcA from <i>Mycobacterium smegmatis</i> . Acta Crystallographica Section D: Structural Biology, 2022, 78, 494-508.	2.3	4
3	Differential lysineâ€mediated allosteric regulation of plant dihydrodipicolinate synthase isoforms. FEBS Journal, 2021, 288, 4973-4986.	4.7	9
4	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. Nature Communications, 2021, 12, 1988.	12.8	16
5	<i>Helicobacter pylori</i> Xanthine–Guanine–Hypoxanthine Phosphoribosyltransferase—A Putative Target for Drug Discovery against Gastrointestinal Tract Infections. Journal of Medicinal Chemistry, 2021, 64, 5710-5729.	6.4	4
6	Towards novel herbicide modes of action by inhibiting lysine biosynthesis in plants. ELife, 2021, 10, .	6.0	15
7	<i>Salmonella enterica</i> BcfH Is a Trimeric Thioredoxin-Like Bifunctional Enzyme with Both Thiol Oxidase and Disulfide Isomerase Activities. Antioxidants and Redox Signaling, 2021, 35, 21-39.	5.4	7
8	Graphene and Graphene Oxide as a Support for Biomolecules in the Development of Biosensors. Nanotechnology, Science and Applications, 2021, Volume 14, 197-220.	4.6	54
9	Identification of two dihydrodipicolinate synthase isoforms from <i>Pseudomonas aeruginosa</i> that differ in allosteric regulation. FEBS Journal, 2020, 287, 386-400.	4.7	15
10	Crystal structure and site-directed mutagenesis of circular bacteriocin plantacyclin B21AG reveals cationic and aromatic residues important for antimicrobial activity. Scientific Reports, 2020, 10, 17398.	3.3	10
11	The basis for non-canonical ROK family function in the N-acetylmannosamine kinase from the pathogen Staphylococcus aureus. Journal of Biological Chemistry, 2020, 295, 3301-3315.	3.4	13
12	Misâ€annotations of a promising antibiotic target in highâ€priority gramâ€negative pathogens. FEBS Letters, 2020, 594, 1453-1463.	2.8	6
13	Structural basis for differentiation between two classes of thiolase: Degradative vs biosynthetic thiolase. Journal of Structural Biology: X, 2020, 4, 100018.	1.3	8
14	Crystal structure of posnjakite formed in the first crystal water-cooling line of the ANSTO Melbourne Australian Synchrotron MX1 Double Crystal Monochromator. Acta Crystallographica Section E: Crystallographic Communications, 2020, 76, 1136-1138.	0.5	0
15	Stereocomplementary Chemoenzymatic Pictet–Spengler Reactions for Formation of Rare Azepino-indole Frameworks: Discovery of Antimalarial Compounds. ACS Catalysis, 2019, 9, 7443-7448.	11.2	31
16	Unique structural features of a bacterial autotransporter adhesin suggest mechanisms for interaction with host macromolecules. Nature Communications, 2019, 10, 1967.	12.8	22
17	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. MBio, 2019, 10, .	4.1	10
18	Lanthanoid Heteroleptic Complexes with Cucurbit[5]uril and Dicarboxylate Ligands: From Discrete Structures to One-Dimensional and Two-Dimensional Polymers. Inorganic Chemistry, 2019, 58, 506-515.	4.0	9

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19	Combining random microseed matrix screening and the magic triangle for the efficient structure solution of a potential lysin from bacteriophage P68. Acta Crystallographica Section D: Structural Biology, 2019, 75, 670-681.	2.3	3
20	MX2: a high-flux undulator microfocus beamline serving both the chemical and macromolecular crystallography communities at the Australian Synchrotron. Journal of Synchrotron Radiation, 2018, 25, 885-891.	2.4	346
21	Crystal structure of TcpK in complex with oriT DNA of the antibiotic resistance plasmid pCW3. Nature Communications, 2018, 9, 3732.	12.8	18
22	Design of Protein-Based Biosensors for Selective Detection of Benzene Groups of Pollutants. ACS Sensors, 2018, 3, 1632-1638.	7.8	27
23	Molecular evolution of an oligomeric biocatalyst functioning in lysine biosynthesis. Biophysical Reviews, 2018, 10, 153-162.	3.2	16
24	Beetle luciferases with naturally red- and blue-shifted emission. Life Science Alliance, 2018, 1, e201800072.	2.8	23
25	Structure Guided Design of Protein Biosensors for Phenolic Pollutants. ACS Sensors, 2017, 2, 411-418.	7.8	25
26	Structure of SgK223 pseudokinase reveals novel mechanisms of homotypic and heterotypic association. Nature Communications, 2017, 8, 1157.	12.8	40
27	Online automated structure solution from multiple data sets. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C787-C787.	0.1	1
28	Functional insights into the mode of DNA and ligand binding of the TetR family regulator TylP from Streptomyces fradiae. Journal of Biological Chemistry, 2017, 292, 15301-15311.	3.4	12
29	Structure-guided design of aromatic biosensors for water quality monitoring. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C97-C97.	0.1	0
30	Crystallographic analysis of β-ketoadipyl-CoA thiolase from <i>Psedomonas putida</i> . Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C250-C250.	0.1	0
31	<i>Campylobacter jejuni</i> adenosine triphosphate phosphoribosyltransferase is an active hexamer that is allosterically controlled by the twisting of a regulatory tail. Protein Science, 2016, 25, 1492-1506.	7.6	15
32	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. Angewandte Chemie, 2016, 128, 8062-8065.	2.0	7
33	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. Angewandte Chemie - International Edition, 2016, 55, 7930-7933.	13.8	45
34	Structural Basis of Selective Aromatic Pollutant Sensing by the Effector Binding Domain of MopR, an NtrC Family Transcriptional Regulator. ACS Chemical Biology, 2016, 11, 2357-2365.	3.4	35
35	Structure and Function of Cyanobacterial DHDPS and DHDPR. Scientific Reports, 2016, 6, 37111.	3.3	23
36	Structural Determinants Defining the Allosteric Inhibition of an Essential Antibiotic Target. Structure, 2016, 24, 1282-1291.	3.3	34

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37	A critical examination of the recently reported crystal structures of the human SMN protein. Human Molecular Genetics, 2016, 25, ddw298.	2.9	13
38	Interdomain Conformational Changes Provide Allosteric Regulation en Route to Chorismate. Journal of Biological Chemistry, 2016, 291, 21836-21847.	3.4	22
39	Titelbild: Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily (Angew. Chem. 28/2016). Angewandte Chemie, 2016, 128, 7995-7995.	2.0	Ο
40	A crystallographic study of human NONO (p54 <sup>nrb</sup> ): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. Acta Crystallographica Section D: Structural Biology, 2016, 72, 761-769.	2.3	11
41	Combining cross-crystal averaging and MRSAD to phase a 4354-amino-acid structure. Acta Crystallographica Section D: Structural Biology, 2016, 72, 182-191.	2.3	1
42	Structural basis of selective aromatic pollutant sensing by MopR, an NtrC family transcriptional regulator. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s251-s252.	0.1	0
43	Automated structure solution from multiple data sets. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s18-s18.	0.1	Ο
44	Quaternary Structure Analyses of an Essential Oligomeric Enzyme. Methods in Enzymology, 2015, 562, 205-223.	1.0	24
45	Functional Coupling of Duplex Translocation to DNA Cleavage in a Type I Restriction Enzyme. PLoS ONE, 2015, 10, e0128700.	2.5	7
46	Stonefish toxin defines an ancient branch of the perforin-like superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15360-15365.	7.1	69
47	Ligand structures of synthetic deoxa-pyranosylamines with raucaffricine and strictosidine glucosidases provide structural insights into their binding and inhibitory behaviours. Journal of Enzyme Inhibition and Medicinal Chemistry, 2015, 30, 472-478.	5.2	1
48	A step towards long-wavelength protein crystallography: subjecting protein crystals to a vacuum. Journal of Applied Crystallography, 2015, 48, 913-916.	4.5	3
49	MX1: a bending-magnet crystallography beamline serving both chemical and macromolecular crystallography communities at the Australian Synchrotron. Journal of Synchrotron Radiation, 2015, 22, 187-190.	2.4	336
50	Cyclic Peptides Incorporating Phosphotyrosine Mimetics as Potent and Specific Inhibitors of the Grb7 Breast Cancer Target. Journal of Medicinal Chemistry, 2015, 58, 7707-7718.	6.4	19
51	The Crystal Structure of a Homodimeric <i>Pseudomonas</i> Glyoxalaseâ€I Enzyme Reveals Asymmetric Metallation Commensurate with Halfâ€of‣ites Activity. Chemistry - A European Journal, 2015, 21, 541-544.	3.3	12
52	Postâ€ŧranslational modification and extended glycosylation pattern of a plant latex peroxidase of native source characterized by <scp>X</scp> â€ray crystallography. FEBS Journal, 2014, 281, 4319-4333.	4.7	9
53	Crystal structure of Clostridium acetobutylicum aspartate kinase (CaAk): An important allosteric enzyme for amino acids production. Biotechnology Reports (Amsterdam, Netherlands), 2014, 3, 73-85.	4.4	12
54	The Three-dimensional Structure of the Extracellular Adhesion Domain of the Sialic Acid-binding Adhesin SabA from Helicobacter pylori. Journal of Biological Chemistry, 2014, 289, 6332-6340.	3.4	54

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55	WXG100 Protein Superfamily Consists of Three Subfamilies and Exhibits an α-Helical C-Terminal Conserved Residue Pattern. PLoS ONE, 2014, 9, e89313.	2.5	92
56	The structure of an ABC toxin particle determined by X-ray crystallography and single particle EM Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1825-C1825.	0.1	0
57	Chemical Crystallography at the Australian Synchrotron MX Beamlines. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1751-C1751.	0.1	0
58	Alternative phasing method in macromolecular crystallography. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C342-C342.	0.1	0
59	The BC component of ABC toxins is an RHS-repeat-containing protein encapsulation device. Nature, 2013, 501, 547-550.	27.8	144
60	In-house UV radiation-damage-induced phasing of selenomethionine-labeled protein structures. Journal of Structural Biology, 2013, 181, 89-94.	2.8	1
61	High speed X-ray analysis of plant enzymes at room temperature. Phytochemistry, 2013, 91, 88-92.	2.9	2
62	Putative dioxygen-binding sites and recognition of tigecycline and minocycline in the tetracycline-degrading monooxygenase TetX. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1758-1767.	2.5	28
63	Cyanuric acid hydrolase: evolutionary innovation by structural concatenation. Molecular Microbiology, 2013, 88, 1149-1163.	2.5	31
64	Importance of Hydrophobic Cavities in Allosteric Regulation of Formylglycinamide Synthetase: Insight from Xenon Trapping and Statistical Coupling Analysis. PLoS ONE, 2013, 8, e77781.	2.5	20
65	Phasing selenomethionine proteins using UV-induced radiation damage. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s87-s87.	0.3	1
66	Cloning to crystallization of dihydrodipicolinate synthase from the intracellular pathogenLegionella pneumophila. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1177-1181.	0.7	3
67	Insights into ubiquitin-conjugating enzyme/ co-activator interactions from the structure of the Pex4p:Pex22p complex. EMBO Journal, 2012, 31, 391-402.	7.8	52
68	Crystal Structure of Perakine Reductase, Founding Member of a Novel Aldo-Keto Reductase (AKR) Subfamily That Undergoes Unique Conformational Changes during NADPH Binding. Journal of Biological Chemistry, 2012, 287, 11213-11221.	3.4	18
69	Nonprocessive [2Â+Â2]e <sup>-</sup> off-loading reductase domains from mycobacterial nonribosomal peptide synthetases. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5681-5686.	7.1	73
70	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
71	Purification, crystallization and preliminary crystallographic analysis of banyan peroxidase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 931-934.	0.7	1
72	Structural insight in histoâ€blood group binding by the F18 fimbrial adhesin FedF. Molecular Microbiology, 2012, 86, 82-95.	2.5	46

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73	Structural basis for modification of flavonol and naphthol glucoconjugates by Nicotiana tabacum malonyltransferase (NtMaT1). Planta, 2012, 236, 781-793.	3.2	23
74	Crystal structure of NAD+-dependent Peptoniphilus asaccharolyticus glutamate dehydrogenase reveals determinants of cofactor specificity. Journal of Structural Biology, 2012, 177, 543-552.	2.8	24
75	The sensor region of the ubiquitous cytosolic sensor kinase, PdtaS, contains PAS and GAF domain sensing modules. Journal of Structural Biology, 2012, 177, 498-505.	2.8	18
76	The crystal structure of the CRISPR-associated protein Csn2 from Streptococcus agalactiae. Journal of Structural Biology, 2012, 178, 350-362.	2.8	24
77	Scaffold Tailoring by a Newly Detected Pictet–Spenglerase Activity of Strictosidine Synthase: From the Common Tryptoline Skeleton to the Rare Piperazino-indole Framework. Journal of the American Chemical Society, 2012, 134, 1498-1500.	13.7	57
78	Structures of Alkaloid Biosynthetic Glucosidases Decode Substrate Specificity. ACS Chemical Biology, 2012, 7, 226-234.	3.4	23
79	The impact of structural biology on alkaloid biosynthesis research. Natural Product Reports, 2012, 29, 1176.	10.3	21
80	Current methods in structural proteomics and its applications in biological sciences. 3 Biotech, 2012, 2, 89-113.	2.2	23
81	Formylglycinamide ribonucleotide amidotransferase from <i>Salmonella typhimurium</i> : role of ATP complexation and the glutaminase domain in catalytic coupling. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 627-636.	2.5	7
82	Structural Insights into the Mechanism of Protein O-Fucosylation. PLoS ONE, 2011, 6, e25365.	2.5	85
83	S-SAD phasing of proteinO-fucosyltransferase-1 at a resolution of 2.6â€Ã in the monoclinic space groupC2. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C65-C65.	0.3	0
84	Structural Characterization of the Multidomain Regulatory Protein Rv1364c from Mycobacterium tuberculosis. Structure, 2011, 19, 56-69.	3.3	19
85	Single isomorphous replacement phasing of selenomethionine-containing proteins using UV-induced radiation damage. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 32-44.	2.5	10
86	On the routine use of soft X-rays in macromolecular crystallography. Part V. Molecular replacement and anomalous scattering. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 729-738.	2.5	4
87	Additional phase information from UV damage of selenomethionine labelled proteins. Journal of Synchrotron Radiation, 2011, 18, 374-380.	2.4	11
88	Crystallization and preliminary X-ray crystallographic studies of an oligomeric species of a refolded C39 peptidase-like domain of the <i>Escherichia coli</i> ABC transporter haemolysin B. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 630-633.	0.7	3
89	Structural Basis for the Oxidation of Protein-bound Sulfur by the Sulfur Cycle Molybdohemo-Enzyme Sulfane Dehydrogenase SoxCD. Journal of Biological Chemistry, 2011, 286, 8349-8360.	3.4	39
90	Phasing selenomethionine proteins using UV induced radiation damage. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C657-C657.	0.3	0

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91	Update on the tutorial for learning and teaching macromolecular crystallography. Journal of Applied Crystallography, 2010, 43, 1230-1237.	4.5	6
92	Expression, purification and X-ray analysis of 1,3-propanediol dehydrogenase (Aq_1145) fromAquifex aeolicusVF5. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 184-186.	0.7	2
93	Update on the tutorial for learning and teaching macromolecular crystallography. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s112-s112.	0.3	0
94	Structural analysis reveals DNA binding properties of Rv2827c, a hypothetical protein from MycobacteriumÂtuberculosis. Journal of Structural and Functional Genomics, 2009, 10, 137-150.	1.2	13
95	The F4 fimbrial chaperone FaeE is stable as a monomer that does not require self-capping of its pilin-interactive surfaces. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 411-420.	2.5	5
96	Structure of the C-terminal domain of nsp4 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 839-846.	2.5	23
97	On the combination of molecular replacement and single-wavelength anomalous diffraction phasing for automated structure determination. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1089-1097.	2.5	158
98	Structure of the motor subunit of type I restriction-modification complex EcoR124I. Nature Structural and Molecular Biology, 2009, 16, 94-95.	8.2	38
99	Structural Basis and Enzymatic Mechanism of the Biosynthesis of C <sub>9</sub> ―from C <sub>10</sub> â€Monoterpenoid Indole Alkaloids. Angewandte Chemie - International Edition, 2009, 48, 5211-5213.	13.8	33
100	The impact of Structural Proteomics on Biotechnology. Biotechnology and Genetic Engineering Reviews, 2009, 26, 353-370.	6.2	4
101	Structure of the C-terminal domain of NSP4 from feline infection peritonitis virus. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s167-s167.	0.3	1
102	Auto-Rickshaw: a tool for online validation of X-ray diffraction experiment. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s115-s116.	0.3	1
103	Purification, crystallization and preliminary X-ray diffraction analysis of aspartate semialdehyde dehydrogenase (Rv3708c) from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 167-170.	0.7	12
104	High crystallizability under air-exclusion conditions of the full-length LysR-type transcriptional regulator TsaR fromComamonas testosteroniT-2 and data-set analysis for a MIRAS structure-solution approach. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 764-769.	0.7	1
105	Purification, crystallization and X-ray diffraction analysis of pavineN-methyltransferase fromThalictrum flavum. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1066-1069.	0.7	2
106	A tutorial for learning and teaching macromolecular crystallography. Journal of Applied Crystallography, 2008, 41, 1161-1172.	4.5	15
107	Automated technologies and novel techniques to accelerate protein crystallography for structural genomics. Proteomics, 2008, 8, 612-625.	2.2	70
108	3D-Structure and function of strictosidine synthase – the key enzyme of monoterpenoid indole alkaloid biosynthesis. Plant Physiology and Biochemistry, 2008, 46, 340-355.	5.8	72

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109	Nonspecific base recognition mediated by water bridges and hydrophobic stacking in ribonuclease I from <i>Escherichia coli</i> . Protein Science, 2008, 17, 681-690.	7.6	10
110	Structural Basis for Parasite-Specific Functions of the Divergent Profilin of Plasmodium falciparum. Structure, 2008, 16, 1638-1648.	3.3	60
111	Strictosidine Synthase:  Mechanism of a Pictetâ^'Spengler Catalyzing Enzyme. Journal of the American Chemical Society, 2008, 130, 710-723.	13.7	190
112	C4-Dicarboxylates Sensing Mechanism Revealed by the Crystal Structures of DctB Sensor Domain. Journal of Molecular Biology, 2008, 383, 49-61.	4.2	75
113	Auto-Rickshaw: an online tool for validation of an X-ray diffraction experiment. Acta Crystallographica Section A: Foundations and Advances, 2008, 64, C78-C78.	0.3	0
114	Molecular Architecture of Strictosidine Glucosidase: The Gateway to the Biosynthesis of the Monoterpenoid Indole Alkaloid Family. Plant Cell, 2007, 19, 2886-2897.	6.6	90
115	The Structure of a Full-length Response Regulator from Mycobacterium tuberculosis in a Stabilized Three-dimensional Domain-swapped, Activated State. Journal of Biological Chemistry, 2007, 282, 37717-37729.	3.4	37
116	Chloroplasts Assemble the Major Subunit FaeG of Escherichia coli F4 (K88) Fimbriae to Strand-swapped Dimers. Journal of Molecular Biology, 2007, 368, 791-799.	4.2	27
117	Crystal Structures of a Poplar Thioredoxin Peroxidase that Exhibits the Structure of Glutathione Peroxidases: Insights into Redox-driven Conformational Changes. Journal of Molecular Biology, 2007, 370, 512-529.	4.2	93
118	Structural biology in plant natural product biosynthesis—architecture of enzymes from monoterpenoid indole and tropane alkaloid biosynthesis. Natural Product Reports, 2007, 24, 1382.	10.3	47
119	Structure-Based Engineering of Strictosidine Synthase: Auxiliary for Alkaloid Libraries. Chemistry and Biology, 2007, 14, 979-985.	6.0	91
120	On the routine use of soft X-rays in macromolecular crystallography. Part IV. Efficient determination of anomalous substructures in biomacromolecules using longer X-ray wavelengths. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 366-380.	2.5	82
121	Structure of the apo form of the catabolite control protein A (CcpA) fromBacillus megateriumwith a DNA-binding domain. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 253-257.	0.7	2
122	Purification, crystallization and preliminary X-ray analysis of the HsdR subunit of theEcoR124I endonuclease fromEscherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 582-585.	0.7	3
123	The molecular architecture of major enzymes from ajmaline biosynthetic pathway. Phytochemistry Reviews, 2007, 6, 15-34.	6.5	37
124	High-resolution structure of NodZ fucosyltransferase involved in the biosynthesis of the nodulation factor Acta Biochimica Polonica, 2007, 54, 537-549.	0.5	25
125	RegX3 – a full-length response regulator that exhibits 3D-domain swapping. Acta Crystallographica Section A: Foundations and Advances, 2007, 63, s114-s114.	0.3	0
126	High-resolution structure of NodZ fucosyltransferase involved in the biosynthesis of the nodulation factor. Acta Biochimica Polonica, 2007, 54, 537-49.	0.5	10

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127	The X-ray Structure of the N-terminal Domain of PILB from Neisseria meningitidis Reveals a Thioredoxin-fold. Journal of Molecular Biology, 2006, 358, 443-454.	4.2	12
128	Heterologous expression, purification, crystallization and preliminary X-ray analysis of raucaffricine glucosidase, a plant enzyme specifically involved inRauvolfiaalkaloid biosynthesis. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 257-260.	0.7	17
129	Crystallization, preliminary crystallographic analysis and phasing of the thiosulfate-binding protein SoxY fromChlorobium limicolaf.thiosulfatophilum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1093-1096.	0.7	2
130	Expression, purification, crystallization and preliminary X-ray analysis of perakine reductase, a new member of the aldo-keto reductase enzyme superfamily from higher plants. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1286-1289.	0.7	13
131	Structural and Functional Aspects of the Sensor Histidine Kinase PrrB from Mycobacterium tuberculosis. Structure, 2006, 14, 275-285.	3.3	41
132	A Catalytic Mechanism Revealed by the Crystal Structures of the Imidazolonepropionase from Bacillus subtilis. Journal of Biological Chemistry, 2006, 281, 36929-36936.	3.4	18
133	The Structural Basis of Signal Transduction for the Response Regulator PrrA from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2006, 281, 9659-9666.	3.4	75
134	The Structure of Rauvolfia serpentina Strictosidine Synthase Is a Novel Six-Bladed β-Propeller Fold in Plant Proteins. Plant Cell, 2006, 18, 907-920.	6.6	126
135	Auto-Rickshaw: an automated crystal structure determination pipeline as an efficient tool for fast validation of an X-ray diffraction experiment. Acta Crystallographica Section A: Foundations and Advances, 2006, 62, s14-s14.	0.3	0
136	Auto-Rickshaw: an automated crystal structure determination platform as an efficient tool for the validation of an X-ray diffraction experiment. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 449-457.	2.5	387
137	On the routine use of soft X-rays in macromolecular crystallography. Part III. The optimal data-collection wavelength. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1263-1272.	2.5	65
138	On the influence of the incident photon energy on the radiation damage in crystalline biological samples. Journal of Synchrotron Radiation, 2005, 12, 304-309.	2.4	34
139	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of DapB (Rv2773c) fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 718-721.	0.7	10
140	Crystal Structure of Vinorine Synthase, the First Representative of the BAHD Superfamily. Journal of Biological Chemistry, 2005, 280, 13576-13583.	3.4	164
141	Structure of  CII: Implications for recognition of direct-repeat DNA by an unusual tetrameric organization. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11242-11247.	7.1	16
142	The Crystal Structure of the Herpes Simplex Virus 1 ssDNA-binding Protein Suggests the Structural Basis for Flexible, Cooperative Single-stranded DNA Binding. Journal of Biological Chemistry, 2005, 280, 2990-2997.	3.4	39
143	On the routine use of soft X-rays in macromolecular crystallography. Part II. Data-collection wavelength and scaling models. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 28-38.	2.5	20
144	Use of dry paraffin oil and Panjelly in the xenon derivatization of protein crystals. Journal of Applied Crystallography, 2002, 35, 117-119.	4.5	7

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145	Phasing possibilities using different wavelengths with a xenon derivative. Journal of Applied Crystallography, 2002, 35, 261-266.	4.5	9
146	Metal binding to porcine pancreatic elastase: calcium or not calcium. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1407-1412.	2.5	12
147	Xenon derivatization of halide-soaked protein crystals. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1413-1420.	2.5	10
148	Use of xenon in practice. Acta Crystallographica Section A: Foundations and Advances, 2002, 58, c28-c28.	0.3	0
149	Novel Cryo-cooling techniques. Acta Crystallographica Section A: Foundations and Advances, 2000, 56, s56-s56.	0.3	0
150	Determinants of Backbone Packing in Globular Proteins: an Analysis of Spatial Neighbours. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 627-637.	2.5	5
151	Structural studies on the 120 kDa motor subunit (HsdR) of the EcoR124I endonuclease from E.coli. , 0, 2007, .		0
152	THE IMPACT OF STRUCTURAL PROTEOMICS ON BIOTECHNOLOGY. , 0, , 353-370.		0