

Santosh Panjekar

List of Publications by Year in descending order

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152
papers

4,847
citations

117453

34
h-index

114278

63
g-index

164
all docs

164
docs citations

164
times ranked

6806
citing authors

#	ARTICLE	IF	CITATIONS
1	β -Methyltryptamine Provoking the Crucial Role of Strictosidine Synthase Tyr151-OH for Its Stereoselective Pictet-Spengler Reactions to Tryptoline-type Alkaloids. <i>ACS Chemical Biology</i> , 2022, 17, 187-197.	1.6	3
2	Crystal structure of the putative cell-wall lipoglycan biosynthesis protein LmcA from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 494-508.	1.1	4
3	Differential lysine-mediated allosteric regulation of plant dihydrodipicolinate synthase isoforms. <i>FEBS Journal</i> , 2021, 288, 4973-4986.	2.2	9
4	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. <i>Nature Communications</i> , 2021, 12, 1988.	5.8	16
5	<i>Helicobacter pylori</i> Xanthine-Guanine-Hypoxanthine Phosphoribosyltransferase: A Putative Target for Drug Discovery against Gastrointestinal Tract Infections. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 5710-5729.	2.9	4
6	Towards novel herbicide modes of action by inhibiting lysine biosynthesis in plants. <i>ELife</i> , 2021, 10, .	2.8	15
7	<i>Salmonella enterica</i> BcfH Is a Trimeric Thioredoxin-Like Bifunctional Enzyme with Both Thiol Oxidase and Disulfide Isomerase Activities. <i>Antioxidants and Redox Signaling</i> , 2021, 35, 21-39.	2.5	7
8	Graphene and Graphene Oxide as a Support for Biomolecules in the Development of Biosensors. <i>Nanotechnology, Science and Applications</i> , 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. <i>FEBS Journal</i> , 2020, 287, 386-400.	2.2	15
10	Crystal structure and site-directed mutagenesis of circular bacteriocin plantacyclin B21AG reveals cationic and aromatic residues important for antimicrobial activity. <i>Scientific Reports</i> , 2020, 10, 17398.	1.6	10
11	The basis for non-canonical ROK family function in the N-acetylmannosamine kinase from the pathogen <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 3301-3315.	1.6	13
12	Misannotations of a promising antibiotic target in high-priority gram-negative pathogens. <i>FEBS Letters</i> , 2020, 594, 1453-1463.	1.3	6
13	Structural basis for differentiation between two classes of thiolase: Degradative vs biosynthetic thiolase. <i>Journal of Structural Biology: X</i> , 2020, 4, 100018.	0.7	8
14	Crystal structure of posnjakite formed in the first crystal water-cooling line of the ANSTO Melbourne Australian Synchrotron MX1 Double Crystal Monochromator. <i>Acta Crystallographica Section E: Crystallographic Communications</i> , 2020, 76, 1136-1138.	0.2	0
15	Stereocomplementary Chemoenzymatic Pictet-Spengler Reactions for Formation of Rare Azepino-indole Frameworks: Discovery of Antimalarial Compounds. <i>ACS Catalysis</i> , 2019, 9, 7443-7448.	5.5	31
16	Unique structural features of a bacterial autotransporter adhesin suggest mechanisms for interaction with host macromolecules. <i>Nature Communications</i> , 2019, 10, 1967.	5.8	22
17	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. <i>MBio</i> , 2019, 10, .	1.8	10
18	Lanthanoid Heteroleptic Complexes with Cucurbit[5]uril and Dicarboxylate Ligands: From Discrete Structures to One-Dimensional and Two-Dimensional Polymers. <i>Inorganic Chemistry</i> , 2019, 58, 506-515.	1.9	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. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 670-681.	1.1	3
20	MX2: a high-flux undulator microfocus beamline serving both the chemical and macromolecular crystallography communities at the Australian Synchrotron. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 885-891.	1.0	346
21	Crystal structure of TcpK in complex with oriT DNA of the antibiotic resistance plasmid pCW3. <i>Nature Communications</i> , 2018, 9, 3732.	5.8	18
22	Design of Protein-Based Biosensors for Selective Detection of Benzene Groups of Pollutants. <i>ACS Sensors</i> , 2018, 3, 1632-1638.	4.0	27
23	Molecular evolution of an oligomeric biocatalyst functioning in lysine biosynthesis. <i>Biophysical Reviews</i> , 2018, 10, 153-162.	1.5	16
24	Beetle luciferases with naturally red- and blue-shifted emission. <i>Life Science Alliance</i> , 2018, 1, e201800072.	1.3	23
25	Structure Guided Design of Protein Biosensors for Phenolic Pollutants. <i>ACS Sensors</i> , 2017, 2, 411-418.	4.0	25
26	Structure of SgK223 pseudokinase reveals novel mechanisms of homotypic and heterotypic association. <i>Nature Communications</i> , 2017, 8, 1157.	5.8	40
27	Online automated structure solution from multiple data sets. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C787-C787.	0.0	1
28	Functional insights into the mode of DNA and ligand binding of the TetR family regulator TylP from <i>Streptomyces fradiae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 15301-15311.	1.6	12
29	Structure-guided design of aromatic biosensors for water quality monitoring. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C97-C97.	0.0	0
30	Crystallographic analysis of $\hat{\text{I}}^2$ -ketoacyl-CoA thiolase from <i>Pseudomonas putida</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C250-C250.	0.0	0
31	<i>Campylobacter jejuni</i> adenosine triphosphate phosphoribosyltransferase is an active hexamer that is allosterically controlled by the twisting of a regulatory tail. <i>Protein Science</i> , 2016, 25, 1492-1506.	3.1	15
32	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. <i>Angewandte Chemie</i> , 2016, 128, 8062-8065.	1.6	7
33	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 7930-7933.	7.2	45
34	Structural Basis of Selective Aromatic Pollutant Sensing by the Effector Binding Domain of MopR, an NtrC Family Transcriptional Regulator. <i>ACS Chemical Biology</i> , 2016, 11, 2357-2365.	1.6	35
35	Structure and Function of Cyanobacterial DHDPS and DHDPR. <i>Scientific Reports</i> , 2016, 6, 37111.	1.6	23
36	Structural Determinants Defining the Allosteric Inhibition of an Essential Antibiotic Target. <i>Structure</i> , 2016, 24, 1282-1291.	1.6	34

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37	A critical examination of the recently reported crystal structures of the human SMN protein. <i>Human Molecular Genetics</i> , 2016, 25, ddw298.	1.4	13
38	Interdomain Conformational Changes Provide Allosteric Regulation en Route to Chorismate. <i>Journal of Biological Chemistry</i> , 2016, 291, 21836-21847.	1.6	22
39	Titelbild: Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the CASA/Snakin Protein Superfamily (<i>Angew. Chem.</i> 28/2016). <i>Angewandte Chemie</i> , 2016, 128, 7995-7995.	1.6	0
40	A crystallographic study of human NONO (p54 ^{nrb}): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 761-769.	1.1	11
41	Combining cross-crystal averaging and MRSAD to phase a 4354-amino-acid structure. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 182-191.	1.1	1
42	Structural basis of selective aromatic pollutant sensing by MopR, an NtrC family transcriptional regulator. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s251-s252.	0.0	0
43	Automated structure solution from multiple data sets. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s18-s18.	0.0	0
44	Quaternary Structure Analyses of an Essential Oligomeric Enzyme. <i>Methods in Enzymology</i> , 2015, 562, 205-223.	0.4	24
45	Functional Coupling of Duplex Translocation to DNA Cleavage in a Type I Restriction Enzyme. <i>PLoS ONE</i> , 2015, 10, e0128700.	1.1	7
46	Stonefish toxin defines an ancient branch of the perforin-like superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15360-15365.	3.3	69
47	Ligand structures of synthetic deoxa-pyranosylamines with raucaffricine and strictosidine glucosidases provide structural insights into their binding and inhibitory behaviours. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2015, 30, 472-478.	2.5	1
48	A step towards long-wavelength protein crystallography: subjecting protein crystals to a vacuum. <i>Journal of Applied Crystallography</i> , 2015, 48, 913-916.	1.9	3
49	MX1: a bending-magnet crystallography beamline serving both chemical and macromolecular crystallography communities at the Australian Synchrotron. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 187-190.	1.0	336
50	Cyclic Peptides Incorporating Phosphotyrosine Mimetics as Potent and Specific Inhibitors of the Grb7 Breast Cancer Target. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 7707-7718.	2.9	19
51	The Crystal Structure of a Homodimeric <i>Pseudomonas</i> Glyoxalase...I Enzyme Reveals Asymmetric Metallation Commensurate with Half-Sites Activity. <i>Chemistry - A European Journal</i> , 2015, 21, 541-544.	1.7	12
52	Post-translational modification and extended glycosylation pattern of a plant latex peroxidase of native source characterized by X-ray crystallography. <i>FEBS Journal</i> , 2014, 281, 4319-4333.	2.2	9
53	Crystal structure of <i>Clostridium acetobutylicum</i> aspartate kinase (CaAk): An important allosteric enzyme for amino acids production. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2014, 3, 73-85.	2.1	12
54	The Three-dimensional Structure of the Extracellular Adhesion Domain of the Sialic Acid-binding Adhesin SabA from <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6332-6340.	1.6	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.	1.1	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.	0.0	0
57	Chemical Crystallography at the Australian Synchrotron MX Beamlines. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1751-C1751.	0.0	0
58	Alternative phasing method in macromolecular crystallography. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C342-C342.	0.0	0
59	The BC component of ABC toxins is an RHS-repeat-containing protein encapsulation device. Nature, 2013, 501, 547-550.	13.7	144
60	In-house UV radiation-damage-induced phasing of selenomethionine-labeled protein structures. Journal of Structural Biology, 2013, 181, 89-94.	1.3	1
61	High speed X-ray analysis of plant enzymes at room temperature. Phytochemistry, 2013, 91, 88-92.	1.4	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.	1.2	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.	1.1	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 pathogen Legionella 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.	3.5	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.	1.6	18
69	Nonprocessive [2 α + α 2] ^e 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.	3.3	73
70	High-resolution structure of Bombyx mori 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 histo-blood group binding by the F18 fimbrial adhesin FedF. Molecular Microbiology, 2012, 86, 82-95.	1.2	46

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73	Structural basis for modification of flavonol and naphthol glucoconjugates by <i>Nicotiana tabacum</i> malonyltransferase (NtMaT1). <i>Planta</i> , 2012, 236, 781-793.	1.6	23
74	Crystal structure of NAD ⁺ -dependent <i>Peptoniphilus asaccharolyticus</i> glutamate dehydrogenase reveals determinants of cofactor specificity. <i>Journal of Structural Biology</i> , 2012, 177, 543-552.	1.3	24
75	The sensor region of the ubiquitous cytosolic sensor kinase, PdtaS, contains PAS and GAF domain sensing modules. <i>Journal of Structural Biology</i> , 2012, 177, 498-505.	1.3	18
76	The crystal structure of the CRISPR-associated protein Csn2 from <i>Streptococcus agalactiae</i> . <i>Journal of Structural Biology</i> , 2012, 178, 350-362.	1.3	24
77	Scaffold Tailoring by a Newly Detected Pictetâ€“Spenglerase Activity of Strictosidine Synthase: From the Common Tryptoline Skeleton to the Rare Piperazino-indole Framework. <i>Journal of the American Chemical Society</i> , 2012, 134, 1498-1500.	6.6	57
78	Structures of Alkaloid Biosynthetic Glucosidases Decode Substrate Specificity. <i>ACS Chemical Biology</i> , 2012, 7, 226-234.	1.6	23
79	The impact of structural biology on alkaloid biosynthesis research. <i>Natural Product Reports</i> , 2012, 29, 1176.	5.2	21
80	Current methods in structural proteomics and its applications in biological sciences. <i>3 Biotech</i> , 2012, 2, 89-113.	1.1	23
81	Formylglycinamide ribonucleotide amidotransferase from <i>Salmonella typhimurium</i> : role of ATP complexation and the glutaminase domain in catalytic coupling. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 627-636.	2.5	7
82	Structural Insights into the Mechanism of Protein O-Fucosylation. <i>PLoS ONE</i> , 2011, 6, e25365.	1.1	85
83	S-SAD phasing of proteinO-fucosyltransferase-1 at a resolution of 2.6â€“Å in the monoclinic space groupC2. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C65-C65.	0.3	0
84	Structural Characterization of the Multidomain Regulatory Protein Rv1364c from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2011, 19, 56-69.	1.6	19
85	Single isomorphous replacement phasing of selenomethionine-containing proteins using UV-induced radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 729-738.	2.5	4
87	Additional phase information from UV damage of selenomethionine labelled proteins. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 374-380.	1.0	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. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 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. <i>Journal of Biological Chemistry</i> , 2011, 286, 8349-8360.	1.6	39
90	Phasing selenomethionine proteins using UV induced radiation damage. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C657-C657.	0.3	0

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91	Update on the tutorial for learning and teaching macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2010, 43, 1230-1237.	1.9	6
92	Expression, purification and X-ray analysis of 1,3-propanediol dehydrogenase (Aq_1145) from <i>Aquifex aeolicus</i> VF5. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 184-186.	0.7	2
93	Update on the tutorial for learning and teaching macromolecular crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s112-s112.	0.3	0
94	Structural analysis reveals DNA binding properties of Rv2827c, a hypothetical protein from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural and Functional Genomics</i> , 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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 411-420.	2.5	5
96	Structure of the C-terminal domain of nsp4 from feline coronavirus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 839-846.	2.5	23
97	On the combination of molecular replacement and single-wavelength anomalous diffraction phasing for automated structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1089-1097.	2.5	158
98	Structure of the motor subunit of type I restriction-modification complex EcoR124I. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 94-95.	3.6	38
99	Structural Basis and Enzymatic Mechanism of the Biosynthesis of C ₉ from C ₁₀ Monoterpenoid Indole Alkaloids. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 5211-5213.	7.2	33
100	The impact of Structural Proteomics on Biotechnology. <i>Biotechnology and Genetic Engineering Reviews</i> , 2009, 26, 353-370.	2.4	4
101	Structure of the C-terminal domain of NSP4 from feline infection peritonitis virus. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s167-s167.	0.3	1
102	Auto-Rickshaw: a tool for online validation of X-ray diffraction experiment. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 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> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 167-170.	0.7	12
104	High crystallizability under air-exclusion conditions of the full-length LysR-type transcriptional regulator TsaR from <i>Comamonas testosteroni</i> T-2 and data-set analysis for a MIRAS structure-solution approach. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 764-769.	0.7	1
105	Purification, crystallization and X-ray diffraction analysis of pavin N-methyltransferase from <i>Thalictrum flavum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1066-1069.	0.7	2
106	A tutorial for learning and teaching macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2008, 41, 1161-1172.	1.9	15
107	Automated technologies and novel techniques to accelerate protein crystallography for structural genomics. <i>Proteomics</i> , 2008, 8, 612-625.	1.3	70
108	3D-Structure and function of strictosidine synthase – the key enzyme of monoterpenoid indole alkaloid biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 340-355.	2.8	72

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109	Nonspecific base recognition mediated by water bridges and hydrophobic stacking in ribonuclease I from <i>Escherichia coli</i> . <i>Protein Science</i> , 2008, 17, 681-690.	3.1	10
110	Structural Basis for Parasite-Specific Functions of the Divergent Profilin of <i>Plasmodium falciparum</i> . <i>Structure</i> , 2008, 16, 1638-1648.	1.6	60
111	Strictosidine Synthase: Mechanism of a Pictet-Spengler Catalyzing Enzyme. <i>Journal of the American Chemical Society</i> , 2008, 130, 710-723.	6.6	190
112	C4-Dicarboxylates Sensing Mechanism Revealed by the Crystal Structures of DctB Sensor Domain. <i>Journal of Molecular Biology</i> , 2008, 383, 49-61.	2.0	75
113	Auto-Rickshaw: an online tool for validation of an X-ray diffraction experiment. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2008, 64, C78-C78.	0.3	0
114	Molecular Architecture of Strictosidine Glucosidase: The Gateway to the Biosynthesis of the Monoterpenoid Indole Alkaloid Family. <i>Plant Cell</i> , 2007, 19, 2886-2897.	3.1	90
115	The Structure of a Full-length Response Regulator from <i>Mycobacterium tuberculosis</i> in a Stabilized Three-dimensional Domain-swapped, Activated State. <i>Journal of Biological Chemistry</i> , 2007, 282, 37717-37729.	1.6	37
116	Chloroplasts Assemble the Major Subunit FaeG of <i>Escherichia coli</i> F4 (K88) Fimbriae to Strand-swapped Dimers. <i>Journal of Molecular Biology</i> , 2007, 368, 791-799.	2.0	27
117	Crystal Structures of a Poplar Thioredoxin Peroxidase that Exhibits the Structure of Glutathione Peroxidases: Insights into Redox-driven Conformational Changes. <i>Journal of Molecular Biology</i> , 2007, 370, 512-529.	2.0	93
118	Structural biology in plant natural product biosynthesis—architecture of enzymes from monoterpenoid indole and tropane alkaloid biosynthesis. <i>Natural Product Reports</i> , 2007, 24, 1382.	5.2	47
119	Structure-Based Engineering of Strictosidine Synthase: Auxiliary for Alkaloid Libraries. <i>Chemistry and Biology</i> , 2007, 14, 979-985.	6.2	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 366-380.	2.5	82
121	Structure of the apo form of the catabolite control protein A (CcpA) from <i>Bacillus megaterium</i> with a DNA-binding domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 253-257.	0.7	2
122	Purification, crystallization and preliminary X-ray analysis of the HsdR subunit of the EcoR124I endonuclease from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 582-585.	0.7	3
123	The molecular architecture of major enzymes from ajmaline biosynthetic pathway. <i>Phytochemistry Reviews</i> , 2007, 6, 15-34.	3.1	37
124	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
125	RegX3—a full-length response regulator that exhibits 3D-domain swapping. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2007, 63, s114-s114.	0.3	0
126	High-resolution structure of NodZ fucosyltransferase involved in the biosynthesis of the nodulation factor. <i>Acta Biochimica Polonica</i> , 2007, 54, 537-49.	0.3	10

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127	The X-ray Structure of the N-terminal Domain of PILB from <i>Neisseria meningitidis</i> Reveals a Thioredoxin-fold. <i>Journal of Molecular Biology</i> , 2006, 358, 443-454.	2.0	12
128	Heterologous expression, purification, crystallization and preliminary X-ray analysis of raucaffricine glucosidase, a plant enzyme specifically involved in <i>Rauvolfia</i> alkaloid biosynthesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 257-260.	0.7	17
129	Crystallization, preliminary crystallographic analysis and phasing of the thiosulfate-binding protein SoxY from <i>Chlorobium limicola</i> f. <i>thiosulfatophilum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 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. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1286-1289.	0.7	13
131	Structural and Functional Aspects of the Sensor Histidine Kinase PrrB from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2006, 14, 275-285.	1.6	41
132	A Catalytic Mechanism Revealed by the Crystal Structures of the Imidazolonepropionase from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 36929-36936.	1.6	18
133	The Structural Basis of Signal Transduction for the Response Regulator PrrA from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 9659-9666.	1.6	75
134	The Structure of <i>Rauvolfia serpentina</i> Strictosidine Synthase Is a Novel Six-Bladed \hat{I}^2 -Propeller Fold in Plant Proteins. <i>Plant Cell</i> , 2006, 18, 907-920.	3.1	126
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