

# Se Won Suh

## List of Publications by Year in descending order

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191  
papers

6,734  
citations

57631

44  
h-index

74018

75  
g-index

192  
all docs

192  
docs citations

192  
times ranked

7670  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for SdgB- and SdgA-mediated glycosylation of staphylococcal adhesive proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1460-1474.	1.1	1
2	Peptidoglycan reshaping by a noncanonical peptidase for helical cell shape in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2020, 11, 458.	5.8	14
3	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>Journal of Hand Surgery Asian-Pacific Volume</i> , The, 2020, , 288-292.	0.2	0
4	Structural basis for the inhibitory effects of a novel reversible covalent ligand on PPAR $\delta$ phosphorylation. <i>Scientific Reports</i> , 2019, 9, 11168.	1.6	12
5	A cytosine modification mechanism revealed by the structure of a ternary complex of deoxycytidylate hydroxymethylase from bacteriophage T4 with its cofactor and substrate. <i>IUCr</i> , 2019, 6, 206-217.	1.0	4
6	Structural Basis for the Enhanced Anti-Diabetic Efficacy of Lobeglitazone on PPAR $\delta$ . <i>Scientific Reports</i> , 2018, 8, 31.	1.6	62
7	Structural basis for the substrate recognition of peptidoglycan pentapeptides by <i>Enterococcus faecalis</i> VanYB. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 335-344.	3.6	5
8	Structural basis for differential activities of enantiomeric PPAR $\delta$ agonists: Binding of S35 to the alternate site. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 674-681.	1.1	40
9	Mechanistic elucidation guided by covalent inhibitors for the development of anti-diabetic PPAR $\delta$ ligands. <i>Chemical Science</i> , 2016, 7, 5523-5529.	3.7	39
10	Crystal structure of Rv2258c from <i>Mycobacterium tuberculosis</i> H37Rv, an S-adenosyl-L-methionine-dependent methyltransferase. <i>Journal of Structural Biology</i> , 2016, 193, 172-180.	1.3	3
11	Structural Basis of the Heterodimer Formation between Cell Shape-Determining Proteins Csd1 and Csd2 from <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2016, 11, e0164243.	1.1	17
12	Structure of Csd3 from <i>Helicobacter pylori</i> , a cell shape-determining metallopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 675-686.	2.5	21
13	The kinetic characterization and X-ray structure of a putative benzoylformate decarboxylase from <i>M. smegmatis</i> highlights the difficulties in the functional annotation of ThDP-dependent enzymes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1001-1009.	1.1	8
14	The Cell Shape-determining Csd6 Protein from <i>Helicobacter pylori</i> Constitutes a New Family of L,d-Carboxypeptidase. <i>Journal of Biological Chemistry</i> , 2015, 290, 25103-25117.	1.6	34
15	Structural basis for methyl-donor-dependent and sequence-specific binding to tRNA substrates by knotted methyltransferase TrmD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4197-205.	3.3	54
16	Structural basis for the recognition of muramyltripeptide by <i>Helicobacter pylori</i> Csd4, a D,L-carboxypeptidase controlling the helical cell shape. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2800-2812.	2.5	20
17	Structure of <i>Mycobacterium smegmatis</i> Eis in complex with paromomycin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1173-1179.	0.4	8
18	Crystal structure of JHP933 from <i>Helicobacter pylori</i> J99 shows two-domain architecture with a DUF1814 family nucleotidyltransferase domain and a helical bundle domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2275-2281.	1.5	3

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19	Crystal structure of PhoU from <i>Pseudomonas aeruginosa</i> , a negative regulator of the Pho regulon. <i>Journal of Structural Biology</i> , 2014, 188, 22-29.	1.3	11
20	Structural Basis for Ovarian Tumor Domain-containing Protein 1 (OTU1) Binding to p97/Valosin-containing Protein (VCP). <i>Journal of Biological Chemistry</i> , 2014, 289, 12264-12274.	1.6	24
21	Structural basis for the inhibition of <i>Mycobacterium tuberculosis</i> LysR, D-lysine transpeptidase by meropenem, a drug effective against extensively drug-resistant strains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 420-431.	2.5	68
22	A docking study of enhanced intracellular survival protein from <i>Mycobacterium tuberculosis</i> with human DUSP16/MKP-7. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 929-932.	1.0	6
23	Structural and functional characterization of HP0377, a thioredoxin-fold protein from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 735-746.	2.5	8
24	High-resolution crystal structure of <i>Streptococcus pyogenes</i> $\beta$ -NAD <sup>+</sup> glycohydrolase in complex with its endogenous inhibitor IFS reveals a highly water-rich interface. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 962-967.	1.0	4
25	Crystal Structure of Pyridoxal Biosynthesis Lyase PdxS from <i>Pyrococcus horikoshii</i> . <i>Molecules and Cells</i> , 2012, 34, 407-412.	1.0	5
26	Helical Repeat Structure of Apoptosis Inhibitor 5 Reveals Protein-Protein Interaction Modules. <i>Journal of Biological Chemistry</i> , 2012, 287, 10727-10737.	1.6	33
27	Structures of the ribosome-inactivating protein from barley seeds reveal a unique activation mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1488-1500.	2.5	8
28	<i>Mycobacterium tuberculosis</i> Eis protein initiates suppression of host immune responses by acetylation of DUSP16/MKP-7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7729-7734.	3.3	167
29	Structures of <i>Staphylococcus aureus</i> peptide deformylase in complex with two classes of new inhibitors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 784-793.	2.5	4
30	Overexpression, crystallization and preliminary X-ray crystallographic analysis of pyridoxal biosynthesis lyase PdxS from <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 440-442.	0.7	2
31	Crystal structures of <i>Pseudomonas aeruginosa</i> guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. <i>Journal of Structural Biology</i> , 2011, 175, 329-338.	1.3	15
32	Crystal structures of YwqE from <i>Bacillus subtilis</i> and CpsB from <i>Streptococcus pneumoniae</i> , unique metal-dependent tyrosine phosphatases. <i>Journal of Structural Biology</i> , 2011, 175, 442-450.	1.3	21
33	Crystal structures of LacD from <i>Staphylococcus aureus</i> and LacD.1 from <i>Streptococcus pyogenes</i> : Insights into substrate specificity and virulence gene regulation. <i>FEBS Letters</i> , 2011, 585, 307-312.	1.3	6
34	Structural and functional characterization of <i>Helicobacter pylori</i> DsbG. <i>FEBS Letters</i> , 2011, 585, 3862-3867.	1.3	23
35	Crystal Structure of Phosphopantetheine Adenylyltransferase from <i>Enterococcus faecalis</i> in the Ligand-Unbound State and in Complex with ATP and Pantetheine. <i>Molecules and Cells</i> , 2011, 32, 431-436.	1.0	11
36	Crystal structure of the catalytic domain of cholesterol $\alpha$ -glucosyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2321-2326.	1.5	13

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37	Crystal structure of FAF1 UBX domain in complex with p97/VCP N domain reveals a conformational change in the conserved FcisP touchâ€turn motif of UBX domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2583-2587.	1.5	25
38	Structural Basis for the Reaction Mechanism of UDP-Glucose Pyrophosphorylase. <i>Molecules and Cells</i> , 2010, 29, 397-406.	1.0	41
39	Overexpression, crystallization and preliminary X-ray crystallographic analysis of <i>Pseudomonas aeruginosa</i> MnmE, a GTPase involved in tRNA modification. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 905-908.	0.7	0
40	Arrest Defective 1 Autoacetylation Is a Critical Step in Its Ability to Stimulate Cancer Cell Proliferation. <i>Cancer Research</i> , 2010, 70, 4422-4432.	0.4	60
41	Crystal structure of Tpa1 from <i>Saccharomyces cerevisiae</i> , a component of the messenger ribonucleoprotein complex. <i>Nucleic Acids Research</i> , 2010, 38, 2099-2110.	6.5	27
42	<i>Helicobacter pylori</i> proinflammatory protein up-regulates NF- $\kappa$ B as a cell-translocating Ser/Thr kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21418-21423.	3.3	49
43	Crystal structures of two archaeal Pelotas reveal inter-domain structural plasticity. <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 600-606.	1.0	3
44	Dimeric and tetrameric forms of enoyl-acyl carrier protein reductase from <i>Bacillus cereus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 400, 517-522.	1.0	14
45	Peptide deformylase inhibitors with retro-amide scaffold: Synthesis and structureâ€activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 4317-4319.	1.0	12
46	Crystal structure of <i>Thermotoga maritima</i> SPOUT superfamily RNA methyltransferase Tm1570 in complex with Sâ€adenosylâ€Lâ€methionine. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 245-249.	1.5	5
47	ATP-dependent DNA ligase from <i>Archaeoglobus fulgidus</i> displays a tightly closed conformation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 544-550.	0.7	22
48	The structure of <i>Staphylococcus aureus</i> phosphopantetheine adenylyltransferase in complex with 3â€phosphoadenosine 5â€phosphosulfate reveals a new ligand-binding mode. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 987-991.	0.7	12
49	Depletion of nucleophosmin via transglutaminase 2 cross-linking increases drug resistance in cancer cells. <i>Cancer Letters</i> , 2009, 274, 201-207.	3.2	28
50	Crystal Structure of the TNF- $\alpha$ -Inducing Protein (Tip1 $\alpha$ ) from <i>Helicobacter pylori</i> : Insights into Its DNA-Binding Activity. <i>Journal of Molecular Biology</i> , 2009, 392, 191-197.	2.0	16
51	Crystal structure of the mouse p53 core domain in zincâ€free state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 280-283.	1.5	6
52	Structural basis of octanoic acid recognition by lipoteâ€protein ligase B. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1620-1625.	1.5	8
53	Structure of 3-deoxy- <i>manno</i> - <i>octulosonate</i> cytidyltransferase from <i>Haemophilus influenzae</i> complexed with the substrate 3-deoxy- <i>manno</i> - <i>octulosonate</i> in the $\beta^2$ -configuration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1292-1294.	2.5	6
54	Crystal structure of UDPâ€Nâ€acetylglucosamine enolpyruvyl transferase from <i>Haemophilus influenzae</i> in complex with UDPâ€Nâ€acetylglucosamine and fosfomycin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1032-1037.	1.5	27

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55	Crystal structure of YlqF, a circularly permuted GTPase: Implications for its GTPase activation in 50 S ribosomal subunit assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1363-1370.	1.5	23
56	Competitive Inhibitors of <i>Helicobacter pylori</i> Type II Dehydroquinase: Synthesis, Biological Evaluation, and NMR Studies. <i>ChemMedChem</i> , 2008, 3, 756-770.	1.6	30
57	HD-ZIP III Activity Is Modulated by Competitive Inhibitors via a Feedback Loop in <i>Arabidopsis</i> Shoot Apical Meristem Development. <i>Plant Cell</i> , 2008, 20, 920-933.	3.1	127
58	The recombination-associated protein RdgC adopts a novel toroidal architecture for DNA binding. <i>Nucleic Acids Research</i> , 2007, 35, 2671-2681.	6.5	7
59	Crystal Structure of d-Erythronate-4-phosphate Dehydrogenase Complexed with NAD. <i>Journal of Molecular Biology</i> , 2007, 366, 1294-1304.	2.0	17
60	Structural and Functional Insights into Dom34, a Key Component of No-Go mRNA Decay. <i>Molecular Cell</i> , 2007, 27, 938-950.	4.5	84
61	Crystal structure of human nucleophosmin core reveals plasticity of the pentamer-pentamer interface. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 672-678.	1.5	94
62	Crystal structure of the <i>Helicobacter pylori</i> enoyl-acyl carrier protein reductase in complex with hydroxydiphenyl ether compounds, triclosan and diclosan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 691-694.	1.5	20
63	Crystal Structure of Visfatin/Pre-B Cell Colony-enhancing Factor 1/Nicotinamide Phosphoribosyltransferase, Free and in Complex with the Anti-cancer Agent FK-866. <i>Journal of Molecular Biology</i> , 2006, 362, 66-77.	2.0	107
64	S2c1-1 Structure and Ribonuclease Activity of Pelota : Implications for the No-go Decay and Translation Regulation(S2-c1: "Crystallographic approach to understand biological) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (supra Seibutsu Butsuri, 2006, 46, S120.	0.0	0
65	Overexpression, crystallization and preliminary X-ray crystallographic analysis of erythronate-4-phosphate dehydrogenase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 139-141.	0.7	3
66	Expression, crystallization and preliminary X-ray crystallographic analyses of two N-terminal acetyltransferase-related proteins from <i>Thermoplasma acidophilum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1127-1130.	0.7	3
67	Overexpression, crystallization and preliminary X-ray crystallographic analysis of phosphopantetheine adenyltransferase from <i>Enterococcus faecalis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1131-1133.	0.7	7
68	Overexpression, crystallization and preliminary X-ray crystallographic analysis of a putative transposase from <i>Thermoplasma acidophilum</i> encoded by the Ta0474 gene. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1147-1149.	0.7	1
69	Crystal Structure of a Metal Ion-bound IS200 Transposase. <i>Journal of Biological Chemistry</i> , 2006, 281, 4261-4266.	1.6	10
70	Crystal Structure of 2-Nitropropane Dioxygenase Complexed with FMN and Substrate. <i>Journal of Biological Chemistry</i> , 2006, 281, 18660-18667.	1.6	40
71	Structure of inorganic pyrophosphatase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1459-1464.	2.5	8
72	Expression, crystallization and preliminary X-ray crystallographic analysis of human agmatinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 889-891.	0.7	3

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73	Crystal Structure of Lipoate-Protein Ligase A Bound with the Activated Intermediate. <i>Journal of Biological Chemistry</i> , 2005, 280, 38081-38089.	1.6	53
74	Crystal Structure of Nicotinic Acid Mononucleotide Adenylyltransferase from <i>Pseudomonas aeruginosa</i> in its Apo and Substrate-complexed Forms Reveals a Fully Open Conformation. <i>Journal of Molecular Biology</i> , 2005, 351, 258-265.	2.0	25
75	Crystal structure of $\hat{\pm}$ -hordothionin at 1.9 Å... resolution. <i>FEBS Letters</i> , 2005, 579, 2301-2306.	1.3	12
76	Crystallization and preliminary X-ray crystallographic analysis of UDP-N-acetylglucosamine enolpyruvyl transferase from <i>Haemophilus influenzae</i> in complex with UDP-N-acetylglucosamine and fosfomycin. <i>Molecules and Cells</i> , 2005, 19, 398-401.	1.0	1
77	Crystal Structure of Agmatinase Reveals Structural Conservation and Inhibition Mechanism of the Ureohydrolase Superfamily. <i>Journal of Biological Chemistry</i> , 2004, 279, 50505-50513.	1.6	43
78	Crystal Structure of T-protein of the Glycine Cleavage System. <i>Journal of Biological Chemistry</i> , 2004, 279, 50514-50523.	1.6	31
79	Mutational analyses of the thermostable NAD <sup>+</sup> -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , 2004, 237, 111-118.	0.7	23
80	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. <i>EMBO Journal</i> , 2004, 23, 2029-2038.	3.5	105
81	Crystal structure of the TM1442 protein from <i>Thermotoga maritima</i> , a homolog of the <i>Bacillus subtilis</i> general stress response anti-anti-sigma factor RsbV. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 176-179.	1.5	10
82	Crystal structure of peptide deformylase from <i>Staphylococcus aureus</i> in complex with actinonin, a naturally occurring antibacterial agent. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 639-642.	1.5	20
83	Crystallization and preliminary X-ray crystallographic analysis of the RecR protein from <i>Deinococcus radiodurans</i> , a member of the RecFOR DNA-repair pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 379-381.	2.5	5
84	Crystallization and preliminary X-ray crystallographic analysis of nicotinic acid mononucleotide adenylyltransferase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 948-949.	2.5	5
85	Crystallization and preliminary X-ray crystallographic study of UDP-glucose pyrophosphorylase (UGPase) from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1447-1449.	2.5	8
86	Crystallization and preliminary X-ray crystallographic analysis of a putative agmatinase from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1890-1892.	2.5	2
87	Crystal Structure of $\hat{2}$ -d-Xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> , a Family 39 Glycoside Hydrolase. <i>Journal of Molecular Biology</i> , 2004, 335, 155-165.	2.0	69
88	Crystal Structure of Chorismate Synthase: A Novel FMN-binding Protein Fold and Functional Insights. <i>Journal of Molecular Biology</i> , 2004, 336, 903-915.	2.0	29
89	Crystal Structure of the Schiff Base Intermediate Prior to Decarboxylation in the Catalytic Cycle of Aspartate $\hat{\pm}$ -Decarboxylase. <i>Journal of Molecular Biology</i> , 2004, 340, 1-7.	2.0	33
90	Mutational analyses of the thermostable NAD <sup>+</sup> -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , 2004, 237, 111-118.	0.7	9

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91	Crystal structure of tRNA(m1G37)methyltransferase: insights into tRNA recognition. <i>EMBO Journal</i> , 2003, 22, 2593-2603.	3.5	124
92	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003, 83, 223-249.	0.8	95
93	Crystallization and preliminary X-ray crystallographic studies of 3-deoxy-manno-octulosonate cytidyltransferase from <i>Haemophilus influenzae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 180-182.	2.5	5
94	Crystallization and preliminary X-ray crystallographic analysis of tRNA(m1G37)methyltransferase from <i>Haemophilus influenzae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 183-184.	2.5	1
95	Crystallization and preliminary X-ray analysis of the Mj0684 gene product, a putative aspartate aminotransferase, from <i>Methanococcus jannaschii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 563-565.	2.5	2
96	Crystallization and preliminary X-ray crystallographic studies of chorismate synthase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 569-571.	2.5	5
97	Crystallization and preliminary X-ray crystallographic studies of phosphopantetheine adenylyltransferase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 561-562.	2.5	7
98	Crystal structure of the type II 3-dehydroquinase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 616-617.	1.5	14
99	Crystal structure of UDP-N-acetylglucosamine acyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 772-774.	1.5	23
100	Crystal Structure of Class I Acetohydroxy Acid Isomeroeductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2003, 328, 505-515.	2.0	41
101	Directed evolution approach to a structural genomics project: Rv2002 from <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 455-460.	3.3	55
102	Î±-Synuclein regulates neuronal survival via Bcl-2 family expression and PI3/Akt kinase pathway. <i>FASEB Journal</i> , 2002, 16, 1-20.	0.2	198
103	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002, 2, 121-141.	2.1	66
104	Crystallization and preliminary X-ray crystallographic analysis of the Rv2002 gene product from <i>Mycobacterium tuberculosis</i> , a Î²-ketoacyl carrier protein reductase homologue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 303-305.	2.5	14
105	Crystallization and preliminary X-ray crystallographic analysis of Î²-xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> , a thermophilic anaerobe. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 531-532.	2.5	1
106	Crystallization and preliminary X-ray crystallographic analysis of aspartate 1-decarboxylase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 861-863.	2.5	5
107	Crystallization and preliminary X-ray crystallographic analysis of UDP-N-acetylglucosamine acyltransferase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 864-866.	2.5	4
108	Crystallization and preliminary X-ray crystallographic analysis of enoyl-acyl carrier protein reductase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1071-1073.	2.5	4

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109	Crystallization and preliminary X-ray crystallographic analysis of peptide deformylase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1874-1875.	2.5	4
110	Crystallization and preliminary X-ray crystallographic analysis of acetohydroxy acid isomeroreductase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2145-2146.	2.5	3
111	Crystal structure of human nucleoside diphosphate kinase A, a metastasis suppressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 340-342.	1.5	27
112	Crystal structure of the MJ0490 gene product of the hyperthermophilic archaeobacterium <i>Methanococcus jannaschii</i> , a novel member of the Lactate/Malate family of dehydrogenases. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 307, 1351-1362.	2.0	32
113	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography. Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2001, 308, 263-278.	2.0	175
114	Crystallization and preliminary X-ray crystallographic analysis of the TM1442 gene product from <i>Thermotoga maritima</i> , a homologue of <i>Bacillus subtilis</i> anti-sigma factors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 276-278.	2.5	5
115	Crystallization and preliminary X-ray crystallographic analysis of type II dehydroquinase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 279-280.	2.5	2
116	Crystallization and preliminary X-ray crystallographic analysis of RNase HIII from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 438-440.	2.5	3
117	Crystallization and preliminary X-ray crystallographic analysis of the surE protein from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 612-613.	2.5	3
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119	Crystallization and preliminary X-ray studies of Trp138Phe/Val185Thr xylose isomerases from <i>Thermotoga neapolitana</i> and <i>Thermoanaerobacterium thermosulfurigenes</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1686-1688.	2.5	4
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