

# Se Won Suh

## List of Publications by Year in descending order

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191  
papers

6,734  
citations

57719

44  
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74108

75  
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192  
all docs

192  
docs citations

192  
times ranked

7670  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>Nature</i> , 1995, 376, 612-616.	13.7	370
2	The crystal structure of a triacylglycerol lipase from <i>Pseudomonas cepacia</i> reveals a highly open conformation in the absence of a bound inhibitor. <i>Structure</i> , 1997, 5, 173-185.	1.6	301
3	Kunitz-type soybean trypsin inhibitor revisited: refined structure of its complex with porcine trypsin reveals an insight into the interaction between a homologous inhibitor from <i>Erythrina caffra</i> and tissue-type plasminogen activator 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1998, 275, 347-363.	2.0	230
4	High-resolution crystal structure of the non-specific lipid-transfer protein from maize seedlings. <i>Structure</i> , 1995, 3, 189-199.	1.6	221
5	Crystal structure and functional analysis of the SurE protein identify a novel phosphatase family. <i>Nature Structural Biology</i> , 2001, 8, 789-794.	9.7	199
6	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
7	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
8	Crystal structure of NAD <sup>+</sup> -dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , 2000, 19, 1119-1129.	3.5	169
9	<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
10	Tertiary structure of plant RuBisCO: domains and their contacts. <i>Science</i> , 1988, 241, 71-74.	6.0	161
11	Structural and mechanistic conservation in DNA ligases. <i>Nucleic Acids Research</i> , 2000, 28, 4051-4058.	6.5	147
12	Rice non-specific lipid transfer protein: the 1.6 Å crystal structure in the unliganded state reveals a small hydrophobic cavity Edited by D. Rees. <i>Journal of Molecular Biology</i> , 1998, 276, 437-448.	2.0	129
13	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
14	Crystal structure of tRNA(m <sup>1</sup> G37)methyltransferase: insights into tRNA recognition. <i>EMBO Journal</i> , 2003, 22, 2593-2603.	3.5	124
15	Surface-enhanced Raman scattering (SERS) of aromatic amino acids and their glyceryl dipeptides in silver sol. <i>Journal of Raman Spectroscopy</i> , 1987, 18, 171-175.	1.2	119
16	Crystal structure of <i>Escherichia coli</i> CyaY protein reveals a previously unidentified fold for the evolutionarily conserved frataxin family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 8932-8937.	3.3	119
17	Crystal structure of carboxylesterase from <i>Pseudomonas fluorescens</i> , an $\alpha/\beta$ hydrolase with broad substrate specificity. <i>Structure</i> , 1997, 5, 1571-1584.	1.6	109
18	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

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19	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
20	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003, 83, 223-249.	0.8	95
21	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
22	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987, 329, 354-356.	13.7	91
23	Crystal structure of the ribosome recycling factor from <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2000, 19, 2362-2370.	3.5	88
24	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
25	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Adenine series. <i>Journal of Raman Spectroscopy</i> , 1986, 17, 381-386.	1.2	82
26	Raman spectroscopy of sulphur-containing amino acids and their derivatives adsorbed on silver. <i>Journal of Raman Spectroscopy</i> , 1991, 22, 91-96.	1.2	73
27	Crystal Structure of $\beta$ -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
28	Structural basis for the inhibition of <i>Mycobacterium tuberculosis</i> L,D-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
29	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
30	Raman spectroscopy of L-tryptophan-containing peptides adsorbed on a silver surface. <i>Journal of Raman Spectroscopy</i> , 1988, 19, 491-495.	1.2	63
31	Structural Basis for the Enhanced Anti-Diabetic Efficacy of Lobeglitazone on PPAR $\beta$ . <i>Scientific Reports</i> , 2018, 8, 31.	1.6	62
32	Structure of ribulose-1,5-bisphosphate carboxylase-oxygenase: Form III crystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1977, 74, 1037-1041.	3.3	61
33	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
34	Crystal structure of a 16 kDa double-headed Bowman-Birk trypsin inhibitor from barley seeds at 1.9 Å resolution. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 293, 1133-1144.	2.0	57
35	Solution structure of a lipid transfer protein extracted from rice seeds. <i>FEBS Journal</i> , 2001, 259, 692-708.	0.2	56
36	Crystallization, molecular replacement solution, and refinement of tetrameric $\beta$ -amylase from sweet potato. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 105-117.	1.5	55

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37	Directed evolution approach to a structural genomics project: Rv2002 from Mycobacterium tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 455-460.	3.3	55
38	Structural basis for methyl-donor-dependent and sequence-specific binding to tRNA substrates by knotted methyltransferase TrmD. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4197-205.	3.3	54
39	Crystal structures of thermostable xylose isomerases from Thermus caldophilus and Thermus thermophilus : possible structural determinants of thermostability 1 Edited by D. Rees. Journal of Molecular Biology, 1999, 288, 623-634.	2.0	53
40	Crystal Structure of Lipoate-Protein Ligase A Bound with the Activated Intermediate. Journal of Biological Chemistry, 2005, 280, 38081-38089.	1.6	53
41	Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from Saccharomyces cerevisiae 1 Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 293, 753-761.	2.0	51
42	Amino acid sequence of a probable amylase/protease inhibitor from rice seeds. Archives of Biochemistry and Biophysics, 1988, 265, 466-475.	1.4	49
43	<i>Helicobacter pylori</i> proinflammatory protein up-regulates NF- $\kappa$ B as a cell-translocating Ser/Thr kinase. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21418-21423.	3.3	49
44	Crystal structure of an uncleaved $\hat{\pm}$ 1 -antitrypsin reveals the conformation of its inhibitory reactive loop. FEBS Letters, 1995, 377, 150-154.	1.3	48
45	Crystal Structure of Agmatinase Reveals Structural Conservation and Inhibition Mechanism of the Ureohydrolase Superfamily. Journal of Biological Chemistry, 2004, 279, 50505-50513.	1.6	43
46	Crystal Structure of Class I Acetohydroxy Acid Isomeroeductase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2003, 328, 505-515.	2.0	41
47	Structural Basis for the Reaction Mechanism of UDP-Glucose Pyrophosphorylase. Molecules and Cells, 2010, 29, 397-406.	1.0	41
48	Crystal Structure of 2-Nitropropane Dioxygenase Complexed with FMN and Substrate. Journal of Biological Chemistry, 2006, 281, 18660-18667.	1.6	40
49	Structural basis for differential activities of enantiomeric PPAR $\hat{\pm}$ agonists: Binding of S35 to the alternate site. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 674-681.	1.1	40
50	Mechanistic elucidation guided by covalent inhibitors for the development of anti-diabetic PPAR $\hat{\pm}$ ligands. Chemical Science, 2016, 7, 5523-5529.	3.7	39
51	Comparison of solution and crystal structures of maize nonspecific lipid transfer protein: A model for a potential in vivo lipid carrier protein. , 1998, 31, 160-171.		37
52	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Guanine series. Journal of Raman Spectroscopy, 1987, 18, 253-258.	1.2	35
53	The Cell Shape-determining Csd6 Protein from Helicobacter pylori Constitutes a New Family of l,d-Carboxypeptidase. Journal of Biological Chemistry, 2015, 290, 25103-25117.	1.6	34
54	Crystal Structure of the Schiff Base Intermediate Prior to Decarboxylation in the Catalytic Cycle of Aspartate $\hat{\pm}$ -Decarboxylase. Journal of Molecular Biology, 2004, 340, 1-7.	2.0	33

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55	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
56	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
57	Crystal structure of deoxycytidylate hydroxymethylase from bacteriophage T4, a component of the deoxyribonucleoside triphosphate-synthesizing complex. <i>EMBO Journal</i> , 1999, 18, 1104-1113.	3.5	31
58	Crystal Structure of T-protein of the Glycine Cleavage System. <i>Journal of Biological Chemistry</i> , 2004, 279, 50514-50523.	1.6	31
59	Crystallization and preliminary X-ray crystallographic analysis of lipase from <i>Pseudomonas cepacia</i> . <i>Journal of Molecular Biology</i> , 1992, 227, 1258-1262.	2.0	30
60	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
61	Crystal structure analyses of uncomplexed ecotin in two crystal forms: Implications for its function and stability. <i>Protein Science</i> , 1996, 5, 2236-2247.	3.1	29
62	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
63	Refined Structure of the Chitinase from Barley Seeds at 2.0 Å Resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 289-298.	2.5	28
64	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
65	Hydrolysis of plasmid DNA catalyzed by Co(III) complex of cyclen attached to polystyrene. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2001, 11, 2401-2404.	1.0	27
66	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
67	Crystal structure of UDP-N-acetylglucosamine enolpyruvyl transferase from <i>Haemophilus influenzae</i> in complex with UDP-N-acetylglucosamine and fosfomycin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1032-1037.	1.5	27
68	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
69	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
70	Crystal structure of FAF1 UBX domain in complex with p97/VCP N domain reveals a conformational change in the conserved FcisP touch-turn motif of UBX domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2583-2587.	1.5	25
71	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
72	Surface-enhanced Raman scattering of nucleic acid components in silver sol: Uracil and its derivatives. <i>Journal of Raman Spectroscopy</i> , 1988, 19, 261-265.	1.2	23

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73	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
74	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
75	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
76	Structural and functional characterization of <i>Helicobacter pylori</i> DsbG. <i>FEBS Letters</i> , 2011, 585, 3862-3867.	1.3	23
77	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
78	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
79	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
80	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
81	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
82	Structural basis for the recognition of muramyl tripeptide by <i>Helicobacter pylori</i> Csd4, a D <sub>1</sub> -L <sub>1</sub> -carboxypeptidase controlling the helical cell shape. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2800-2812.	2.5	20
83	A crystal form of ribulose-1,5-bisphosphate carboxylase/oxygenase from <i>Nicotiana tabacum</i> in the activated state. <i>Journal of Molecular Biology</i> , 1987, 197, 363-365.	2.0	18
84	Molecular Symmetry of the ClpP Component of the ATP-dependent Clp Protease, an <i>Escherichia coli</i> Homolog of 20 S Proteasome. <i>Journal of Molecular Biology</i> , 1996, 262, 71-76.	2.0	18
85	Isolation of a root-specific cDNA encoding a ns-LTP-like protein from the roots of bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo	2.0	18
86	Determination of the three-dimensional structure of hordothionin- $\hat{\pm}$ by nuclear magnetic resonance. <i>Biochemical Journal</i> , 1996, 313, 885-892.	1.7	17
87	Crystal Structure of d-Erythronate-4-phosphate Dehydrogenase Complexed with NAD. <i>Journal of Molecular Biology</i> , 2007, 366, 1294-1304.	2.0	17
88	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
89	Crystal Structure of the TNF- $\hat{\pm}$ -Inducing Protein (Tip $\hat{\pm}$ ) from <i>Helicobacter pylori</i> : Insights into Its DNA-Binding Activity. <i>Journal of Molecular Biology</i> , 2009, 392, 191-197.	2.0	16
90	Crystallization and a preliminary X-ray crystallographic study of $\hat{\pm}$ -amylase from <i>Bacillus licheniformis</i> . <i>Archives of Biochemistry and Biophysics</i> , 1991, 291, 255-257.	1.4	15

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91	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
92	Surface-enhanced Raman scattering of cytosine and its derivatives in silver sol. <i>Journal of Raman Spectroscopy</i> , 1990, 21, 237-241.	1.2	14
93	Crystallization and preliminary X-ray crystallographic analysis of the Rv2002 gene product from <i>Mycobacterium tuberculosis</i> , a l <sup>2</sup> -ketoacyl carrier protein reductase homologue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 303-305.	2.5	14
94	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
95	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
96	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
97	Cloning and expression of the gene for xylose isomerase from <i>Thermus flavus</i> AT62 in <i>Escherichia coli</i> . <i>Applied Biochemistry and Biotechnology</i> , 1997, 62, 15-27.	1.4	13
98	HBV Polymerase Interacts Independently with N-Terminal and C-Terminal Fragments of Hsp90 <sup>β</sup> . <i>Biochemical and Biophysical Research Communications</i> , 2000, 274, 203-211.	1.0	13
99	Crystal structure of the catalytic domain of cholesterol 14 $\alpha$ -glucosyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2321-2326.	1.5	13
100	Molecular cloning of the Ecotin gene in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1991, 287, 53-56.	1.3	12
101	Computational Studies of Essential Dynamics of <i>Pseudomonas cepacia</i> Lipase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 18, 297-309.	2.0	12
102	Crystal structure of $\beta$ -hordothionin at 1.9 Å... resolution. <i>FEBS Letters</i> , 2005, 579, 2301-2306.	1.3	12
103	The structure of <i>Staphylococcus aureus</i> phosphopantetheine adenyltransferase in complex with 3 <sup>phosphoadenosine 5<sup>phosphosulfate</sup></sup> reveals a new ligand-binding mode. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 987-991.	0.7	12
104	Peptide deformylase inhibitors with retro-amide scaffold: Synthesis and structure-activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 4317-4319.	1.0	12
105	Structural basis for the inhibitory effects of a novel reversible covalent ligand on PPAR <sup>γ</sup> phosphorylation. <i>Scientific Reports</i> , 2019, 9, 11168.	1.6	12
106	Crystal Structure of Phosphopantetheine Adenyltransferase 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
107	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
108	Preliminary X-ray crystallographic and Raman studies on gramicidin S · 2HCl. <i>Archives of Biochemistry and Biophysics</i> , 1985, 243, 563-569.	1.4	10

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109	Hydrolysis of the IciA protein, an inhibitor of DNA replication initiation, by protease Do in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1993, 327, 17-20.	1.3	10
110	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
111	Crystal Structure of a Metal Ion-bound IS200 Transposase. <i>Journal of Biological Chemistry</i> , 2006, 281, 4261-4266.	1.6	10
112	Purothionin from wheat endosperm reversibly blocks myogenic differentiation of chick embryonic muscle cells in culture. <i>Experimental Cell Research</i> , 1989, 183, 501-507.	1.2	9
113	Crystallization and preliminary X-ray crystallographic analysis of arylesterase from <i>Pseudomonas fluorescens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 213-215.	1.5	9
114	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
115	Crystallization and preliminary X-ray crystallographic analysis of <i>Escherichia coli</i> CyaY, a structural homologue of human frataxin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 920-921.	2.5	8
116	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
117	Structure of inorganic pyrophosphatase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1459-1464.	2.5	8
118	Structural basis of octanoic acid recognition by lipoteichoate protein ligase B. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1620-1625.	1.5	8
119	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
120	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
121	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
122	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
123	A Raman spectroscopic study on 5'-rGMP gel and self-aggregate. <i>Biopolymers</i> , 1986, 25, 753-762.	1.2	7
124	Crystallization and Preliminary X-ray Crystallographic Analysis of the Protease Inhibitor Ecotin. <i>Journal of Molecular Biology</i> , 1993, 229, 1157-1158.	2.0	7
125	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
126	Overexpression, crystallization and preliminary X-ray crystallographic analysis of phosphopantetheine adenylyltransferase from <i>Enterococcus faecalis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1131-1133.	0.7	7



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127	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
128	Crystallization and Preliminary X-ray Crystallographic Analysis of Probable Amylase/Protease Inhibitor-B from Rice Seeds. <i>Journal of Molecular Biology</i> , 1993, 229, 255-257.	2.0	6
129	Crystallization and preliminary X-ray crystallographic analysis of human nucleoside diphosphate kinase A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 504-505.	2.5	6
130	Crystal structure of the mouse p53 core domain in zinc-free state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 280-283.	1.5	6
131	Structure of 3-deoxy-manno-octulosonate cytidyltransferase from <i>Haemophilus influenzae</i> complexed with the substrate 3-deoxy-manno-octulosonate in the $\beta^2$ -configuration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1292-1294.	2.5	6
132	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
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