

# Se Won Suh

## List of Publications by Citations

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190  
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192  
ext. papers

6,268  
ext. citations

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4.96  
L-index

#	Paper	IF	Citations
190	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>Nature</i> , <b>1995</b> , 376, 612-6	50.4	332
189	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> , <b>1997</b> , 5, 173-85	5.2	275
188	High-resolution crystal structure of the non-specific lipid-transfer protein from maize seedlings. <i>Structure</i> , <b>1995</b> , 3, 189-99	5.2	212
187	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. <i>Journal of Molecular Biology</i> , <b>1998</b> , 275, 347-63	6.5	204
186	Crystal structure and functional analysis of the SurE protein identify a novel phosphatase family. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 789-94		177
185	Alpha-synuclein regulates neuronal survival via Bcl-2 family expression and PI3/Akt kinase pathway. <i>FASEB Journal</i> , <b>2002</b> , 16, 1826-8	0.9	169
184	Crystal structure of NAD(+)-dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , <b>2000</b> , 19, 1119-29	13	154
183	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography. <i>Journal of Molecular Biology</i> , <b>2001</b> , 308, 263-78	6.5	145
182	Tertiary structure of plant RuBisCO: domains and their contacts. <i>Science</i> , <b>1988</b> , 241, 71-4	33.3	142
181	<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> , <b>2012</b> , 109, 7729-34	11.5	137
180	Rice non-specific lipid transfer protein: the 1.6 Å crystal structure in the unliganded state reveals a small hydrophobic cavity. <i>Journal of Molecular Biology</i> , <b>1998</b> , 276, 437-48	6.5	117
179	Crystal structure of tRNA(m1G37)methyltransferase: insights into tRNA recognition. <i>EMBO Journal</i> , <b>2003</b> , 22, 2593-603	13	111
178	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> , <b>2000</b> , 97, 8932-7	11.5	104
177	Surface-enhanced Raman scattering (SERS) of aromatic amino acids and their glycyI dipeptides in silver sol. <i>Journal of Raman Spectroscopy</i> , <b>1987</b> , 18, 171-175	2.3	103
176	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> , <b>2008</b> , 20, 920-33	11.6	97
175	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. <i>EMBO Journal</i> , <b>2004</b> , 23, 2029-38	13	94
174	Crystal structure of carboxylesterase from <i>Pseudomonas fluorescens</i> , an alpha/beta hydrolase with broad substrate specificity. <i>Structure</i> , <b>1997</b> , 5, 1571-84	5.2	93

173	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> , <b>2006</b> , 362, 66-77	6.5	87
172	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. <i>Tuberculosis</i> , <b>2003</b> , 83, 223-49	2.6	86
171	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , <b>1987</b> , 329, 354-6	50.4	83
170	Crystal structure of the ribosome recycling factor from Escherichia coli. <i>EMBO Journal</i> , <b>2000</b> , 19, 2362-70	3	80
169	Structural and functional insights into Dom34, a key component of no-go mRNA decay. <i>Molecular Cell</i> , <b>2007</b> , 27, 938-50	17.6	78
168	Crystal structure of human nucleophosmin-core reveals plasticity of the pentamer-pentamer interface. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69, 672-8	4.2	72
167	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Adenine series. <i>Journal of Raman Spectroscopy</i> , <b>1986</b> , 17, 381-386	2.3	71
166	Raman spectroscopy of sulphur-containing amino acids and their derivatives adsorbed on silver. <i>Journal of Raman Spectroscopy</i> , <b>1991</b> , 22, 91-96	2.3	67
165	The TB structural genomics consortium: providing a structural foundation for drug discovery. <i>Current Drug Targets Infectious Disorders</i> , <b>2002</b> , 2, 121-41		60
164	Crystal structure of beta-D-xylosidase from Thermoanaerobacterium saccharolyticum, a family 39 glycoside hydrolase. <i>Journal of Molecular Biology</i> , <b>2004</b> , 335, 155-65	6.5	59
163	Raman spectroscopy of L-tryptophan-containing peptides adsorbed on a silver surface. <i>Journal of Raman Spectroscopy</i> , <b>1988</b> , 19, 491-495	2.3	57
162	Structural basis for the inhibition of Mycobacterium tuberculosis L,D-transpeptidase by meropenem, a drug effective against extensively drug-resistant strains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 420-31		53
161	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> , <b>1977</b> , 74, 1037-41	11.5	52
160	Arrest defective 1 autoacetylation is a critical step in its ability to stimulate cancer cell proliferation. <i>Cancer Research</i> , <b>2010</b> , 70, 4422-32	10.1	50
159	Solution structure of a lipid transfer protein extracted from rice seeds. Comparison with homologous proteins. <i>FEBS Journal</i> , <b>1999</b> , 259, 692-708		50
158	Crystal structure of a 16 kDa double-headed Bowman-Birk trypsin inhibitor from barley seeds at 1.9 Å resolution. <i>Journal of Molecular Biology</i> , <b>1999</b> , 293, 1133-44	6.5	50
157	Crystallization, molecular replacement solution, and refinement of tetrameric beta-amylase from sweet potato. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 21, 105-17	4.2	50
156	Directed evolution approach to a structural genomics project: Rv2002 from Mycobacterium tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 455-60	11.5	48

155	Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , <b>1999</b> , 293, 753-61	6.5	48
154	Crystal structures of thermostable xylose isomerases from <i>Thermus caldophilus</i> and <i>Thermus thermophilus</i> : possible structural determinants of thermostability. <i>Journal of Molecular Biology</i> , <b>1999</b> , 288, 623-34	6.5	46
153	Amino acid sequence of a probable amylase/protease inhibitor from rice seeds. <i>Archives of Biochemistry and Biophysics</i> , <b>1988</b> , 265, 466-75	4.1	45
152	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> , <b>2015</b> , 112, E4197-205	11.5	44
151	Crystal structure of an uncleaved alpha 1-antitrypsin reveals the conformation of its inhibitory reactive loop. <i>FEBS Letters</i> , <b>1995</b> , 377, 150-4	3.8	44
150	<i>Helicobacter pylori</i> proinflammatory protein up-regulates NF-kappaB as a cell-translocating Ser/Thr kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 21418-23	11.5	43
149	Crystal structure of lipoate-protein ligase A bound with the activated intermediate: insights into interaction with lipoyl domains. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 38081-9	5.4	42
148	Structural Basis for the Enhanced Anti-Diabetic Efficacy of Lobeglitazone on PPAR $\alpha$ <i>Scientific Reports</i> , <b>2018</b> , 8, 31	4.9	41
147	Crystal structure of agmatinase reveals structural conservation and inhibition mechanism of the ureohydrolase superfamily. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 50505-13	5.4	37
146	Crystal structure of class I acetohydroxy acid isomeroreductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , <b>2003</b> , 328, 505-15	6.5	36
145	Crystal structure of 2-nitropropane dioxygenase complexed with FMN and substrate. Identification of the catalytic base. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 18660-7	5.4	35
144	Comparison of solution and crystal structures of maize nonspecific lipid transfer protein: a model for a potential in vivo lipid carrier protein. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1998</b> , 31, 160-71	4.7	34
143	Structural basis for the reaction mechanism of UDP-glucose pyrophosphorylase. <i>Molecules and Cells</i> , <b>2010</b> , 29, 397-405	3.5	31
142	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Guanine series. <i>Journal of Raman Spectroscopy</i> , <b>1987</b> , 18, 253-258	2.3	31
141	Structural basis for differential activities of enantiomeric PPAR $\alpha$ agonists: Binding of S35 to the alternate site. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2017</b> , 1865, 674-681	4	29
140	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. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 1351-62	6.5	29
139	Mechanistic elucidation guided by covalent inhibitors for the development of anti-diabetic PPAR $\alpha$ ligands. <i>Chemical Science</i> , <b>2016</b> , 7, 5523-5529	9.4	29
138	Competitive inhibitors of <i>Helicobacter pylori</i> type II dehydroquinase: synthesis, biological evaluation, and NMR studies. <i>ChemMedChem</i> , <b>2008</b> , 3, 756-70	3.7	28

137	Crystal structure of T-protein of the glycine cleavage system. Cofactor binding, insights into H-protein recognition, and molecular basis for understanding nonketotic hyperglycinemia. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 50514-23	5.4	26
136	Crystal structure of the schiff base intermediate prior to decarboxylation in the catalytic cycle of aspartate alpha-decarboxylase. <i>Journal of Molecular Biology</i> , <b>2004</b> , 340, 1-7	6.5	26
135	Crystal structure of deoxycytidylate hydroxymethylase from bacteriophage T4, a component of the deoxyribonucleoside triphosphate-synthesizing complex. <i>EMBO Journal</i> , <b>1999</b> , 18, 1104-13	13	26
134	Crystallization and preliminary X-ray crystallographic analysis of lipase from <i>Pseudomonas cepacia</i> . <i>Journal of Molecular Biology</i> , <b>1992</b> , 227, 1258-62	6.5	26
133	Crystal structure of chorismate synthase: a novel FMN-binding protein fold and functional insights. <i>Journal of Molecular Biology</i> , <b>2004</b> , 336, 903-15	6.5	25
132	Crystal structure analyses of uncomplexed ecotin in two crystal forms: implications for its function and stability. <i>Protein Science</i> , <b>1996</b> , 5, 2236-47	6.3	25
131	Crystal structure of human nucleoside diphosphate kinase A, a metastasis suppressor. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 46, 340-2	4.2	24
130	Refined structure of the chitinase from barley seeds at 2.0 a resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1996</b> , 52, 289-98		24
129	Crystal structure of Tpa1 from <i>Saccharomyces cerevisiae</i> , a component of the messenger ribonucleoprotein complex. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 2099-110	20.1	23
128	Depletion of nucleophosmin via transglutaminase 2 cross-linking increases drug resistance in cancer cells. <i>Cancer Letters</i> , <b>2009</b> , 274, 201-7	9.9	23
127	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> , <b>2008</b> , 71, 1032-7	4.2	23
126	Crystal structure of UDP-N-acetylglucosamine acyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53, 772-4	4.2	23
125	Hydrolysis of plasmid DNA catalyzed by Co(III) complex of cyclen attached to polystyrene. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2001</b> , 11, 2401-4	2.9	23
124	Structural basis for ovarian tumor domain-containing protein 1 (OTU1) binding to p97/valosin-containing protein (VCP). <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 12264-74	5.4	22
123	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> , <b>2011</b> , 79, 2583-7	4.2	22
122	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> , <b>2008</b> , 72, 1363-70	4.2	21
121	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> , <b>2005</b> , 351, 258-65	6.5	21
120	Structural and functional characterization of <i>Helicobacter pylori</i> DsbG. <i>FEBS Letters</i> , <b>2011</b> , 585, 3862-7	3.8	20

119	ATP-dependent DNA ligase from <i>Archaeoglobus fulgidus</i> displays a tightly closed conformation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2009</b> , 65, 544-50		20
118	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> , <b>2007</b> , 69, 691-4	4.2	20
117	Mutational analyses of the thermostable NAD <sup>+</sup> -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , <b>2004</b> , 237, 111-118	2.9	20
116	Surface-enhanced Raman scattering of nucleic acid components in silver sol: Uracil and its derivatives. <i>Journal of Raman Spectroscopy</i> , <b>1988</b> , 19, 261-265	2.3	20
115	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> , <b>2015</b> , 290, 25103-17	5.4	19
114	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> , <b>2004</b> , 57, 639-42	4.2	18
113	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> , <b>2011</b> , 175, 442-50	3.4	17
112	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> , <b>1996</b> , 262, 71-6	6.5	17
111	Determination of the three-dimensional structure of hordothionin-alpha by nuclear magnetic resonance. <i>Biochemical Journal</i> , <b>1996</b> , 313 ( Pt 3), 885-92	3.8	17
110	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> , <b>1987</b> , 197, 363-5	6.5	17
109	Isolation of a root-specific cDNA encoding a ns-LTP-like protein from the roots of bean ( <i>Phaseolus vulgaris</i> L.) seedlings. <i>Plant Molecular Biology</i> , <b>1996</b> , 30, 1059-66	4.6	16
108	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> , <b>2014</b> , 70, 2800-12		15
107	Helical repeat structure of apoptosis inhibitor 5 reveals protein-protein interaction modules. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 10727-37	5.4	15
106	Crystal structure of D-erythronate-4-phosphate dehydrogenase complexed with NAD. <i>Journal of Molecular Biology</i> , <b>2007</b> , 366, 1294-304	6.5	15
105	Crystallization and a preliminary X-ray crystallographic study of alpha-amylase from <i>Bacillus licheniformis</i> . <i>Archives of Biochemistry and Biophysics</i> , <b>1991</b> , 291, 255-7	4.1	15
104	Crystal structure of the TNF-alpha-Inducing protein (Tipalpha) from <i>Helicobacter pylori</i> : Insights into Its DNA-binding activity. <i>Journal of Molecular Biology</i> , <b>2009</b> , 392, 191-7	6.5	13
103	Crystallization and preliminary X-ray crystallographic analysis of the Rv2002 gene product from <i>Mycobacterium tuberculosis</i> , a beta-ketoacyl carrier protein reductase homologue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 303-5		13
102	HBV polymerase interacts independently with N-terminal and C-terminal fragments of Hsp90beta. <i>Biochemical and Biophysical Research Communications</i> , <b>2000</b> , 274, 203-11	3.4	13

101	Surface-enhanced Raman scattering of cytosine and its derivatives in silver sol. <i>Journal of Raman Spectroscopy</i> , <b>1990</b> , 21, 237-241	2.3	13
100	Crystal structure of the catalytic domain of cholesterol- $\beta$ -glucosyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 2321-6	4.2	12
99	Peptide deformylase inhibitors with retro-amide scaffold: synthesis and structure-activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2010</b> , 20, 4317-9	2.9	12
98	Crystal structure of the type II 3-dehydroquinase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 51, 616-7	4.2	12
97	Computational studies of essential dynamics of <i>Pseudomonas cepacia</i> lipase. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2000</b> , 18, 297-309	3.6	12
96	Structure of Csd3 from <i>Helicobacter pylori</i> , a cell shape-determining metallopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 675-86		11
95	Dimeric and tetrameric forms of enoyl-acyl carrier protein reductase from <i>Bacillus cereus</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2010</b> , 400, 517-22	3.4	11
94	The structure of <i>Staphylococcus aureus</i> phosphopantetheine adenylyltransferase in complex with 3Pphosphoadenosine 5Pphosphosulfate reveals a new ligand-binding mode. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2009</b> , 65, 987-91		11
93	Structural Basis of the Heterodimer Formation between Cell Shape-Determining Proteins Csd1 and Csd2 from <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , <b>2016</b> , 11, e0164243	3.7	11
92	Crystal structures of <i>Pseudomonas aeruginosa</i> guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. <i>Journal of Structural Biology</i> , <b>2011</b> , 175, 329-38	3.4	10
91	Crystal structure of alpha-hordothionin at 1.9 Angstrom resolution. <i>FEBS Letters</i> , <b>2005</b> , 579, 2301-6	3.8	10
90	Crystal structure of a metal ion-bound IS200 transposase. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 4263-6	3.6	10
89	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> , <b>2004</b> , 56, 176-9	4.2	10
88	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> , <b>2011</b> , 32, 431-5	3.5	9
87	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> , <b>1997</b> , 62, 15-27	3.2	9
86	Purothionin from wheat endosperm reversibly blocks myogenic differentiation of chick embryonic muscle cells in culture. <i>Experimental Cell Research</i> , <b>1989</b> , 183, 501-7	4.2	9
85	Molecular cloning of the ecotin gene in <i>Escherichia coli</i> . <i>FEBS Letters</i> , <b>1991</b> , 287, 53-6	3.8	9
84	Crystal structure of PhoU from <i>Pseudomonas aeruginosa</i> , a negative regulator of the Pho regulon. <i>Journal of Structural Biology</i> , <b>2014</b> , 188, 22-9	3.4	8

83	Structures of the ribosome-inactivating protein from barley seeds reveal a unique activation mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1488-500		8
82	Structural and functional characterization of HP0377, a thioredoxin-fold protein from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 735-46		8
81	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> , <b>2004</b> , 60, 1447-9		8
80	Structure of inorganic pyrophosphatase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2005</b> , 61, 1459-64		8
79	Hydrolysis of the IciA protein, an inhibitor of DNA replication initiation, by protease Do in <i>Escherichia coli</i> . <i>FEBS Letters</i> , <b>1993</b> , 327, 17-20	3.8	8
78	Structural basis for the inhibitory effects of a novel reversible covalent ligand on PPAR $\alpha$ phosphorylation. <i>Scientific Reports</i> , <b>2019</b> , 9, 11168	4.9	7
77	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> , <b>2006</b> , 62, 1131-3		7
76	Crystallization and preliminary X-ray crystallographic analysis of the protease inhibitor ecotin. <i>Journal of Molecular Biology</i> , <b>1993</b> , 229, 1157-8	6.5	7
75	Crystallization and preliminary X-ray crystallographic analysis of arylesterase from <i>Pseudomonas fluorescens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1993</b> , 15, 213-5	4.2	7
74	A Raman spectroscopic study on 5'-rGMP gel and self-aggregate. <i>Biopolymers</i> , <b>1986</b> , 25, 753-762	2.2	7
73	Preliminary X-ray crystallographic and Raman studies on gramicidin S.2HCl. <i>Archives of Biochemistry and Biophysics</i> , <b>1985</b> , 243, 563-9	4.1	7
72	Peptidoglycan reshaping by a noncanonical peptidase for helical cell shape in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 458	17.4	6
71	Structure of <i>Mycobacterium smegmatis</i> Eis in complex with paromomycin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1173-9	1.1	6
70	Crystal structure of the mouse p53 core domain in zinc-free state. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 280-3	4.2	6
69	Structural basis of octanoic acid recognition by lipoate-protein ligase B. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 1620-5	4.2	6
68	Crystallization and preliminary X-ray crystallographic studies of phosphopantetheine adenylyltransferase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 561-2		6
67	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> , <b>2000</b> , 56, 920-1		6
66	Mutational analyses of the thermostable NAD <sup>+</sup> -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , <b>2004</b> , 237, 111-8	2.9	6



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35	Crystal structure of Rv2258c from <i>Mycobacterium tuberculosis</i> H37Rv, an S-adenosyl-L-methionine-dependent methyltransferase. <i>Journal of Structural Biology</i> , <b>2016</b> , 193, 172-180 <sup>3,4</sup>		2
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