

Se Won Suh

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/3242192/se-won-suh-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

190
papers

5,799
citations

42
h-index

70
g-index

192
ext. papers

6,268
ext. citations

6.5
avg, IF

4.96
L-index

#	Paper	IF	Citations
190	Structural basis for SdgB- and SdgA-mediated glycosylation of staphylococcal adhesive proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1460-1474	5.5	
189	Peptidoglycan reshaping by a noncanonical peptidase for helical cell shape in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2020 , 11, 458	17.4	6
188	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>Journal of Hand Surgery Asian-Pacific Volume, The</i> , 2020 , 288-292	0.5	
187	Structural basis for the inhibitory effects of a novel reversible covalent ligand on PPAR α phosphorylation. <i>Scientific Reports</i> , 2019 , 9, 11168	4.9	7
186	A cytosine modification mechanism revealed by the structure of a ternary complex of deoxycytidylate hydroxymethylase from bacteriophage T4 with its cofactor and substrate. <i>IUCrJ</i> , 2019 , 6, 206-217	4.7	4
185	Structural Basis for the Enhanced Anti-Diabetic Efficacy of Lobeglitazone on PPAR α . <i>Scientific Reports</i> , 2018 , 8, 31	4.9	41
184	Structural basis for the substrate recognition of peptidoglycan pentapeptides by <i>Enterococcus faecalis</i> VanY. <i>International Journal of Biological Macromolecules</i> , 2018 , 119, 335-344	7.9	3
183	Structural basis for differential activities of enantiomeric PPAR α agonists: Binding of S35 to the alternate site. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 674-681	4	29
182	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 ^{3,4}		2
181	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	3.7	11
180	Mechanistic elucidation guided by covalent inhibitors for the development of anti-diabetic PPAR α ligands. <i>Chemical Science</i> , 2016 , 7, 5523-5529	9.4	29
179	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	11.5	44
178	Structure of Csd3 from <i>Helicobacter pylori</i> , a cell shape-determining metallopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 675-86		11
177	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, 1001-9	4	4
176	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, 25103-17	5.4	19
175	Structure of <i>Mycobacterium smegmatis</i> Eis in complex with paromomycin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1173-9	1.1	6
174	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, 2275-81	4.2	3

173	Crystal structure of PhoU from <i>Pseudomonas aeruginosa</i> , a negative regulator of the Pho regulon. <i>Journal of Structural Biology</i> , 2014 , 188, 22-9	3.4	8
172	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, 12264-74	5.4	22
171	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, 2800-12		15
170	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, 420-31		53
169	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, 929-32	2.4	5
168	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, 735-46		8
167	High-resolution crystal structure of <i>Streptococcus pyogenes</i> ENAD+ glycohydrolase in complex with its endogenous inhibitor IFS reveals a highly water-rich interface. <i>Journal of Synchrotron Radiation</i> , 2013 , 20, 962-7	2.4	1
166	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, 784-93		4
165	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, 440-2		2
164	Crystal structure of pyridoxal biosynthesis lyase PdxS from <i>Pyrococcus horikoshii</i> . <i>Molecules and Cells</i> , 2012 , 34, 407-12	3.5	5
163	Helical repeat structure of apoptosis inhibitor 5 reveals protein-protein interaction modules. <i>Journal of Biological Chemistry</i> , 2012 , 287, 10727-37	5.4	15
162	Structures of the ribosome-inactivating protein from barley seeds reveal a unique activation mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 1488-500		8
161	<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, 7729-34	11.5	137
160	Crystal structures of <i>Pseudomonas aeruginosa</i> guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. <i>Journal of Structural Biology</i> , 2011 , 175, 329-38	3.4	10
159	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, 442-50	3.4	17
158	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, 307-12	3.8	4
157	Structural and functional characterization of <i>Helicobacter pylori</i> DsbG. <i>FEBS Letters</i> , 2011 , 585, 3862-7	3.8	20
156	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, 431-5	3.5	9

155	Crystal structure of the catalytic domain of cholesterol- β -glucosyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2321-6	4.2	12
154	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, 2583-7	4.2	22
153	Arrest defective 1 autoacetylation is a critical step in its ability to stimulate cancer cell proliferation. <i>Cancer Research</i> , 2010 , 70, 4422-32	10.1	50
152	Crystal structure of Tpa1 from <i>Saccharomyces cerevisiae</i> , a component of the messenger ribonucleoprotein complex. <i>Nucleic Acids Research</i> , 2010 , 38, 2099-110	20.1	23
151	<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> , 2010 , 107, 21418-23	11.5	43
150	Crystal structures of two archaeal Pelotas reveal inter-domain structural plasticity. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 399, 600-6	3.4	3
149	Dimeric and tetrameric forms of enoyl-acyl carrier protein reductase from <i>Bacillus cereus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010 , 400, 517-22	3.4	11
148	Peptide deformylase inhibitors with retro-amide scaffold: synthesis and structure-activity relationships. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010 , 20, 4317-9	2.9	12
147	Structural basis for the reaction mechanism of UDP-glucose pyrophosphorylase. <i>Molecules and Cells</i> , 2010 , 29, 397-405	3.5	31
146	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, 905-8		
145	Crystal structure of <i>Thermotoga maritima</i> SPOUT superfamily RNA methyltransferase Tm1570 in complex with S-adenosyl-L-methionine. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 245-9	4.2	2
144	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, 544-50		20
143	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> , 2009 , 65, 987-91		11
142	Depletion of nucleophosmin via transglutaminase 2 cross-linking increases drug resistance in cancer cells. <i>Cancer Letters</i> , 2009 , 274, 201-7	9.9	23
141	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> , 2009 , 392, 191-7	6.5	13
140	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, 920-33	11.6	97
139	Crystal structure of the mouse p53 core domain in zinc-free state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 280-3	4.2	6
138	Structural basis of octanoic acid recognition by lipoate-protein ligase B. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 1620-5	4.2	6

137	Structure of 3-deoxy-manno-octulosonate cytidyltransferase from Haemophilus influenzae complexed with the substrate 3-deoxy-manno-octulosonate in the beta-configuration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 1292-4		5
136	Crystal structure of UDP-N-acetylglucosamine enolpyruvyl transferase from Haemophilus influenzae in complex with UDP-N-acetylglucosamine and fosfomycin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1032-7	4.2	23
135	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, 1363-70	4.2	21
134	Competitive inhibitors of Helicobacter pylori type II dehydroquinase: synthesis, biological evaluation, and NMR studies. <i>ChemMedChem</i> , 2008 , 3, 756-70	3.7	28
133	Crystal structure of human nucleophosmin-core reveals plasticity of the pentamer-pentamer interface. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 672-8	4.2	72
132	Crystal structure of the Helicobacter pylori enoyl-acyl carrier protein reductase in complex with hydroxydiphenyl ether compounds, triclosan and diclosan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 691-4	4.2	20
131	The recombination-associated protein RdgC adopts a novel toroidal architecture for DNA binding. <i>Nucleic Acids Research</i> , 2007 , 35, 2671-81	20.1	5
130	Crystal structure of D-erythronate-4-phosphate dehydrogenase complexed with NAD. <i>Journal of Molecular Biology</i> , 2007 , 366, 1294-304	6.5	15
129	Structural and functional insights into Dom34, a key component of no-go mRNA decay. <i>Molecular Cell</i> , 2007 , 27, 938-50	17.6	78
128	Crystal structure of 2-nitropropane dioxygenase complexed with FMN and substrate. Identification of the catalytic base. <i>Journal of Biological Chemistry</i> , 2006 , 281, 18660-7	5.4	35
127	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	6.5	87
126	S2c1-1 Structure and Ribonuclease Activity of Pelota : Implications for the No-go Decay and Translation Regulation(S2-c1: "Crystallographic approach to understand biological supramacromolecular assemblies",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). <i>Cellular and Molecular Life Sciences</i> , 2006 , 62, 5120	0	
125	Overexpression, crystallization and preliminary X-ray crystallographic analysis of erythronate-4-phosphate dehydrogenase from Pseudomonas aeruginosa. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 139-41		2
124	Expression, crystallization and preliminary X-ray crystallographic analyses of two N-terminal acetyltransferase-related proteins from Thermoplasma acidophilum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 1127-30		2
123	Overexpression, crystallization and preliminary X-ray crystallographic analysis of phosphopantetheine adenylyltransferase from Enterococcus faecalis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 1131-3		7
122	Overexpression, crystallization and preliminary X-ray crystallographic analysis of a putative transposase from Thermoplasma acidophilum encoded by the Ta0474 gene. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 1147-9		1
121	Crystal structure of a metal ion-bound IS200 transposase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 4263-6		10
120	Crystal structure of nicotinic acid mononucleotide adenylyltransferase from Pseudomonas aeruginosa in its Apo and substrate-complexed forms reveals a fully open conformation. <i>Journal of Molecular Biology</i> , 2005 , 351, 258-65	6.5	21

119	Crystal structure of alpha-hordothionin at 1.9 Angstrom resolution. <i>FEBS Letters</i> , 2005 , 579, 2301-6	3.8	10
118	Structure of inorganic pyrophosphatase from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1459-64		8
117	Expression, crystallization and preliminary X-ray crystallographic analysis of human agmatinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 889-91		1
116	Crystal structure of lipoate-protein ligase A bound with the activated intermediate: insights into interaction with lipoyl domains. <i>Journal of Biological Chemistry</i> , 2005 , 280, 38081-9	5.4	42
115	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	3.5	1
114	Crystal structure of agmatinase reveals structural conservation and inhibition mechanism of the ureohydrolase superfamily. <i>Journal of Biological Chemistry</i> , 2004 , 279, 50505-13	5.4	37
113	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> , 2004 , 279, 50514-23	5.4	26
112	Mutational analyses of the thermostable NAD ⁺ -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , 2004 , 237, 111-118	2.9	20
111	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. <i>EMBO Journal</i> , 2004 , 23, 2029-38	13	94
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, 176-9	4.2	10
109	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, 639-42	4.2	18
108	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, 379-81		4
107	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, 948-9		5
106	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, 1447-9		8
105	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, 1890-2		2
104	Crystal structure of beta-D-xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> , a family 39 glycoside hydrolase. <i>Journal of Molecular Biology</i> , 2004 , 335, 155-65	6.5	59
103	Crystal structure of chorismate synthase: a novel FMN-binding protein fold and functional insights. <i>Journal of Molecular Biology</i> , 2004 , 336, 903-15	6.5	25
102	Crystal structure of the schiff base intermediate prior to decarboxylation in the catalytic cycle of aspartate alpha-decarboxylase. <i>Journal of Molecular Biology</i> , 2004 , 340, 1-7	6.5	26

101	Mutational analyses of the thermostable NAD ⁺ -dependent DNA ligase from <i>Thermus filiformis</i> . <i>FEMS Microbiology Letters</i> , 2004 , 237, 111-8	2.9	6
100	Crystal structure of tRNA(m1G37)methyltransferase: insights into tRNA recognition. <i>EMBO Journal</i> , 2003 , 22, 2593-603	13	111
99	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003 , 83, 223-49	2.6	86
98	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, 180-2		2
97	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, 183-4		1
96	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, 563-5		1
95	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, 569-71		4
94	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, 561-2		6
93	Crystal structure of the type II 3-dehydroquinase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 51, 616-7	4.2	12
92	Crystal structure of UDP-N-acetylglucosamine acyltransferase from <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 772-4	4.2	23
91	Crystal structure of class I acetohydroxy acid isomeroeductase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2003 , 328, 505-15	6.5	36
90	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, 455-60	11.5	48
89	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> , 2002 , 58, 303-5		13
88	Crystallization and preliminary X-ray crystallographic analysis of beta-xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> , a thermophilic anaerobe. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 531-2		1
87	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, 861-3		3
86	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, 864-6		3
85	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, 1071-3		3
84	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, 1874-5		4

83	Crystallization and preliminary X-ray crystallographic analysis of acetohydroxy acid isomeroeductase from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 2145-6		3
82	Crystal structure of human nucleoside diphosphate kinase A, a metastasis suppressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 46, 340-2	4.2	24
81	Alpha-synuclein regulates neuronal survival via Bcl-2 family expression and PI3/Akt kinase pathway. <i>FASEB Journal</i> , 2002 , 16, 1826-8	0.9	169
80	The TB structural genomics consortium: providing a structural foundation for drug discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002 , 2, 121-41		60
79	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-anti-sigma factors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 276-8		4
78	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, 279-80		2
77	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, 438-40		2
76	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, 612-3		2
75	Crystallization and preliminary X-ray crystallographic analysis of deoxyuridine triphosphate nucleotidohydrolase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1147-9		0
74	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, 1686-8		4
73	Hydrolysis of plasmid DNA catalyzed by Co(III) complex of cyclen attached to polystyrene. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2001 , 11, 2401-4	2.9	23
72	Crystal structure and functional analysis of the SurE protein identify a novel phosphatase family. <i>Nature Structural Biology</i> , 2001 , 8, 789-94		177
71	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> , 2001 , 307, 1351-62	6.5	29
70	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> , 2001 , 308, 263-78	6.5	145
69	Crystallization and preliminary x-ray crystallographic analysis of NAD ⁺ -dependent DNA ligase from <i>Thermus filiformis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 357-8		2
68	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		3
67	Overexpression, crystallization and preliminary X-ray crystallographic analysis of dihydrofolate reductase from bacteriophage T4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 775-7		
66	Crystallization and preliminary X-ray diffraction analysis of <i>Saccharomyces cerevisiae</i> Ygr203p, a homologue of Acr2 arsenate reductase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 778-80		2

65	Crystallization and preliminary X-ray crystallographic analysis of Escherichia coli CyaY, a structural homologue of human frataxin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 920-1		6
64	Nucleoside diphosphate kinase from the hyperthermophilic archaeon Methanococcus jannaschii: overexpression, crystallization and preliminary X-ray crystallographic analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1485-7		3
63	Lactate dehydrogenase from the hyperthermophilic archaeon Methanococcus jannaschii: overexpression, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 81-3		2
62	Crystallization and preliminary crystallographic studies of ribosome recycling factor from Escherichia coli. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 84-5		2
61	Crystal structure of the ribosome recycling factor from Escherichia coli. <i>EMBO Journal</i> , 2000 , 19, 2362-70	13	80
60	Crystal structure of NAD(+)-dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , 2000 , 19, 1119-29	13	154
59	Crystal structure of Escherichia coli 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, 8932-7	11.5	104
58	HBV polymerase interacts independently with N-terminal and C-terminal fragments of Hsp90beta. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 274, 203-11	3.4	13
57	Computational studies of essential dynamics of Pseudomonas cepacia lipase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000 , 18, 297-309	3.6	12
56	Solution structure of a lipid transfer protein extracted from rice seeds. Comparison with homologous proteins. <i>FEBS Journal</i> , 1999 , 259, 692-708		50
55	A thermostable xylose isomerase from Thermus caldophilus: biochemical characterization, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 294-6		3
54	Crystallization and preliminary X-ray crystallographic analysis of deoxycytidylate hydroxymethylase from bacteriophage T4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1061-3		1
53	Crystallization and preliminary X-ray crystallographic analysis of the protease inhibitor ecotin in complex with chymotrypsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1091-2		1
52	Crystallization and preliminary X-ray analysis of Saccharomyces cerevisiae Ypd1p, a key intermediate in phosphorelay signal transduction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1219-21		2
51	Crystallization and preliminary X-ray analysis of a complex between the Bowman-Birk trypsin inhibitor from barley and porcine pancreatic trypsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1244-6		1
50	Crystal structure of deoxycytidylate hydroxymethylase from bacteriophage T4, a component of the deoxyribonucleoside triphosphate-synthesizing complex. <i>EMBO Journal</i> , 1999 , 18, 1104-13	13	26
49	Crystal structures of thermostable xylose isomerases from Thermus caldophilus and Thermus thermophilus: possible structural determinants of thermostability. <i>Journal of Molecular Biology</i> , 1999 , 288, 623-34	6.5	46
48	Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from Saccharomyces cerevisiae. <i>Journal of Molecular Biology</i> , 1999 , 293, 753-61	6.5	48

47	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> , 1999 , 293, 1133-44	6.5	50
46	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> , 1998 , 31, 160-71	4.7	34
45	Preliminary X-ray crystallographic analysis of Bowman-Birk trypsin inhibitor from barley seeds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 441-3		3
44	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> , 1998 , 275, 347-63	6.5	204
43	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> , 1998 , 276, 437-48	6.5	117
42	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, 173-85	5.2	275
41	Crystal structure of carboxylesterase from <i>Pseudomonas fluorescens</i> , an alpha/beta hydrolase with broad substrate specificity. <i>Structure</i> , 1997 , 5, 1571-84	5.2	93
40	Mutational analysis for the role of C-terminal region of ecotin, a dimeric inhibitor of pancreatic serine proteases. <i>IUBMB Life</i> , 1997 , 42, 799-807	4.7	
39	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	3.2	9
38	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, 71-6	6.5	17
37	Crystal structure of <i>Bacillus licheniformis</i> α-Amylase at 1.7 Å resolution. <i>Progress in Biotechnology</i> , 1996 , 12, 163-170		1
36	Determination of the three-dimensional structure of hordothionin-α by nuclear magnetic resonance. <i>Biochemical Journal</i> , 1996 , 313 (Pt 3), 885-92	3.8	17
35	Refined structure of the chitinase from barley seeds at 2.0 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996 , 52, 289-98		24
34	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> , 1996 , 30, 1059-66	4.6	16
33	Crystal structure analyses of uncomplexed ecotin in two crystal forms: implications for its function and stability. <i>Protein Science</i> , 1996 , 5, 2236-47	6.3	25
32	Crystallization, molecular replacement solution, and refinement of tetrameric beta-amylase from sweet potato. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 21, 105-17	4.2	50
31	Crystal structure of <i>Thermus aquaticus</i> DNA polymerase. <i>Nature</i> , 1995 , 376, 612-6	50.4	332
30	Crystal structure of an uncleaved alpha 1-antitrypsin reveals the conformation of its inhibitory reactive loop. <i>FEBS Letters</i> , 1995 , 377, 150-4	3.8	44

29	Crystallization and preliminary X-ray crystallographic analysis of DNA polymerase from <i>Thermus aquaticus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995 , 51, 1086-8		1
28	High-resolution crystal structure of the non-specific lipid-transfer protein from maize seedlings. <i>Structure</i> , 1995 , 3, 189-99	5.2	212
27	Crystallization and preliminary X-ray crystallographic analysis of phospholipid transfer protein from maize seedlings. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 80-3	4.2	3
26	Crystallization and preliminary X-ray crystallographic study of ribosome-inactivating protein from barley seeds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994 , 50, 910-2		1
25	Crystallization and preliminary X-ray crystallographic analysis of carboxylesterase from <i>Pseudomonas fluorescens</i> . <i>Archives of Biochemistry and Biophysics</i> , 1993 , 302, 417-9	4.1	4
24	Crystallization and preliminary X-ray crystallographic analysis of alpha-amylase from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 1993 , 229, 235-8	6.5	3
23	Crystallization and preliminary X-ray crystallographic analysis of probable amylase/protease inhibitor-B from rice seeds. <i>Journal of Molecular Biology</i> , 1993 , 229, 255-7	6.5	5
22	Crystallization and preliminary X-ray crystallographic analysis of the protease inhibitor ecotin. <i>Journal of Molecular Biology</i> , 1993 , 229, 1157-8	6.5	7
21	Crystallization and preliminary X-ray crystallographic analysis of arylesterase from <i>Pseudomonas fluorescens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 213-5	4.2	7
20	Crystallization and preliminary X-ray crystallographic analysis of chitinase from barley seeds. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 17, 107-9	4.2	3
19	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	3.8	8
18	Crystallization and preliminary X-ray crystallographic analysis of lipase from <i>Pseudomonas cepacia</i> . <i>Journal of Molecular Biology</i> , 1992 , 227, 1258-62	6.5	26
17	Raman spectroscopy of sulphur-containing amino acids and their derivatives adsorbed on silver. <i>Journal of Raman Spectroscopy</i> , 1991 , 22, 91-96	2.3	67
16	Crystallization and a preliminary X-ray crystallographic study of alpha-amylase from <i>Bacillus licheniformis</i> . <i>Archives of Biochemistry and Biophysics</i> , 1991 , 291, 255-7	4.1	15
15	Molecular cloning of the ecotin gene in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1991 , 287, 53-6	3.8	9
14	Surface-enhanced Raman scattering of cytosine and its derivatives in silver sol. <i>Journal of Raman Spectroscopy</i> , 1990 , 21, 237-241	2.3	13
13	Purothionin from wheat endosperm reversibly blocks myogenic differentiation of chick embryonic muscle cells in culture. <i>Experimental Cell Research</i> , 1989 , 183, 501-7	4.2	9
12	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	2.3	20

11	Raman spectroscopy of L-tryptophan-containing peptides adsorbed on a silver surface. <i>Journal of Raman Spectroscopy</i> , 1988 , 19, 491-495	2.3	57
10	Amino acid sequence of a probable amylase/protease inhibitor from rice seeds. <i>Archives of Biochemistry and Biophysics</i> , 1988 , 265, 466-75	4.1	45
9	Tertiary structure of plant RuBisCO: domains and their contacts. <i>Science</i> , 1988 , 241, 71-4	33.3	142
8	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, 363-5	6.5	17
7	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	2.3	103
6	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Guanine series. <i>Journal of Raman Spectroscopy</i> , 1987 , 18, 253-258	2.3	31
5	Sliding-layer conformational change limited by the quaternary structure of plant RuBisCO. <i>Nature</i> , 1987 , 329, 354-6	50.4	83
4	A Raman spectroscopic study on 5'-rGMP gel and self-aggregate. <i>Biopolymers</i> , 1986 , 25, 753-762	2.2	7
3	Surface-enhanced Raman scattering (SERS) of nucleic acid components in silver sol: Adenine series. <i>Journal of Raman Spectroscopy</i> , 1986 , 17, 381-386	2.3	71
2	Preliminary X-ray crystallographic and Raman studies on gramicidin S.2HCl. <i>Archives of Biochemistry and Biophysics</i> , 1985 , 243, 563-9	4.1	7
1	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, 1037-41	11.5	52