

Hyun Kyu Song

List of Publications by Year in descending order

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141
papers

11,088
citations

81743

39
h-index

30848

102
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143
all docs

143
docs citations

143
times ranked

21388
citing authors

#	ARTICLE	IF	CITATIONS
1	LC3B is an RNA-binding protein to trigger rapid mRNA degradation during autophagy. <i>Nature Communications</i> , 2022, 13, 1436.	5.8	39
2	Mitochondrial protease ClpP supplementation ameliorates diet-induced NASH in mice. <i>Journal of Hepatology</i> , 2022, 77, 735-747.	1.8	8
3	LAG-3xPD-L1 bispecific antibody potentiates antitumor responses of T cells through dendritic cell activation. <i>Molecular Therapy</i> , 2022, 30, 2800-2816.	3.7	29
4	Structural insights into ClpP protease side exit pore opening by a pH drop coupled with substrate hydrolysis. <i>EMBO Journal</i> , 2022, 41, e109755.	3.5	8
5	TRAF6-mediated ubiquitination of MST1/STK4 attenuates the TLR4-NF- κ B signaling pathway in macrophages. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2315-2328.	2.4	10
6	Tyrosyltyrosylcysteine-Directed Synthesis of Chiral Cobalt Oxide Nanoparticles and Peptide Conformation Analysis. <i>ACS Nano</i> , 2021, 15, 979-988.	7.3	19
7	UXT chaperone prevents proteotoxicity by acting as an autophagy adaptor for p62-dependent aggregation. <i>Nature Communications</i> , 2021, 12, 1955.	5.8	9
8	Phospholipid transfer function of PTPIP51 at mitochondria-associated ER membranes. <i>EMBO Reports</i> , 2021, 22, e51323.	2.0	54
9	Translation mediated by the nuclear cap-binding complex is confined to the perinuclear region via a CTIF- α -DDX19B interaction. <i>Nucleic Acids Research</i> , 2021, 49, 8261-8276.	6.5	10
10	Dynamics and Entropy of Cyclohexane Rings Control pH-Responsive Reactivity. <i>JACS</i> , 2021, 143, 2070-2079.	3.6	3
11	Structural basis for the N-degron specificity of ClpS1 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2021, 30, 700-708.	3.1	15
12	Aminopeptidases trim Xaa-Pro proteins, initiating their degradation by the Pro/N-degron pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
13	Crystal structure of yeast Gid10 in complex with Pro/N-degron. <i>Biochemical and Biophysical Research Communications</i> , 2021, 582, 86-92.	1.0	9
14	Use of the LC3B-fusion technique for biochemical and structural studies of proteins involved in the N-degron pathway. <i>Journal of Biological Chemistry</i> , 2020, 295, 2590-2600.	1.6	14
15	Metabolic engineering of <i>Escherichia coli</i> to produce a monophosphoryl lipid A adjuvant. <i>Metabolic Engineering</i> , 2020, 57, 193-202.	3.6	16
16	Enhancing Protein Crystallization under a Magnetic Field. <i>Crystals</i> , 2020, 10, 821.	1.0	9
17	Targeted Degradation of Transcription Coactivator SRC-1 through the N-degron Pathway. <i>Angewandte Chemie</i> , 2020, 132, 17701-17708.	1.6	2
18	Targeted Degradation of Transcription Coactivator SRC-1 through the N-degron Pathway. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 17548-17555.	7.2	22

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19	A host dTMP-bound structure of T4 phage dCMP hydroxymethylase mutant using an X-ray free electron laser. <i>Scientific Reports</i> , 2019, 9, 16316.	1.6	2
20	Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. <i>Journal of Molecular Biology</i> , 2019, 431, 3647-3661.	2.0	26
21	Endoribonucleolytic Cleavage of m6A-Containing RNAs by RNase P/MRP Complex. <i>Molecular Cell</i> , 2019, 74, 494-507.e8.	4.5	371
22	MST1 Negatively Regulates TNF α -Induced NF- κ B Signaling through Modulating LUBAC Activity. <i>Molecular Cell</i> , 2019, 73, 1138-1149.e6.	4.5	39
23	eIF4A3 Phosphorylation by CDKs Affects NMD during the Cell Cycle. <i>Cell Reports</i> , 2019, 26, 2126-2139.e9.	2.9	36
24	pH-dependent regulation of SQSTM1/p62 during autophagy. <i>Autophagy</i> , 2019, 15, 180-181.	4.3	12
25	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
26	Structural studies of a novel ubiquitin-modifying enzyme, SdeA, using various tools. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a78-a78.	0.0	0
27	Unveiling the pathway to Z-DNA in the protein-induced B α €Z transition. <i>Nucleic Acids Research</i> , 2018, 46, 4129-4137.	6.5	36
28	Structural and Biochemical Study of the Mono-ADP-Ribosyltransferase Domain of SdeA, a Ubiquitylating/Deubiquitylating Enzyme from <i>Legionella pneumophila</i> . <i>Journal of Molecular Biology</i> , 2018, 430, 2843-2856.	2.0	24
29	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. <i>Nature Communications</i> , 2018, 9, 3291.	5.8	62
30	The C-terminal region of ATG101 bridges ULK1 and PtdIns3K complex in autophagy initiation. <i>Autophagy</i> , 2018, 14, 2104-2116.	4.3	40
31	PELI1 Selectively Targets Kinase-Active RIP3 for Ubiquitylation-Dependent Proteasomal Degradation. <i>Molecular Cell</i> , 2018, 70, 920-935.e7.	4.5	77
32	A Structural View of Xenophagy, a Battle between Host and Microbes. <i>Molecules and Cells</i> , 2018, 41, 27-34.	1.0	34
33	Structural insight into degradation mechanism of N-end rule substrates by p62/SQSTM1 selective autophagy adaptor. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a313-a313.	0.0	0
34	ACCORD: an assessment tool to determine the orientation of homodimeric coiled-coils. <i>Scientific Reports</i> , 2017, 7, 43318.	1.6	6
35	Structural Characterization of <sc>RNA</sc> Recognition Motif ϵ 2 Domain of <sc>SART3</sc>. <i>Bulletin of the Korean Chemical Society</i> , 2017, 38, 444-447.	1.0	1
36	A novel conformation of the LC3-interacting region motif revealed by the structure of a complex between LC3B and RavZ. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 1093-1099.	1.0	26

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37	The 1:2 complex between RavZ and LC3 reveals a mechanism for deconjugation of LC3 on the phagophore membrane. <i>Autophagy</i> , 2017, 13, 70-81.	4.3	37
38	An assessment tool for determination of coiled-coil orientation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a118-a118.	0.0	0
39	Structural Studies of Peptide Binding Interaction of HCV IRES Domain IV. <i>Journal of the Korean Magnetic Resonance Society</i> , 2017, 21, 109-113.	0.1	0
40	Structure biology of selective autophagy receptors. <i>BMB Reports</i> , 2016, 49, 73-80.	1.1	54
41	A facile method to prepare large quantities of active caspase-3 overexpressed by auto-induction in the C41(DE3) strain. <i>Protein Expression and Purification</i> , 2016, 126, 104-108.	0.6	7
42	The structure of the pleiotropic transcription regulator CodY provides insight into its GTP-sensing mechanism. <i>Nucleic Acids Research</i> , 2016, 44, gkw775.	6.5	18
43	Structural basis for dual specificity of yeast N-terminal amidase in the N-end rule pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12438-12443.	3.3	22
44	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
45	Structural Characterization of pre-miRNA 155. <i>Journal of the Korean Magnetic Resonance Society</i> , 2016, 20, 46-49.	0.1	0
46	A key lysine residue in the AXH domain of ataxin-1 is essential for its ubiquitylation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 356-364.	1.1	14
47	mTRAQ-based quantitative analysis combined with peptide fractionation based on cysteinyl peptide enrichment. <i>Analytical Biochemistry</i> , 2015, 477, 41-49.	1.1	3
48	PEA α 15 facilitates EGFR dephosphorylation <i>via</i> ERK sequestration at increased ER α PM contacts in TNBC cells. <i>FEBS Letters</i> , 2015, 589, 1033-1039.	1.3	11
49	Mitochondrial ATP synthase activity is impaired by suppressed <i>O</i> -GlcNAcylation in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2015, 24, 6492-6504.	1.4	74
50	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. <i>Autophagy</i> , 2015, 11, 75-87.	4.3	59
51	Swapping of interaction partners with ATG5 for autophagosome maturation. <i>BMB Reports</i> , 2015, 48, 129-130.	1.1	9
52	Insulin activates EGFR by stimulating its interaction with IGF-1R in low-EGFR-expressing TNBC cells. <i>BMB Reports</i> , 2015, 48, 342-347.	1.1	9
53	Direct recognition of the C-terminal polylysine residues of nonstop protein by Ltn1, an E3 ubiquitin ligase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 453, 642-647.	1.0	2
54	Crystallization and preliminary X-ray analysis of the C-terminal fragment of Ski7 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1252-1255.	0.4	1

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55	Expansion of the clinicopathological and mutational spectrum of Perry syndrome. <i>Parkinsonism and Related Disorders</i> , 2014, 20, 388-393.	1.1	24
56	eIF4AIII enhances translation of nuclear cap-binding complex-bound mRNAs by promoting disruption of secondary structures in 5'UTR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4577-86.	3.3	62
57	Insights into the Molecular Evolution of HslU ATPase through Biochemical and Mutational Analyses. <i>PLoS ONE</i> , 2014, 9, e103027.	1.1	2
58	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. <i>Nature Communications</i> , 2013, 4, 1613.	5.8	91
59	Differential in vitro and cellular effects of iron chelators for hypoxia inducible factor hydroxylases. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 864-873.	1.2	29
60	MG53-induced IRS-1 ubiquitination negatively regulates skeletal myogenesis and insulin signalling. <i>Nature Communications</i> , 2013, 4, 2354.	5.8	140
61	In vivo fluorescence imaging for cancer diagnosis using receptor-targeted epidermal growth factor-based nanoprobe. <i>Biomaterials</i> , 2013, 34, 9149-9159.	5.7	33
62	Crystal structure of the single cystathionine β -synthase domain-containing protein CBSX1 from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 265-271.	1.0	5
63	Change in single cystathionine β -synthase domain-containing protein from a bent to flat conformation upon adenosine monophosphate binding. <i>Journal of Structural Biology</i> , 2013, 183, 40-46.	1.3	14
64	Renal Protective Effects of Toll-like Receptor 4 Signaling Blockade in Type 2 Diabetic Mice. <i>Endocrinology</i> , 2013, 154, 2144-2155.	1.4	79
65	Rapid degradation of replication-dependent histone mRNAs largely occurs on mRNAs bound by nuclear cap-binding proteins 80 and 20. <i>Nucleic Acids Research</i> , 2013, 41, 1307-1318.	6.5	29
66	Structural and Biochemical Analyses of the Eukaryotic Heat Shock Locus V (HslV) from <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 23234-23243.	1.6	8
67	Structure of the autophagic E2 enzyme Atg10. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1409-1417.	2.5	26
68	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
69	Backbone resonances assignment of 19 kDa CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. <i>Biomolecular NMR Assignments</i> , 2012, 6, 109-113.	0.4	3
70	Crystal structure of <i>Pyrococcus furiosus</i> PF2050, a member of the DUF2666 protein family. <i>FEBS Letters</i> , 2012, 586, 1384-1388.	1.3	0
71	Insights into noncanonical E1 enzyme activation from the structure of autophagic E1 Atg7 with Atg8. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1323-1330.	3.6	89
72	Crystal structure of ubiquitin-like small archaeal modifier protein 1 (SAMP1) from <i>Haloferax volcanii</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 112-117.	1.0	22

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73	Crystal Structure of a Coiled-Coil Domain from Human ROCK I. <i>PLoS ONE</i> , 2011, 6, e18080.	1.1	31
74	Ubiquitin Ligases of the N-End Rule Pathway: Assessment of Mutations in UBR1 That Cause the Johanson-Blizzard Syndrome. <i>PLoS ONE</i> , 2011, 6, e24925.	1.1	40
75	Structural Insights into the Conformational Diversity of ClpP from <i>Bacillus subtilis</i> . <i>Molecules and Cells</i> , 2011, 32, 589-596.	1.0	49
76	Single Cystathionine β -Synthase Domain-Containing Proteins Modulate Development by Regulating the Thioredoxin System in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 3577-3594.	3.1	92
77	Crystal structure of PRY-SPRY domain of human TRIM72. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 790-795.	1.5	37
78	Dab1 binds to Fe65 and diminishes the effect of Fe65 or LRP1 on APP processing. <i>Journal of Cellular Biochemistry</i> , 2010, 111, 508-519.	1.2	16
79	Structures of ClpP in complex with acyldepsipeptide antibiotics reveal its activation mechanism. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 471-478.	3.6	194
80	Structural basis for the recognition of N-end rule substrates by the UBR box of ubiquitin ligases. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1175-1181.	3.6	128
81	Expression, purification and biochemical characterization of the N-terminal regions of human TIC3 and HRASLS3 proteins. <i>Protein Expression and Purification</i> , 2010, 71, 103-107.	0.6	17
82	Identification of a novel ubiquitin binding site of STAM1 VHS domain by NMR spectroscopy. <i>FEBS Letters</i> , 2009, 583, 287-292.	1.3	22
83	A simple technique to convert sitting-drop vapor diffusion into hanging-drop vapor diffusion by solidifying the reservoir solution with agarose. <i>Journal of Applied Crystallography</i> , 2009, 42, 975-976.	1.9	10
84	Biochemical and structural characterization of 5-methylthioadenosine nucleosidases from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 619-624.	1.0	6
85	A degradation signal recognition in prokaryotes. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 246-249.	1.0	6
86	Purification, crystallization and preliminary X-ray diffraction analysis of a cystathionine β -synthase domain-containing protein, CDCP2, from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 825-827.	0.7	4
87	Real-time imaging of NF-AT nucleocytoplasmic shuttling with a photoswitchable fluorescence protein in live cells. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2008, 1780, 1403-1407.	1.1	8
88	A Role for a Menthone Reductase in Resistance against Microbial Pathogens in Plants. <i>Plant Physiology</i> , 2008, 148, 383-401.	2.3	97
89	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
90	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 962-967.	1.0	26

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91	Structural Basis of SspB-tail Recognition by the Zinc Binding Domain of ClpX. <i>Journal of Molecular Biology</i> , 2007, 367, 514-526.	2.0	43
92	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
93	Tumoral acidic extracellular pH targeting of pH-responsive MPEG-poly(β^2 -amino ester) block copolymer micelles for cancer therapy. <i>Journal of Controlled Release</i> , 2007, 123, 109-115.	4.8	281
94	STAM α -AMSH interaction facilitates the deubiquitination activity in the C-terminal AMSH. <i>Biochemical and Biophysical Research Communications</i> , 2006, 351, 612-618.	1.0	25
95	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 ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 582 Seibutsu Butsuri, 2006. 46. S120.	0.0	0
96	Crystal structure of 5 β -methylthioadenosine nucleosidase from <i>Arabidopsis thaliana</i> at 1.5-Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 519-523.	1.5	11
97	Crystal Structure of the FERM Domain of Focal Adhesion Kinase. <i>Journal of Biological Chemistry</i> , 2006, 281, 252-259.	1.6	108
98	Characterization of the HslU chaperone affinity for HslV protease. <i>Protein Science</i> , 2005, 14, 1357-1362.	3.1	16
99	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
100	Crystal Structure of the Bowman α -Birk Inhibitor from Barley Seeds in Ternary Complex with Porcine Trypsin. <i>Journal of Molecular Biology</i> , 2004, 343, 173-186.	2.0	29
101	Origins of Peptide Selectivity and Phosphoinositide Binding Revealed by Structures of Disabled-1 PTB Domain Complexes. <i>Structure</i> , 2003, 11, 569-579.	1.6	117
102	SAP couples Fyn to SLAM immune receptors. <i>Nature Cell Biology</i> , 2003, 5, 155-160.	4.6	259
103	Homotetrameric Structure of the SNAP-23 N-terminal Coiled-coil Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 13462-13467.	1.6	17
104	Structural Basis of Degradation Signal Recognition by SspB, a Specificity-Enhancing Factor for the ClpXP Proteolytic Machine. <i>Molecular Cell</i> , 2003, 12, 75-86.	4.5	56
105	Proteomics-based Target Identification. <i>Journal of Biological Chemistry</i> , 2003, 278, 52964-52971.	1.6	132
106	Functional interactions of HslV (ClpQ) with the ATPase HslU (ClpY). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7396-7401.	3.3	65
107	Isolation and characterization of the prokaryotic proteasome homolog HslVU (ClpQY) from <i>Thermotoga maritima</i> and the crystal structure of HslV. <i>Biophysical Chemistry</i> , 2002, 100, 437-452.	1.5	24
108	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

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109	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography ¹ Edited by D. Rees. <i>Journal of Molecular Biology</i> , 2001, 308, 263-278.	2.0	175
110	The Quaternary Arrangement of HslU and HslV in a Cocrystal: A Response to Wang, Yale. <i>Journal of Structural Biology</i> , 2001, 135, 281-293.	1.3	13
111	Crystal Structure of <i>Klebsiella aerogenes</i> UreE, a Nickel-binding Metallochaperone for Urease Activation. <i>Journal of Biological Chemistry</i> , 2001, 276, 49359-49364.	1.6	86
112	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
113	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, 778-780.	2.5	3
114	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
115	Nucleoside diphosphate kinase from the hyperthermophilic archaeon <i>Methanococcus jannaschii</i> : overexpression, crystallization and preliminary X-ray crystallographic analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1485-1487.	2.5	3
116	The structures of HslU and the ATP-dependent protease HslU/HslV. <i>Nature</i> , 2000, 403, 800-805.	13.7	406
117	Docking of components in a bacterial complex. <i>Nature</i> , 2000, 408, 667-668.	13.7	40
118	Docking of components in a bacterial complex. <i>Nature</i> , 2000, 408, 668-668.	13.7	5
119	Crystal structure of NAD ⁺ -dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , 2000, 19, 1119-1129.	3.5	169
120	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
121	Mutational studies on HslU and its docking mode with HslV. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 14103-14108.	3.3	136
122	A thermostable xylose isomerase from <i>Thermus caldophilus</i> : biochemical characterization, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 294-296.	2.5	5
123	Crystallization and preliminary X-ray crystallographic analysis of deoxycytidylate hydroxymethylase from bacteriophage T4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1061-1063.	2.5	1
124	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, 1091-1092.	2.5	1
125	Crystallization and preliminary X-ray analysis of <i>Saccharomyces cerevisiae</i> Ypd1p, a key intermediate in phosphorelay signal transduction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1219-1221.	2.5	2
126	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, 1244-1246.	2.5	1

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127	Crystal structure of deoxycytidylate hydroxymethylase from bacteriophage T4, a component of the deoxyribonucleoside triphosphate-synthesizing complex. EMBO Journal, 1999, 18, 1104-1113.	3.5	31
128	Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from <i>Saccharomyces cerevisiae</i> . Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 293, 753-761.	2.0	51
129	Crystal structure of a 16 kda double-headed bowman-birk trypsin inhibitor from barley seeds at 1.9 Å resolution. Edited by R. Huber. Journal of Molecular Biology, 1999, 293, 1133-1144.	2.0	57
130	Preliminary X-ray crystallographic analysis of Bowman-Birk trypsin inhibitor from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 441-443.	2.5	3
131	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. Edited by R. Huber. Journal of Molecular Biology, 1998, 275, 347-363.	2.0	230
132	The crystal structure of a triacylglycerol lipase from <i>Pseudomonas cepacia</i> reveals a highly open conformation in the absence of a bound inhibitor. Structure, 1997, 5, 173-185.	1.6	301
133	Crystal structure of carboxylesterase from <i>Pseudomonas fluorescens</i> , an $\hat{1}\hat{2}$ hydrolase with broad substrate specificity. Structure, 1997, 5, 1571-1584.	1.6	109
134	Crystal structure of <i>Bacillus licheniformis</i> $\hat{1}\hat{2}$ -Amylase at 1.7 resolution. Progress in Biotechnology, 1996, 12, 163-170.	0.2	1
135	Refined Structure of the Chitinase from Barley Seeds at 2.0 Å Resolution. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 289-298.	2.5	28
136	Crystal structure analyses of uncomplexed ecotin in two crystal forms: Implications for its function and stability. Protein Science, 1996, 5, 2236-2247.	3.1	29
137	Crystallization and preliminary X-ray crystallographic analysis of DNA polymerase from <i>Thermus aquaticus</i> . Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 1086-1088.	2.5	1
138	Crystallization, molecular replacement solution, and refinement of tetrameric $\hat{1}\hat{2}$ -amylase from sweet potato. Proteins: Structure, Function and Bioinformatics, 1995, 21, 105-117.	1.5	55
139	Crystal structure of an uncleaved $\hat{1}\hat{2}$ -antitrypsin reveals the conformation of its inhibitory reactive loop. FEBS Letters, 1995, 377, 150-154.	1.3	48
140	Crystallization and preliminary X-ray crystallographic study of ribosome-inactivating protein from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 910-912.	2.5	1
141	Crystallization and preliminary X-ray crystallographic analysis of chitinase from barley seeds. Proteins: Structure, Function and Bioinformatics, 1993, 17, 107-109.	1.5	5