

Hyun Kyu Song

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136
papers

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38
h-index

94
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143
ext. papers

10,128
ext. citations

8.8
avg, IF

5.29
L-index

#	Paper	IF	Citations
136	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016 , 12, 1-222	10.2	3838
135	The structures of HslU and the ATP-dependent protease HslU-HslV. <i>Nature</i> , 2000 , 403, 800-5	50.4	378
134	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
133	Tumoral acidic extracellular pH targeting of pH-responsive MPEG-poly(beta-amino ester) block copolymer micelles for cancer therapy. <i>Journal of Controlled Release</i> , 2007 , 123, 109-15	11.7	261
132	SAP couples Fyn to SLAM immune receptors. <i>Nature Cell Biology</i> , 2003 , 5, 155-60	23.4	237
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. <i>Journal of Molecular Biology</i> , 1998 , 275, 347-63	6.5	204
130	Endoribonucleolytic Cleavage of mA-Containing RNAs by RNase P/MRP Complex. <i>Molecular Cell</i> , 2019 , 74, 494-507.e8	17.6	189
129	Structures of ClpP in complex with acyldepsipeptide antibiotics reveal its activation mechanism. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 471-8	17.6	169
128	Crystal structure of NAD(+)-dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , 2000 , 19, 1119-29	13	154
127	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
126	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, 14103-8	11.5	129
125	Proteomics-based target identification: bengamides as a new class of methionine aminopeptidase inhibitors. <i>Journal of Biological Chemistry</i> , 2003 , 278, 52964-71	5.4	113
124	Origins of peptide selectivity and phosphoinositide binding revealed by structures of disabled-1 PTB domain complexes. <i>Structure</i> , 2003 , 11, 569-79	5.2	104
123	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, 8932-7	11.5	104
122	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, 1175-81	17.6	103
121	MG53-induced IRS-1 ubiquitination negatively regulates skeletal myogenesis and insulin signalling. <i>Nature Communications</i> , 2013 , 4, 2354	17.4	102
120	Crystal structure of the FERM domain of focal adhesion kinase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 252-9	5.4	97

119	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. <i>EMBO Journal</i> , 2004 , 23, 2029-38	13	94
118	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
117	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
116	Crystal structure of <i>Klebsiella aerogenes</i> UreE, a nickel-binding metallochaperone for urease activation. <i>Journal of Biological Chemistry</i> , 2001 , 276, 49359-64	5.4	77
115	Insights into noncanonical E1 enzyme activation from the structure of autophagic E1 Atg7 with Atg8. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1323-30	17.6	70
114	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. <i>Nature Communications</i> , 2013 , 4, 1613	17.4	64
113	Renal protective effects of toll-like receptor 4 signaling blockade in type 2 diabetic mice. <i>Endocrinology</i> , 2013 , 154, 2144-55	4.8	63
112	A role for a menthone reductase in resistance against microbial pathogens in plants. <i>Plant Physiology</i> , 2008 , 148, 383-401	6.6	62
111	Single cystathionine β -synthase domain-containing proteins modulate development by regulating the thioredoxin system in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011 , 23, 3577-94	11.6	59
110	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, 7396-401	11.5	59
109	Mitochondrial ATP synthase activity is impaired by suppressed O-GlcNAcylation in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2015 , 24, 6492-504	5.6	57
108	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
107	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
106	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	11.5	48
105	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> , 1999 , 293, 753-61	6.5	48
104	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. <i>Autophagy</i> , 2015 , 11, 75-87	10.2	47
103	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	17.6	46
102	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

101	Structure biology of selective autophagy receptors. <i>BMB Reports</i> , 2016 , 49, 73-80	5.5	42
100	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. <i>Nature Communications</i> , 2018 , 9, 3291	17.4	41
99	PELI1 Selectively Targets Kinase-Active RIP3 for Ubiquitylation-Dependent Proteasomal Degradation. <i>Molecular Cell</i> , 2018 , 70, 920-935.e7	17.6	41
98	Structural basis of SspB-tail recognition by the zinc binding domain of ClpX. <i>Journal of Molecular Biology</i> , 2007 , 367, 514-26	6.5	38
97	Structural insights into the conformational diversity of ClpP from <i>Bacillus subtilis</i> . <i>Molecules and Cells</i> , 2011 , 32, 589-95	3.5	36
96	Docking of components in a bacterial complex. <i>Nature</i> , 2000 , 408, 667-8	50.4	36
95	In vivo fluorescence imaging for cancer diagnosis using receptor-targeted epidermal growth factor-based nanoprobe. <i>Biomaterials</i> , 2013 , 34, 9149-59	15.6	31
94	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	3.7	31
93	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	10.2	29
92	Crystal structure of PRY-SPRY domain of human TRIM72. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 790-5	4.2	29
91	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, 1307-18	20.1	27
90	Crystal structure of the Bowman-Birk inhibitor from barley seeds in ternary complex with porcine trypsin. <i>Journal of Molecular Biology</i> , 2004 , 343, 173-86	6.5	27
89	A Structural View of Xenophagy, a Battle between Host and Microbes. <i>Molecules and Cells</i> , 2018 , 41, 27-34	3.5	27
88	Crystal structure of a coiled-coil domain from human ROCK I. <i>PLoS ONE</i> , 2011 , 6, e18080	3.7	26
87	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
86	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
85	STAM-AMSH interaction facilitates the deubiquitination activity in the C-terminal AMSH. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 351, 612-8	3.4	24
84	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

83	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
82	Differential in vitro and cellular effects of iron chelators for hypoxia inducible factor hydroxylases. <i>Journal of Cellular Biochemistry</i> , 2013 , 114, 864-73	4.7	23
81	Unveiling the pathway to Z-DNA in the protein-induced B-Z transition. <i>Nucleic Acids Research</i> , 2018 , 46, 4129-4137	20.1	23
80	The C-terminal region of ATG101 bridges ULK1 and PtdIns3K complex in autophagy initiation. <i>Autophagy</i> , 2018 , 14, 2104-2116	10.2	22
79	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 354, 962-7	3.4	22
78	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	11.5	21
77	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, 112-7	3.4	21
76	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> , 2003 , 100, 437-52	3.5	21
75	eIF4A3 Phosphorylation by CDKs Affects NMD during the Cell Cycle. <i>Cell Reports</i> , 2019 , 26, 2126-2139.e9	10.6	21
74	Identification of a novel ubiquitin binding site of STAM1 VHS domain by NMR spectroscopy. <i>FEBS Letters</i> , 2009 , 583, 287-92	3.8	20
73	Expansion of the clinicopathological and mutational spectrum of Perry syndrome. <i>Parkinsonism and Related Disorders</i> , 2014 , 20, 388-93	3.6	19
72	MST1 Negatively Regulates TNF-Induced NF- κ B Signaling through Modulating LUBAC Activity. <i>Molecular Cell</i> , 2019 , 73, 1138-1149.e6	17.6	18
71	Structure of the autophagic E2 enzyme Atg10. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 1409-17		18
70	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	3.4	17
69	Expression, purification and biochemical characterization of the N-terminal regions of human TIG3 and HRASLS3 proteins. <i>Protein Expression and Purification</i> , 2010 , 71, 103-7	2	17
68	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	6.5	17
67	Characterization of the HslU chaperone affinity for HslV protease. <i>Protein Science</i> , 2005 , 14, 1357-62	6.3	16
66	Homotetrameric structure of the SNAP-23 N-terminal coiled-coil domain. <i>Journal of Biological Chemistry</i> , 2003 , 278, 13462-7	5.4	15

65	The structure of the pleiotropic transcription regulator CodY provides insight into its GTP-sensing mechanism. <i>Nucleic Acids Research</i> , 2016 , 44, 9483-9493	20.1	14
64	Dab1 binds to Fe65 and diminishes the effect of Fe65 or LRP1 on APP processing. <i>Journal of Cellular Biochemistry</i> , 2010 , 111, 508-19	4.7	13
63	Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. <i>Journal of Molecular Biology</i> , 2019 , 431, 3647-3661	6.5	12
62	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, 356-64	4	12
61	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, 40-6	3.4	11
60	Crystal structure of 5Qmethylthioadenosine nucleosidase from <i>Arabidopsis thaliana</i> at 1.5-Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 519-23	4.2	11
59	The quaternary arrangement of HslU and HslV in a cocrystal: a response to Wang, Yale. <i>Journal of Structural Biology</i> , 2001 , 135, 281-93	3.4	11
58	PEA-15 facilitates EGFR dephosphorylation via ERK sequestration at increased ER-PM contacts in TNBC cells. <i>FEBS Letters</i> , 2015 , 589, 1033-9	3.8	10
57	pH-dependent regulation of SQSTM1/p62 during autophagy. <i>Autophagy</i> , 2019 , 15, 180-181	10.2	10
56	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	5.4	9
55	Phospholipid transfer function of PTPIP51 at mitochondria-associated ER membranes. <i>EMBO Reports</i> , 2021 , 22, e51323	6.5	9
54	Structural basis for the N-degron specificity of ClpS1 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2021 , 30, 700-708	6.3	9
53	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
52	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, 23234-43	5.4	8
51	Targeted Degradation of Transcription Coactivator SRC-1 through the N-Degron Pathway. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 17548-17555	16.4	7
50	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	3.8	7
49	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, 1403-7	4	7
48	Swapping of interaction partners with ATG5 for autophagosome maturation. <i>BMB Reports</i> , 2015 , 48, 129-30	5.5	7

47	Insulin activates EGFR by stimulating its interaction with IGF-1R in low-EGFR-expressing TNBC cells. <i>BMB Reports</i> , 2015 , 48, 342-7	5.5	7
46	Tyrosyltyrosylcysteine-Directed Synthesis of Chiral Cobalt Oxide Nanoparticles and Peptide Conformation Analysis. <i>ACS Nano</i> , 2021 , 15, 979-988	16.7	7
45	Biochemical and structural characterization of 5Qmethylthioadenosine nucleosidases from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009 , 381, 619-24	3.4	6
44	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, 920-1		6
43	Crystal structure of yeast <i>Gid10</i> in complex with Pro/N-degron. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 582, 86-92	3.4	6
42	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	2	6
41	ACCORD: an assessment tool to determine the orientation of homodimeric coiled-coils. <i>Scientific Reports</i> , 2017 , 7, 43318	4.9	5
40	A degradation signal recognition in prokaryotes. <i>Journal of Synchrotron Radiation</i> , 2008 , 15, 246-9	2.4	5
39	The recombination-associated protein <i>RdgC</i> adopts a novel toroidal architecture for DNA binding. <i>Nucleic Acids Research</i> , 2007 , 35, 2671-81	20.1	5
38	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,	11.5	5
37	Metabolic engineering of <i>Escherichia coli</i> to produce a monophosphoryl lipid A adjuvant. <i>Metabolic Engineering</i> , 2020 , 57, 193-202	9.7	5
36	Purification, crystallization and preliminary X-ray diffraction analysis of a cystathionine beta-synthase domain-containing protein, <i>CDCP2</i> , from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 825-7		4
35	Docking of components in a bacterial complex. <i>Nature</i> , 2000 , 408, 668-668	50.4	4
34	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
33	Translation mediated by the nuclear cap-binding complex is confined to the perinuclear region via a CTIF-DDX19B interaction. <i>Nucleic Acids Research</i> , 2021 , 49, 8261-8276	20.1	4
32	MTRAQ-based quantitative analysis combined with peptide fractionation based on cysteinyl peptide enrichment. <i>Analytical Biochemistry</i> , 2015 , 477, 41-9	3.1	3
31	Crystal structure of the single cystathionine β -synthase domain-containing protein <i>CBSX1</i> from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013 , 430, 265-71	3.4	3
30	Backbone resonances assignment of 19 kDa CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, <i>Bub1</i> . <i>Biomolecular NMR Assignments</i> , 2012 , 6, 109-13	0.7	3

29	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
28	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
27	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, 1485-7		3
26	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, 294-6		3
25	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
24	Enhancing Protein Crystallization under a Magnetic Field. <i>Crystals</i> , 2020 , 10, 821	2.3	3
23	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	10.3	3
22	LAG-3xPD-L1 bispecific antibody potentiates antitumor responses of T cells through dendritic cell activation.. <i>Molecular Therapy</i> , 2022 ,	11.7	3
21	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	4.9	2
20	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
19	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, 1219-21		2
18	Insights into the molecular evolution of HslU ATPase through biochemical and mutational analyses. <i>PLoS ONE</i> , 2014 , 9, e103027	3.7	2
17	UXT chaperone prevents proteotoxicity by acting as an autophagy adaptor for p62-dependent aggrephagy. <i>Nature Communications</i> , 2021 , 12, 1955	17.4	2
16	Dynamics and Entropy of Cyclohexane Rings Control pH-Responsive Reactivity. <i>Jacs Au</i> , 2021 , 1, 2070-2079		2
15	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, 642-7	3.4	1
14	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, 1252-5	1.1	1
13	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
12	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

11	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
10	Crystal structure of Bacillus licheniformis α -Amylase at 1.7 resolution. <i>Progress in Biotechnology</i> , 1996 , 12, 163-170		1
9	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
8	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
7	Targeted Degradation of Transcription Coactivator SRC-1 through the N-Degron Pathway. <i>Angewandte Chemie</i> , 2020 , 132, 17701-17708	3.6	1
6	LC3B is an RNA-binding protein to trigger rapid mRNA degradation during autophagy.. <i>Nature Communications</i> , 2022 , 13, 1436	17.4	1
5	Structural insights into ClpP protease side exit pore-opening by a pH drop coupled with substrate hydrolysis.. <i>EMBO Journal</i> , 2022 , e109755	13	1
4	Structural Characterization of RNA Recognition Motif-2 Domain of SART3. <i>Bulletin of the Korean Chemical Society</i> , 2017 , 38, 444-447	1.2	
3	Crystal structure of <i>Pyrococcus furiosus</i> PF2050, a member of the DUF2666 protein family. <i>FEBS Letters</i> , 2012 , 586, 1384-8	3.8	
2	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>Seibutsu Batsuri</i> , 2006 , 46, S120	0	
1	Structural Characterization of pre-miRNA 155. <i>Journal of the Korean Magnetic Resonance Society</i> , 2016 , 20, 46-49		