Hyun Kyu Song

List of Publications by Year
in descending order

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		81900	30922
141	11,088	39	102
papers	citations	h-index	g-index

143	143	143	21388
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	The structures of HslU and the ATP-dependent protease HslUâ€“HslV. Nature, 2000, 403, 800-805.	27.8	406
3	Endoribonucleolytic Cleavage of m6A-Containing RNAs by RNase P/MRP Complex. Molecular Cell, 2019, 74, 494-507.e8.	9.7	371
4	The crystal structure of a triacylglycerol lipase from Pseudomonas cepacia reveals a highly open conformation in the absence of a bound inhibitor. Structure, 1997, 5, 173-185.	3.3	301
5	Tumoral acidic extracellular pH targeting of pH-responsive MPEG-poly(Î²-amino ester) block copolymer micelles for cancer therapy. Journal of Controlled Release, 2007, 123, 109-115.	9.9	281
6	SAP couples Fyn to SLAM immune receptors. Nature Cell Biology, 2003, 5, 155-160.	10.3	259
7	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 Erythrina caffra and tissue-type plasminogen activator 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 275, 347-363.	4.2	230
8	Structures of ClpP in complex with acyldepsipeptide antibiotics reveal its activation mechanism. Nature Structural and Molecular Biology, 2010, 17, 471-478.	8.2	194
9	Structural basis of non-specific lipid binding in maize lipid-transfer protein complexes revealed by high-resolution X-ray crystallography1 1Edited by D. Rees. Journal of Molecular Biology, 2001, 308, 263-278.	4.2	175
10	Crystal structure of NAD+-dependent DNA ligase: modular architecture and functional implications. EMBO Journal, 2000, 19, 1119-1129.	7.8	169
11	MG53-induced IRS-1 ubiquitination negatively regulates skeletal myogenesis and insulin signalling. Nature Communications, 2013, 4, 2354.	12.8	140
12	Mutational studies on HslU and its docking mode with HslV. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14103-14108.	7.1	136
13	Proteomics-based Target Identification. Journal of Biological Chemistry, 2003, 278, 52964-52971.	3.4	132
14	Structural basis for the recognition of N-end rule substrates by the UBR box of ubiquitin ligases. Nature Structural and Molecular Biology, 2010, 17, 1175-1181.	8.2	128
15	Crystal structure of Escherichia coli CyaY protein reveals a previously unidentified fold for the evolutionarily conserved frataxin family. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 8932-8937.	7.1	119
16	Origins of Peptide Selectivity and Phosphoinositide Binding Revealed by Structures of Disabled-1 PTB Domain Complexes. Structure, 2003, 11, 569-579.	3.3	117
17	Crystal structure of carboxylesterase from Pseudomonas fluorescens, an Î±/Î² hydrolase with broad substrate specificity. Structure, 1997, 5, 1571-1584.	3.3	109
18	Crystal Structure of the FERM Domain of Focal Adhesion Kinase. Journal of Biological Chemistry, 2006, 281, 252-259.	3.4	108

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19	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. EMBO Journal, 2004, 23, 2029-2038.	7.8	105
20	A Role for a Menthone Reductase in Resistance against Microbial Pathogens in Plants Â Â. Plant Physiology, 2008, 148, 383-401.	4.8	97
21	Single Cystathionine Î²-Synthase Domainâ€“Containing Proteins Modulate Development by Regulating the Thioredoxin System in <i>Arabidopsis</i> Â Â. Plant Cell, 2011, 23, 3577-3594.	6.6	92
22	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. Nature Communications, 2013, 4, 1613.	12.8	91
23	Insights into noncanonical E1 enzyme activation from the structure of autophagic E1 Atg7 with Atg8. Nature Structural and Molecular Biology, 2011, 18, 1323-1330.	8.2	89
24	Crystal Structure of Klebsiella aerogenesUreE, a Nickel-binding Metallochaperone for Urease Activation. Journal of Biological Chemistry, 2001, 276, 49359-49364.	3.4	86
25	Structural and Functional Insights into Dom34, a Key Component of No-Go mRNA Decay. Molecular Cell, 2007, 27, 938-950.	9.7	84
26	Renal Protective Effects of Toll-like Receptor 4 Signaling Blockade in Type 2 Diabetic Mice. Endocrinology, 2013, 154, 2144-2155.	2.8	79
27	PELI1 Selectively Targets Kinase-Active RIP3 for Ubiquitylation-Dependent Proteasomal Degradation. Molecular Cell, 2018, 70, 920-935.e7.	9.7	77
28	Mitochondrial ATP synthase activity is impaired by suppressed<i>O</i>-GlcNAcylation in Alzheimer's disease. Human Molecular Genetics, 2015, 24, 6492-6504.	2.9	74
29	Functional interactions of HslV (ClpQ) with the ATPase HslU (ClpY). Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7396-7401.	7.1	65
30	eIF4AIII enhances translation of nuclear cap-binding complexâ€“bound mRNAs by promoting disruption of secondary structures in 5â€²UTR. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4577-86.	7.1	62
31	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. Nature Communications, 2018, 9, 3291.	12.8	62
32	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. Autophagy, 2015, 11, 75-87.	9.1	59
33	Crystal structure of a 16 kda double-headed bowman-birk trypsin inhibitor from barley seeds at 1.9 Ã… resolution 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 293, 1133-1144.	4.2	57
34	Structural Basis of Degradation Signal Recognition by SspB, a Specificity-Enhancing Factor for the ClpXP Proteolytic Machine. Molecular Cell, 2003, 12, 75-86.	9.7	56
35	Crystallization, molecular replacement solution, and refinement of tetrameric Î²-amylase from sweet potato. Proteins: Structure, Function and Bioinformatics, 1995, 21, 105-117.	2.6	55
36	Structure biology of selective autophagy receptors. BMB Reports, 2016, 49, 73-80.	2.4	54

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37	Phospholipid transfer function of PTPIP51 at mitochondriaâ€associated ER membranes. EMBO Reports, 2021, 22, e51323.	4.5	54
38	Insights into eukaryotic multistep phosphorelay signal transduction revealed by the crystal structure of Ypd1p from Saccharomyces cerevisiae 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 293, 753-761.	4.2	51
39	Structural Insights into the Conformational Diversity of ClpP from Bacillus subtilis. Molecules and Cells, 2011, 32, 589-596.	2.6	49
40	Crystal structure of an uncleaved Î± 1 -antitrypsin reveals the conformation of its inhibitory reactive loop. FEBS Letters, 1995, 377, 150-154.	2.8	48
41	Structural Basis of SspB-tail Recognition by the Zinc Binding Domain of ClpX. Journal of Molecular Biology, 2007, 367, 514-526.	4.2	43
42	Docking of components in a bacterial complex. Nature, 2000, 408, 667-668.	27.8	40
43	Ubiquitin Ligases of the N-End Rule Pathway: Assessment of Mutations in UBR1 That Cause the Johanson-Blizzard Syndrome. PLoS ONE, 2011, 6, e24925.	2.5	40
44	The C-terminal region of ATG101 bridges ULK1 and PtdIns3K complex in autophagy initiation. Autophagy, 2018, 14, 2104-2116.	9.1	40
45	MST1 Negatively Regulates TNFÎ±-Induced NF-ÎºB Signaling through Modulating LUBAC Activity. Molecular Cell, 2019, 73, 1138-1149.e6.	9.7	39
46	LC3B is an RNA-binding protein to trigger rapid mRNA degradation during autophagy. Nature Communications, 2022, 13, 1436.	12.8	39
47	Crystal structure of PRYâ€SPRY domain of human TRIM72. Proteins: Structure, Function and Bioinformatics, 2010, 78, 790-795.	2.6	37
48	The 1:2 complex between RavZ and LC3 reveals a mechanism for deconjugation of LC3 on the phagophore membrane. Autophagy, 2017, 13, 70-81.	9.1	37
49	Unveiling the pathway to Z-DNA in the protein-induced Bâ€“Z transition. Nucleic Acids Research, 2018, 46, 4129-4137.	14.5	36
50	eIF4A3 Phosphorylation by CDKs Affects NMD during the Cell Cycle. Cell Reports, 2019, 26, 2126-2139.e9.	6.4	36
51	A Structural View of Xenophagy, a Battle between Host and Microbes. Molecules and Cells, 2018, 41, 27-34.	2.6	34
52	InÂvivo fluorescence imaging for cancer diagnosis using receptor-targeted epidermal growth factor-based nanoprobe. Biomaterials, 2013, 34, 9149-9159.	11.4	33
53	Crystal structure of deoxycytidylate hydroxymethylase from bacteriophage T4, a component of the deoxyribonucleoside triphosphate-synthesizing complex. EMBO Journal, 1999, 18, 1104-1113.	7.8	31
54	Crystal Structure of a Coiled-Coil Domain from Human ROCK I. PLoS ONE, 2011, 6, e18080.	2.5	31

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55	Crystal structure analyses of uncomplexed ecotin in two crystal forms: Implications for its function and stability. Protein Science, 1996, 5, 2236-2247.	7.6	29
56	Crystal Structure of the Bowmanâ€"Birk Inhibitor from Barley Seeds in Ternary Complex with Porcine Trypsin. Journal of Molecular Biology, 2004, 343, 173-186.	4.2	29
57	Differential in vitro and cellular effects of iron chelators for hypoxia inducible factor hydroxylases. Journal of Cellular Biochemistry, 2013, 114, 864-873.	2.6	29
58	Rapid degradation of replication-dependent histone mRNAs largely occurs on mRNAs bound by nuclear cap-binding proteins 80 and 20. Nucleic Acids Research, 2013, 41, 1307-1318.	14.5	29
59	LAG-3xPD-L1 bispecific antibody potentiates antitumor responses of TÂcells through dendritic cell activation. Molecular Therapy, 2022, 30, 2800-2816.	8.2	29
60	Refined Structure of the Chitinase from Barley Seeds at 2.0 Ã… Resolution. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 289-298.	2.5	28
61	Crystal structure of human nucleoside diphosphate kinase A, a metastasis suppressor. Proteins: Structure, Function and Bioinformatics, 2002, 46, 340-342.	2.6	27
62	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. Biochemical and Biophysical Research Communications, 2007, 354, 962-967.	2.1	26
63	Structure of the autophagic E2 enzyme Atg10. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1409-1417.	2.5	26
64	A novel conformation of the LC3-interacting region motif revealed by the structure of a complex between LC3B and RavZ. Biochemical and Biophysical Research Communications, 2017, 490, 1093-1099.	2.1	26
65	Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. Journal of Molecular Biology, 2019, 431, 3647-3661.	4.2	26
66	STAMâ€"AMSH interaction facilitates the deubiquitination activity in the C-terminal AMSH. Biochemical and Biophysical Research Communications, 2006, 351, 612-618.	2.1	25
67	Isolation and characterization of the prokaryotic proteasome homolog HslVU (ClpQY) from Thermotoga maritima and the crystal structure of HslV. Biophysical Chemistry, 2002, 100, 437-452.	2.8	24
68	Expansion of the clinicopathological and mutational spectrum of Perry syndrome. Parkinsonism and Related Disorders, 2014, 20, 388-393.	2.2	24
69	Structural and Biochemical Study of the Mono-ADP-Ribosyltransferase Domain of SdeA, a Ubiquitylating/Deubiquitylating Enzyme from Legionella pneumophila. Journal of Molecular Biology, 2018, 430, 2843-2856.	4.2	24
70	Identification of a novel ubiquitin binding site of STAM1 VHS domain by NMR spectroscopy. FEBS Letters, 2009, 583, 287-292.	2.8	22
71	Crystal structure of ubiquitin-like small archaeal modifier protein 1 (SAMP1) from Haloferax volcanii. Biochemical and Biophysical Research Communications, 2011, 405, 112-117.	2.1	22
72	Structural basis for dual specificity of yeast N-terminal amidase in the N-end rule pathway. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12438-12443.	7.1	22

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73	Targeted Degradation of Transcription Coactivator SRCâ€•1 through the Nâ€•Degron Pathway. Angewandte Chemie - International Edition, 2020, 59, 17548-17555.	13.8	22
74	Tyrosyltyrosylcysteine-Directed Synthesis of Chiral Cobalt Oxide Nanoparticles and Peptide Conformation Analysis. ACS Nano, 2021, 15, 979-988.	14.6	19
75	The structure of the pleiotropic transcription regulator CodY provides insight into its GTP-sensing mechanism. Nucleic Acids Research, 2016, 44, gkw775.	14.5	18
76	Homotetrameric Structure of the SNAP-23 N-terminal Coiled-coil Domain. Journal of Biological Chemistry, 2003, 278, 13462-13467.	3.4	17
77	Expression, purification and biochemical characterization of the N-terminal regions of human TIG3 and HRASLS3 proteins. Protein Expression and Purification, 2010, 71, 103-107.	1.3	17
78	Characterization of the HslU chaperone affinity for HslV protease. Protein Science, 2005, 14, 1357-1362.	7.6	16
79	Dab1 binds to Fe65 and diminishes the effect of Fe65 or LRP1 on APP processing. Journal of Cellular Biochemistry, 2010, 111, 508-519.	2.6	16
80	Metabolic engineering of Escherichia coli to produce a monophosphoryl lipid A adjuvant. Metabolic Engineering, 2020, 57, 193-202.	7.0	16
81	Structural basis for the Nâ€•degron specificity of <scp>ClpS1</scp> from <scp><i>Arabidopsis thaliana</i></scp>. Protein Science, 2021, 30, 700-708.	7.6	15
82	Change in single cystathionine Î²-synthase domain-containing protein from a bent to flat conformation upon adenosine monophosphate binding. Journal of Structural Biology, 2013, 183, 40-46.	2.8	14
83	A key lysine residue in the AXH domain of ataxin-1 is essential for its ubiquitylation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 356-364.	2.3	14
84	Use of the LC3B-fusion technique for biochemical and structural studies of proteins involved in the N-degron pathway. Journal of Biological Chemistry, 2020, 295, 2590-2600.	3.4	14
85	The Quaternary Arrangement of HslU and HslV in a Cocrystal: A Response to Wang, Yale. Journal of Structural Biology, 2001, 135, 281-293.	2.8	13
86	Aminopeptidases trim Xaa-Pro proteins, initiating their degradation by the Pro/N-degron pathway. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
87	pH-dependent regulation of SQSTM1/p62 during autophagy. Autophagy, 2019, 15, 180-181.	9.1	12
88	Crystal structure of 5â€²-methylthioadenosine nucleosidase from Arabidopsis thaliana at 1.5-Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2006, 65, 519-523.	2.6	11
89	PEAâ€•15 facilitates EGFR dephosphorylation <i>via</i> ERK sequestration at increased ERâ€“PM contacts in TNBC cells. FEBS Letters, 2015, 589, 1033-1039.	2.8	11
90	A simple technique to convert sitting-drop vapor diffusion into hanging-drop vapor diffusion by solidifying the reservoir solution with agarose. Journal of Applied Crystallography, 2009, 42, 975-976.	4.5	10

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91	TRAF6-mediated ubiquitination of MST1/STK4 attenuates the TLR4-NF-Î°B signaling pathway in macrophages. Cellular and Molecular Life Sciences, 2021, 78, 2315-2328.	5.4	10
92	Translation mediated by the nuclear cap-binding complex is confined to the perinuclear region via a CTIFâ€"DDX19B interaction. Nucleic Acids Research, 2021, 49, 8261-8276.	14.5	10
93	Enhancing Protein Crystallization under a Magnetic Field. Crystals, 2020, 10, 821.	2.2	9
94	UXT chaperone prevents proteotoxicity by acting as an autophagy adaptor for p62-dependent aggrephagy. Nature Communications, 2021, 12, 1955.	12.8	9
95	Swapping of interaction partners with ATG5 for autophagosome maturation. BMB Reports, 2015, 48, 129-130.	2.4	9
96	Insulin activates EGFR by stimulating its interaction with IGF-1R in low-EGFR-expressing TNBC cells. BMB Reports, 2015, 48, 342-347.	2.4	9
97	Crystal structure of yeast Gid10 in complex with Pro/N-degron. Biochemical and Biophysical Research Communications, 2021, 582, 86-92.	2.1	9
98	Crystallization and preliminary X-ray crystallographic analysis ofEscherichia coliCyaY, a structural homologue of human frataxin. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 920-921.	2.5	8
99	Real-time imaging of NF-AT nucleocytoplasmic shuttling with a photoswitchable fluorescence protein in live cells. Biochimica Et Biophysica Acta - General Subjects, 2008, 1780, 1403-1407.	2.4	8
100	Structures of the ribosome-inactivating protein from barley seeds reveal a unique activation mechanism. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1488-1500.	2.5	8
101	Structural and Biochemical Analyses of the Eukaryotic Heat Shock Locus V (HslV) from Trypanosoma brucei. Journal of Biological Chemistry, 2013, 288, 23234-23243.	3.4	8
102	Mitochondrial protease ClpP supplementation ameliorates diet-induced NASH in mice. Journal of Hepatology, 2022, 77, 735-747.	3.7	8
103	Structural insights into ClpP protease side exit poreâ€opening by a pH drop coupled with substrate hydrolysis. EMBO Journal, 2022, 41, e109755.	7.8	8
104	The recombination-associated protein RdgC adopts a novel toroidal architecture for DNA binding. Nucleic Acids Research, 2007, 35, 2671-2681.	14.5	7
105	A facile method to prepare large quantities of active caspase-3 overexpressed by auto-induction in the C41(DE3) strain. Protein Expression and Purification, 2016, 126, 104-108.	1.3	7
106	Crystallization and preliminary X-ray crystallographic analysis of human nucleoside diphosphate kinase A. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 504-505.	2.5	6
107	A degradation signal recognition in prokaryotes. Journal of Synchrotron Radiation, 2008, 15, 246-249.	2.4	6
108	Biochemical and structural characterization of 5â€²-methylthioadenosine nucleosidases from Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2009, 381, 619-624.	2.1	6

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109	ACCORD: an assessment tool to determine the orientation of homodimeric coiled-coils. Scientific Reports, 2017, 7, 43318.	3.3	6
110	Crystallization and preliminary X-ray crystallographic analysis of chitinase from barley seeds. Proteins: Structure, Function and Bioinformatics, 1993, 17, 107-109.	2.6	5
111	A thermostable xylose isomerase fromThermus caldophilus: biochemical characterization, crystallization and preliminary X-ray analysis. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 294-296.	2.5	5
112	Docking of components in a bacterial complex. Nature, 2000, 408, 668-668.	27.8	5
113	Crystal structure of the single cystathionine Î²-synthase domain-containing protein CBSX1 from Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2013, 430, 265-271.	2.1	5
114	Purification, crystallization and preliminary X-ray diffraction analysis of a cystathionine Î²-synthase domain-containing protein, CDCP2, fromArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 825-827.	0.7	4
115	A cytosine modification mechanism revealed by the structure of a ternary complex of deoxycytidylate hydroxymethylase from bacteriophage T4 with its cofactor and substrate. IUCrJ, 2019, 6, 206-217.	2.2	4
116	Preliminary X-ray crystallographic analysis of Bowmanâ€“Birk trypsin inhibitor from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 441-443.	2.5	3
117	Crystallization and preliminary X-ray diffraction analysis ofSaccharomyces cerevisiaeYgr203p, a homologue of Acr2 arsenate reductase. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 778-780.	2.5	3
118	Nucleoside diphosphate kinase from the hyperthermophilic archaeonMethanococcus jannaschii: overexpression, crystallization and preliminary X-ray crystallographic analysis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1485-1487.	2.5	3
119	Backbone resonances assignment of 19ÂkDa CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. Biomolecular NMR Assignments, 2012, 6, 109-113.	0.8	3
120	mTRAQ-based quantitative analysis combined with peptide fractionation based on cysteinyl peptide enrichment. Analytical Biochemistry, 2015, 477, 41-49.	2.4	3
121	Dynamics and Entropy of Cyclohexane Rings Control pH-Responsive Reactivity. Jacs Au, 2021, 1, 2070-2079.	7.9	3
122	Crystallization and preliminary X-ray analysis of Saccharomyces cerevisiae Ypd1p, a key intermediate in phosphorelay signal transduction. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1219-1221.	2.5	2
123	Direct recognition of the C-terminal polylysine residues of nonstop protein by Ltn1, an E3 ubiquitin ligase. Biochemical and Biophysical Research Communications, 2014, 453, 642-647.	2.1	2
124	A host dTMP-bound structure of T4 phage dCMP hydroxymethylase mutant using an X-ray free electron laser. Scientific Reports, 2019, 9, 16316.	3.3	2
125	Targeted Degradation of Transcription Coactivator SRCâ€1 through the Nâ€Degron Pathway. Angewandte Chemie, 2020, 132, 17701-17708.	2.0	2
126	Insights into the Molecular Evolution of HslU ATPase through Biochemical and Mutational Analyses. PLoS ONE, 2014, 9, e103027.	2.5	2

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127	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
128	Crystallization and preliminary X-ray crystallographic analysis of DNA polymerase fromThermus aquaticus. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 1086-1088.	2.5	1
129	Crystal structure of Bacillus licheniformis Î±-Amylase at 1.7resolution. Progress in Biotechnology, 1996, 12, 163-170.	0.2	1
130	Crystallization and preliminary X-ray crystallographic analysis of deoxycytidylate hydroxymethylase from bacteriophage T4. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1061-1063.	2.5	1
131	Crystallization and preliminary X-ray crystallographic analysis of the protease inhibitor ecotin in complex with chymotrypsin. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1091-1092.	2.5	1
132	Crystallization and preliminary X-ray analysis of a complex between the Bowmanâ€"Birk trypsin inhibitor from barley and porcine pancreatic trypsin. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1244-1246.	2.5	1
133	Crystallization and preliminary X-ray analysis of the C-terminal fragment of Ski7 fromSaccharomyces cerevisiae. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1252-1255.	0.8	1
134	Structural Characterization of <scp>RNA</scp> Recognition Motifâ€2 Domain of <scp>SART3</scp>. Bulletin of the Korean Chemical Society, 2017, 38, 444-447.	1.9	1
135	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 50 422 Seibutsu Butsuri, 2006, 46, S120.	0.1	0
136	Crystal structure of <i>Pyrococcus furiosus</i> PF2050, a member of the DUF2666 protein family. FEBS Letters, 2012, 586, 1384-1388.	2.8	0
137	Structural Characterization of pre-miRNA 155. Journal of the Korean Magnetic Resonance Society, 2016, 20, 46-49.	0.1	0
138	An assessment tool for determination of coiled-coil orientation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a118-a118.	0.1	0
139	Structural Studies of Peptide Binding Interaction of HCV IRES Domain IV. Journal of the Korean Magnetic Resonance Society, 2017, 21, 109-113.	0.1	0
140	Structural insight into degradation mechanism of N-end rule substrates by p62/SQSTM1 selective autophagy adaptor. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a313-a313.	0.1	0
141	Structural studies of a novel ubiquitin-modifying enzyme, SdeA, using various tools. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a78-a78.	0.1	0