

Hyun Kyu Song

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/327441/hyun-kyu-song-publications-by-year.pdf>

Version: 2024-04-20

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.

136
papers

8,936
citations

38
h-index

94
g-index

143
ext. papers

10,128
ext. citations

8.8
avg, IF

5.29
L-index

#	Paper	IF	Citations
136	LC3B is an RNA-binding protein to trigger rapid mRNA degradation during autophagy.. <i>Nature Communications</i> , 2022 , 13, 1436	17.4	1
135	LAG-3xPD-L1 bispecific antibody potentiates antitumor responses of T cells through dendritic cell activation.. <i>Molecular Therapy</i> , 2022 ,	11.7	3
134	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
133	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
132	Crystal structure of yeast Gid10 in complex with Pro/N-degron. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 582, 86-92	3.4	6
131	UXT chaperone prevents proteotoxicity by acting as an autophagy adaptor for p62-dependent aggrephagy. <i>Nature Communications</i> , 2021 , 12, 1955	17.4	2
130	Phospholipid transfer function of PTPIP51 at mitochondria-associated ER membranes. <i>EMBO Reports</i> , 2021 , 22, e51323	6.5	9
129	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
128	Tyrosyltyrosylcysteine-Directed Synthesis of Chiral Cobalt Oxide Nanoparticles and Peptide Conformation Analysis. <i>ACS Nano</i> , 2021 , 15, 979-988	16.7	7
127	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
126	Dynamics and Entropy of Cyclohexane Rings Control pH-Responsive Reactivity. <i>Jacs Au</i> , 2021 , 1, 2070-2079		2
125	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
124	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
123	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
122	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
121	Enhancing Protein Crystallization under a Magnetic Field. <i>Crystals</i> , 2020 , 10, 821	2.3	3
120	Targeted Degradation of Transcription Coactivator SRC-1 through the N-Degron Pathway. <i>Angewandte Chemie</i> , 2020 , 132, 17701-17708	3.6	1

119	Endoribonucleolytic Cleavage of mA-Containing RNAs by RNase P/MRP Complex. <i>Molecular Cell</i> , 2019 , 74, 494-507.e8	17.6	189
118	MST1 Negatively Regulates TNF α -Induced NF- κ B Signaling through Modulating LUBAC Activity. <i>Molecular Cell</i> , 2019 , 73, 1138-1149.e6	17.6	18
117	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
116	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
115	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
114	eIF4A3 Phosphorylation by CDKs Affects NMD during the Cell Cycle. <i>Cell Reports</i> , 2019 , 26, 2126-2139.e9	10.6	21
113	pH-dependent regulation of SQSTM1/p62 during autophagy. <i>Autophagy</i> , 2019 , 15, 180-181	10.2	10
112	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. <i>Nature Communications</i> , 2018 , 9, 3291	17.4	41
111	The C-terminal region of ATG101 bridges ULK1 and PtdIns3K complex in autophagy initiation. <i>Autophagy</i> , 2018 , 14, 2104-2116	10.2	22
110	PEL1 Selectively Targets Kinase-Active RIP3 for Ubiquitylation-Dependent Proteasomal Degradation. <i>Molecular Cell</i> , 2018 , 70, 920-935.e7	17.6	41
109	A Structural View of Xenophagy, a Battle between Host and Microbes. <i>Molecules and Cells</i> , 2018 , 41, 27-34	3.5	27
108	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
107	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
106	ACCORD: an assessment tool to determine the orientation of homodimeric coiled-coils. <i>Scientific Reports</i> , 2017 , 7, 43318	4.9	5
105	Structural Characterization of RNA Recognition Motif-2 Domain of SART3. <i>Bulletin of the Korean Chemical Society</i> , 2017 , 38, 444-447	1.2	
104	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
103	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
102	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

101	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016 , 12, 1-222	10.2	3838
100	Structural Characterization of pre-miRNA 155. <i>Journal of the Korean Magnetic Resonance Society</i> , 2016 , 20, 46-49		
99	Structure biology of selective autophagy receptors. <i>BMB Reports</i> , 2016 , 49, 73-80	5.5	42
98	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
97	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
96	MTRAQ-based quantitative analysis combined with peptide fractionation based on cysteinyl peptide enrichment. <i>Analytical Biochemistry</i> , 2015 , 477, 41-9	3.1	3
95	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
94	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
93	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. <i>Autophagy</i> , 2015 , 11, 75-87	10.2	47
92	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
91	Swapping of interaction partners with ATG5 for autophagosome maturation. <i>BMB Reports</i> , 2015 , 48, 129-30	5.5	7
90	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
89	Expansion of the clinicopathological and mutational spectrum of Perry syndrome. <i>Parkinsonism and Related Disorders</i> , 2014 , 20, 388-93	3.6	19
88	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
87	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
86	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
85	Insights into the molecular evolution of HslU ATPase through biochemical and mutational analyses. <i>PLoS ONE</i> , 2014 , 9, e103027	3.7	2
84	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. <i>Nature Communications</i> , 2013 , 4, 1613	17.4	64

83	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
82	MG53-induced IRS-1 ubiquitination negatively regulates skeletal myogenesis and insulin signalling. <i>Nature Communications</i> , 2013 , 4, 2354	17.4	102
81	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
80	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, 265-71	3.4	3
79	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
78	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
77	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
76	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
75	Structure of the autophagic E2 enzyme Atg10. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 1409-17		18
74	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
73	Backbone resonances assignment of 19 kDa CD1 domain of human mitotic checkpoint serine/threonine-protein kinase, Bub1. <i>Biomolecular NMR Assignments</i> , 2012 , 6, 109-13	0.7	3
72	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	
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, 1323-30	17.6	70
70	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
69	Crystal structure of a coiled-coil domain from human ROCK I. <i>PLoS ONE</i> , 2011 , 6, e18080	3.7	26
68	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
67	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
66	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

65	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
64	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
63	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
62	Crystal structure of PRY-SPRY domain of human TRIM72. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 790-5	4.2	29
61	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
60	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
59	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
58	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
57	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
56	A role for a menthone reductase in resistance against microbial pathogens in plants. <i>Plant Physiology</i> , 2008 , 148, 383-401	6.6	62
55	A degradation signal recognition in prokaryotes. <i>Journal of Synchrotron Radiation</i> , 2008 , 15, 246-9	2.4	5
54	Purification, crystallization and preliminary X-ray diffraction analysis of a cystathionine beta-synthase domain-containing protein, CDCP2, from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 825-7		4
53	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
52	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
51	Structural characterization of the photoswitchable fluorescent protein Dronpa-C62S. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 354, 962-7	3.4	22
50	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
49	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
48	Crystal structure of the FERM domain of focal adhesion kinase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 252-9	5.4	97

47	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
46	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, 5120	0	
45	Crystal structure of 5Qmethylthioadenosine nucleosidase from Arabidopsis thaliana at 1.5-A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 519-23	4.2	11
44	Characterization of the HslU chaperone affinity for HslV protease. <i>Protein Science</i> , 2005 , 14, 1357-62	6.3	16
43	Ring-shaped architecture of RecR: implications for its role in homologous recombinational DNA repair. <i>EMBO Journal</i> , 2004 , 23, 2029-38	13	94
42	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
41	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
40	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
39	SAP couples Fyn to SLAM immune receptors. <i>Nature Cell Biology</i> , 2003 , 5, 155-60	23.4	237
38	Homotetrameric structure of the SNAP-23 N-terminal coiled-coil domain. <i>Journal of Biological Chemistry</i> , 2003 , 278, 13462-7	5.4	15
37	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
36	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
35	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
34	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
33	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
32	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
31	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
30	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

29	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
28	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
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	The structures of HslU and the ATP-dependent protease HslU-HslV. <i>Nature</i> , 2000 , 403, 800-5	50.4	378
25	Docking of components in a bacterial complex. <i>Nature</i> , 2000 , 408, 667-8	50.4	36
24	Docking of components in a bacterial complex. <i>Nature</i> , 2000 , 408, 668-668	50.4	4
23	Crystal structure of NAD(+)-dependent DNA ligase: modular architecture and functional implications. <i>EMBO Journal</i> , 2000 , 19, 1119-29	13	154
22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	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
14	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
13	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
12	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

11	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
10	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
9	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
8	Crystal structure of <i>Bacillus licheniformis</i> α -Amylase at 1.7 resolution. <i>Progress in Biotechnology</i> , 1996 , 12, 163-170		1
7	Refined structure of the chitinase from barley seeds at 2.0 a resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996 , 52, 289-98		24
6	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
5	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
4	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
3	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
2	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
1	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