

# Kyoung-Seok Ryu

## List of Publications by Year in descending order

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68  
papers

1,397  
citations

331670

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361022

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docs citations

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times ranked

2228  
citing authors

#	ARTICLE	IF	CITATIONS
1	MUL1-RING recruits the substrate, p53-TAD as a complex with UBE2D2-UB conjugate. FEBS Journal, 2022, 289, 3568-3586.	4.7	2
2	Repositioning Food and Drug Administration-Approved Drugs for Inhibiting Biliverdin IX $\alpha$ Reductase B as a Novel Thrombocytopenia Therapeutic Target. Journal of Medicinal Chemistry, 2022, 65, 2548-2557.	6.4	1
3	Separation of native and C106-oxidized DJ-1 proteins by using column chromatography. Protein Expression and Purification, 2022, 195-196, 106092.	1.3	1
4	Structure of neuroendocrine regulatory peptide $\alpha$ 2 in membrane-mimicking environments. Peptide Science, 2021, 113, e24206.	1.8	2
5	NMR spectroscopy uncovers direct interaction between BAF60A and p53. Biochemical and Biophysical Research Communications, 2021, 534, 815-821.	2.1	1
6	Systematic Approach to Find the Global Minimum of Relaxation Dispersion Data for Protein-Induced B $\alpha$ -Z Transition of DNA. International Journal of Molecular Sciences, 2021, 22, 3517.	4.1	2
7	Probing the Neuraminidase Activity of Influenza Virus Using a Cytolysin A Protein Nanopore. Analytical Chemistry, 2020, 92, 14303-14308.	6.5	16
8	NMR mapping of the highly flexible regions of $^{13}\text{C}/^{15}\text{N}$ -labeled antibody TTAC-0001-Fab. Journal of Biomolecular NMR, 2020, 74, 311-319.	2.8	2
9	Determinants of PB1 Domain Interactions in Auxin Response Factor ARF5 and Repressor IAA17. Journal of Molecular Biology, 2020, 432, 4010-4022.	4.2	16
10	The RING domain of mitochondrial E3 ubiquitin ligase 1 and its complex with Ube2D2: crystallization and X-ray diffraction. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 1-7.	0.8	4
11	Diverse Structural Conversion and Aggregation Pathways of Alzheimer's Amyloid- $\beta$ (1-40). ACS Nano, 2019, 13, 8766-8783.	14.6	33
12	Structural Basis for Cell-Wall Recognition by Bacteriophage PBC5 Endolysin. Structure, 2019, 27, 1355-1365.e4.	3.3	17
13	Solution structure of MUL1-RING domain and its interaction with p53 transactivation domain. Biochemical and Biophysical Research Communications, 2019, 516, 533-539.	2.1	9
14	Unique Unfoldase/Aggregase Activity of a Molecular Chaperone Hsp33 in its Holding-Inactive State. Journal of Molecular Biology, 2019, 431, 1468-1480.	4.2	7
15	NMR Dynamics Study Reveals the Z $\beta$ Domain of Human ADAR1 Associates with and Dissociates from Z-RNA More Slowly than Z-DNA. ACS Chemical Biology, 2019, 14, 245-255.	3.4	20
16	NMR Investigation of the Interaction between the RecQ C-Terminal Domain of Human Bloom Syndrome Protein and G-Quadruplex DNA from the Human c-Myc Promoter. Journal of Molecular Biology, 2019, 431, 794-806.	4.2	11
17	Nonenzymatic acetylation of ubiquitin Lys side chains is modulated by their neighboring residues. FEBS Journal, 2018, 285, 1277-1289.	4.7	7
18	Interaction of replication protein A with two acidic peptides from human Bloom syndrome protein. FEBS Letters, 2018, 592, 547-558.	2.8	23

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19	Solution structure and dynamics of <i>Xanthomonas albilineans</i> Cas2 provide mechanistic insight on nuclease activity. FEBS Letters, 2018, 592, 147-155.	2.8	2
20	Zinc-mediated Reversible Multimerization of Hsp31 Enhances the Activity of Holding Chaperone. Journal of Molecular Biology, 2018, 430, 1760-1772.	4.2	7
21	Total Synthesis of Xanthoangelol B and Its Various Fragments: Toward Inhibition of Virulence Factor Production of <i>Staphylococcus aureus</i> . Journal of Medicinal Chemistry, 2018, 61, 10473-10487.	6.4	11
22	Evidence of link between quorum sensing and sugar metabolism in <i>Escherichia coli</i> revealed via cocrystal structures of LsrK and HPr. Science Advances, 2018, 4, eaar7063.	10.3	68
23	Biophysical characterization of Ca <sup>2+</sup> -binding of S100A5 and Ca <sup>2+</sup> -induced interaction with RAGE. Biochemical and Biophysical Research Communications, 2017, 483, 332-338.	2.1	5
24	NMR elucidation of reduced B-Z transition activity of PKZ protein kinase at high NaCl concentration. Biochemical and Biophysical Research Communications, 2017, 482, 335-340.	2.1	8
25	C-terminal dimerization of apo-cyclic <i>AMP</i> receptor protein validated in solution. FEBS Letters, 2017, 591, 1064-1070.	2.8	2
26	Backbone resonance assignments of the <i>Escherichia coli</i> 62 kDa protein, Hsp31. Biomolecular NMR Assignments, 2017, 11, 159-163.	0.8	3
27	Increasing the soluble expression and crystallization of the <i>Escherichia coli</i> quorum-sensing protein LsrK. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 253-258.	0.8	3
28	Amphiphilic Peptide Nanorods Based on Oligo-Phenylalanine as a Biocompatible Drug Carrier. Bioconjugate Chemistry, 2017, 28, 2266-2276.	3.6	19
29	Solution structure of the Z-DNA binding domain of PKR-like protein kinase from <i>Carassius auratus</i> and quantitative analyses of the intermediate complex during B $\rightarrow$ Z transition. Nucleic Acids Research, 2016, 44, 2936-2948.	14.5	25
30	The role of the KRSIK motif of human angiogenin in heparin and DNA binding. RSC Advances, 2016, 6, 82644-82647.	3.6	1
31	<sup>1</sup> H NMR study of the antifreeze activities of active and inactive isoforms of a type III antifreeze protein. FEBS Letters, 2016, 590, 4202-4212.	2.8	5
32	Comparative studies on manual and automatic backbone chemical shift assignments of <sup>2</sup> H/ <sup>13</sup> C/ <sup>15</sup> N-labeled Ube2g1. Journal of Analytical Science and Technology, 2015, 6, .	2.1	1
33	Semi-Empirical Structure Determination of <i>Escherichia coli</i> Hsp33 and Identification of Dynamic Regulatory Elements for the Activation Process. Journal of Molecular Biology, 2015, 427, 3850-3861.	4.2	18
34	Structural convergence of unstructured p53 family transactivation domains in MDM2 recognition. Cell Cycle, 2015, 14, 533-543.	2.6	25
35	Differential Ubiquitin Binding by the Acidic Loops of Ube2g1 and Ube2r1 Enzymes Distinguishes Their Lys-48-ubiquitylation Activities. Journal of Biological Chemistry, 2015, 290, 2251-2263.	3.4	22
36	Per-deuteration and NMR experiments for the backbone assignment of 62 kDa protein, Hsp31. Journal of the Korean Magnetic Resonance Society, 2015, 19, 112-118.	0.1	2

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37	Stereospecific mechanism of <i>DJ1</i> glyoxalases inferred from their hemithioacetal-containing crystal structures. <i>FEBS Journal</i> , 2014, 281, 5447-5462.	4.7	36
38	Solution structure of the RecQ C-terminal domain of human Bloom syndrome protein. <i>Journal of Biomolecular NMR</i> , 2014, 58, 141-147.	2.8	9
39	Probing the Rate-Limiting Step for Intramolecular Transfer of a Transcription Factor between Specific Sites on the Same DNA Molecule by <sup>15</sup> N-Exchange NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2014, 136, 14369-14372.	13.7	7
40	Structural alteration of <i>Escherichia coli</i> Hsp31 by thermal unfolding increases chaperone activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 621-628.	2.3	7
41	Crystal Structures of the LsrR Proteins Complexed with Phospho-AI-2 and Two Signal-Interrupting Analogues Reveal Distinct Mechanisms for Ligand Recognition. <i>Journal of the American Chemical Society</i> , 2013, 135, 15526-15535.	13.7	21
42	Insights into the regulation of human Rev1 for translesion synthesis polymerases revealed by the structural studies on its polymerase-interacting domain. <i>Journal of Molecular Cell Biology</i> , 2013, 5, 204-206.	3.3	14
43	Mechanism of anchoring of OmpA protein to the cell wall peptidoglycan of the gram-negative bacterial outer membrane. <i>FASEB Journal</i> , 2012, 26, 219-228.	0.5	164
44	Srs2 possesses a non-canonical PIP box in front of its SBM for precise recognition of SUMOylated PCNA. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 258-261.	3.3	14
45	Structural insights into the dual-targeting mechanism of Nutlin-3. <i>Biochemical and Biophysical Research Communications</i> , 2012, 420, 48-53.	2.1	22
46	Structural analysis of <i>Escherichia coli</i> C5 protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 963-967.	2.6	2
47	Verification of the interdomain contact site in the inactive monomer, and the domain-swapped fold in the active dimer of Hsp33 in solution. <i>FEBS Letters</i> , 2012, 586, 411-415.	2.8	7
48	Molecular Mimicry-Based Repositioning of Nutlin-3 to Anti-Apoptotic Bcl-2 Family Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 1244-1247.	13.7	36
49	Structural characterization reveals that a PilZ domain protein undergoes substantial conformational change upon binding to cyclic dimeric guanosine monophosphate. <i>Protein Science</i> , 2011, 20, 270-277.	7.6	19
50	Backbone assignment of the OmpA-like domain of peptidoglycan-associated lipoprotein from <i>Acinetobacter baumannii</i> . <i>Journal of Analytical Science and Technology</i> , 2011, 2, 52-58.	2.1	1
51	Backbone NMR assignment of a hypothetical protein MJ0754 from <i>Methanococcus jannaschii</i> DSM 2661. <i>Journal of Analytical Science and Technology</i> , 2011, 2, 46-51.	2.1	0
52	The Human Cdc34 Carboxyl Terminus Contains a Non-covalent Ubiquitin Binding Activity That Contributes to SCF-dependent Ubiquitination. <i>Journal of Biological Chemistry</i> , 2010, 285, 17754-17762.	3.4	24
53	Structure of PP4397 Reveals the Molecular Basis for Different c-di-GMP Binding Modes by Pilz Domain Proteins. <i>Journal of Molecular Biology</i> , 2010, 398, 97-110.	4.2	94
54	Codon optimization enhances protein expression of human peptide deformylase in <i>E. coli</i> . <i>Protein Expression and Purification</i> , 2010, 70, 224-230.	1.3	24

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55	60th residues of ubiquitin and Nedd8 are located out of E2-binding surfaces, but are important for K48 ubiquitin-linkage. <i>FEBS Letters</i> , 2009, 583, 3323-3328.	2.8	19
56	Structure of the Cdt1 C-terminal domain: Conservation of the winged helix fold in replication licensing factors. <i>Protein Science</i> , 2009, 18, 2252-2264.	7.6	33
57	Structure and interaction of ubiquitin-associated domain of human Fas-associated factor 1. <i>Protein Science</i> , 2009, 18, 2265-2276.	7.6	22
58	Crystal Structures and Enzyme Mechanisms of a Dual Fucose Mutarotase/Ribose Pyranase. <i>Journal of Molecular Biology</i> , 2009, 391, 178-191.	4.2	8
59	Biotinoyl domain of human acetyl-CoA carboxylase: Structural insights into the carboxyl transfer mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 613-624.	2.6	19
60	Direct characterization of E2-dependent target specificity and processivity using an artificial p27-linker-E2 ubiquitination system. <i>BMB Reports</i> , 2008, 41, 852-857.	2.4	9
61	Characterization and role of fucose mutarotase in mammalian cells. <i>Glycobiology</i> , 2007, 17, 955-962.	2.5	22
62	Structural insight into dimeric interaction of the SARAH domains from Mst1 and RASSF family proteins in the apoptosis pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9236-9241.	7.1	124
63	Solution structure and backbone dynamics of the XPC-binding domain of the human DNA repair protein hHR23B. <i>FEBS Journal</i> , 2005, 272, 2467-2476.	4.7	12
64	Biophysical Characterization of the Interaction Domains and Mapping of the Contact Residues in the XPF-ERCC1 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 28644-28652.	3.4	38
65	Structural Insights into the Monosaccharide Specificity of Escherichia coli Rhamnose Mutarotase. <i>Journal of Molecular Biology</i> , 2005, 349, 153-162.	4.2	26
66	NMR Application Probes a Novel and Ubiquitous Family of Enzymes That Alter Monosaccharide Configuration. <i>Journal of Biological Chemistry</i> , 2004, 279, 25544-25548.	3.4	34
67	NMR Analysis of Enzyme-Catalyzed and Free-Equilibrium Mutarotation Kinetics of Monosaccharides. <i>Journal of the American Chemical Society</i> , 2004, 126, 9180-9181.	13.7	25
68	Binding Surface Mapping of Intra- and Interdomain Interactions among hHR23B, Ubiquitin, and Polyubiquitin Binding Site 2 of S5a. <i>Journal of Biological Chemistry</i> , 2003, 278, 36621-36627.	3.4	104