

Ji-Joon Song

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

6,094
citations

331670

21
h-index

161849

54
g-index

63
all docs

63
docs citations

63
times ranked

6891
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structure of the human somatostatin receptor 2 complex with its agonist somatostatin delineates the ligand-binding specificity. <i>ELife</i> , 2022, 11, .	6.0	10
2	RUNX3 methylation drives hypoxia-induced cell proliferation and antiapoptosis in early tumorigenesis. <i>Cell Death and Differentiation</i> , 2021, 28, 1251-1269.	11.2	16
3	Cisplatin fastens chromatin irreversibly even at a high chloride concentration. <i>Nucleic Acids Research</i> , 2021, 49, 12035-12047.	14.5	5
4	Single-Molecule Imaging Reveals the Mechanism Underlying Histone Loading of <i>Schizosaccharomyces pombe</i> AAA+ ATPase Abo1. <i>Molecules and Cells</i> , 2021, 44, 79-87.	2.6	4
5	Antigen-Presenting, Self-Assembled Protein Nanobarrels as an Adjuvant-Free Vaccine Platform against Influenza Virus. <i>ACS Nano</i> , 2021, 15, 10722-10732.	14.6	14
6	Targeting the Nuclear Receptor-Binding SET Domain Family of Histone Lysine Methyltransferases for Cancer Therapy: Recent Progress and Perspectives. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 14913-14929.	6.4	13
7	A Novel N-terminal Region to Chromodomain in CHD7 is Required for the Efficient Remodeling Activity. <i>Journal of Molecular Biology</i> , 2021, 433, 167114.	4.2	4
8	Cryo-EM structure of <i>Vibrio cholerae</i> aldehyde-alcohol dehydrogenase spiroosomes. <i>Biochemical and Biophysical Research Communications</i> , 2021, 536, 38-44.	2.1	3
9	Purification of full-length recombinant human huntingtin proteins with allelic series of polyglutamine lengths. <i>STAR Protocols</i> , 2021, 2, 100886.	1.2	4
10	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020, 28, 1035-1050.e8.	3.3	24
11	Yeast Chd1p Unwraps the Exit Side DNA upon ATP Binding to Facilitate the Nucleosome Translocation Occurring upon ATP Hydrolysis. <i>Biochemistry</i> , 2020, 59, 4481-4487.	2.5	2
12	Quantification of purified endogenous miRNAs with high sensitivity and specificity. <i>Nature Communications</i> , 2020, 11, 6033.	12.8	55
13	Aldehyde-alcohol dehydrogenase undergoes structural transition to form extended spiroosomes for substrate channeling. <i>Communications Biology</i> , 2020, 3, 298.	4.4	16
14	Spectral and photochemical diversity of tandem cysteine cyanobacterial phytochromes. <i>Journal of Biological Chemistry</i> , 2020, 295, 6754-6766.	3.4	8
15	Identification of the Antidepressant Vilazodone as an Inhibitor of Inositol Polyphosphate Multikinase by Structure-Based Drug Repositioning. <i>Molecules and Cells</i> , 2020, 43, 222-227.	2.6	5
16	EMPAS: Electron Microscopy Screening for Endogenous Protein Architectures. <i>Molecules and Cells</i> , 2020, 43, 804-812.	2.6	0
17	The crystal structure of Capicua HMG-box domain complexed with the ETV5-DNA and its implications for Capicua-mediated cancers. <i>FEBS Journal</i> , 2019, 286, 4951-4963.	4.7	7
18	Prolonged half-life of small-sized therapeutic protein using serum albumin-specific protein binder. <i>Journal of Controlled Release</i> , 2019, 315, 31-39.	9.9	18

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19	Editorial overview: The future after the cryo-EM resolution revolution. <i>Current Opinion in Structural Biology</i> , 2019, 58, iii-iv.	5.7	1
20	Aldehyde-alcohol dehydrogenase forms a high-order spiroosome architecture critical for its activity. <i>Nature Communications</i> , 2019, 10, 4527.	12.8	39
21	The big picture of chromatin biology by cryo-EM. <i>Current Opinion in Structural Biology</i> , 2019, 58, 76-87.	5.7	12
22	Structural Basis of MRG15-Mediated Activation of the ASH1L Histone Methyltransferase by Releasing an Autoinhibitory Loop. <i>Structure</i> , 2019, 27, 846-852.e3.	3.3	24
23	Structural basis of recognition and destabilization of the histone H2B ubiquitinated nucleosome by the DOT1L histone H3 Lys79 methyltransferase. <i>Genes and Development</i> , 2019, 33, 620-625.	5.9	73
24	Structural basis of nucleosome assembly by the Abo1 AAA+ATPase histone chaperone. <i>Nature Communications</i> , 2019, 10, 5764.	12.8	36
25	Novel DNA Aptamers that Bind to Mutant Huntingtin and Modify Its Activity. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 416-428.	5.1	16
26	Integrative Structural Investigation on the Architecture of Human Importin4_Histone H3/H4_Asf1a Complex and Its Histone H3 Tail Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 822-841.	4.2	17
27	Mechanisms of the Binding/Dissociation Acceleration of the Target-Guide Interaction by <i>Thermus thermophilus</i> Argonaute. <i>Bulletin of the Korean Chemical Society</i> , 2018, 39, 167-173.	1.9	5
28	Targeting protein and peptide therapeutics to the heart via tannic acid modification. <i>Nature Biomedical Engineering</i> , 2018, 2, 304-317.	22.5	202
29	Regulation and function of H3K36 di-methylation by the trithorax-group protein complex AMC. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	33
30	Structural insights into the oligomerization of FtsH periplasmic domain from <i>Thermotoga maritima</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1201-1207.	2.1	2
31	Biophysical characterization of the basic cluster in the transcription repression domain of human MeCP2 with AT-rich DNA. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 145-150.	2.1	4
32	ANKRD9 is associated with tumor suppression as a substrate receptor subunit of ubiquitin ligase. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 3145-3153.	3.8	13
33	Hydrophobic Residues near the Bilin Chromophore-Binding Pocket Modulate Spectral Tuning of Insert-Cys Subfamily Cyanobacteriochromes. <i>Scientific Reports</i> , 2017, 7, 40576.	3.3	13
34	RNA activation-independent DNA targeting of the Type III CRISPR-Cas system by a Csm complex. <i>EMBO Reports</i> , 2017, 18, 826-840.	4.5	23
35	Arabidopsis FRIGIDA stimulates EFS histone H3 Lys36 methyltransferase activity. <i>Plant Cell Reports</i> , 2017, 36, 1183-1185.	5.6	7
36	Structure-based nuclear import mechanism of histones H3 and H4 mediated by Kap123. <i>ELife</i> , 2017, 6, .	6.0	18

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37	Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016, 6, 26702.	3.3	26
38	Crystal structure of <i>Arabidopsis thaliana</i> SNC1 TIR domain. <i>Biochemical and Biophysical Research Communications</i> , 2016, 481, 146-152.	2.1	18
39	Structural Analysis of FRIGIDA Flowering-Time Regulator. <i>Molecular Plant</i> , 2016, 9, 618-620.	8.3	6
40	Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184.	6.0	52
41	Reconstitution and Crystallization of Sir 3/4 in a Complex with Nucleosome. <i>Bulletin of the Korean Chemical Society</i> , 2015, 36, 2793-2794.	1.9	0
42	Human Argonaute 2 Has Diverse Reaction Pathways on Target RNAs. <i>Molecular Cell</i> , 2015, 59, 117-124.	9.7	166
43	AUF1 promotes let-7b loading on Argonaute 2. <i>Genes and Development</i> , 2015, 29, 1599-1604.	5.9	41
44	Genomic Survey and Biochemical Analysis of Recombinant Candidate Cyanobacteriochromes Reveals Enrichment for Near UV/Violet Sensors in the Halotolerant and Alkaliphilic Cyanobacterium <i>Microcoleus</i> IPPAS B353. <i>Journal of Biological Chemistry</i> , 2015, 290, 28502-28514.	3.4	36
45	Structural basis of the phosphorylation dependent complex formation of neurodegenerative disease protein Ataxin-1 and RBM17. <i>Biochemical and Biophysical Research Communications</i> , 2014, 449, 399-404.	2.1	8
46	Dynamic Anchoring of the 3'-End of the Guide Strand Controls the Target Dissociation of Argonaute-Guide Complex. <i>Journal of the American Chemical Society</i> , 2013, 135, 16865-16871.	13.7	47
47	<i>Brucella</i> Immunogenic BP26 Forms a Channel-like Structure. <i>Journal of Molecular Biology</i> , 2013, 425, 1119-1126.	4.2	13
48	Structural basis of protein complex formation and reconfiguration by polyglutamine disease protein Ataxin-1 and Capicua. <i>Genes and Development</i> , 2013, 27, 590-595.	5.9	40
49	The Coded Functions of Noncoding RNAs for Gene Regulation. <i>Molecules and Cells</i> , 2011, 31, 491-496.	2.6	21
50	Crystal Structure of the Human Histone Methyltransferase ASH1L Catalytic Domain and Its Implications for the Regulatory Mechanism. <i>Journal of Biological Chemistry</i> , 2011, 286, 8369-8374.	3.4	105
51	Huntingtin facilitates polycomb repressive complex 2. <i>Human Molecular Genetics</i> , 2010, 19, 573-583.	2.9	169
52	WDR5 Interacts with Mixed Lineage Leukemia (MLL) Protein via the Histone H3-binding Pocket. <i>Journal of Biological Chemistry</i> , 2008, 283, 35258-35264.	3.4	155
53	Structural basis of histone H4 recognition by p53. <i>Genes and Development</i> , 2008, 22, 1313-1318.	5.9	133
54	Purified Argonaute2 and an siRNA form recombinant human RISC. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 340-349.	8.2	658

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55	Argonaute2 Is the Catalytic Engine of Mammalian RNAi. Science, 2004, 305, 1437-1441.	12.6	2,370
56	Crystal Structure of Argonaute and Its Implications for RISC Slicer Activity. Science, 2004, 305, 1434-1437.	12.6	1,283