

Jeong-Yong Suh

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

1,685
citations

257450

24
h-index

289244

40
g-index

60
all docs

60
docs citations

60
times ranked

2547
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	14.5	5
2	Asp149 and Asp152 in chicken and human ANP32A play an essential role in the interaction with influenza viral polymerase. FASEB Journal, 2021, 35, e21630.	0.5	7
3	Structural Investigation of Self-Assembly and Target Binding of Anti-CRISPR AcrIIIC2. CRISPR Journal, 2021, 4, 448-458.	2.9	1
4	Beneficial effect on rapid skin wound healing through carboxylic acid-treated chicken eggshell membrane. Materials Science and Engineering C, 2021, 128, 112350.	7.3	17
5	Structural and mechanistic insights into the CRISPR inhibition of AcrIF7. Nucleic Acids Research, 2020, 48, 9959-9968.	14.5	13
6	Intrinsic disorder is essential for Cas9 inhibition of anti-CRISPR AcrIIIA5. Nucleic Acids Research, 2020, 48, 7584-7594.	14.5	12
7	A Coil-to-Helix Transition Serves as a Binding Motif for hSNF5 and BAF155 Interaction. International Journal of Molecular Sciences, 2020, 21, 2452.	4.1	3
8	Determinants of PB1 Domain Interactions in Auxin Response Factor ARF5 and Repressor IAA17. Journal of Molecular Biology, 2020, 432, 4010-4022.	4.2	16
9	Anti-CRISPR AcrIIIC3 discriminates between Cas9 orthologs via targeting the variable surface of the HNH nuclease domain. FEBS Journal, 2019, 286, 4661-4674.	4.7	27
10	Structural Basis for Cell-Wall Recognition by Bacteriophage PBC5 Endolysin. Structure, 2019, 27, 1355-1365.e4.	3.3	17
11	Crystal structure of an anti-CRISPR protein, AcrIIIA1. Nucleic Acids Research, 2018, 46, 485-492.	14.5	34
12	CRISPR RNA and anti-CRISPR protein binding to the Xanthomonas albilineans Csy1-Csy2 heterodimer in the type I-F CRISPR-Cas system. Journal of Biological Chemistry, 2018, 293, 2744-2754.	3.4	17
13	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
14	Chicken NANOG self-associates via a novel folding-upon-binding mechanism. FASEB Journal, 2018, 32, 2563-2573.	0.5	5
15	The transgenic chicken derived anti-CD20 monoclonal antibodies exhibits greater anti-cancer therapeutic potential with enhanced Fc effector functions. Biomaterials, 2018, 167, 58-68.	11.4	18
16	Solution structure and dynamics of anti-CRISPR AcrIIIA4, the Cas9 inhibitor. Scientific Reports, 2018, 8, 3883.	3.3	31
17	Chicken Nanog Protein Self-Associates via a Novel Folding-upon-Binding Mechanism. Biophysical Journal, 2018, 114, 567a.	0.5	0
18	Facilitated Protein Association via Engineered Target Search Pathways Visualized by Paramagnetic NMR Spectroscopy. Structure, 2018, 26, 887-893.e2.	3.3	11

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19	Evidence of link between quorum sensing and sugar metabolism in <i>Escherichia coli</i> revealed via cocrystal structures of LsrK and HPr. <i>Science Advances</i> , 2018, 4, eaar7063.	10.3	68
20	Mechanism Underlying Green Discolouration of Myoglobin Induced by Atmospheric Pressure Plasma. <i>Scientific Reports</i> , 2018, 8, 9790.	3.3	32
21	Biophysical characterization of Ca ²⁺ -binding of S100A5 and Ca ²⁺ -induced interaction with RAGE. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 332-338.	2.1	5
22	Structural and dynamic insights into the role of conformational switching in the nuclease activity of the <i>Xanthomonas albilineans</i> Cas2 in CRISPR-mediated adaptive immunity. <i>Structural Dynamics</i> , 2017, 4, 054701.	2.3	8
23	Precise gene editing of chicken Na ⁺ /H ⁺ exchange type 1 (chNHE1) confers resistance to avian leukosis virus subgroup J (ALV-J). <i>Developmental and Comparative Immunology</i> , 2017, 77, 340-349.	2.3	32
24	Dimerization facilitates the conformational transitions for bacterial phosphotransferase enzyme I autophosphorylation in an allosteric manner. <i>FEBS Open Bio</i> , 2017, 7, 1208-1216.	2.3	0
25	Exosome Cofactors Connect Transcription Termination to RNA Processing by Guiding Terminated Transcripts to the Appropriate Exonuclease within the Nuclear Exosome. <i>Journal of Biological Chemistry</i> , 2016, 291, 13229-13242.	3.4	36
26	Biophysical characterization of the domain association between cytosolic A and B domains of the mannitol transporter enzymes MtlA and MtlB in the presence and absence of a connecting linker. <i>Protein Science</i> , 2016, 25, 1803-1811.	7.6	0
27	Catalytic hydrothermal conversion of macroalgae-derived alginate: effect of pH on production of furfural and valuable organic acids under subcritical water conditions. <i>Journal of Molecular Catalysis A</i> , 2015, 399, 106-113.	4.8	31
28	¹ H, ¹⁵ N, and ¹³ C backbone assignments and secondary structure of the cytoplasmic domain A of mannitol transporter MtlA from <i>Thermoanaerobacter tengcongensis</i> phosphotransferase system. <i>Journal of the Korean Magnetic Resonance Society</i> , 2015, 19, 42-48.	0.1	4
29	The Diarylheptanoid Hirsutenone Sensitizes Chemoresistant Ovarian Cancer Cells to Cisplatin via Modulation of Apoptosis-inducing Factor and X-linked Inhibitor of Apoptosis. <i>Journal of Biological Chemistry</i> , 2014, 289, 1723-1731.	3.4	28
30	Structural basis for the auxin-induced transcriptional regulation by Aux/IAA17. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18613-18618.	7.1	69
31	An Unusual Protein-Protein Interaction through Coupled Unfolding and Binding. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 9784-9787.	13.8	12
32	Crystal structure of toxin HP0892 from <i>Helicobacter pylori</i> with two Zn(II) at 1.8 Å resolution. <i>Protein Science</i> , 2014, 23, 819-832.	7.6	3
33	Piceatannol Enhances Cisplatin Sensitivity in Ovarian Cancer via Modulation of p53, X-linked Inhibitor of Apoptosis Protein (XIAP), and Mitochondrial Fission. <i>Journal of Biological Chemistry</i> , 2013, 288, 23740-23750.	3.4	86
34	Thermodynamic dissection of large-scale domain motions coupled with ligand binding of enzyme I. <i>Protein Science</i> , 2013, 22, 1602-1611.	7.6	3
35	Probing Target Search Pathways during Protein-Protein Association by Rational Mutations Based on Paramagnetic Relaxation Enhancement. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 3384-3388.	13.8	5
36	An Improved Quantitative Approach for the Assessment of Mitochondrial Fragmentation in Chemoresistant Ovarian Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e74008.	2.5	34

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37	Calorimetric and spectroscopic investigation of the interaction between the C-terminal domain of Enzyme I and its ligands. <i>Protein Science</i> , 2012, 21, 1726-1733.	7.6	4
38	Molecular determinants of ovarian cancer chemoresistance: new insights into an old conundrum. <i>Annals of the New York Academy of Sciences</i> , 2012, 1271, 58-67.	3.8	76
39	Active site phosphoryl groups in the biphosphorylated phosphotransferase complex reveal dynamics in a millisecond time scale. <i>FEBS Letters</i> , 2012, 586, 1439-1444.	2.8	2
40	Bio-inspired Design and Potential Biomedical Applications of a Novel Class of High-Affinity Peptides. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 1890-1894.	13.8	69
41	Peptide Switch Is Essential for Sirt1 Deacetylase Activity. <i>Molecular Cell</i> , 2011, 44, 203-213.	9.7	89
42	Mechanistic details of a protein-protein association pathway revealed by paramagnetic relaxation enhancement titration measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1379-1384.	7.1	80
43	Solution Structure of the 128 kDa Enzyme I Dimer from <i>Escherichia coli</i> and Its 146 kDa Complex with HPr Using Residual Dipolar Couplings and Small- and Wide-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2010, 132, 13026-13045.	13.7	118
44	Using the Experimentally Determined Components of the Overall Rotational Diffusion Tensor To Restrain Molecular Shape and Size in NMR Structure Determination of Globular Proteins and Protein-Protein Complexes. <i>Journal of the American Chemical Society</i> , 2009, 131, 9522-9531.	13.7	27
45	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. <i>Nature</i> , 2008, 455, 693-696.	27.8	123
46	Impact of Phosphorylation on Structure and Thermodynamics of the Interaction between the N-terminal Domain of Enzyme I and the Histidine Phosphocarrier Protein of the Bacterial Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2008, 283, 18980-18989.	3.4	30
47	Solution NMR Structure of the Barrier-to-Autointegration Factor-Emerin Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 14525-14535.	3.4	75
48	Intramolecular domain-domain association/dissociation and phosphoryl transfer in the mannitol transporter of <i>Escherichia coli</i> are not coupled. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3153-3158.	7.1	22
49	Role of Electrostatic Interactions in Transient Encounter Complexes in Protein-Protein Association Investigated by Paramagnetic Relaxation Enhancement. <i>Journal of the American Chemical Society</i> , 2007, 129, 12954-12955.	13.7	73
50	Solution Structure of a Post-transition State Analog of the Phosphotransfer Reaction between the A and B Cytoplasmic Domains of the Mannitol Transporter II Mannitol of the <i>Escherichia coli</i> Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2006, 281, 8939-8949.	3.4	27
51	Solution NMR Structure of the 48-kDa IIAMannose-HPr Complex of the <i>Escherichia coli</i> Mannose Phosphotransferase System. <i>Journal of Biological Chemistry</i> , 2005, 280, 20775-20784.	3.4	54
52	Visualization of the Phosphorylated Active Site Loop of the Cytoplasmic B Domain of the Mannitol Transporter II Mannitol of the <i>Escherichia coli</i> Phosphotransferase System by NMR Spectroscopy and Residual Dipolar Couplings. <i>Journal of Molecular Biology</i> , 2005, 353, 1129-1136.	4.2	10
53	Assignments of ¹ H and ¹⁵ N resonances of the <i>Pseudomonas aeruginosa</i> K122-4 pilin monomer. <i>Journal of Biomolecular NMR</i> , 2001, 19, 385-386.	2.8	4
54	Structural and functional implications of a proline residue in the antimicrobial peptide gaegurin. <i>FEBS Journal</i> , 1999, 266, 665-674.	0.2	51

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55	Unusually stable helical kink in the antimicrobial peptide - A derivative of gaegurin. FEBS Letters, 1996, 392, 309-312.	2.8	50