

Hyung-Sik Won

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

468
citations

840776

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Oxidative Dimerization of PHD2 is Responsible for its Inactivation and Contributes to Metabolic Reprogramming via HIF-1 α Activation. <i>Scientific Reports</i> , 2016, 6, 18928.	3.3	113
2	Structural overview on the allosteric activation of cyclic AMP receptor protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1299-1308.	2.3	61
3	Action mechanism and structural requirements of the antimicrobial peptides, gaegurins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 1620-1629.	2.6	43
4	Structural Determinants for the Membrane Interaction of Novel Bioactive Undecapeptides Derived from Gaegurin 5. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 4886-4895.	6.4	41
5	Diverse Structural Conversion and Aggregation Pathways of Alzheimer's Amyloid- β (1-40). <i>ACS Nano</i> , 2019, 13, 8766-8783.	14.6	33
6	Anti-Inflammatory Action of an Antimicrobial Model Peptide That Suppresses the TRIF-Dependent Signaling Pathway via Inhibition of Toll-Like Receptor 4 Endocytosis in Lipopolysaccharide-Stimulated Macrophages. <i>PLoS ONE</i> , 2015, 10, e0126871.	2.5	33
7	Rational discovery of antimetastatic agents targeting the intrinsically disordered region of MBD2. <i>Science Advances</i> , 2019, 5, eaav9810.	10.3	21
8	Semi-Empirical Structure Determination of Escherichia coli Hsp33 and Identification of Dynamic Regulatory Elements for the Activation Process. <i>Journal of Molecular Biology</i> , 2015, 427, 3850-3861.	4.2	18
9	Structures of inactive CRP species reveal the atomic details of the allosteric transition that discriminates cyclic nucleotide second messengers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1726-1742.	2.5	17
10	Structure-based functional identification of Helicobacter pylori HP0268 as a nuclease with both DNA nicking and RNase activities. <i>Nucleic Acids Research</i> , 2015, 43, 5194-5207.	14.5	13
11	Dimerization of TRAF-interacting protein (TRAIIP) regulates the mitotic progression. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 864-869.	2.1	13
12	Application of Solution NMR to Structural Studies on α -Helical Integral Membrane Proteins. <i>Molecules</i> , 2017, 22, 1347.	3.8	12
13	Structural changes of antitoxin HigA from Shigella flexneri by binding of its cognate toxin HigB. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 99-108.	7.5	9
14	Interdomain interaction of cyclic AMP receptor protein in the absence of cyclic AMP. <i>Journal of Biochemistry</i> , 2008, 143, 163-167.	1.7	8
15	Unique Unfoldase/Aggregase Activity of a Molecular Chaperone Hsp33 in its Holding-Inactive State. <i>Journal of Molecular Biology</i> , 2019, 431, 1468-1480.	4.2	7
16	Insights into the Vastly Different Effects of Eutectic Solvents on the Stability of Phenolic Compounds. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 5268-5272.	4.6	5
17	Bacterial production and structure-functional validation of a recombinant antigen-binding fragment (Fab) of an anti-cancer therapeutic antibody targeting epidermal growth factor receptor. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10521-10529.	3.6	4
18	Structural identification of the lipopolysaccharide-binding capability of a cupin-family protein from <i>Helicobacter pylori</i> . <i>FEBS Letters</i> , 2016, 590, 2997-3004.	2.8	4

#	ARTICLE	IF	CITATIONS
19	Molecular Targeting of VEGF with a Suramin Fragment-DOCA Conjugate by Mimicking the Action of Low Molecular Weight Heparins. <i>Biomolecules</i> , 2021, 11, 46.	4.0	4
20	C-terminal dimerization of apo-cyclic AMP receptor protein validated in solution. <i>FEBS Letters</i> , 2017, 591, 1064-1070.	2.8	2
21	Molecular Effects of Elongation Factor Ts and Trigger Factor on the Unfolding and Aggregation of Elongation Factor Tu Induced by the Prokaryotic Molecular Chaperone Hsp33. <i>Biology</i> , 2021, 10, 1171.	2.8	2
22	Thermal denaturation of the apo-cyclic AMP receptor protein and noncovalent interactions between its domains. <i>Molecules and Cells</i> , 2008, 26, 61-6.	2.6	2
23	Crystal structure and functional characterization of SF216 from <i>Shigella flexneri</i> . <i>FEBS Letters</i> , 2017, 591, 3692-3703.	2.8	1
24	Crystal Structure of <i>Shigella flexneri</i> SF173 Reveals a Dimeric Helical Bundle Conformation. <i>Crystals</i> , 2018, 8, 97.	2.2	1
25	Structural Interplays in the Flexible N-Terminus and Scaffolding Domain of Human Membrane Protein Caveolin 3. <i>Membranes</i> , 2021, 11, 82.	3.0	1