

Hyung Ho Lee

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

829
citations

759233

12
h-index

526287

27
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41
all docs

41
docs citations

41
times ranked

1538
citing authors

#	ARTICLE	IF	CITATIONS
1	Midbody Targeting of the ESCRT Machinery by a Noncanonical Coiled Coil in CEP55. <i>Science</i> , 2008, 322, 576-580.	12.6	228
2	Crystal structure of human nucleophosmin core reveals plasticity of the pentamer-pentamer interface. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 672-678.	2.6	94
3	Structural and Functional Insights into Dom34, a Key Component of No-Go mRNA Decay. <i>Molecular Cell</i> , 2007, 27, 938-950.	9.7	84
4	Crystal Structure of \hat{I}^2 -Arrestin 2 in Complex with CXCR7 Phosphopeptide. <i>Structure</i> , 2020, 28, 1014-1023.e4.	3.3	38
5	Structural and functional insights into the regulation mechanism of CK2 by IP ₆ and the intrinsically disordered protein Nopp140. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19360-19365.	7.1	35
6	Crystal Structure of T-protein of the Glycine Cleavage System. <i>Journal of Biological Chemistry</i> , 2004, 279, 50514-50523.	3.4	31
7	Structural and biochemical insights into the role of testis-expressed gene 14 (TEX14) in forming the stable intercellular bridges of germ cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12372-12377.	7.1	28
8	Structural Insights into the FtsQ/FtsB/FtsL Complex, a Key Component of the Divisome. <i>Scientific Reports</i> , 2018, 8, 18061.	3.3	28
9	Fine-tuning of amino sugar homeostasis by EliANtr in <i>Salmonella Typhimurium</i> . <i>Scientific Reports</i> , 2016, 6, 33055.	3.3	26
10	Structural insights into the efficient CO ₂ -reducing activity of an NAD-dependent formate dehydrogenase from <i>Thiobacillus</i> sp. KNK65MA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 313-323.	2.5	23
11	FOXL2 directs DNA double-strand break repair pathways by differentially interacting with Ku. <i>Nature Communications</i> , 2020, 11, 2010.	12.8	21
12	Crystal structure of the <i>Helicobacter pylori</i> enoyl-acyl carrier protein reductase in complex with hydroxydiphenyl ether compounds, triclosan and diclosan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 691-694.	2.6	20
13	Over-activation of a nonessential bacterial protease DegP as an antibiotic strategy. <i>Communications Biology</i> , 2020, 3, 547.	4.4	20
14	Noncanonical DNA-binding mode of repressor and its disassembly by antirepressor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2480-8.	7.1	14
15	Peptidoglycan reshaping by a noncanonical peptidase for helical cell shape in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2020, 11, 458.	12.8	14
16	The structure of <i>Staphylococcus aureus</i> phosphopantetheine adenylyltransferase in complex with 3 $\hat{\epsilon}$ -phosphoadenosine 5 $\hat{\epsilon}$ -phosphosulfate reveals a new ligand-binding mode. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 987-991.	0.7	12
17	Crystal structure of a putative oligopeptide-binding periplasmic protein from a hyperthermophile. <i>Extremophiles</i> , 2016, 20, 723-731.	2.3	11
18	Intracellular delivery of immunoglobulin G at nanomolar concentrations with domain Z-fused multimeric \hat{I}^2 -helical cell penetrating peptides. <i>Journal of Controlled Release</i> , 2021, 330, 161-172.	9.9	11

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19	Crystal Structure of a Metal Ion-bound IS200 Transposase. <i>Journal of Biological Chemistry</i> , 2006, 281, 4261-4266.	3.4	10
20	Crystal structures of human NSDHL and development of its novel inhibitor with the potential to suppress EGFR activity. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 207-225.	5.4	9
21	Molecular dynamics study with mutation shows that N-terminal domain structural reorientation in Niemann-Pick type C1 is required for proper alignment of cholesterol transport. <i>Journal of Neurochemistry</i> , 2021, 156, 967-978.	3.9	8
22	Crystal structures of Uso1 membrane tether reveal an alternative conformation in the globular head domain. <i>Scientific Reports</i> , 2020, 10, 9544.	3.3	7
23	Discovery of a transdermally deliverable pentapeptide for activating AdipoR1 to promote hair growth. <i>EMBO Molecular Medicine</i> , 2021, 13, e13790.	6.9	7
24	Structural and Biochemical Studies Reveal a Putative FtsZ Recognition Site on the Z-ring Stabilizer ZapD. <i>Molecules and Cells</i> , 2016, 39, 814-820.	2.6	7
25	Structural insights into the apo-structure of Cpf1 protein from <i>Francisella novicida</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 775-781.	2.1	6
26	Structural and Biophysical Analyses of Human N-Myc Downstream-Regulated Gene 3 (NDRG3) Protein. <i>Biomolecules</i> , 2020, 10, 90.	4.0	6
27	Thermodynamic Models for Assembly of Intrinsically Disordered Protein Hubs with Multiple Interaction Partners. <i>Journal of the American Chemical Society</i> , 2021, 143, 12509-12523.	13.7	6
28	The role of the FliD C-terminal domain in pentamer formation and interaction with FliT. <i>Scientific Reports</i> , 2017, 7, 4418.	3.3	5
29	Dissecting the structural features of β -arrestins as multifunctional proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140603.	2.3	4
30	Crystallization and preliminary X-ray crystallographic analysis of Z-ring-associated protein (ZapD) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 194-198.	0.8	3
31	Structural and functional studies of a metallo- β -lactamase unveil a new type of structurally encoded nickel-containing heterodinuclear site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2054-2065.	2.5	3
32	Crystal structure of proteolyzed VapBC and DNA-bound VapBC from <i>Salmonella enterica</i> Typhimurium LT2 and VapC as a putative Ca ²⁺ -dependent ribonuclease. <i>FASEB Journal</i> , 2020, 34, 3051-3068.	0.5	3
33	Biochemical Characterization of the Num1-Mdm36 Complex at the Mitochondria-Plasma Membrane Contact Site. <i>Molecules and Cells</i> , 2021, 44, 207-213.	2.6	2
34	Structural Basis for Recognition of L-lysine, L-ornithine, and L-2,4-diamino Butyric Acid by Lysine Cyclodeaminase. <i>Molecules and Cells</i> , 2018, 41, 331-341.	2.6	2
35	Biochemical and Molecular Modeling Studies of the Interaction between Human CEP55 and TEX14. <i>Bulletin of the Korean Chemical Society</i> , 2016, 37, 847-854.	1.9	1
36	Phosphatidylserine-induced dissociation of the heterodimeric PstB2p/Pbi1p complex in yeast phosphatidylserine trafficking system. <i>Biochemical and Biophysical Research Communications</i> , 2019, 517, 285-290.	2.1	1

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37	Structure-based inhibitor design for reshaping bacterial morphology. <i>Communications Biology</i> , 2022, 5, 395.	4.4	1
38	S2c1-1 Structure and Ribonuclease Activity of Pelota : Implications for the No-go Decay and Translation Regulation (S2-c1: "Crystallographic approach to understand biological) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (supra Seibutsu Butsuri, 2006, 46, S120.	0.1	0
39	Structural characterization of a putative diguanylate cyclase conserved in hyperthermophiles. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 114-119.	2.1	0
40	Structural and functional studies of SAV1707 from <i>Staphylococcus aureus</i> elucidate its distinct metal-dependent activity and a crucial residue for catalysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 587-598.	2.3	0