

Sangkee Rhee

List of Publications by Year in descending order

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52
papers

1,515
citations

430874

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h-index

315739

38
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53
all docs

53
docs citations

53
times ranked

2180
citing authors

#	ARTICLE	IF	CITATIONS
1	The Molecular Basis of Substrate Channeling. <i>Journal of Biological Chemistry</i> , 1999, 274, 12193-12196.	3.4	325
2	Crystal Structures of a Mutant (Î²K87T) Tryptophan Synthase Î±2Î²2Complex with Ligands Bound to the Active Sites of the Î±- and Î²-Subunits Reveal Ligand-Induced Conformational Changes. <i>Biochemistry</i> , 1997, 36, 7664-7680.	2.5	154
3	Crystal Structure of d-Psicose 3-epimerase from <i>Agrobacterium tumefaciens</i> and its Complex with True Substrate d-Fructose: A Pivotal Role of Metal in Catalysis, an Active Site for the Non-phosphorylated Substrate, and its Conformational Changes. <i>Journal of Molecular Biology</i> , 2006, 361, 920-931.	4.2	102
4	Small-molecule inhibitor binding to an <i>N</i> -acyl-homoserine lactone synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12089-12094.	7.1	102
5	Refinement and Comparisons of the Crystal Structures of Pig Cytosolic Aspartate Aminotransferase and Its Complex with 2-Methylaspartate. <i>Journal of Biological Chemistry</i> , 1997, 272, 17293-17302.	3.4	94
6	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
7	<i>Oryza sativa</i> COI Homologues Restore Jasmonate Signal Transduction in <i>Arabidopsis coi1-1</i> Mutants. <i>PLoS ONE</i> , 2013, 8, e52802.	2.5	68
8	Cryocrystallography and Microspectrophotometry of a Mutant (Î²D60N) Tryptophan Synthase Î±2Î²2Complex Reveals Allosteric Roles of Î±Asp60. <i>Biochemistry</i> , 1998, 37, 10653-10659.	2.5	44
9	Structural and Functional Insights into Intramolecular Fructosyl Transfer by Inulin Fructotransferase. <i>Journal of Biological Chemistry</i> , 2007, 282, 8414-8423.	3.4	44
10	Structural and Functional Basis for (S)-Allantoin Formation in the Ureide Pathway. <i>Journal of Biological Chemistry</i> , 2007, 282, 23457-23464.	3.4	40
11	Structural and functional analysis of PucM, a hydrolase in the ureide pathway and a member of the transthyretin-related protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9790-9795.	7.1	38
12	Crystal Structure of Metal-Dependent Allantoinase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2009, 387, 1067-1074.	4.2	37
13	Autoregulation of <i>ZEB2</i> expression for zearalenone production in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2015, 97, 942-956.	2.5	26
14	Crystal Structures and Mutagenesis of Sucrose Hydrolase from <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> : Insight into the Exclusively Hydrolytic Amylosucrase Fold. <i>Journal of Molecular Biology</i> , 2008, 380, 636-647.	4.2	25
15	Structural and Functional Insights into O-Methyltransferase from <i>Bacillus cereus</i> . <i>Journal of Molecular Biology</i> , 2008, 382, 987-997.	4.2	25
16	Structural and Functional Basis for Substrate Specificity and Catalysis of Levan Fructotransferase. <i>Journal of Biological Chemistry</i> , 2012, 287, 31233-31241.	3.4	25
17	Structure of bacteriophage <i>SPN1</i> <i>S</i> endolysin reveals an unusual two-module fold for the peptidoglycan lytic and binding activity. <i>Molecular Microbiology</i> , 2014, 92, 316-325.	2.5	23
18	Crystal Structure and Functional Analysis of the Exradiol Dioxygenase LapB from a Long-chain Alkylphenol Degradation Pathway in <i>Pseudomonas</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 34321-34330.	3.4	22

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19	Structural and Functional Analysis of Phytotoxin Toxoflavin-Degrading Enzyme. <i>PLoS ONE</i> , 2011, 6, e22443.	2.5	18
20	Structural Basis for a Cofactor-dependent Oxidation Protection and Catalysis of Cyanobacterial Succinic Semialdehyde Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2013, 288, 15760-15770.	3.4	17
21	Binding study of AfsK, a Ser/Thr kinase from <i>Streptomyces coelicolor</i> A3(2) and S-adenosyl-L-methionine. <i>FEMS Microbiology Letters</i> , 2007, 266, 236-240.	1.8	15
22	Role of the N-Terminal Domain of Endoinulinase from <i>Arthrobacter</i> sp. S37 in Regulation of Enzyme Catalysis. <i>Journal of Biochemistry</i> , 2005, 138, 27-33.	1.7	13
23	The crystal structure of type III effector protein XopQ from <i>Xanthomonas oryzae</i> complexed with adenosine diphosphate ribose. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2910-2914.	2.6	13
24	Crystal structure and functional analysis of isocitrate lyases from <i>Magnaporthe oryzae</i> and <i>Fusarium graminearum</i> . <i>Journal of Structural Biology</i> , 2016, 194, 395-403.	2.8	13
25	Structural and Functional Insights into (S)-Ureidoglycine Aminohydrolase, Key Enzyme of Purine Catabolism in <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 18796-18805.	3.4	12
26	Mutational analysis of the active site residues of a D-psicose 3-epimerase from <i>Agrobacterium tumefaciens</i> . <i>Biotechnology Letters</i> , 2010, 32, 261-268.	2.2	11
27	Crystal structure of the effector protein HopA1 from <i>Pseudomonas syringae</i> . <i>Journal of Structural Biology</i> , 2015, 189, 276-280.	2.8	11
28	Initiation of cytosolic plant purine nucleotide catabolism involves a monospecific xanthosine monophosphate phosphatase. <i>Nature Communications</i> , 2021, 12, 6846.	12.8	10
29	Structural Basis for Bacterial Quorum Sensing-mediated Oxalogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 11465-11475.	3.4	9
30	Structural Insights into the Substrate Specificity of (S)-Ureidoglycolate Amidohydrolase and Its Comparison with Allantoate Amidohydrolase. <i>Journal of Molecular Biology</i> , 2014, 426, 3028-3040.	4.2	9
31	Crystal structure of chloramphenicol-metabolizing enzyme EstDL136 from a metagenome. <i>PLoS ONE</i> , 2019, 14, e0210298.	2.5	9
32	Structural basis for the substrate specificity and catalytic features of pseudouridine kinase from <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2021, 49, 491-503.	14.5	9
33	Structural Insights into an Oxalate-producing Serine Hydrolase with an Unusual Oxanion Hole and Additional Lyase Activity. <i>Journal of Biological Chemistry</i> , 2016, 291, 15185-15195.	3.4	8
34	Importance of Conserved and Variable C-terminal Residues for the Activity and Thermal Stability of the β Subunit of Tryptophan Synthase. <i>Journal of Biological Chemistry</i> , 1997, 272, 7859-7866.	3.4	7
35	Crystal structure of toll-like receptor 2-activating lipoprotein IIpA from <i>Vibrio vulnificus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1020-1025.	2.6	7
36	Gene Context Analysis Reveals Functional Divergence between Hypothetically Equivalent Enzymes of the Purine-Ureide Pathway. <i>Biochemistry</i> , 2014, 53, 735-745.	2.5	7

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37	Structural and mutational analyses of the bifunctional arginine dihydrolase and ornithine cyclodeaminase AgrE from the cyanobacterium Anabaena. <i>Journal of Biological Chemistry</i> , 2020, 295, 5751-5760.	3.4	7
38	Crystal structure of the effector protein XOO4466 from <i>Xanthomonas oryzae</i> . <i>Journal of Structural Biology</i> , 2013, 184, 361-366.	2.8	6
39	Crystal structure and mutational analyses of ribokinase from <i>Arabidopsis thaliana</i> . <i>Journal of Structural Biology</i> , 2019, 206, 110-118.	2.8	6
40	A triclosan resistance protein from the soil metagenome is a novel enoyl acyl carrier protein reductase: Structure-guided functional analysis. <i>FEBS Journal</i> , 2020, 287, 4710-4728.	4.7	6
41	Structure and substrate specificity determinants of NfnB, a dinitroaniline herbicide catabolizing nitroreductase from <i>Sphingopyxis</i> sp. strain HMH. <i>Journal of Biological Chemistry</i> , 2021, 297, 101143.	3.4	6
42	Diatom Allantoin Synthase Provides Structural Insights into Natural Fusion Protein Therapeutics. <i>ACS Chemical Biology</i> , 2018, 13, 2237-2246.	3.4	5
43	Crystal structure of the indole-3-acetic acid-catabolizing enzyme DAO1 from <i>Arabidopsis thaliana</i> . <i>Journal of Structural Biology</i> , 2020, 212, 107632.	2.8	4
44	Structural and Functional Insights into (S)-Ureidoglycolate Dehydrogenase, a Metabolic Branch Point Enzyme in Nitrogen Utilization. <i>PLoS ONE</i> , 2012, 7, e52066.	2.5	4
45	Crystallization and preliminary X-ray diffraction analysis of BcOMT2 from <i>Bacillus cereus</i> : a family of O-methyltransferase. <i>Journal of Microbiology and Biotechnology</i> , 2007, 17, 369-72.	2.1	4
46	Substrate-binding loop interactions with pseudouridine trigger conformational changes that promote catalytic efficiency of pseudouridine kinase PUK1. <i>Journal of Biological Chemistry</i> , 2022, 298, 101869.	3.4	4
47	Title is missing!. <i>Biotechnology Letters</i> , 2002, 24, 1869-1874.	2.2	1
48	Crystal structure of inositol 1,3,4,5,6-pentakisphosphate 2-kinase from <i>Cryptococcus neoformans</i> . <i>Journal of Structural Biology</i> , 2017, 200, 118-123.	2.8	1
49	Structural and functional basis for substrate specificity and catalysis of levan fructotransferase. <i>FASEB Journal</i> , 2013, 27, lb219.	0.5	0
50	Crystal structure and inhibition studies of isocitrate lyase. <i>FASEB Journal</i> , 2013, 27, lb220.	0.5	0
51	Structural Basis for Bacterial Quorum Sensing-mediated Oxalogenesis. <i>FASEB Journal</i> , 2015, 29, 895.2.	0.5	0
52	Structural and biochemical basis for the substrate specificity of Pad-1, an indole-3-pyruvic acid aminotransferase in auxin homeostasis. <i>Journal of Structural Biology</i> , 2022, , 107857.	2.8	0