

Sangkee Rhee

List of Publications by Year in descending order

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52
papers

1,515
citations

430874

18
h-index

315739

38
g-index

53
all docs

53
docs citations

53
times ranked

2180
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Initiation of cytosolic plant purine nucleotide catabolism involves a monospecific xanthosine monophosphate phosphatase. <i>Nature Communications</i> , 2021, 12, 6846. | 12.8 | 10 |
| 6 | 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 |
| 7 | Structural and mutational analyses of the bifunctional arginine dihydrolase and ornithine cyclodeaminase AgrE from the cyanobacterium <i>Anabaena</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 5751-5760. | 3.4 | 7 |
| 8 | 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 |
| 9 | Crystal structure of chloramphenicol-metabolizing enzyme EstDL136 from a metagenome. <i>PLoS ONE</i> , 2019, 14, e0210298. | 2.5 | 9 |
| 10 | 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 |
| 11 | Diatom Allantoin Synthase Provides Structural Insights into Natural Fusion Protein Therapeutics. <i>ACS Chemical Biology</i> , 2018, 13, 2237-2246. | 3.4 | 5 |
| 12 | 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 |
| 13 | Structural Insights into an Oxalate-producing Serine Hydrolase with an Unusual Oxyanion Hole and Additional Lyase Activity. <i>Journal of Biological Chemistry</i> , 2016, 291, 15185-15195. | 3.4 | 8 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | Structural Basis for Bacterial Quorum Sensing-mediated Oxalogenesis. <i>FASEB Journal</i> , 2015, 29, 895.2. | 0.5 | 0 |
| 18 | Structural Basis for Bacterial Quorum Sensing-mediated Oxalogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 11465-11475. | 3.4 | 9 |

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|----|---|-----|-----------|
| 19 | Structural basis for the auxin-induced transcriptional regulation by Aux/IAA17. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18613-18618. | 7.1 | 69 |
| 20 | Structure of bacteriophage <i>SPN1</i> endolysin reveals an unusual two-module fold for the peptidoglycan lytic and binding activity. Molecular Microbiology, 2014, 92, 316-325. | 2.5 | 23 |
| 21 | Structural Insights into the Substrate Specificity of (S)-Ureidoglycolate Amidohydrolase and Its Comparison with Allantoate Amidohydrolase. Journal of Molecular Biology, 2014, 426, 3028-3040. | 4.2 | 9 |
| 22 | Gene Context Analysis Reveals Functional Divergence between Hypothetically Equivalent Enzymes of the Purine Ureide Pathway. Biochemistry, 2014, 53, 735-745. | 2.5 | 7 |
| 23 | The crystal structure of type III effector protein XopQ from <i>Xanthomonas oryzae</i> complexed with adenosine diphosphate ribose. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2910-2914. | 2.6 | 13 |
| 24 | Crystal structure of the effector protein XOO4466 from <i>Xanthomonas oryzae</i> . Journal of Structural Biology, 2013, 184, 361-366. | 2.8 | 6 |
| 25 | Structural Basis for a Cofactor-dependent Oxidation Protection and Catalysis of Cyanobacterial Succinic Semialdehyde Dehydrogenase. Journal of Biological Chemistry, 2013, 288, 15760-15770. | 3.4 | 17 |
| 26 | <i>Oryza sativa</i> COI Homologues Restore Jasmonate Signal Transduction in <i>Arabidopsis coi1-1</i> Mutants. PLoS ONE, 2013, 8, e52802. | 2.5 | 68 |
| 27 | Structural and functional basis for substrate specificity and catalysis of levan fructotransferase. FASEB Journal, 2013, 27, lb219. | 0.5 | 0 |
| 28 | Crystal structure and inhibition studies of isocitrate lyase. FASEB Journal, 2013, 27, lb220. | 0.5 | 0 |
| 29 | Structural and Functional Insights into (S)-Ureidoglycine Aminohydrolase, Key Enzyme of Purine Catabolism in <i>Arabidopsis thaliana</i> . Journal of Biological Chemistry, 2012, 287, 18796-18805. | 3.4 | 12 |
| 30 | Structural and Functional Basis for Substrate Specificity and Catalysis of Levan Fructotransferase. Journal of Biological Chemistry, 2012, 287, 31233-31241. | 3.4 | 25 |
| 31 | Structural and Functional Insights into (S)-Ureidoglycolate Dehydrogenase, a Metabolic Branch Point Enzyme in Nitrogen Utilization. PLoS ONE, 2012, 7, e52066. | 2.5 | 4 |
| 32 | Structural and Functional Analysis of Phytotoxin Toxoflavin-Degrading Enzyme. PLoS ONE, 2011, 6, e22443. | 2.5 | 18 |
| 33 | Crystal structure of toll-like receptor activating lipoprotein IlpA from <i>Vibrio vulnificus</i> . Proteins: Structure, Function and Bioinformatics, 2011, 79, 1020-1025. | 2.6 | 7 |
| 34 | Small-molecule inhibitor binding to an <i>N</i> -acyl-homoserine lactone synthase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12089-12094. | 7.1 | 102 |
| 35 | Mutational analysis of the active site residues of a d-psicose 3-epimerase from <i>Agrobacterium tumefaciens</i> . Biotechnology Letters, 2010, 32, 261-268. | 2.2 | 11 |
| 36 | Crystal Structure and Functional Analysis of the Exradiol Dioxygenase LapB from a Long-chain Alkylphenol Degradation Pathway in <i>Pseudomonas</i> . Journal of Biological Chemistry, 2009, 284, 34321-34330. | 3.4 | 22 |

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|----|---|-----|-----------|
| 37 | Crystal Structure of Metal-Dependent Allantoinase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2009, 387, 1067-1074. | 4.2 | 37 |
| 38 | 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 |
| 39 | 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 |
| 40 | Structural and Functional Insights into Intramolecular Fructosyl Transfer by Inulin Fructotransferase. <i>Journal of Biological Chemistry</i> , 2007, 282, 8414-8423. | 3.4 | 44 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | Title is missing!. <i>Biotechnology Letters</i> , 2002, 24, 1869-1874. | 2.2 | 1 |
| 48 | The Molecular Basis of Substrate Channeling. <i>Journal of Biological Chemistry</i> , 1999, 274, 12193-12196. | 3.4 | 325 |
| 49 | Cryocrystallography and Microspectrophotometry of a Mutant (Î±D60N) Tryptophan Synthase Î±2Î²2Complex Reveals Allosteric Roles of Î±Asp60. <i>Biochemistry</i> , 1998, 37, 10653-10659. | 2.5 | 44 |
| 50 | 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 |
| 51 | Importance of Conserved and Variable C-terminal Residues for the Activity and Thermal Stability of the Î² Subunit of Tryptophan Synthase. <i>Journal of Biological Chemistry</i> , 1997, 272, 7859-7866. | 3.4 | 7 |
| 52 | 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 |