Jungwook Kim

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structural and functional characterization of <scp>TrmM</scp> in <scp> m ⁶ A </scp> modification of bacterial <scp>tRNA</scp> . Protein Science, 2022, 31, e4319.	7.6	2
2	Structural snapshots of CmoB in various states during wobble uridine modification of tRNA. Biochemical and Biophysical Research Communications, 2021, 534, 604-609.	2.1	2
3	Structural insights into phosphatidylethanolamine formation in bacterial membrane biogenesis. Scientific Reports, 2021, 11, 5785.	3.3	19
4	Unique anticodon loop conformation with the flipped-out wobble nucleotide in the crystal structure of unbound tRNA ^{Val} . Rna, 2021, 27, 1330-1338.	3.5	1
5	Structural basis for the inhibition of PDK2 by novel ATP- and lipoyl-binding site targeting compounds. Biochemical and Biophysical Research Communications, 2020, 527, 778-784.	2.1	2
6	Structural and biochemical characterization of Rv0187, an O-methyltransferase from Mycobacterium tuberculosis. Scientific Reports, 2019, 9, 8059.	3.3	17
7	Identification of a novel tRNA wobble uridine modifying activity in the biosynthesis of 5-methoxyuridine. Nucleic Acids Research, 2018, 46, 9160-9169.	14.5	13
8	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. Nucleic Acids Research, 2015, 43, 4602-4613.	14.5	23
9	Experimental Strategies for Functional Annotation and Metabolism Discovery: Targeted Screening of Solute Binding Proteins and Unbiased Panning of Metabolomes. Biochemistry, 2015, 54, 909-931.	2.5	95
10	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. PLoS Biology, 2014, 12, e1001843.	5.6	79
11	Global structures of IgG isotypes expressing identical variable regions. Molecular Immunology, 2013, 56, 588-598.	2.2	28
12	Structural basis for hypermodification of the wobble uridine in tRNA by bifunctional enzyme MnmC. BMC Structural Biology, 2013, 13, 5.	2.3	13
13	Structure-Guided Discovery of New Deaminase Enzymes. Journal of the American Chemical Society, 2013, 135, 13927-13933.	13.7	16
14	The Gate That Governs Sulfotransferase Selectivity. Biochemistry, 2013, 52, 415-424.	2.5	64
15	Structure-guided discovery of the metabolite carboxy-SAM that modulates tRNA function. Nature, 2013, 498, 123-126.	27.8	84
16	Testing the Sulfotransferase Molecular Pore Hypothesis. Journal of Biological Chemistry, 2013, 288, 8619-8626.	3.4	27
17	Structural Determinants for the Stereoselective Hydrolysis of Chiral Substrates by Phosphotriesterase. Biochemistry, 2010, 49, 7988-7997.	2.5	25
18	Structure of Diethyl Phosphate Bound to the Binuclear Metal Center of Phosphotriesterase. Biochemistry, 2008, 47, 9497-9504.	2.5	67

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19	Structural and Kinetic Characterization of Escherichia coli TadA, the Wobble-Specific tRNA Deaminase. Biochemistry, 2006, 45, 6407-6416.	2.5	72
20	Long-range allosteric transitions in carbamoyl phosphate synthetase. Protein Science, 2004, 13, 2398-2405.	7.6	19
21	Perforation of the Tunnel Wall in Carbamoyl Phosphate Synthetase Derails the Passage of Ammonia between Sequential Active Sitesâ€. Biochemistry, 2004, 43, 5334-5340.	2.5	23
22	Access to the carbamate tunnel of carbamoyl phosphate synthetase. Archives of Biochemistry and Biophysics, 2004, 425, 33-41.	3.0	19
23	The catalytic mechanism of galactose mutarotase. Protein Science, 2003, 12, 1051-1059.	7.6	34
24	Structural and Kinetic Studies of Sugar Binding to Galactose Mutarotase from Lactococcus lactis. Journal of Biological Chemistry, 2002, 277, 45458-45465.	3.4	28
25	Structural Defects within the Carbamate Tunnel of Carbamoyl Phosphate Synthetaseâ€. Biochemistry, 2002, 41, 12575-12581.	2.5	10
26	Allosteric Control of the Oligomerization of Carbamoyl Phosphate Synthetase from <i>Escherichia coli</i> . Biochemistry, 2001, 40, 11030-11036.	2.5	24