

Takato Yano

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

420
citations

840776

11
h-index

752698

20
g-index

22
all docs

22
docs citations

22
times ranked

609
citing authors

#	ARTICLE	IF	CITATIONS
1	Disruption of <i>Thermus thermophilus</i> genes by homologous recombination using a thermostable kanamycin-resistant marker. <i>FEBS Letters</i> , 2001, 506, 231-234.	2.8	92
2	ER stress stimulates production of the key antimicrobial peptide, cathelicidin, by forming a previously unidentified intracellular S1P signaling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1334-42.	7.1	77
3	Proteome-wide identification of lysine succinylation in thermophilic and mesophilic bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 232-242.	2.3	40
4	High-throughput Screening of Small Molecule Inhibitors of the <i>Streptococcus</i> Quorum-sensing Signal Pathway. <i>Scientific Reports</i> , 2017, 7, 4029.	3.3	27
5	Sulfur Modifications of the Wobble U34 in tRNAs and their Intracellular Localization in Eukaryotic Cells. <i>Biomolecules</i> , 2017, 7, 17.	4.0	18
6	The GYAG endonuclease domain of <i>Arabidopsis</i> MutS homolog 1 specifically binds to branched DNA structures. <i>FEBS Letters</i> , 2018, 592, 4066-4077.	2.8	18
7	Structural Features and Functional Dependency on $\hat{2}$ -Clamp Define Distinct Subfamilies of Bacterial Mismatch Repair Endonuclease MutL. <i>Journal of Biological Chemistry</i> , 2016, 291, 16990-17000.	3.4	17
8	Heme-dependent Inactivation of 5-Aminolevulinatase Synthase from <i>Caulobacter crescentus</i> . <i>Scientific Reports</i> , 2018, 8, 14228.	3.3	17
9	The Lon protease-like domain in the bacterial RecA paralog RadA is required for DNA binding and repair. <i>Journal of Biological Chemistry</i> , 2017, 292, 9801-9814.	3.4	15
10	tRNA Wobble Modification Affects Leaf Cell Development in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 2026-2039.	3.1	14
11	Both Sphingosine Kinase 1 and 2 Coordinately Regulate Cathelicidin Antimicrobial Peptide Production during Keratinocyte Differentiation. <i>Journal of Investigative Dermatology</i> , 2019, 139, 492-494.	0.7	13
12	Crystal structure and DNA-binding property of the ATPase domain of bacterial mismatch repair endonuclease MutL from <i>Aquifex aeolicus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1178-1187.	2.3	12
13	Indispensable residue for uridine binding in the uridine-cytidine kinase family. <i>Biochemistry and Biophysics Reports</i> , 2017, 11, 93-98.	1.3	11
14	Neutron crystallography of copper amine oxidase reveals keto/enolate interconversion of the quinone cofactor and unusual proton sharing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10818-10824.	7.1	11
15	<i>In crystallo</i> thermodynamic analysis of conformational change of the topaquinone cofactor in bacterial copper amine oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 135-140.	7.1	10
16	The crystal structure of homoserine dehydrogenase complexed with α -homoserine and NADPH in a closed form. <i>Journal of Biochemistry</i> , 2019, 165, 185-195.	1.7	9
17	Multiple zinc ions maintain the open conformation of the catalytic site in the α -DNA mismatch repair endonuclease MutL from <i>Aquifex aeolicus</i> . <i>FEBS Letters</i> , 2018, 592, 1611-1619.	2.8	6
18	Archaeal MutS5 tightly binds to Holliday junction similarly to eukaryotic MutS $\hat{3}$. <i>FEBS Journal</i> , 2017, 284, 3470-3483.	4.7	5

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19	Biochemical characterization of mismatch-binding protein MutS1 and nicking endonuclease MutL from a euryarchaeon <i>Methanosaeta thermophila</i> . <i>DNA Repair</i> , 2019, 75, 29-38.	2.8	3
20	A Lynch syndrome-associated mutation at a Bergerat ATP-binding fold destabilizes the structure of the DNA mismatch repair endonuclease MutL. <i>Journal of Biological Chemistry</i> , 2020, 295, 11643-11655.	3.4	2
21	Microcrystal preparation for serial femtosecond X-ray crystallography of bacterial copper amine oxidase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 356-363.	0.8	2
22	Structural and functional insights into the mechanism by which MutS2 recognizes a DNA junction. <i>Structure</i> , 2022, , .	3.3	1