

# Tamotsu Kanai

## List of Publications by Year in descending order

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78  
papers

2,560  
citations

236925

25  
h-index

206112

48  
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78  
all docs

78  
docs citations

78  
times ranked

2213  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of high-level expression of A1-ATPase on H <sub>2</sub> production in <i>Thermococcus kodakarensis</i> . <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 149-158.	2.2	0
2	Thermophilic Degradation of Hemicellulose, a Critical Feedstock in the Production of Bioenergy and Other Value-Added Products. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	13
3	Distinct Modified Nucleosides in tRNA <sup>Trp</sup> from the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> and Requirement of tRNA <sup>2</sup> G10/m <sup>2</sup> G10 Methytransferase (Archaeal Trm11) for Survival at High Temperatures. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	15
4	The TK0271 Protein Activates Transcription of Aromatic Amino Acid Biosynthesis Genes in the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> . <i>MBio</i> , 2019, 10, .	4.1	0
5	Crystal structures of an archaeal chitinase ChiD and its ligand complexes. <i>Glycobiology</i> , 2018, 28, 418-426.	2.5	3
6	Identification of the glucosamine kinase in the chitinolytic pathway of <i>Thermococcus kodakarensis</i> . <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 320-326.	2.2	11
7	Structure of a [NiFe] hydrogenase maturation protease Hycl provides insights into its substrate selectivity. <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 782-788.	2.1	4
8	Crystal structures of a [NiFe] hydrogenase large subunit HyhL in an immature state in complex with a Ni chaperone HypA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7045-7050.	7.1	27
9	Engineering of the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> for Chitin-Dependent Hydrogen Production. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	17
10	An archaeal RNA binding protein, FAU-1, is a novel ribonuclease related to rRNA stability in <i>Pyrococcus</i> and <i>Thermococcus</i> . <i>Scientific Reports</i> , 2017, 7, 12674.	3.3	4
11	Pcal_1311, an alcohol dehydrogenase homologue from <i>Pyrobaculum calidifontis</i> , displays NADH-dependent high aldehyde reductase activity. <i>Extremophiles</i> , 2017, 21, 1101-1110.	2.3	2
12	Possible function of the second RecJ-like protein in stalled replication fork repair by interacting with Hef. <i>Scientific Reports</i> , 2017, 7, 16949.	3.3	8
13	Gene regulation of two ferredoxin:NADP <sup>+</sup> oxidoreductases by the redox-responsive regulator SurR in <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2017, 21, 903-917.	2.3	6
14	Genetic analyses of the functions of [NiFe]-hydrogenase maturation endopeptidases in the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2017, 21, 27-39.	2.3	9
15	The Cdc45/RecJ-like protein forms a complex with GINS and MCM, and is important for DNA replication in <i>Thermococcus kodakarensis</i> . <i>Nucleic Acids Research</i> , 2017, 45, 10693-10705.	14.5	22
16	A Structurally Novel Chitinase from the Chitin-Degrading Hyperthermophilic Archaeon <i>Thermococcus chitonophagus</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 3554-3562.	3.1	15
17	Crystal structure of a [NiFe] hydrogenase maturation protease HybD from <i>Thermococcus kodakarensis</i> KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1321-1327.	2.6	13
18	Crystal structures of chitin binding domains of chitinase from <i>Thermococcus kodakarensis</i> KOD1. <i>FEBS Letters</i> , 2016, 590, 298-304.	2.8	22

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19	Sodium-Driven Energy Conversion for Flagellar Rotation of the Earliest Divergent Hyperthermophilic Bacterium. <i>Biophysical Journal</i> , 2016, 110, 468a.	0.5	0
20	Crystal structure of the TK2203 protein from <i>Thermococcus kodakarensis</i> , a putative extradiol dioxygenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 427-433.	0.8	3
21	Sodium-driven energy conversion for flagellar rotation of the earliest divergent hyperthermophilic bacterium. <i>Scientific Reports</i> , 2015, 5, 12711.	3.3	27
22	Structural studies of a novel type of chitinase from archaea. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s216-s216.	0.1	0
23	Overproduction of the membrane-bound [NiFe]-hydrogenase in <i>Thermococcus kodakarensis</i> and its effect on hydrogen production. <i>Frontiers in Microbiology</i> , 2015, 6, 847.	3.5	22
24	Structural basis of a Ni acquisition cycle for [NiFe] hydrogenase by Ni-metallochaperone HypA and its enhancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7701-7706.	7.1	54
25	<i>Polymorphobacter multimanifer</i> gen. nov., sp. nov., a polymorphic bacterium isolated from antarctic white rock. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2034-2040.	1.7	30
26	The X-ray crystal structure of the euryarchaeal RNA polymerase in an open-clamp configuration. <i>Nature Communications</i> , 2014, 5, 5132.	12.8	36
27	Different roles of two transcription factor B proteins in the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2014, 18, 573-588.	2.3	9
28	Genetic studies on the virus-like regions in the genome of hyperthermophilic archaeon, <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2013, 17, 153-160.	2.3	8
29	Identification and Structure of a Novel Archaeal HypB for [NiFe] Hydrogenase Maturation. <i>Journal of Molecular Biology</i> , 2013, 425, 1627-1640.	4.2	20
30	Hydrogen Production by the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i>. <i>Journal of the Japan Petroleum Institute</i> , 2013, 56, 267-279.	0.6	2
31	An Archaeal Histone Is Required for Transformation of <i>Thermococcus kodakarensis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 6864-6874.	2.2	43
32	Characterization and in vitro interaction study of a [NiFe] hydrogenase large subunit from the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> KOD1. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 192-196.	2.1	16
33	Comparative analyses of the two proliferating cell nuclear antigens from the hyperthermophilic archaeon, <i>Thermococcus kodakarensis</i>. <i>Genes To Cells</i> , 2012, 17, 923-937.	1.2	25
34	Salt Has a Biphasic Effect on the Higher-Order Structure of a DNA~Protamine Complex. <i>Journal of Physical Chemistry B</i> , 2011, 115, 4453-4459.	2.6	17
35	Biochemical and genetical analyses of the three mcm genes from the hyperthermophilic archaeon, <i>Thermococcus kodakarensis</i> . <i>Genes To Cells</i> , 2011, 16, 1176-1189.	1.2	32
36	Application of hyperthermophiles and their enzymes. <i>Current Opinion in Biotechnology</i> , 2011, 22, 618-626.	6.6	76

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37	Synthesis and in situ insertion of a site-specific fluorescently labeled membrane protein into cell-sized liposomes. <i>Analytical Biochemistry</i> , 2011, 418, 97-101.	2.4	14
38	Structural basis for branching enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 547-557.	2.6	54
39	Pseudouridine at position 55 in tRNA controls the contents of other modified nucleotides for low-temperature adaptation in the extreme-thermophilic eubacterium <i>Thermus thermophilus</i> . <i>Nucleic Acids Research</i> , 2011, 39, 2304-2318.	14.5	80
40	Distinct Physiological Roles of the Three [NiFe]-Hydrogenase Orthologs in the Hyperthermophilic Archaeon <i>Thermococcus kodakaraensis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3109-3116.	2.2	69
41	Dual Biosynthesis Pathway for Longer-Chain Polyamines in the Hyperthermophilic Archaeon <i>Thermococcus kodakaraensis</i> . <i>Journal of Bacteriology</i> , 2010, 192, 4991-5001.	2.2	49
42	N <sup>7</sup> -Methylguanine at position 46 (m <sup>7</sup> G46) in tRNA from <i>Thermus thermophilus</i> is required for cell viability at high temperatures through a tRNA modification network. <i>Nucleic Acids Research</i> , 2010, 38, 942-957.	14.5	93
43	Identification of the Phr-dependent heat shock regulon in the hyperthermophilic archaeon, <i>Thermococcus kodakaraensis</i> . <i>Journal of Biochemistry</i> , 2010, 147, 361-370.	1.7	23
44	GFP synthesis in giant liposomes using the in vitro translation system of <i>Thermococcus kodakaraensis</i> . , 2009, , .		0
45	The Fur iron regulator-like protein is cryptic in the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> . <i>FEMS Microbiology Letters</i> , 2009, 295, 117-128.	1.8	15
46	Protein Synthesis in Giant Liposomes Using the <i>In Vitro</i> Translation System of <i>Thermococcus kodakaraensis</i> . <i>IEEE Transactions on Nanobioscience</i> , 2009, 8, 325-331.	3.3	19
47	Controlling the higher-order structure of DNA-protamine complex. , 2009, , .		0
48	Stabilization of tRNA (m <sup>1</sup> G37) methyltransferase [TrmD] from <i>Aquifex aeolicus</i> by an intersubunit disulfide bond formation. <i>Genes To Cells</i> , 2008, 13, 807-816.	1.2	10
49	Archaeal RNA polymerase subunits E and F are not required for transcription <i>in vitro</i> , but a <i>Thermococcus kodakaraensis</i> mutant lacking subunit F is temperature-sensitive. <i>Molecular Microbiology</i> , 2008, 70, 623-633.	2.5	43
50	Expression Profiles and Physiological Roles of Two Types of Prefoldins from the Hyperthermophilic Archaeon <i>Thermococcus kodakaraensis</i> . <i>Journal of Molecular Biology</i> , 2008, 382, 298-311.	4.2	25
51	Effective approaches for the production of heterologous proteins using the <i>Thermococcus kodakaraensis</i> -based translation system. <i>Journal of Biotechnology</i> , 2008, 133, 177-182.	3.8	11
52	Synthesis of multiple gene products from a single polycistronic mRNA using the <i>Thermococcus kodakaraensis</i> -based translation system. , 2008, , .		0
53	A Global Transcriptional Regulator in <i>Thermococcus kodakaraensis</i> Controls the Expression Levels of Both Glycolytic and Gluconeogenic Enzyme-encoding Genes. <i>Journal of Biological Chemistry</i> , 2007, 282, 33659-33670.	3.4	79
54	Cell-free synthesis of GFP under high temperature conditions. , 2007, , .		0

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55	A highly productive system for cell-free protein synthesis using a lysate of the hyperthermophilic archaeon, <i>Thermococcus kodakaraensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 1153-1161.	3.6	19
56	A Novel Branching Enzyme of the GH-57 Family in the Hyperthermophilic Archaeon <i>Thermococcus kodakaraensis</i> KOD1. <i>Journal of Bacteriology</i> , 2006, 188, 5915-5924.	2.2	92
57	Cell-free protein synthesis at high temperature using a lysate of a hyperthermophile. , 2006, , .		0
58	Cell-free protein synthesis at high temperatures using the lysate of a hyperthermophile. <i>Journal of Biotechnology</i> , 2006, 126, 186-195.	3.8	43
59	Complete genome sequence of the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> KOD1 and comparison with <i>Pyrococcus</i> genomes. <i>Genome Research</i> , 2005, 15, 352-363.	5.5	376
60	Continuous hydrogen production by the hyperthermophilic archaeon, <i>Thermococcus kodakaraensis</i> KOD1. <i>Journal of Biotechnology</i> , 2005, 116, 271-282.	3.8	148
61	Expression of acetylcholine (ACh) and ACh-synthesizing activity in Archaea. <i>Life Sciences</i> , 2005, 77, 1935-1944.	4.3	26
62	Description of <i>Thermococcus kodakaraensis</i> sp. nov., a well studied hyperthermophilic archaeon previously reported as <i>Pyrococcus</i> sp. KOD1. <i>Archaea</i> , 2004, 1, 263-267.	2.3	261
63	Among Multiple Phosphomannomutase Gene Orthologues, Only One Gene Encodes a Protein with Phosphoglucomutase and Phosphomannomutase Activities in <i>Thermococcus kodakaraensis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 6070-6076.	2.2	29
64	Characterization of a Cytosolic NiFe-Hydrogenase from the Hyperthermophilic Archaeon <i>Thermococcus kodakaraensis</i> KOD1. <i>Journal of Bacteriology</i> , 2003, 185, 1705-1711.	2.2	44
65	Variant Forms of $\beta$ -Fetoprotein Transcripts Expressed in Human Hematopoietic Progenitors. <i>Journal of Biological Chemistry</i> , 2002, 277, 27629-27635.	3.4	37
66	The Unique Pentagonal Structure of an Archaeal Rubisco Is Essential for Its High Thermostability. <i>Journal of Biological Chemistry</i> , 2002, 277, 31656-31662.	3.4	59
67	A Novel Candidate for the True Fructose-1,6-bisphosphatase in Archaea. <i>Journal of Biological Chemistry</i> , 2002, 277, 30649-30655.	3.4	71
68	Novel and convenient methods for <i>Candida tropicalis</i> gene disruption using a mutated hygromycin B resistance gene. <i>Archives of Microbiology</i> , 2001, 176, 364-369.	2.2	13
69	Repression of fatty-acyl-CoA oxidase-encoding gene expression is not necessarily a determinant of high-level production of dicarboxylic acids in industrial dicarboxylic-acid-producing <i>Candida tropicalis</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 478-485.	3.6	21
70	An n-Alkane-Responsive Promoter Element Found in the Gene Encoding the Peroxisomal Protein of <i>Candida tropicalis</i> Does Not Contain a C 6 Zinc Cluster DNA-Binding Motif. <i>Journal of Bacteriology</i> , 2000, 182, 2492-2497.	2.2	9
71	Expression of the SNF1 gene from <i>Candida tropicalis</i> is required for growth on various carbon sources, including glucose. <i>Archives of Microbiology</i> , 1999, 172, 256-263.	2.2	12
72	A regulatory factor, Fil1p, involved in derepression of the isocitrate lyase gene in <i>Saccharomyces cerevisiae</i> . A possible mitochondrial protein necessary for protein synthesis in mitochondria. <i>FEBS Journal</i> , 1998, 256, 212-220.	0.2	21

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73	Derepression of Gene Expression Mediated by the 5' Upstream Region of the Isocitrate Lyase Gene of <i>Candida Tropicalis</i> is Controlled by two Distinct Regulatory Pathways in <i>Saccharomyces Cerevisiae</i> . <i>FEBS Journal</i> , 1997, 243, 748-752.	0.2	13
74	Analysis of carbon source-regulated gene expression by the upstream region of the <i>Candida tropicalis</i> malate synthase gene in <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1997, 1350, 80-88.	2.4	3
75	A novel heterologous gene expression system in <i>Saccharomyces cerevisiae</i> using the isocitrate lyase gene promoter from <i>Candida tropicalis</i> . <i>Applied Microbiology and Biotechnology</i> , 1996, 44, 759-765.	3.6	39
76	Effects of carbon source on the application of a novel foreign gene expression system in <i>Saccharomyces cerevisiae</i> using the upstream region of the <i>Candida tropicalis</i> isocitrate lyase gene (UPR-ICL). <i>Journal of Bioscience and Bioengineering</i> , 1995, 80, 529-533.	0.9	13
77	The upstream region of the isocitrate lyase gene (UPR-ICL) of <i>Candida tropicalis</i> induces gene expression in both <i>Saccharomyces cerevisiae</i> and <i>Escherichia coli</i> by acetate via two distinct promoters. <i>Archives of Microbiology</i> , 1995, 163, 322-328.	2.2	13
78	The upstream region of the isocitrate lyase gene (UPR-ICL) of <i>Candida tropicalis</i> induces gene expression in both <i>Saccharomyces cerevisiae</i> and <i>Escherichia coli</i> by acetate via two distinct promoters. <i>Archives of Microbiology</i> , 1995, 163, 322-328.	2.2	3