Tamotsu Kanai

List of Publications by Year in descending order

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Version: 2024-02-01

78	2,560	236925	206112
papers	citations	25 h-index	48 g-index

78	78	78	2213
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Complete genome sequence of the hyperthermophilic archaeon Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus genomes. Genome Research, 2005, 15, 352-363.	5.5	376
2	Description ofThermococcus kodakaraensissp. nov., a well studied hyperthermophilic archaeon previously reported asPyrococcussp. KOD1. Archaea, 2004, 1, 263-267.	2.3	261
3	Continuous hydrogen production by the hyperthermophilic archaeon, Thermococcus kodakaraensis KOD1. Journal of Biotechnology, 2005, 116, 271-282.	3.8	148
4	N 7-Methylguanine at position 46 (m7G46) in tRNA from Thermus thermophilus is required for cell viability at high temperatures through a tRNA modification network. Nucleic Acids Research, 2010, 38, 942-957.	14.5	93
5	A Novel Branching Enzyme of the GH-57 Family in the Hyperthermophilic Archaeon Thermococcus kodakaraensis KOD1. Journal of Bacteriology, 2006, 188, 5915-5924.	2.2	92
6	Pseudouridine at position 55 in tRNA controls the contents of other modified nucleotides for low-temperature adaptation in the extreme-thermophilic eubacterium Thermus thermophilus. Nucleic Acids Research, 2011, 39, 2304-2318.	14.5	80
7	A Global Transcriptional Regulator in Thermococcus kodakaraensis Controls the Expression Levels of Both Glycolytic and Gluconeogenic Enzyme-encoding Genes. Journal of Biological Chemistry, 2007, 282, 33659-33670.	3.4	79
8	Application of hyperthermophiles and their enzymes. Current Opinion in Biotechnology, 2011, 22, 618-626.	6.6	76
9	A Novel Candidate for the True Fructose-1,6-bisphosphatase in Archaea. Journal of Biological Chemistry, 2002, 277, 30649-30655.	3.4	71
10	Distinct Physiological Roles of the Three [NiFe]-Hydrogenase Orthologs in the Hyperthermophilic Archaeon Thermococcus kodakarensis. Journal of Bacteriology, 2011, 193, 3109-3116.	2.2	69
11	The Unique Pentagonal Structure of an Archaeal Rubisco Is Essential for Its High Thermostability. Journal of Biological Chemistry, 2002, 277, 31656-31662.	3.4	59
12	Structural basis for branchingâ€enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon Thermococcus Kodakaraensis KOD1. Proteins: Structure, Function and Bioinformatics, 2011, 79, 547-557.	2.6	54
13	Structural basis of a Ni acquisition cycle for [NiFe] hydrogenase by Ni-metallochaperone HypA and its enhancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7701-7706.	7.1	54
14	Dual Biosynthesis Pathway for Longer-Chain Polyamines in the Hyperthermophilic Archaeon Thermococcus kodakarensis. Journal of Bacteriology, 2010, 192, 4991-5001.	2.2	49
15	Characterization of a Cytosolic NiFe-Hydrogenase from the Hyperthermophilic Archaeon Thermococcus kodakaraensis KOD1. Journal of Bacteriology, 2003, 185, 1705-1711.	2.2	44
16	Cell-free protein synthesis at high temperatures using the lysate of a hyperthermophile. Journal of Biotechnology, 2006, 126, 186-195.	3.8	43
17	Archaeal RNA polymerase subunits E and F are not required for transcription in vitro, but a Thermococcus kodakarensis mutant lacking subunit F is temperatureâ€sensitive. Molecular Microbiology, 2008, 70, 623-633.	2.5	43
18	An Archaeal Histone Is Required for Transformation of Thermococcus kodakarensis. Journal of Bacteriology, 2012, 194, 6864-6874.	2.2	43

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19	A novel heterologous gene expression system in Saccharomyces cerevisiae using the isocitrate lyase gene promoter from Candida tropicalis. Applied Microbiology and Biotechnology, 1996, 44, 759-765.	3.6	39
20	Variant Forms of Î±-Fetoprotein Transcripts Expressed in Human Hematopoietic Progenitors. Journal of Biological Chemistry, 2002, 277, 27629-27635.	3.4	37
21	The X-ray crystal structure of the euryarchaeal RNA polymerase in an open-clamp configuration. Nature Communications, 2014, 5, 5132.	12.8	36
22	Biochemical and genetical analyses of the three mcm genes from the hyperthermophilic archaeon, Thermococcus kodakarensis. Genes To Cells, 2011, 16, 1176-1189.	1.2	32
23	Polymorphobacter multimanifer gen. nov., sp. nov., a polymorphic bacterium isolated from antarctic white rock. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2034-2040.	1.7	30
24	Among Multiple Phosphomannomutase Gene Orthologues, Only One Gene Encodes a Protein with Phosphoglucomutase and Phosphomannomutase Activities in Thermococcus kodakaraensis. Journal of Bacteriology, 2004, 186, 6070-6076.	2.2	29
25	Sodium-driven energy conversion for flagellar rotation of the earliest divergent hyperthermophilic bacterium. Scientific Reports, 2015, 5, 12711.	3.3	27
26	Crystal structures of a [NiFe] hydrogenase large subunit HyhL in an immature state in complex with a Ni chaperone HypA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7045-7050.	7.1	27
27	Expression of acetylcholine (ACh) and ACh-synthesizing activity in Archaea. Life Sciences, 2005, 77, 1935-1944.	4.3	26
28	Expression Profiles and Physiological Roles of Two Types of Prefoldins from the Hyperthermophilic Archaeon Thermococcus kodakaraensis. Journal of Molecular Biology, 2008, 382, 298-311.	4.2	25
29	Comparative analyses of the two proliferating cell nuclear antigens from the hyperthermophilic archaeon, Thermococcus kodakarensis. Genes To Cells, 2012, 17, 923-937.	1.2	25
30	Identification of the Phr-dependent heat shock regulon in the hyperthermophilic archaeon, Thermococcus kodakaraensis. Journal of Biochemistry, 2010, 147, 361-370.	1.7	23
31	Overproduction of the membrane-bound [NiFe]-hydrogenase in Thermococcus kodakarensis and its effect on hydrogen production. Frontiers in Microbiology, 2015, 6, 847.	3.5	22
32	Crystal structures of chitin binding domains of chitinase from ThermococcusÂkodakarensis <scp>KOD</scp>1. FEBS Letters, 2016, 590, 298-304.	2.8	22
33	The Cdc45/RecJ-like protein forms a complex with GINS and MCM, and is important for DNA replication in Thermococcus kodakarensis. Nucleic Acids Research, 2017, 45, 10693-10705.	14.5	22
34	A regulatory factor, Fil1p, involved in derepression of the isocitrate lyase gene in Saccharomyces cerevisiae . A possible mitochondrial protein necessary for protein synthesis in mitochondria. FEBS Journal, 1998, 256, 212-220.	0.2	21
35	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 Candida tropicalis. Applied Microbiology and Biotechnology, 2001, 56, 478-485.	3.6	21
36	Identification and Structure of a Novel Archaeal HypB for [NiFe] Hydrogenase Maturation. Journal of Molecular Biology, 2013, 425, 1627-1640.	4.2	20

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37	A highly productive system for cell-free protein synthesis using a lysate of the hyperthermophilic archaeon, Thermococcus kodakaraensis. Applied Microbiology and Biotechnology, 2007, 74, 1153-1161.	3.6	19
38	Protein Synthesis in Giant Liposomes Using theIn VitroTranslation System ofThermococcus kodakaraensis. IEEE Transactions on Nanobioscience, 2009, 8, 325-331.	3.3	19
39	Salt Has a Biphasic Effect on the Higher-Order Structure of a DNAâ^'Protamine Complex. Journal of Physical Chemistry B, 2011, 115, 4453-4459.	2.6	17
40	Engineering of the Hyperthermophilic Archaeon Thermococcus kodakarensis for Chitin-Dependent Hydrogen Production. Applied and Environmental Microbiology, 2017, 83, .	3.1	17
41	Characterization and in vitro interaction study of a [NiFe] hydrogenase large subunit from the hyperthermophilic archaeon Thermococcus kodakarensis KOD1. Biochemical and Biophysical Research Communications, 2012, 417, 192-196.	2.1	16
42	The Fur iron regulator-like protein is cryptic in the hyperthermophilic archaeonThermococcus kodakaraensis. FEMS Microbiology Letters, 2009, 295, 117-128.	1.8	15
43	A Structurally Novel Chitinase from the Chitin-Degrading Hyperthermophilic Archaeon Thermococcus chitonophagus. Applied and Environmental Microbiology, 2016, 82, 3554-3562.	3.1	15
44	Distinct Modified Nucleosides in tRNA ^{Trp} from the Hyperthermophilic Archaeon Thermococcus kodakarensis and Requirement of tRNA m ² G10/m ² ₂ G10 Methyltransferase (Archaeal Trm11) for Survival at High Temperatures. Journal of Bacteriology, 2019, 201, .	2.2	15
45	Synthesis and in situ insertion of a site-specific fluorescently labeled membrane protein into cell-sized liposomes. Analytical Biochemistry, 2011, 418, 97-101.	2.4	14
46	Effects of carbon source on the application of a novel foreign gene expression system in Saccharomyces cerevisiae using the upstream region of the Candida tropicalis isocitrate lyase gene (UPR-ICL). Journal of Bioscience and Bioengineering, 1995, 80, 529-533.	0.9	13
47	The upstream region of the isocitrate lyase gene (UPR-ICL) of Candida tropicalis induces gene expression in both Saccharomyces cerevisiae and Escherichia coli by acetate via two distinct promoters. Archives of Microbiology, 1995, 163, 322-328.	2.2	13
48	Derepression of Gene Expression Mediated by the 5' Upstream Region of the Isocitrate Lyase Gene of Candida Tropicalis is Controlled by two Distinct Regulatory Pathways in Saccharomyces Cerevisiae. FEBS Journal, 1997, 243, 748-752.	0.2	13
49	Novel and convenient methods for Candida tropicalis gene disruption using a mutated hygromycin B resistance gene. Archives of Microbiology, 2001, 176, 364-369.	2.2	13
50	Crystal structure of a [NiFe] hydrogenase maturation protease HybD fromThermococcus kodakarensisKOD1. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1321-1327.	2.6	13
51	Thermophilic Degradation of Hemicellulose, a Critical Feedstock in the Production of Bioenergy and Other Value-Added Products. Applied and Environmental Microbiology, 2020, 86, .	3.1	13
52	Expression of the SNF1 gene from Candida tropicalis is required for growth on various carbon sources, including glucose. Archives of Microbiology, 1999, 172, 256-263.	2.2	12
53	Effective approaches for the production of heterologous proteins using the Thermococcus kodakaraensis-based translation system. Journal of Biotechnology, 2008, 133, 177-182.	3.8	11
54	Identification of the glucosamine kinase in the chitinolytic pathway of Thermococcus kodakarensis. Journal of Bioscience and Bioengineering, 2018, 125, 320-326.	2.2	11

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55	Stabilization of tRNA (m¹G37) methyltransferase [TrmD] from Aquifex aeolicus by an intersubunit disulfide bond formation. Genes To Cells, 2008, 13, 807-816.	1.2	10
56	An n -Alkane-Responsive Promoter Element Found in the Gene Encoding the Peroxisomal Protein of Candida tropicalis Does Not Contain a C 6 Zinc Cluster DNA-Binding Motif. Journal of Bacteriology, 2000, 182, 2492-2497.	2.2	9
57	Different roles of two transcription factor B proteins in the hyperthermophilic archaeon Thermococcus kodakarensis. Extremophiles, 2014, 18, 573-588.	2.3	9
58	Genetic analyses of the functions of [NiFe]-hydrogenase maturation endopeptidases in the hyperthermophilic archaeon Thermococcus kodakarensis. Extremophiles, 2017, 21, 27-39.	2.3	9
59	Genetic studies on the virus-like regions in the genome of hyperthermophilic archaeon, Thermococcus kodakarensis. Extremophiles, 2013, 17, 153-160.	2.3	8
60	Possible function of the second RecJ-like protein in stalled replication fork repair by interacting with Hef. Scientific Reports, 2017, 7, 16949.	3.3	8
61	Gene regulation of two ferredoxin:NADP+ oxidoreductases by the redox-responsive regulator SurR in Thermococcus kodakarensis. Extremophiles, 2017, 21, 903-917.	2.3	6
62	An archaeal RNA binding protein, FAU-1, is a novel ribonuclease related to rRNA stability in Pyrococcus and Thermococcus. Scientific Reports, 2017, 7, 12674.	3.3	4
63	Structure of a [NiFe] hydrogenase maturation protease HycI provides insights into its substrate selectivity. Biochemical and Biophysical Research Communications, 2018, 498, 782-788.	2.1	4
64	Analysis of carbon source-regulated gene expression by the upstream region of the Candida tropicalis malate synthase gene in Saccharomyces cerevisiae. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1997, 1350, 80-88.	2.4	3
65	Crystal structure of the TK2203 protein fromThermococcus kodakarensis, a putative extradiol dioxygenase. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 427-433.	0.8	3
66	Crystal structures of an archaeal chitinase ChiD and its ligand complexes. Glycobiology, 2018, 28, 418-426.	2.5	3
67	The upstream region of the isocitrate lyase gene (UPR-ICL) of Candida tropicalis induces gene expression in both Saccharomyces cerevisiae and Escherichia coli by acetate via two distinct promoters. Archives of Microbiology, 1995, 163, 322-328.	2.2	3
68	Pcal_1311, an alcohol dehydrogenase homologue from Pyrobaculum calidifontis, displays NADH-dependent high aldehyde reductase activity. Extremophiles, 2017, 21, 1101-1110.	2.3	2
69	Hydrogen Production by the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i>. Journal of the Japan Petroleum Institute, 2013, 56, 267-279.	0.6	2
70	Cell-free protein synthesis at high temperature using a lysate of a hyperthermophile. , 2006, , .		0
71	Cell-free synthesis of GFP under high temperature conditions. , 2007, , .		0
72	Synthesis of multiple gene products from a single polycistronic mRNA using the Thermococcus kodakaraensis-based translation system. , 2008, , .		0

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73	GFP synthesis in giant liposomes using the in vitro translation system of Thermococcus kodakaraensis. , 2009, , .		0
74	Controlling the higher-order structure of DNA-protamine complex. , 2009, , .		0
75	Structural studies of a novel type of chitinase from archaea. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s216-s216.	0.1	0
76	Sodium-Driven Energy Conversion for Flagellar Rotation of the Earliest Divergent Hyperthermophilic Bacterium. Biophysical Journal, 2016, 110, 468a.	0.5	0
77	The TK0271 Protein Activates Transcription of Aromatic Amino Acid Biosynthesis Genes in the Hyperthermophilic Archaeon Thermococcus kodakarensis. MBio, 2019, 10, .	4.1	0
78	Effects of high-level expression of A1-ATPase on H2 production in Thermococcus kodakarensis. Journal of Bioscience and Bioengineering, 2020, 130, 149-158.	2.2	0