

Tsutomu Nakamura

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Rebuilding Ring-Type Assembly of Peroxiredoxin by Chemical Modification. <i>Bioconjugate Chemistry</i> , 2021, 32, 153-160.	1.8	3
2	Structural analysis and reaction mechanism of malate dehydrogenase from <i>Geobacillus stearothermophilus</i> . <i>Journal of Biochemistry</i> , 2021, 170, 97-105.	0.9	6
3	Increasing loop flexibility affords low-temperature adaptation of a moderate thermophilic malate dehydrogenase from <i>Geobacillus stearothermophilus</i> . <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	1.0	2
4	Crystal structure of acetylxylan esterase from <i>Caldanaerobacter subterraneus</i> subsp. <i>tengcongensis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 399-406.	0.4	1
5	Polyploid engineering by increasing mutant gene dosage in yeasts. <i>Microbial Biotechnology</i> , 2021, 14, 979-992.	2.0	4
6	Disassembly of the ring-type decameric structure of peroxiredoxin from <i>Aeropyrum pernix</i> K1 by amino acid mutation. <i>Protein Science</i> , 2020, 29, 1138-1147.	3.1	4
7	Distinct molecular assembly of homologous peroxiredoxins from <i>Pyrococcus horikoshii</i> and <i>Thermococcus kodakaraensis</i> . <i>Journal of Biochemistry</i> , 2019, 166, 89-95.	0.9	4
8	Application of chromosomal gene insertion into <i>Escherichia coli</i> for expression of recombinant proteins. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 266-272.	1.1	4
9	Alteration of molecular assembly of peroxiredoxins from hyperthermophilic archaea. <i>Journal of Biochemistry</i> , 2017, 162, 415-422.	0.9	8
10	Heat-induced native dimerization prevents amyloid formation by variable domain from immunoglobulin light chain. <i>FEBS Journal</i> , 2017, 284, 3114-3127.	2.2	4
11	Substrate recognition of N,N ² -diacetylchitobiose deacetylase from <i>Pyrococcus horikoshii</i> . <i>Journal of Structural Biology</i> , 2016, 195, 286-293.	1.3	6
12	Multiple crystal forms of N,N ² -diacetylchitobiose deacetylase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 657-662.	0.4	6
13	Solution structure of the chitin-binding domain 1 (ChBD1) of a hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Journal of Biochemistry</i> , 2014, 155, 115-122.	0.9	12
14	Expression from engineered <i>Escherichia coli</i> chromosome and crystallographic study of archaeal N,N ² -diacetylchitobiose deacetylase. <i>FEBS Journal</i> , 2014, 281, 2584-2596.	2.2	22
15	Structure of peroxiredoxin from the anaerobic hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 719-722.	0.7	12
16	Expression, refolding, and purification of active diacetylchitobiose deacetylase from <i>Pyrococcus horikoshii</i> . <i>Protein Expression and Purification</i> , 2012, 84, 265-269.	0.6	15
17	Characterization and crystal structure of the thermophilic ROK hexokinase from <i>Thermus thermophilus</i> . <i>Journal of Bioscience and Bioengineering</i> , 2012, 114, 150-154.	1.1	19
18	Growth of Protein Crystals by Syringe-Type Top-Seeded Solution Growth. <i>Crystal Growth and Design</i> , 2011, 11, 1486-1492.	1.4	7

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19	Crystal structure of the cambialistic superoxide dismutase from <i>Aeropyrum pernix</i> K1 - insights into the enzyme mechanism and stability. <i>FEBS Journal</i> , 2011, 278, 598-609.	2.2	20
20	Crystallization and preliminary crystallographic analysis of a putative glucokinase/hexokinase from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1559-1562.	0.7	1
21	Growth of large protein crystals by a large-scale hanging-drop method. <i>Journal of Applied Crystallography</i> , 2010, 43, 937-939.	1.9	4
22	Kinetic and crystallographic analyses of the catalytic domain of chitinase from <i>Pyrococcus furiosus</i> - the role of conserved residues in the active site. <i>FEBS Journal</i> , 2010, 277, 2683-2695.	2.2	30
23	Crystal structure of peroxiredoxin from <i>Aeropyrum pernix</i> K1 complexed with its substrate, hydrogen peroxide. <i>Journal of Biochemistry</i> , 2010, 147, 109-115.	0.9	54
24	Kinetic and crystallographic analyses of the catalytic domain of chitinase from <i>Pyrococcus furiosus</i> - the role of conserved residues in the active site. <i>FEBS Journal</i> , 2010, 277, 2683-2695.	2.2	13
25	Mass Spectrometric Analysis Using Ruthenium (II)-Labeling for Identification of Glycosyl Hydrolase Product. <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 428-430.	0.6	3
26	Tertiary Structure and Carbohydrate Recognition by the Chitin-Binding Domain of a Hyperthermophilic Chitinase from <i>Pyrococcus furiosus</i> . <i>Journal of Molecular Biology</i> , 2008, 381, 670-680.	2.0	59
27	Oxidation of archaeal peroxiredoxin involves a hypervalent sulfur intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6238-6242.	3.3	57
28	The First Crystal Structure of L-Threonine Dehydrogenase. <i>Journal of Molecular Biology</i> , 2007, 366, 857-867.	2.0	36
29	Structure of the catalytic domain of the hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 7-11.	0.7	24
30	Crystallization and X-ray diffraction analysis of a catalytic domain of hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 791-793.	0.7	6
31	NMR assignment of the chitin-binding domain of a hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Journal of Biomolecular NMR</i> , 2006, 36, 70-70.	1.6	3
32	Amyloid fibril formation by the CAD domain of caspase-activated DNase. <i>Biopolymers</i> , 2005, 79, 39-47.	1.2	6
33	Crystallization and preliminary X-ray diffraction analysis of thioredoxin peroxidase from the aerobic hyperthermophilic archaeon <i>Aeropyrum pernix</i> K1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 323-325.	0.7	10
34	Crystallization and preliminary X-ray diffraction analysis of a chitin-binding domain of hyperthermophilic chitinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 476-478.	0.7	10
35	Crystal structure of thioredoxin peroxidase from aerobic hyperthermophilic archaeon <i>Aeropyrum pernix</i> K1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 822-826.	1.5	27
36	Identification of the Region Responsible for Fibril Formation in the CAD Domain of Caspase-Activated DNase. <i>Journal of Biochemistry</i> , 2005, 138, 815-819.	0.9	0

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37	Screening for Stable Mutants with Amino Acid Pairs Substituted for the Disulfide Bond between Residues 14 and 38 of Bovine Pancreatic Trypsin Inhibitor (BPTI). <i>Journal of Biological Chemistry</i> , 2002, 277, 51043-51048.	1.6	23
38	Thermostable and active phosphoenolpyruvate carboxylase from <i>Thermus</i> sp. even after proteolytic cleavage. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2002, 17, 215-222.	1.8	2
39	Systematic circular permutation of an entire protein reveals essential folding elements. <i>Nature Structural Biology</i> , 2000, 7, 580-585.	9.7	111
40	Circular Permutation Analysis as a Method for Distinction of Functional Elements in the M20 Loop of <i>Escherichia coli</i> Dihydrofolate Reductase. <i>Journal of Biological Chemistry</i> , 1999, 274, 19041-19047.	1.6	31
41	Molecular characterization of recombinant phosphoenolpyruvate carboxylase from an extreme thermophile. <i>Studies in Surface Science and Catalysis</i> , 1998, 114, 605-608.	1.5	1
42	Phosphoenolpyruvate carboxylase of <i>Thermus</i> sp.: role of a divergent glycine-rich region. <i>Biotechnology Letters</i> , 1997, 19, 335-340.	1.1	2
43	Cloning and Sequence Analysis of the Gene for Phosphoenolpyruvate Carboxylase from an Extreme Thermophile, <i>Thermus</i> sp1. <i>Journal of Biochemistry</i> , 1995, 118, 319-324.	0.9	26