

Tomohiro Tamura

List of Publications by Year in descending order

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153
papers

6,837
citations

53660

45
h-index

66788

78
g-index

154
all docs

154
docs citations

154
times ranked

5756
citing authors

#	ARTICLE	IF	CITATIONS
1	Ornithine decarboxylase is degraded by the 26S proteasome without ubiquitination. <i>Nature</i> , 1992, 360, 597-599.	13.7	767
2	Interferon- β Induces Different Subunit Organizations and Functional Diversity of Proteasomes1. <i>Journal of Biochemistry</i> , 1994, 115, 257-269.	0.9	370
3	Less Body Fat Accumulation in Rats Fed a Safflower Oil Diet Than in Rats Fed a Beef Tallow Diet. <i>Journal of Nutrition</i> , 1990, 120, 1291-1296.	1.3	238
4	Self-compartmentalizing proteases. <i>Trends in Biochemical Sciences</i> , 1997, 22, 399-404.	3.7	223
5	cDNA cloning and interferon gamma down-regulation of proteasomal subunits X and Y. <i>Science</i> , 1994, 265, 1231-1234.	6.0	194
6	Newly identified pair of proteasomal subunits regulated reciprocally by interferon gamma.. <i>Journal of Experimental Medicine</i> , 1996, 183, 1807-1816.	4.2	194
7	The first characterization of a eubacterial proteasome: the 20S complex of <i>Rhodococcus</i> . <i>Current Biology</i> , 1995, 5, 766-774.	1.8	190
8	Molecular Characterization of the "26S" Proteasome Complex from Rat Liver. <i>Journal of Structural Biology</i> , 1993, 111, 200-211.	1.3	142
9	ATP-dependent reversible association of proteasomes with multiple protein components to form 26S complexes that degrade ubiquitinated proteins in human HL-60 cells. <i>FEBS Letters</i> , 1991, 284, 206-210.	1.3	137
10	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 149-154.	3.3	136
11	Total cellular glycomics allows characterizing cells and streamlining the discovery process for cellular biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2105-2110.	3.3	130
12	Possible mechanism of nuclear translocation of proteasomes. <i>FEBS Letters</i> , 1990, 271, 41-46.	1.3	123
13	Isolation and Characterization of a Rolling-Circle-Type Plasmid from <i>Rhodococcus erythropolis</i> and Application of the Plasmid to Multiple-Recombinant-Protein Expression. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5557-5568.	1.4	119
14	Demonstration that a human 26S proteolytic complex consists of a proteasome and multiple associated protein components and hydrolyzes ATP and ubiquitin-ligated proteins by closely linked mechanisms. <i>FEBS Journal</i> , 1992, 206, 567-578.	0.2	115
15	The Role of Tricorn Protease and Its Aminopeptidase-Interacting Factors in Cellular Protein Degradation. <i>Cell</i> , 1998, 95, 637-648.	13.5	112
16	Replacement of proteasome subunits X and Y by LMP7 and LMP2 induced by interferon- β for acquirement of the functional diversity responsible for antigen processing. <i>FEBS Letters</i> , 1994, 343, 85-88.	1.3	111
17	Paired termini stabilize antisense RNAs and enhance conditional gene silencing in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2006, 34, e138-e138.	6.5	104
18	Tricorn Protease--The Core of a Modular Proteolytic System. <i>Science</i> , 1996, 274, 1385-1389.	6.0	102

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19	Purification and Characterization of the 26S Proteasome Complex Catalyzing ATP-Dependent Breakdown of Ubiquitin-Ligated Prot from Rat Liver1. <i>Journal of Biochemistry</i> , 1993, 113, 754-768.	0.9	84
20	Conditional gene silencing of multiple genes with antisense RNAs and generation of a mutator strain of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2009, 37, e103-e103.	6.5	83
21	Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multi-catalytic proteinase complexes). <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1991, 1089, 95-102.	2.4	80
22	Molecular Structures of 20S and 26S Proteasomes. <i>Enzyme & Protein</i> , 1993, 47, 241-251.	1.6	77
23	A novel system for expressing recombinant proteins over a wide temperature range from 4 to 35°C. <i>Biotechnology and Bioengineering</i> , 2004, 86, 136-148.	1.7	75
24	Prevalence, Molecular Characterization, and Antimicrobial Susceptibility of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from Milk and Dairy Products. <i>Foodborne Pathogens and Disease</i> , 2016, 13, 156-162.	0.8	75
25	Tricorn Protease Exists as an Icosahedral Supermolecule In Vivo. <i>Molecular Cell</i> , 1997, 1, 59-65.	4.5	74
26	The 20S Proteasome of <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5448-5453.	1.0	73
27	Occurrence, genetic characterization and antimicrobial resistance of <i>Salmonella</i> isolated from chicken meat and giblets. <i>Epidemiology and Infection</i> , 2015, 143, 997-1003.	1.0	70
28	Venomous protease of aphid soldier for colony defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11338-11343.	3.3	69
29	VAT, the <i>Thermoplasma</i> Homolog of Mammalian p97/VCP, Is an N Domain-regulated Protein Unfoldase*. <i>Journal of Biological Chemistry</i> , 2005, 280, 42856-42862.	1.6	65
30	Prevalence, molecular identification and antimicrobial resistance profile of <i>Salmonella</i> serovars isolated from retail beef products in Mansoura, Egypt. <i>Food Control</i> , 2014, 38, 209-214.	2.8	62
31	Subunit topology of the <i>Rhodococcus</i> proteasome. <i>FEBS Letters</i> , 1997, 400, 83-90.	1.3	61
32	Regulation of branched-chain amino acid catabolism in rat models for spontaneous type 2 diabetes mellitus. <i>Biochemical and Biophysical Research Communications</i> , 2008, 373, 94-98.	1.0	61
33	Purification, characterization, and directed evolution study of a vitamin D3 hydroxylase from <i>Pseudonocardia autotrophica</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 385, 170-175.	1.0	61
34	cDNA cloning and sequencing of component C9 of proteasomes from rat hepatoma cells. <i>FEBS Letters</i> , 1990, 264, 279-282.	1.3	60
35	Cloning, sequencing and expression of VAT, a CDC48/p97 ATPase homologue from the archaeon <i>Thermoplasma acidophilum</i> . <i>FEBS Letters</i> , 1997, 404, 263-268.	1.3	59
36	Sequential Enzymatic Epoxidation Involved in Polyether Lasalocid Biosynthesis. <i>Journal of the American Chemical Society</i> , 2012, 134, 7246-7249.	6.6	59

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37	Genetic and biochemical characterization of the dioxygenase involved in lateral dioxygenation of dibenzofuran from <i>Rhodococcus opacus</i> strain SAO101. <i>Applied Microbiology and Biotechnology</i> , 2006, 73, 474-484.	1.7	54
38	Mos is degraded by the 26S proteasome in a ubiquitin-dependent fashion. <i>FEBS Letters</i> , 1993, 324, 345-348.	1.3	53
39	Effect of High-Fat Diet on the Gene Expression of Pancreatic GLUT2 and Glucokinase in Rats. <i>Biochemical and Biophysical Research Communications</i> , 1995, 208, 1092-1098.	1.0	53
40	A Quinoline Antibiotic from <i>Rhodococcus erythropolis</i> JCM 6824. <i>Journal of Antibiotics</i> , 2008, 61, 680-682.	1.0	53
41	cDNA cloning and sequencing of component C5 of proteasomes from rat hepatoma cells. <i>FEBS Letters</i> , 1990, 264, 91-94.	1.3	51
42	cDNA cloning and sequencing of component C8 of proteasomes from rat hepatoma cells. <i>Biochemical and Biophysical Research Communications</i> , 1990, 171, 676-683.	1.0	49
43	Eubacterial proteasomes. <i>Molecular Biology Reports</i> , 1997, 24, 125-131.	1.0	48
44	Actinomycetes as host cells for production of recombinant proteins. <i>Microbial Cell Factories</i> , 2005, 4, 7.	1.9	48
45	Molecular Characterization and Antimicrobial Resistance Profile of Methicillin-Resistant <i>Staphylococcus aureus</i> in Retail Chicken. <i>Journal of Food Protection</i> , 2015, 78, 1879-1884.	0.8	47
46	Effects of Endurance Training of Gene Expression on Insulin Signal Transduction Pathway. <i>Biochemical and Biophysical Research Communications</i> , 1995, 210, 766-773.	1.0	42
47	Structural Evidence for Enhancement of Sequential Vitamin D3 Hydroxylation Activities by Directed Evolution of Cytochrome P450 Vitamin D3 Hydroxylase. <i>Journal of Biological Chemistry</i> , 2010, 285, 31193-31201.	1.6	40
48	Regulation of hepatic branched-chain α -keto acid dehydrogenase kinase in a rat model for type 2 diabetes mellitus at different stages of the disease. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 303-307.	1.0	40
49	A Single Mutation at the Ferredoxin Binding Site of P450 Vdh Enables Efficient Biocatalytic Production of 25-Hydroxyvitamin D ₃ . <i>ChemBioChem</i> , 2013, 14, 2284-2291.	1.3	40
50	Prevalence, genetic characterization and virulence genes of sorbitol-fermenting <i>Escherichia coli</i> O157:H- and <i>E. coli</i> O157:H7 isolated from retail beef. <i>International Journal of Food Microbiology</i> , 2013, 165, 295-301.	2.1	40
51	Separation of yeast proteasome subunits. <i>Biochemical and Biophysical Research Communications</i> , 1989, 164, 1253-1261.	1.0	39
52	Mutational analysis of conserved AAA+residues in the archaeal Lon protease from <i>Thermoplasma acidophilum</i> . <i>FEBS Letters</i> , 2004, 574, 161-166.	1.3	39
53	Characterization of LtsA from <i>Rhodococcus erythropolis</i> , an Enzyme with Glutamine Amidotransferase Activity. <i>Journal of Bacteriology</i> , 2005, 187, 2582-2591.	1.0	39
54	Downregulation of the skeletal muscle pyruvate dehydrogenase complex in the Otsuka Long-Evans Tokushima Fatty rat both before and after the onset of diabetes mellitus. <i>Life Sciences</i> , 2004, 75, 2117-2130.	2.0	36

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55	Structure-guided mutagenesis for the improvement of substrate specificity of <i>Bacillus megaterium</i> glucose dehydrogenase IV. <i>FEBS Journal</i> , 2012, 279, 3264-3275.	2.2	36
56	Tricorn protease (TRI) interacting factor 1 from <i>Thermoplasma acidophilum</i> is a proline iminopeptidase. <i>FEBS Letters</i> , 1996, 398, 101-105.	1.3	34
57	Molecular Cloning of cDNAs for Rat Proteasomes: Deduced Primary Structures of Four Other Subunits. <i>Journal of Biochemistry</i> , 1992, 112, 530-534.	0.9	33
58	Crystal structure of cytochrome P450 MoxA from <i>Nonomuraea recticatena</i> (CYP105). <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 876-882.	1.0	33
59	Three Types of Antibiotics Produced from <i>Rhodococcus erythropolis</i> Strains. <i>Microbes and Environments</i> , 2008, 23, 167-171.	0.7	33
60	Sequence analyses and inter-species comparisons of three novel human proteasomal subunits, HsN3, HsC7-I and HsC10-II, confirm potential proteolytic active-site residues. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1994, 1219, 361-368.	2.4	32
61	Preparation and characterization of EGCCase I, applicable to the comprehensive analysis of GSLs, using a rhodococcal expression system. <i>Journal of Lipid Research</i> , 2012, 53, 2242-2251.	2.0	32
62	Mechanism of Activation of Branched-Chain α -Keto Acid Dehydrogenase Complex by Exercise. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 752-756.	1.0	31
63	PR3 encoding an essential subunit of yeast proteasomes homologous to mammalian proteasome subunit C5. <i>Biochemical and Biophysical Research Communications</i> , 1992, 182, 452-460.	1.0	29
64	A Vector Library for Silencing Central Carbon Metabolism Genes with Antisense RNAs in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 564-573.	1.4	29
65	Improved method for preparation of ubiquitin-ligated lysozyme as substrate of ATP-dependent proteolysis. <i>FEBS Letters</i> , 1991, 292, 154-158.	1.3	28
66	Phylogenetic analysis of <i>Rhodococcus erythropolis</i> based on the variation of ribosomal proteins as observed by matrix-assisted laser desorption ionization-mass spectrometry without using genome information. <i>Journal of Bioscience and Bioengineering</i> , 2009, 108, 348-353.	1.1	28
67	Cloning and Heterologous Expression of the Aurachin RE Biosynthesis Gene Cluster Afford a New Cytochrome P450 for Quinoline N -Hydroxylation. <i>ChemBioChem</i> , 2013, 14, 1085-1093.	1.3	28
68	Construction of random transposition mutagenesis system in <i>Rhodococcus erythropolis</i> using IS1415. <i>Journal of Biotechnology</i> , 2006, 121, 13-22.	1.9	27
69	SUG1, a Component of the 26 S Proteasome, Is an ATPase Stimulated by Specific RNAs. <i>Journal of Biological Chemistry</i> , 1997, 272, 23201-23205.	1.6	26
70	A new carbon catabolite repression mutation of <i>Escherichia coli</i> , <i>mlc</i> ⁻ , and its use for producing isobutanol. <i>Journal of Bioscience and Bioengineering</i> , 2012, 114, 38-44.	1.1	26
71	cDNA cloning of rat proteasome subunit RC1, a homologue of RING10 located in the human MHC class II region. <i>FEBS Letters</i> , 1992, 301, 65-68.	1.3	25
72	Quantitative GSL-glycome analysis of human whole serum based on an EGCCase digestion and glycoblotting method. <i>Journal of Lipid Research</i> , 2015, 56, 2399-2407.	2.0	25

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73	Heterologous production of kasugamycin, an aminoglycoside antibiotic from <i>Streptomyces kasugaensis</i> , in <i>Streptomyces lividans</i> and <i>Rhodococcus erythropolis</i> L-88 by constitutive expression of the biosynthetic gene cluster. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4259-4268.	1.7	23
74	Gene expression of insulin signal-transduction pathway intermediates is lower in rats fed a beef tallow diet than in rats fed a safflower oil diet. <i>Metabolism: Clinical and Experimental</i> , 1996, 45, 1080-1088.	1.5	22
75	Capsids of Tricorn Protease Studied by Electron Cryomicroscopy. <i>Journal of Structural Biology</i> , 1999, 128, 65-68.	1.3	22
76	Anodized gold surface enables mediator-free and low-overpotential electrochemical oxidation of NADH: A facile method for the development of an NAD ⁺ -dependent enzyme biosensor. <i>Sensors and Actuators B: Chemical</i> , 2019, 288, 512-518.	4.0	22
77	Isolation and characterization of the <i>Rhodococcus opacusthiostrepton</i> -inducible <i>genestipALandtipAS</i> : application for recombinant protein expression in <i>Rhodococcus</i> . <i>FEMS Microbiology Letters</i> , 2004, 237, 35-40.	0.7	20
78	Enzymatic Characterization of an Amine Oxidase from <i>Arthrobacter</i> sp. Used to Measure Phosphatidylethanolamine. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 2732-2738.	0.6	20
79	Analysis of Bacterial Glucose Dehydrogenase Homologs from Thermoacidophilic Archaeon <i>Thermoplasma acidophilum</i> : Finding and Characterization of Aldo-hexose Dehydrogenase. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004, 68, 2451-2456.	0.6	19
80	Activation of hepatic branched-chain α -keto acid dehydrogenase complex by tumor necrosis factor- α in rats. <i>Biochemical and Biophysical Research Communications</i> , 2005, 328, 973-978.	1.0	19
81	Permeabilization induced by lipid II-targeting lantibiotic nisin and its effect on the bioconversion of vitamin D3 to 25-hydroxyvitamin D3 by <i>Rhodococcus erythropolis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 393-398.	1.0	19
82	Isolation and Characterization of α -Type HC3 and β -Type HC5 Subunit Genes of Human Proteasomes. <i>Journal of Molecular Biology</i> , 1994, 244, 117-124.	2.0	18
83	Structural Insights into Unique Substrate Selectivity of <i>Thermoplasma acidophilum</i> d-Aldo-hexose Dehydrogenase. <i>Journal of Molecular Biology</i> , 2007, 367, 1034-1046.	2.0	18
84	Recombinant ATPases of the yeast 26S proteasome activate protein degradation by the 20S proteasome. <i>FEBS Letters</i> , 2004, 565, 39-42.	1.3	17
85	A multipurpose transposon-based vector system mediates protein expression in <i>Rhodococcus erythropolis</i> . <i>Gene</i> , 2007, 386, 173-182.	1.0	16
86	De Novo Genome Project for the Aromatic Degradar <i>Rhodococcus pyridinivorans</i> Strain AK37. <i>Journal of Bacteriology</i> , 2012, 194, 1247-1248.	1.0	16
87	Multiple-Gene Silencing Using Antisense RNAs in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2012, 815, 307-319.	0.4	16
88	Prevalence, identification and molecular characterization of <i>Cronobacter sakazakii</i> isolated from retail meat products. <i>Food Control</i> , 2015, 53, 206-211.	2.8	16
89	Bifunctional quorum-quenching and antibiotic-acylase MacQ forms a 170-kDa capsule-shaped molecule containing spacer polypeptides. <i>Scientific Reports</i> , 2017, 7, 8946.	1.6	16
90	Developing a codon optimization method for improved expression of recombinant proteins in actinobacteria. <i>Scientific Reports</i> , 2019, 9, 8338.	1.6	16

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91	Gene silencing in <i>Escherichia coli</i> using antisense RNAs expressed from doxycycline-inducible vectors. <i>Letters in Applied Microbiology</i> , 2013, 56, 436-442.	1.0	15
92	Expression of Bovine Lactoferrin C-lobe in <i>Rhodococcus erythropolis</i> and Its Purification and Characterization. <i>Bioscience, Biotechnology and Biochemistry</i> , 2006, 70, 2641-2645.	0.6	14
93	New Vector System for Random, Single-Step Integration of Multiple Copies of DNA into the <i>Rhodococcus</i> Genome. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2531-2539.	1.4	14
94	SCO4008, a Putative TetR Transcriptional Repressor from <i>Streptomyces coelicolor</i> A3(2), Regulates Transcription of sco4007 by Multidrug Recognition. <i>Journal of Molecular Biology</i> , 2013, 425, 3289-3300.	2.0	14
95	Structure of the quinoline N-hydroxylating cytochrome P450 RauA, an essential enzyme that confers antibiotic activity on aurachin alkaloids. <i>FEBS Letters</i> , 2014, 588, 105-110.	1.3	14
96	Chemoenzymatically prepared konjac ceramide inhibits NGF-induced neurite outgrowth by a semaphorin 3A-like action. <i>Biochemistry and Biophysics Reports</i> , 2016, 5, 160-167.	0.7	14
97	cDNA cloning of rat proteasome subunit RC10-II, assumed to be responsible for trypsin-like catalytic activity. <i>FEBS Letters</i> , 1993, 336, 462-466.	1.3	13
98	Construction of a novel expression vector in <i>Pseudonocardia autotrophica</i> and its application to efficient biotransformation of compactin to pravastatin, a specific HMG-CoA reductase inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2011, 404, 511-516.	1.0	13
99	cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential for chymotrypsin-like activity. <i>FEBS Letters</i> , 1993, 332, 52-56.	1.3	12
100	Structural and functional analysis of the TetR-family transcriptional regulator SCO0332 from <i>Streptomyces coelicolor</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 198-205.	2.5	12
101	Occurrence, serotypes and virulence genes of non-O157 Shiga toxin-producing <i>Escherichia coli</i> in fresh beef, ground beef, and beef burger. <i>Food Control</i> , 2014, 37, 182-187.	2.8	12
102	Structural insights into the mechanism of the drastic changes in enzymatic activity of the cytochrome P450 vitamin D ₃ hydroxylase (CYP107BR1) caused by a mutation distant from the active site. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 266-275.	0.4	12
103	Tricorn Protease in Bacteria: Characterization of the Enzyme from <i>Streptomyces coelicolor</i> . <i>Biological Chemistry</i> , 2001, 382, 449-58.	1.2	11
104	Crystallization and preliminary X-ray diffraction studies of vitamin D ₃ hydroxylase, a novel cytochrome P450 isolated from <i>Pseudonocardia autotrophica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 372-375.	0.7	11
105	<i>Rhodococcus</i> Prokaryotic Ubiquitin-Like Protein (Pup) Is Degraded by Deaminase of Pup (Dop). <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1959-1966.	0.6	11
106	Crystal structure of human p120 homologue protein PH1374 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 814-816.	1.5	10
107	Characterization of a Novel Intracellular Endopeptidase of the $\hat{I}\pm/\hat{I}^2$ Hydrolase Family from <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 2003, 185, 496-503.	1.0	9
108	Size distribution of native cytosolic proteins of <i>Thermoplasma acidophilum</i> . <i>Proteomics</i> , 2009, 9, 3783-3786.	1.3	9

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109	Crystal structure of hypothetical protein PH0828 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 862-865.	1.5	8
110	Gene expression analysis using a modified HiCEP method applicable to prokaryotes: A study of the response of <i>Rhodococcus</i> to isoniazid and ethambutol. <i>Journal of Biotechnology</i> , 2006, 123, 259-272.	1.9	8
111	Leucine-induced activation of translational initiation is partly regulated by the branched-chain α -keto acid dehydrogenase complex in C2C12 cells. <i>Biochemical and Biophysical Research Communications</i> , 2006, 343, 1244-1250.	1.0	8
112	Advances in the Development of Genetic Tools for the Genus <i>Rhodococcus</i> . <i>Nihon Hosenkin Gakkai Shi = Actinomycetologica</i> , 2006, 20, 55-61.	0.3	8
113	Bacterial triacylglycerol lipase is a potential cholesterol esterase: Identification of a key determinant for sterol-binding specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 578-586.	3.6	8
114	Isolation and characterization of the <i>Rhodococcus opacus</i> thiostrepton-inducible genes <i>tipAL</i> and <i>tipAS</i> : application for recombinant protein expression in <i>Rhodococcus</i> . <i>FEMS Microbiology Letters</i> , 2004, 237, 35-40.	0.7	8
115	Cell-free protein synthesis using cell extract of <i>Pseudomonas fluorescens</i> and CspA promoter. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 671-676.	1.0	7
116	The β -propeller domain of the trilobed protease from <i>Pyrococcus furiosus</i> reveals an open Velcro topology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 179-187.	2.5	7
117	A novel nucleoside kinase from <i>Burkholderia thailandensis</i> . <i>FEBS Journal</i> , 2008, 275, 5865-5872.	2.2	7
118	Identification of a methanol-inducible promoter from <i>Rhodococcus erythropolis</i> PR4 and its use as an expression vector. <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 596-603.	1.1	7
119	Structural and genomic DNA analysis of the putative TetR transcriptional repressor SCO7518 from <i>Streptomyces coelicolor</i> A3(2). <i>FEBS Letters</i> , 2014, 588, 4311-4318.	1.3	7
120	Structural insights into the substrate stereospecificity of d-threo-3-hydroxyaspartate dehydratase from <i>Delftia</i> sp. HT23: a useful enzyme for the synthesis of optically pure l-threo- and d-erythro-3-hydroxyaspartate. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7137-7150.	1.7	7
121	Identification of a novel bacteriocin-like protein and structural gene from <i>Rhodococcus erythropolis</i> JCM 2895, using suppression-subtractive hybridization. <i>Journal of Antibiotics</i> , 2018, 71, 872-879.	1.0	7
122	Konjac Ceramide (kCer) Regulates NGF-Induced Neurite Outgrowth via the Sema3A Signaling Pathway. <i>Journal of Oleo Science</i> , 2018, 67, 77-86.	0.6	7
123	A Novel Enzymatic Method for Measuring Mizoribine β -Monophosphate Levels in Serum. <i>Journal of Bioscience and Bioengineering</i> , 2008, 106, 511-514.	1.1	6
124	Protein and Gene Structures of 20S and 26S Proteasomes. <i>Advances in Experimental Medicine and Biology</i> , 1996, 389, 187-195.	0.8	6
125	Purification, Crystallization, and Preliminary X-ray Diffraction Analysis of the Tricorn Protease Hexamer from <i>Thermoplasma acidophilum</i> . <i>Journal of Structural Biology</i> , 2001, 134, 83-87.	1.3	5
126	Structures of <i>Burkholderia thailandensis</i> nucleoside kinase: implications for the catalytic mechanism and nucleoside selectivity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 945-956.	2.5	5

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127	Production of recombinant extracellular cholesterol esterase using consistently active promoters in <i>Burkholderia stabilis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1974-1984.	0.6	5
128	Crystal structure of PH0010 from <i>Pyrococcus horikoshii</i> , which is highly homologous to human AMMECR 1C-terminal region. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 501-503.	1.5	4
129	C-terminal tail derived from the neighboring subunit is critical for the activity of <i>Thermoplasma acidophilum</i> aldohexose dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 801-807.	1.5	4
130	Characterization of Konjac Ceramide (kCer) Binding to Sema3A Receptor Nrp1. <i>Journal of Oleo Science</i> , 2018, 67, 87-94.	0.6	4
131	Konjac ceramide (kCer) regulates keratinocyte migration by Sema3A-like repulsion mechanism. <i>Biochemistry and Biophysics Reports</i> , 2019, 17, 132-138.	0.7	4
132	Neurite Outgrowth and Morphological Changes Induced by 8-trans Unsaturation of Sphingadienine in kCer Molecular Species. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2116.	1.8	4
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