Tomohiro Tamura

List of Publications by Year
in descending order

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153
papers

6,837
citations

53660
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all docs

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154
times ranked

5756
citing authors

#	ARTICLE	IF	CITATIONS
1	Konjac Ceramide (kCer)-Mediated Signal Transduction of the Sema3A Pathway Promotes HaCaT Keratinocyte Differentiation. Biology, 2022, 11, 121.	1.3	3
2	Bacterial triacylglycerol lipase is a potential cholesterol esterase: Identification of a key determinant for sterol-binding specificity. International Journal of Biological Macromolecules, 2021, 167, 578-586.	3.6	8
3	Nrp1 is Activated by Konjac Ceramide Binding-Induced Structural Rigidification of the a1a2 Domain. Cells, 2020, 9, 517.	1.8	2
4	Electrochemically boosted cytochrome P450 reaction that efficiently produces 25-hydroxyvitamin D3. Journal of Catalysis, 2020, 384, 30-36.	3.1	4
5	Konjac ceramide (kCer) regulates keratinocyte migration by Sema3A-like repulsion mechanism. Biochemistry and Biophysics Reports, 2019, 17, 132-138.	0.7	4
6	Production of recombinant extracellular cholesterol esterase using consistently active promoters in Burkholderia stabilis. Bioscience, Biotechnology and Biochemistry, 2019, 83, 1974-1984.	0.6	5
7	Developing a codon optimization method for improved expression of recombinant proteins in actinobacteria. Scientific Reports, 2019, 9, 8338.	1.6	16
8	Neurite Outgrowth and Morphological Changes Induced by 8-trans Unsaturation of Sphingadienine in kCer Molecular Species. International Journal of Molecular Sciences, 2019, 20, 2116.	1.8	4
9	Genome Sequence of Rhodococcus erythropolis Type Strain JCM 3201. Microbiology Resource Announcements, 2019, 8, .	0.3	1
10	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. Sensors and Actuators B: Chemical, 2019, 288, 512-518.	4.0	22
11	Characterization and application of a novel nicotinamide mononucleotide adenylyltransferase from Thermus thermophilus HB8. Journal of Bioscience and Bioengineering, 2018, 125, 385-389.	1.1	1
12	Complete Genome Sequence of an Efficient Vitamin D 3 -Hydroxylating Bacterium, Pseudonocardia autotrophica NBRC 12743. Microbiology Resource Announcements, 2018, 7, .	0.3	2
13	Characterization of Konjac Ceramide (kCer) Binding to Sema3A Receptor Nrp1. Journal of Oleo Science, 2018, 67, 87-94.	0.6	4
14	Identification of a novel bacteriocin-like protein and structural gene from Rhodococcus erythropolis JCM 2895, using suppression-subtractive hybridization. Journal of Antibiotics, 2018, 71, 872-879.	1.0	7
15	Konjac Ceramide (kCer) Regulates NGF-Induced Neurite Outgrowth via the Sema3A Signaling Pathway. Journal of Oleo Science, 2018, 67, 77-86.	0.6	7
16	Heterologous production of kasugamycin, an aminoglycoside antibiotic from Streptomyces kasugaensis, in Streptomyces lividans and Rhodococcus erythropolis L-88 by constitutive expression of the biosynthetic gene cluster. Applied Microbiology and Biotechnology, 2017, 101, 4259-4268.	1.7	23
17	Structural insights into the mechanism of the drastic changes in enzymatic activity of the cytochrome P450 vitamin D₃hydroxylase (CYP107BR1) caused by a mutation distant from the active site. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 266-275.	0.4	12
18	Bifunctional quorum-quenching and antibiotic-acylase MacQ forms a 170-kDa capsule-shaped molecule containing spacer polypeptides. Scientific Reports, 2017, 7, 8946.	1.6	16

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19	Complete Genome Sequence of Burkholderia stabilis FERMP-21014. Genome Announcements, 2017, 5, .	0.8	3
20	Chemoenzymatically prepared konjac ceramide inhibits NGF-induced neurite outgrowth by a semaphorin 3A-like action. Biochemistry and Biophysics Reports, 2016, 5, 160-167.	0.7	14
21	Prevalence, Molecular Characterization, and Antimicrobial Susceptibility of Methicillin-Resistant<i>Staphylococcus aureus</i>Isolated from Milk and Dairy Products. Foodborne Pathogens and Disease, 2016, 13, 156-162.	0.8	75
22	Prevalence, identification and molecular characterization of Cronobacter sakazakii isolated from retail meat products. Food Control, 2015, 53, 206-211.	2.8	16
23	Occurrence, genetic characterization and antimicrobial resistance of<i>Salmonella</i>isolated from chicken meat and giblets. Epidemiology and Infection, 2015, 143, 997-1003.	1.0	70
24	Structural insights into the substrate stereospecificity of d-threo-3-hydroxyaspartate dehydratase from Delftia sp. HT23: a useful enzyme for the synthesis of optically pure l-threo- and d-erythro-3-hydroxyaspartate. Applied Microbiology and Biotechnology, 2015, 99, 7137-7150.	1.7	7
25	Molecular Characterization and Antimicrobial Resistance Profile of Methicillin-Resistant Staphylococcus aureus in Retail Chicken. Journal of Food Protection, 2015, 78, 1879-1884.	0.8	47
26	Quantitative GSL-glycome analysis of human whole serum based on an EGCase digestion and glycoblotting method. Journal of Lipid Research, 2015, 56, 2399-2407.	2.0	25
27	Prevalence, molecular identification and antimicrobial resistance profile of Salmonella serovars isolated from retail beef products in Mansoura, Egypt. Food Control, 2014, 38, 209-214.	2.8	62
28	Structural and genomic DNA analysis of the putative TetR transcriptional repressor SCO7518 from <i>Streptomyces coelicolor</i> A3(2). FEBS Letters, 2014, 588, 4311-4318.	1.3	7
29	Occurrence, serotypes and virulence genes of non-O157 Shiga toxin-producing Escherichia coli in fresh beef, ground beef, and beef burger. Food Control, 2014, 37, 182-187.	2.8	12
30	Structure of the quinoline Nâ€hydroxylating cytochrome P450 RauA, an essential enzyme that confers antibiotic activity on aurachin alkaloids. FEBS Letters, 2014, 588, 105-110.	1.3	14
31	Protein complex purification from Thermoplasma acidophilum using a phage display library. Journal of Microbiological Methods, 2014, 98, 15-22.	0.7	3
32	A Vector Library for Silencing Central Carbon Metabolism Genes with Antisense RNAs in Escherichia coli. Applied and Environmental Microbiology, 2014, 80, 564-573.	1.4	29
33	Gene silencing in <i>Escherichia coli</i> using antisense RNAs expressed from doxycycline-inducible vectors. Letters in Applied Microbiology, 2013, 56, 436-442.	1.0	15
34	A Single Mutation at the Ferredoxin Binding Site of P450 Vdh Enables Efficient Biocatalytic Production of 25â€Hydroxyvitamin D₃. ChemBioChem, 2013, 14, 2284-2291.	1.3	40
35	Prevalence, genetic characterization and virulence genes of sorbitol-fermenting Escherichia coli O157:H- and E. coli O157:H7 isolated from retail beef. International Journal of Food Microbiology, 2013, 165, 295-301.	2.1	40
36	Structural and genomic DNA analysis of a putative transcription factor SCO5550 from Streptomyces coelicolor A3(2): Regulating the expression of gene sco5551 as a transcriptional activator with a novel dimer shape. Biochemical and Biophysical Research Communications, 2013, 435, 28-33.	1.0	3

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37	SCO4008, a Putative TetR Transcriptional Repressor from Streptomyces coelicolor A3(2), Regulates Transcription of sco4007 by Multidrug Recognition. Journal of Molecular Biology, 2013, 425, 3289-3300.	2.0	14
38	Cloning and Heterologous Expression of the Aurachin RE Biosynthesis Gene Cluster Afford a New Cytochrome P450 for Quinoline Nâ€Hydroxylation. ChemBioChem, 2013, 14, 1085-1093.	1.3	28
39	Crystallization and preliminary X-ray diffraction studies ofD-threo-3-hydroxyaspartate dehydratase isolated fromDelftiasp. HT23. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1131-1134.	0.7	1
40	Total cellular glycomics allows characterizing cells and streamlining the discovery process for cellular biomarkers. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2105-2110.	3.3	130
41	Tricorn Protease. , 2013, , 3614-3616.		0
42	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 149-154.	3.3	136
43	Preparation and characterization of EGCase I, applicable to the comprehensive analysis of GSLs, using a rhodococcal expression system. Journal of Lipid Research, 2012, 53, 2242-2251.	2.0	32
44	Structureâ€guided mutagenesis for the improvement of substrate specificity of <i>Bacillusâ€ƒmegaterium</i> glucose 1â€dehydrogenase IV. FEBS Journal, 2012, 279, 3264-3275.	2.2	36
45	De Novo Genome Project for the Aromatic Degrader Rhodococcus pyridinivorans Strain AK37. Journal of Bacteriology, 2012, 194, 1247-1248.	1.0	16
46	Multiple-Gene Silencing Using Antisense RNAs in Escherichia coli. Methods in Molecular Biology, 2012, 815, 307-319.	0.4	16
47	Sphingomyelinase C from Streptomyces sp. A9107: Unusual primary structure for bacterial sphingomyelinase C. Journal of Bioscience and Bioengineering, 2012, 114, 398-401.	1.1	0
48	RhodococcusProkaryotic Ubiquitin-Like Protein (Pup) Is Degraded by Deaminase of Pup (Dop). Bioscience, Biotechnology and Biochemistry, 2012, 76, 1959-1966.	0.6	11
49	Sequential Enzymatic Epoxidation Involved in Polyether Lasalocid Biosynthesis. Journal of the American Chemical Society, 2012, 134, 7246-7249.	6.6	59
50	A new carbon catabolite repression mutation of Escherichia coli, mlcâˆ—, and its use for producing isobutanol. Journal of Bioscience and Bioengineering, 2012, 114, 38-44.	1.1	26
51	Efficient production of active form of vitamin D3 by microbial conversion. Synthesiology, 2012, 4, 227-235.	0.2	1
52	Identification of a methanol-inducible promoter from Rhodococcus erythropolis PR4 and its use as an expression vector. Journal of Bioscience and Bioengineering, 2012, 113, 596-603.	1.1	7
53	Construction of a novel expression vector in Pseudonocardia autotrophica and its application to efficient biotransformation of compactin to pravastatin, a specific HMG-CoA reductase inhibitor. Biochemical and Biophysical Research Communications, 2011, 404, 511-516.	1.0	13
54	Permeabilization induced by lipid II-targeting lantibiotic nisin and its effect on the bioconversion of vitamin D3 to 25-hydroxyvitamin D3 by Rhodococcus erythropolis. Biochemical and Biophysical Research Communications, 2011, 405, 393-398.	1.0	19

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55	Enzymatic assay method for measuring mizoribine levels in serum. Journal of Bioscience and Bioengineering, 2011, 112, 205-207.	1.1	1
56	Structures of<i>Burkholderia thailandensis</i>nucleoside kinase: implications for the catalytic mechanism and nucleoside selectivity. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 945-956.	2.5	5
57	Efficient production of active form of vitamin D3 by microbial conversion. Synthesiology, 2011, 4, 222-229.	0.2	1
58	Structural Evidence for Enhancement of Sequential Vitamin D3 Hydroxylation Activities by Directed Evolution of Cytochrome P450 Vitamin D3 Hydroxylase. Journal of Biological Chemistry, 2010, 285, 31193-31201.	1.6	40
59	New Vector System for Random, Single-Step Integration of Multiple Copies of DNA into the <i>Rhodococcus</i> Genome. Applied and Environmental Microbiology, 2010, 76, 2531-2539.	1.4	14
60	Regulation of hepatic branched-chain Î±-keto acid dehydrogenase kinase in a rat model for type 2 diabetes mellitus at different stages of the disease. Biochemical and Biophysical Research Communications, 2010, 393, 303-307.	1.0	40
61	Phylogenetic analysis of Rhodococcus erythropolis based on the variation of ribosomal proteins as observed by matrix-assisted laser desorption ionization-mass spectrometry without using genome information. Journal of Bioscience and Bioengineering, 2009, 108, 348-353.	1.1	28
62	Câ€terminal tail derived from the neighboring subunit is critical for the activity of <i>Thermoplasma acidophilum</i><scp>D</scp>â€aldohexose dehydrogenase. Proteins: Structure, Function and Bioinformatics, 2009, 74, 801-807.	1.5	4
63	Size distribution of native cytosolic proteins of Thermoplasma acidophilum. Proteomics, 2009, 9, 3783-3786.	1.3	9
64	Crystallization and preliminary X-ray diffraction studies of vitamin D₃hydroxylase, a novel cytochrome P450 isolated from<i>Pseudonocardia autotrophica</i>. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 372-375.	0.7	11
65	Purification, characterization, and directed evolution study of a vitamin D3 hydroxylase from Pseudonocardia autotrophica. Biochemical and Biophysical Research Communications, 2009, 385, 170-175.	1.0	61
66	Conditional gene silencing of multiple genes with antisense RNAs and generation of a mutator strain of Escherichia coli. Nucleic Acids Research, 2009, 37, e103-e103.	6.5	83
67	Selective Protein Patterning Based on the Micro-Structured Organosilane Self-Assembled Monolayer by Vacuum Ultraviolet Light Lithography. Journal of Nanoscience and Nanotechnology, 2009, 9, 7318-23.	0.9	0
68	Structural and functional analysis of the TetR-family transcriptional regulator SCO0332 from<i>Streptomyces coelicolor</i>. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 198-205.	2.5	12
69	A novel nucleoside kinase from <i>Burkholderiaâ€ƒthailandensis</i>. FEBS Journal, 2008, 275, 5865-5872.	2.2	7
70	A Quinoline Antibiotic from Rhodococcus erythropolis JCM 6824. Journal of Antibiotics, 2008, 61, 680-682.	1.0	53
71	Regulation of branched-chain amino acid catabolism in rat models for spontaneous type 2 diabetes mellitus. Biochemical and Biophysical Research Communications, 2008, 373, 94-98.	1.0	61
72	A Novel Enzymatic Method for Measuring Mizoribine 5â€²-Monophosphate Levels in Serum. Journal of Bioscience and Bioengineering, 2008, 106, 511-514.	1.1	6

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73	Enzymatic Characterization of an Amine Oxidase from<i>Arthrobacter</i>sp. Used to Measure Phosphatidylethanolamine. Bioscience, Biotechnology and Biochemistry, 2008, 72, 2732-2738.	0.6	20
74	Three Types of Antibiotics Produced from Rhodococcus erythropolis Strains. Microbes and Environments, 2008, 23, 167-171.	0.7	33
75	Crystal Structure of SCO6571 from Streptomyces coelicolor A3(2). Protein and Peptide Letters, 2008, 15, 709-712.	0.4	1
76	Crystal structure of cytochrome P450 MoxA from Nonomuraea recticatena (CYP105). Biochemical and Biophysical Research Communications, 2007, 361, 876-882.	1.0	33
77	A multipurpose transposon-based vector system mediates protein expression in Rhodococcus erythropolis. Gene, 2007, 386, 173-182.	1.0	16
78	Structural Insights into Unique Substrate Selectivity of Thermoplasma acidophilum d-Aldohexose Dehydrogenase. Journal of Molecular Biology, 2007, 367, 1034-1046.	2.0	18
79	The Î²-propeller domain of the trilobed protease fromPyrococcus furiosusreveals an open Velcro topology. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 179-187.	2.5	7
80	Construction of random transposition mutagenesis system in Rhodococcus erythropolis using IS1415. Journal of Biotechnology, 2006, 121, 13-22.	1.9	27
81	Gene expression analysis using a modified HiCEP method applicable to prokaryotes: A study of the response of Rhodococcus to isoniazid and ethambutol. Journal of Biotechnology, 2006, 123, 259-272.	1.9	8
82	Leucine-induced activation of translational initiation is partly regulated by the branched-chain Î±-keto acid dehydrogenase complex in C2C12 cells. Biochemical and Biophysical Research Communications, 2006, 343, 1244-1250.	1.0	8
83	Participation of proteasome-associating complex PC500 in starfish oocyte maturation as revealed by monoclonal antibodies. Biochemical and Biophysical Research Communications, 2006, 349, 694-700.	1.0	1
84	Advances in the Development of Genetic Tools for the Genus Rhodococcus. Nihon Hosenkin Gakkai Shi = Actinomycetologica, 2006, 20, 55-61.	0.3	8
85	Crystallization and preliminary crystallographic analysis of NAD+-preferring aldohexose dehydrogenase from the thermoacidophilic archaeonThermoplasma acidophilum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 586-589.	0.7	1
86	Genetic and biochemical characterization of the dioxygenase involved in lateral dioxygenation of dibenzofuran from Rhodococcus opacus strain SAO101. Applied Microbiology and Biotechnology, 2006, 73, 474-484.	1.7	54
87	Paired termini stabilize antisense RNAs and enhance conditional gene silencing in Escherichia coli. Nucleic Acids Research, 2006, 34, e138-e138.	6.5	104
88	Expression of Bovine Lactoferrin C-lobe inRhodococcus erythropolisand Its Purification and Characterization. Bioscience, Biotechnology and Biochemistry, 2006, 70, 2641-2645.	0.6	14
89	Largeâ€loop antisense RNA hairpins provide stabilized and highly efficient antisense regulators in Escherichia coli. FASEB Journal, 2006, 20, A538.	0.2	0
90	Characterization of LtsA from Rhodococcus erythropolis , an Enzyme with Glutamine Amidotransferase Activity. Journal of Bacteriology, 2005, 187, 2582-2591.	1.0	39

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91	VAT, the Thermoplasma Homolog of Mammalian p97/VCP, Is an N Domain-regulated Protein Unfoldase*. Journal of Biological Chemistry, 2005, 280, 42856-42862.	1.6	65
92	Activation of hepatic branched-chain Î±-keto acid dehydrogenase complex by tumor necrosis factor-Î± in rats. Biochemical and Biophysical Research Communications, 2005, 328, 973-978.	1.0	19
93	Actinomycetes as host cells for production of recombinant proteins. Microbial Cell Factories, 2005, 4, 7.	1.9	48
94	Venomous protease of aphid soldier for colony defense. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11338-11343.	3.3	69
95	Isolation and Characterization of a Rolling-Circle-Type Plasmid from Rhodococcus erythropolis and Application of the Plasmid to Multiple-Recombinant-Protein Expression. Applied and Environmental Microbiology, 2004, 70, 5557-5568.	1.4	119
96	Isolation and characterization of theRhodococcus opacusthiostrepton-inducible genestipALandtipAS: application for recombinant protein expression inRhodococcus. FEMS Microbiology Letters, 2004, 237, 35-40.	0.7	20
97	Crystal structure of hypothetical protein PH0828 fromPyrococcus horikoshii. Proteins: Structure, Function and Bioinformatics, 2004, 57, 862-865.	1.5	8
98	Crystal structure of PH0010 from Pyrococcus horikoshii, which is highly homologous to human AMMECR 1C-terminal region. Proteins: Structure, Function and Bioinformatics, 2004, 58, 501-503.	1.5	4
99	Crystal structure of human p120 homologue protein PH1374 from Pyrococcus horikoshii. Proteins: Structure, Function and Bioinformatics, 2004, 54, 814-816.	1.5	10
100	A novel system for expressing recombinant proteins over a wide temperature range from 4 to 35Â°C. Biotechnology and Bioengineering, 2004, 86, 136-148.	1.7	75
101	Analysis of Bacterial Glucose Dehydrogenase Homologs from Thermoacidophilic ArchaeonThermoplasma acidophilum: Finding and Characterization of Aldohexose Dehydrogenase. Bioscience, Biotechnology and Biochemistry, 2004, 68, 2451-2456.	0.6	19
102	Recombinant ATPases of the yeast 26S proteasome activate protein degradation by the 20S proteasome. FEBS Letters, 2004, 565, 39-42.	1.3	17
103	Mutational analysis of conserved AAA+residues in the archaeal Lon protease fromThermoplasma acidophilum. FEBS Letters, 2004, 574, 161-166.	1.3	39
104	Cell-free protein synthesis using cell extract of Pseudomonas fluorescens and CspA promoter. Biochemical and Biophysical Research Communications, 2004, 319, 671-676.	1.0	7
105	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. Life Sciences, 2004, 75, 2117-2130.	2.0	36
106	Isolation and characterization of the Rhodococcus opacus thiostrepton-inducible genes tipAL and tipAS: application for recombinant protein expression in Rhodococcus. FEMS Microbiology Letters, 2004, 237, 35-40.	0.7	8
107	Characterization of a Novel Intracellular Endopeptidase of the Î±/Î² Hydrolase Family from Streptomyces coelicolor A3(2). Journal of Bacteriology, 2003, 185, 496-503.	1.0	9
108	Mechanism of Activation of Branched-Chain Î±-Keto Acid Dehydrogenase Complex by Exercise. Biochemical and Biophysical Research Communications, 2001, 287, 752-756.	1.0	31

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109	Purification, Crystallization, and Preliminary X-ray Diffraction Analysis of the Tricorn Protease Hexamer from Thermoplasma acidophilum. Journal of Structural Biology, 2001, 134, 83-87.	1.3	5
110	Tricorn Protease in Bacteria: Characterization of the Enzyme from Streptomyces coelicolor. Biological Chemistry, 2001, 382, 449-58.	1.2	11
111	Capsids of Tricorn Protease Studied by Electron Cryomicroscopy. Journal of Structural Biology, 1999, 128, 65-68.	1.3	22
112	The Role of Tricorn Protease and Its Aminopeptidase-Interacting Factors in Cellular Protein Degradation. Cell, 1998, 95, 637-648.	13.5	112
113	The 20S Proteasome of <i>Streptomyces coelicolor</i>. Journal of Bacteriology, 1998, 180, 5448-5453.	1.0	73
114	SUG1, a Component of the 26 S Proteasome, Is an ATPase Stimulated by Specific RNAs. Journal of Biological Chemistry, 1997, 272, 23201-23205.	1.6	26
115	Tricorn Protease Exists as an Icosahedral Supermolecule In Vivo. Molecular Cell, 1997, 1, 59-65.	4.5	74
116	Subunit topology of the Rhodococcus proteasome. FEBS Letters, 1997, 400, 83-90.	1.3	61
117	Cloning, sequencing and expression of VAT, a CDC48/p97 ATPase homologue from the archaeon Thermoplasma acidophilum. FEBS Letters, 1997, 404, 263-268.	1.3	59
118	Self-compartmentalizing proteases. Trends in Biochemical Sciences, 1997, 22, 399-404.	3.7	223
119	Eubacterial proteasomes. Molecular Biology Reports, 1997, 24, 125-131.	1.0	48
120	2-D Crystallization of theRhodococcus20S Proteasome. Journal of Structural Biology, 1996, 116, 438-442.	1.3	1
121	Tricorn protease (TRI) interacting factor 1 fromThermoplasma acidophilumis a proline iminopeptidase. FEBS Letters, 1996, 398, 101-105.	1.3	34
122	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. Metabolism: Clinical and Experimental, 1996, 45, 1080-1088.	1.5	22
123	Tricorn Protease--The Core of a Modular Proteolytic System. Science, 1996, 274, 1385-1389.	6.0	102
124	Newly identified pair of proteasomal subunits regulated reciprocally by interferon gamma.. Journal of Experimental Medicine, 1996, 183, 1807-1816.	4.2	194
125	Protein and Gene Structures of 20S and 26S Proteasomes. Advances in Experimental Medicine and Biology, 1996, 389, 187-195.	0.8	6
126	The first characterization of a eubacterial proteasome: the 20S complex of Rhodococcus. Current Biology, 1995, 5, 766-774.	1.8	190

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127	Effect of High-Fat Diet on the Gene Expression of Pancreatic GLUT2 and Glucokinase in Rats. Biochemical and Biophysical Research Communications, 1995, 208, 1092-1098.	1.0	53
128	Effects of Endurance Training of Gene Expression on Insulin Signal Transduction Pathway. Biochemical and Biophysical Research Communications, 1995, 210, 766-773.	1.0	42
129	cDNA cloning and interferon gamma down-regulation of proteasomal subunits X and Y. Science, 1994, 265, 1231-1234.	6.0	194
130	Sequence analyses and inter-species comparisons of three novel human proteasomal subunits, HsN3, HsC7-I and HsC10-II, confine potential proteolytic active-site residues. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1219, 361-368.	2.4	32
131	Isolation and Characterization of Î±-Type HC3 and Î²-Type HC5 Subunit Genes of Human Proteasomes. Journal of Molecular Biology, 1994, 244, 117-124.	2.0	18
132	Replacement of proteasome subunits X and Y by LMP7 and LMP2 induced by interferon-Î³ for acquirement of the functional diversity responsible for antigen processing. FEBS Letters, 1994, 343, 85-88.	1.3	111
133	Interferon-Î³ Induces Different Subunit Organizations and Functional Diversity of Proteasomes1. Journal of Biochemistry, 1994, 115, 257-269.	0.9	370
134	Mos is degraded by the 26S proteasome in a ubiquitin-dependent fashion. FEBS Letters, 1993, 324, 345-348.	1.3	53
135	cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential for chymotrypsin-like activity. FEBS Letters, 1993, 332, 52-56.	1.3	12
136	cDNA cloning of rat proteasome subunit RC10-II, assumed to be responsible for trypsin-like catalytic activity. FEBS Letters, 1993, 336, 462-466.	1.3	13
137	Molecular Characterization of the "26S" Proteasome Complex from Rat Liver. Journal of Structural Biology, 1993, 111, 200-211.	1.3	142
138	Purification and Characterization of the 26S Proteasome Complex Catalyzing ATP-Dependent Breakdown of Ubiquitin-Ligated Prot from Rat Liver1. Journal of Biochemistry, 1993, 113, 754-768.	0.9	84
139	Molecular Structures of 20S and 26S Proteasomes. Enzyme & Protein, 1993, 47, 241-251.	1.6	77
140	PRS3 encoding an essential subunit of yeast proteasomes homologous to mammalian proteasome subunit C5. Biochemical and Biophysical Research Communications, 1992, 182, 452-460.	1.0	29
141	cDNA cloning of rat proteasome subunit RC1, a homologue of RING10 located in the human MHC class II region. FEBS Letters, 1992, 301, 65-68.	1.3	25
142	Molecular Cloning of cDNAs for Rat Proteasomes: Deduced Primary Structures of Four Other Subunits1. Journal of Biochemistry, 1992, 112, 530-534.	0.9	33
143	Ornithine decarboxylase is degraded by the 26S proteasome without ubiquitination. Nature, 1992, 360, 597-599.	13.7	767
144	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. FEBS Journal, 1992, 206, 567-578.	0.2	115

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145	ATP-dependent reversible association of proteasomes with multiple protein components to form 26S complexes that degrade ubiquitinated proteins in human HL-60 cells. FEBS Letters, 1991, 284, 206-210.	1.3	137
146	Improved method for preparation of ubiquitin‐ligated lysozyme as substrate of ATP‐dependent proteolysis. FEBS Letters, 1991, 292, 154-158.	1.3	28
147	Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multi-catalytic proteinase complexes). Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1991, 1089, 95-102.	2.4	80
148	Less Body Fat Accumulation in Rats Fed a Safflower Oil Diet Than in Rats Fed a Beef Tallow Diet. Journal of Nutrition, 1990, 120, 1291-1296.	1.3	238
149	cDNA cloning and sequencing of component C9 of proteasomes from rat hepatoma cells. FEBS Letters, 1990, 264, 279-282.	1.3	60
150	Possible mechanism of nuclear translocation of proteasomes. FEBS Letters, 1990, 271, 41-46.	1.3	123
151	cDNA cloning and sequencing of component C5 of proteasomes from rat hepatoma cells. FEBS Letters, 1990, 264, 91-94.	1.3	51
152	cDNA cloning and sequencing of component C8 of proteasomes from rat hepatoma cells. Biochemical and Biophysical Research Communications, 1990, 171, 676-683.	1.0	49
153	Separation of yeast proteasome subunits. Biochemical and Biophysical Research Communications, 1989, 164, 1253-1261.	1.0	39