

Teru Ogura

List of Publications by Year in descending order

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125
papers

6,682
citations

76294

40
h-index

66879

78
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129
all docs

129
docs citations

129
times ranked

5354
citing authors

#	ARTICLE	IF	CITATIONS
1	Hierarchical Model for the Role of J-Domain Proteins in Distinct Cellular Functions. <i>Journal of Molecular Biology</i> , 2021, 433, 166750.	2.0	7
2	Split conformation of <i>Chaetomium thermophilum</i> Hsp104 disaggregase. <i>Structure</i> , 2021, 29, 721-730.e6.	1.6	2
3	Distinct roles and actions of protein disulfide isomerase family enzymes in catalysis of nascent-chain disulfide bond formation. <i>IScience</i> , 2021, 24, 102296.	1.9	5
4	A AAA ATPase Cdc48 with a cofactor Ubx2 facilitates ubiquitylation of a mitochondrial fusion-promoting factor Fzo1 for proteasomal degradation. <i>Journal of Biochemistry</i> , 2020, 167, 279-286.	0.9	14
5	The Cdc48-20S proteasome degrades a class of endogenous proteins in a ubiquitin-independent manner. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 835-840.	1.0	3
6	Cyclization of Single-Chain Fv Antibodies Markedly Suppressed Their Characteristic Aggregation Mediated by Inter-Chain VH-VL Interactions. <i>Molecules</i> , 2019, 24, 2620.	1.7	20
7	Dynamic assembly of protein disulfide isomerase in catalysis of oxidative folding. <i>Nature Chemical Biology</i> , 2019, 15, 499-509.	3.9	58
8	Functional characterization of UBXM-6, a C-terminal cofactor of CDC-48, in <i>C.Âlegans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 462-468.	1.0	0
9	Development of transgenic <i>Caenorhabditis elegans</i> expressing human transthyretin as a model for drug screening. <i>Scientific Reports</i> , 2018, 8, 17884.	1.6	8
10	Expression, Functional Characterization, and Preliminary Crystallization of the Cochaperone Prefoldin from the Thermophilic Fungus <i>Chaetomium thermophilum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2452.	1.8	4
11	A newly isolated Pex7-binding, atypical PTS2 protein P7BP2 is a novel dynein-type AAA+ protein. <i>Journal of Biochemistry</i> , 2018, 164, 437-447.	0.9	2
12	Inhibitory effects of Myricetin derivatives on curli-dependent biofilm formation in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2018, 8, 8452.	1.6	48
13	Biological and Pathological Implications of an Alternative ATP-Powered Proteasomal Assembly With Cdc48 and the 20S Peptidase. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 56.	1.6	8
14	Multitasking of Hsp70 chaperone in the biogenesis of bacterial functional amyloids. <i>Communications Biology</i> , 2018, 1, 52.	2.0	16
15	Two Cdc48 cofactors Ubp3 and Ubx2 regulate mitochondrial morphology and protein turnover. <i>Journal of Biochemistry</i> , 2018, 164, 349-358.	0.9	12
16	The Highly Dynamic Nature of ERdj5 Is Key to Efficient Elimination of Aberrant Protein Oligomers through ER-Associated Degradation. <i>Structure</i> , 2017, 25, 846-857.e4.	1.6	25
17	Deviation of the typical AAA substrate-threading pore prevents fatal protein degradation in yeast Cdc48. <i>Scientific Reports</i> , 2017, 7, 5475.	1.6	22
18	Production of Single-Chain Fv Antibodies Specific for GA-Pyridine, an Advanced Glycation End-Product (AGE), with Reduced Inter-Domain Motion. <i>Molecules</i> , 2017, 22, 1695.	1.7	9

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19	Imaging of bacterial multicellular behaviour in biofilms in liquid by atmospheric scanning electron microscopy. <i>Scientific Reports</i> , 2016, 6, 25889.	1.6	66
20	Thioflavin T as a fluorescence probe for monitoring RNA metabolism at molecular and cellular levels. <i>Nucleic Acids Research</i> , 2015, 43, e92-e92.	6.5	73
21	Characterization of C-terminal adaptors, UFD-2 and UFD-3, of CDC-48 on the polyglutamine aggregation in <i>C.Âelegans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 459, 154-160.	1.0	5
22	Microtubule Severing by Katanin p60 AAA+ ATPase Requires the C-terminal Acidic Tails of Both Î±- and Î²-Tubulins and Basic Amino Acid Residues in the AAA+ Ring Pore. <i>Journal of Biological Chemistry</i> , 2015, 290, 11762-11770.	1.6	37
23	Novel Strategy for Biofilm Inhibition by Using Small Molecules Targeting Molecular Chaperone DnaK. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 633-641.	1.4	72
24	A conserved Î± helix of Bcs1, a mitochondrial AAA chaperone, is required for the Respiratory Complex III maturation. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 997-1002.	1.0	6
25	Serial block-face scanning electron microscopy for three-dimensional analysis of morphological changes in mitochondria regulated by Cdc48p/p97 ATPase. <i>Journal of Structural Biology</i> , 2014, 187, 187-193.	1.3	22
26	Whole-cell imaging of the budding yeast <i>Saccharomyces cerevisiae</i> by high-voltage scanning transmission electron tomography. <i>Ultramicroscopy</i> , 2014, 146, 39-45.	0.8	28
27	High-Speed Atomic Force Microscopic Observation of ATP-Dependent Rotation of the AAA+ Chaperone p97. <i>Structure</i> , 2013, 21, 1992-2002.	1.6	40
28	FtsH Protease. , 2013, , 685-692.		3
29	FtsH Protease-Mediated Regulation of Various Cellular Functions. <i>Sub-Cellular Biochemistry</i> , 2013, 66, 53-69.	1.0	19
30	The C-terminal Î±-helix of SPAS-1, a <i>Caenorhabditis elegans</i> spastin homologue, is crucial for microtubule severing. <i>Journal of Structural Biology</i> , 2012, 179, 138-142.	1.3	1
31	Cdc48p/p97-mediated regulation of mitochondrial morphology is Vms1p-independent. <i>Journal of Structural Biology</i> , 2012, 179, 112-120.	1.3	35
32	fidgetin homolog FIGL-1, a nuclear-localized AAA ATPase, binds to SUMO. <i>Journal of Structural Biology</i> , 2012, 179, 143-151.	1.3	9
33	CDC-48/p97 is required for proper meiotic chromosome segregation via controlling AIR-2/Aurora B kinase localization in <i>Caenorhabditis elegans</i> . <i>Journal of Structural Biology</i> , 2012, 179, 104-111.	1.3	12
34	Editorial. <i>Journal of Structural Biology</i> , 2012, 179, 77.	1.3	1
35	Phosphorylation of Kif26b Promotes Its Polyubiquitination and Subsequent Proteasomal Degradation during Kidney Development. <i>PLoS ONE</i> , 2012, 7, e39714.	1.1	22
36	Recent advances in p97/VCP/Cdc48 cellular functions. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 130-137.	1.9	165

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37	Positive Cooperativity of the p97 AAA ATPase Is Critical for Essential Functions. <i>Journal of Biological Chemistry</i> , 2011, 286, 15815-15820.	1.6	42
38	<i>Caenorhabditis elegans</i> UBX cofactors for CDC-48/p97 control spermatogenesis. <i>Genes To Cells</i> , 2010, 15, 1201-1215.	0.5	22
39	AAA+ Chaperone ClpX Regulates Dynamics of Prokaryotic Cytoskeletal Protein FtsZ. <i>Journal of Biological Chemistry</i> , 2010, 285, 6648-6657.	1.6	44
40	ATP-bound form of the D1 AAA domain inhibits an essential function of Cdc48p/p97 This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 109-117.	0.9	31
41	FtsH cleavage of non-native conformations of proteins. <i>Journal of Structural Biology</i> , 2010, 171, 117-124.	1.3	11
42	High-Speed Atomic Force Microscopy Techniques for Observing Dynamic Biomolecular Processes. <i>Methods in Enzymology</i> , 2010, 475, 541-564.	0.4	66
43	3P-254 Direct observation of structural changes in p97 during the ATPase cycle using High-speed AFM(Bioimaging,The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009, 49, S193.	0.0	0
44	<i>Caenorhabditis elegans</i> p97 controls germline-specific sex determination by controlling the TRA-1 level in a CUL-2-dependent manner. <i>Journal of Cell Science</i> , 2009, 122, 3663-3672.	1.2	21
45	Conserved aromatic and basic amino acid residues in the pore region of <i>Caenorhabditis elegans</i> spastin play critical roles in microtubule severing. <i>Genes To Cells</i> , 2009, 14, 925-940.	0.5	13
46	p97 homologs from <i>Caenorhabditis elegans</i> , CDC-48.1 and CDC-48.2, suppress the aggregate formation of huntingtin exon1 containing expanded polyQ repeat. <i>Genes To Cells</i> , 2008, 13, 827-838.	0.5	33
47	Involvement of HMG-12 and CAR-1 in the cdc-48.1 expression of <i>Caenorhabditis elegans</i> . <i>Developmental Biology</i> , 2008, 318, 348-359.	0.9	5
48	From the common molecular basis of the AAA protein to various energy-dependent and -independent activities of AAA proteins. <i>Biochemical Society Transactions</i> , 2008, 36, 68-71.	1.6	11
49	Differential expression pattern of UBX family genes in <i>Caenorhabditis elegans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 545-552.	1.0	9
50	<i>Caenorhabditis elegans</i> p97/CDC-48 is crucial for progression of meiosis I. <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 920-924.	1.0	27
51	The <i>C. elegans</i> homologue of the spastic paraplegia protein, spastin, disassembles microtubules. <i>Biochemical and Biophysical Research Communications</i> , 2007, 359, 157-162.	1.0	23
52	<i>C. elegans</i> RBX-2-CUL-5- and RBX-1-CUL-2-based complexes are redundant for oogenesis and activation of the MAP kinase MPK-1. <i>FEBS Letters</i> , 2007, 581, 145-150.	1.3	17
53	ER E3 ubiquitin ligase HRD-1 and its specific partner chaperone BiP play important roles in ERAD and developmental growth in <i>Caenorhabditis elegans</i> . <i>Genes To Cells</i> , 2007, 12, 1063-1073.	0.5	52
54	Comparative analysis of expression of two p97 homologues in <i>Caenorhabditis elegans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2006, 345, 746-753.	1.0	19

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55	Flavodoxin, a new fluorescent substrate for monitoring proteolytic activity of FtsH lacking a robust unfolding activity. <i>Journal of Structural Biology</i> , 2006, 156, 115-119.	1.3	5
56	Characterization of mutants of the Escherichia coli AAA protease, FtsH, carrying a mutation in the central pore region. <i>Journal of Structural Biology</i> , 2006, 156, 109-114.	1.3	21
57	Mutational analysis of the functional motifs in the ATPase domain of Caenorhabditis elegans fidgetin homologue FIGL-1: Firm evidence for an intersubunit catalysis mechanism of ATP hydrolysis by AAA ATPases. <i>Journal of Structural Biology</i> , 2006, 156, 93-100.	1.3	16
58	An AAA protease FtsH can initiate proteolysis from internal sites of a model substrate, apo-flavodoxin. <i>Genes To Cells</i> , 2006, 11, 261-268.	0.5	25
59	Allelic characterization of the leaf-variegated mutation var2 identifies the conserved amino acid residues of FtsH that are important for ATP hydrolysis and proteolysis. <i>Plant Molecular Biology</i> , 2004, 56, 705-716.	2.0	34
60	Identification of a cysteine residue important for the ATPase activity of C. elegans fidgetin homologue. <i>FEBS Letters</i> , 2004, 578, 191-197.	1.3	14
61	Spectrometric analysis of degradation of a physiological substrate β -galactosidase by Escherichia coli AAA protease FtsH. <i>Journal of Structural Biology</i> , 2004, 146, 148-154.	1.3	19
62	Analysis of the two p97/VCP/Cdc48p proteins of Caenorhabditis elegans and their suppression of polyglutamine-induced protein aggregation. <i>Journal of Structural Biology</i> , 2004, 146, 242-250.	1.3	62
63	Conserved arginine residues implicated in ATP hydrolysis, nucleotide-sensing, and inter-subunit interactions in AAA and AAA+ ATPases. <i>Journal of Structural Biology</i> , 2004, 146, 106-112.	1.3	233
64	FtsH protease. , 2004, , 794-798.		3
65	Dissecting Various ATP-Dependent Steps Involved in Proteasomal Degradation. <i>Molecular Cell</i> , 2003, 11, 3-5.	4.5	29
66	Conserved Pore Residues in the AAA Protease FtsH Are Important for Proteolysis and Its Coupling to ATP Hydrolysis. <i>Journal of Biological Chemistry</i> , 2003, 278, 50182-50187.	1.6	120
67	The AAA ATPase: Structure and Mechanisms of Remodeling of Protein Substrates. <i>Seibutsu Butsuri</i> , 2003, 43, 244-247.	0.0	0
68	The Crystal Structure of the AAA Domain of the ATP-Dependent Protease FtsH of Escherichia coli at 1.5 Å... Resolution. <i>Structure</i> , 2002, 10, 1073-1083.	1.6	127
69	Mutational analysis of the functional motifs of RuvB, an AAA+ class helicase and motor protein for Holliday junction branch migration. <i>Molecular Microbiology</i> , 2002, 36, 528-538.	1.2	43
70	Crystallization of the AAA domain of the ATP-dependent protease FtsH of Escherichia coli. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1066-1067.	2.5	7
71	AAA+superfamily ATPases: common structure-diverse function. <i>Genes To Cells</i> , 2001, 6, 575-597.	0.5	864
72	Probing the mechanism of ATP hydrolysis and substrate translocation in the AAA protease FtsH by modelling and mutagenesis. <i>Molecular Microbiology</i> , 2001, 39, 890-903.	1.2	53

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73	The C Terminus of σ_{32} Is Not Essential for Degradation by FtsH. <i>Journal of Bacteriology</i> , 2001, 183, 5911-5917.	1.0	34
74	A colicin-tolerant <i>Escherichia coli</i> mutant that confers Hfl phenotype carries two mutations in the region coding for the C-terminal domain of FtsH (HflB). <i>FEMS Microbiology Letters</i> , 2000, 183, 115-117.	0.7	6
75	Structural and functional studies on an FtsH inhibitor from <i>Bacillus subtilis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2000, 1475, 353-359.	1.1	33
76	Evidence for an active role of the DnaK chaperone system in the degradation of σ_{32} . <i>FEBS Letters</i> , 2000, 478, 271-275.	1.3	33
77	Dissecting the Role of a Conserved Motif (the Second Region of Homology) in the AAA Family of ATPases. <i>Journal of Biological Chemistry</i> , 1999, 274, 26225-26232.	1.6	179
78	Balanced biosynthesis of major membrane components through regulated degradation of the committed enzyme of lipid A biosynthesis by the AAA protease FtsH (HflB) in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1999, 31, 833-844.	1.2	234
79	Second transmembrane segment of FtsH plays a role in its proteolytic activity and homo-oligomerization. <i>FEBS Letters</i> , 1999, 460, 554-558.	1.3	16
80	Regulation of the Heat Shock Response by the DnaK Chaperone System and the FtsH Protease in <i>E. coli</i> . <i>Seibutsu Butsuri</i> , 1999, 39, 295-300.	0.0	0
81	Autoregulation of the partition genes of the mini-F plasmid and the intracellular localization of their products in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1998, 257, 392-403.	2.4	69
82	Levels of DnaK and DnaJ provide tight control of heat shock gene expression and protein repair in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1998, 30, 567-581.	1.2	185
83	Heat shock regulation in the <i>ftsH</i> null mutant of <i>Escherichia coli</i> : dissection of stability and activity control mechanisms of σ_{32} in vivo. <i>Molecular Microbiology</i> , 1998, 30, 583-593.	1.2	118
84	Roles of the Periplasmic Domain of <i>Escherichia coli</i> FtsH (HflB) in Protein Interactions and Activity Modulation. <i>Journal of Biological Chemistry</i> , 1998, 273, 22326-22333.	1.6	44
85	Characterization of the <i>ftsH</i> gene of <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 971-978.	0.7	46
86	RNase E polypeptides lacking a carboxyl-terminal half suppress a <i>mukB</i> mutation in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1996, 178, 3917-3925.	1.0	140
87	Carboxyl terminal region of the MukB protein in <i>Escherichia coli</i> is essential for DNA binding activity. <i>FEMS Microbiology Letters</i> , 1996, 143, 211-216.	0.7	17
88	Identification of the <i>cpdA</i> Gene Encoding Cyclic 3',5'-Adenosine Monophosphate Phosphodiesterase in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 25423-25429.	1.6	96
89	Carboxyl terminal region of the MukB protein in <i>Escherichia coli</i> is essential for DNA binding activity. <i>FEMS Microbiology Letters</i> , 1996, 143, 211-216.	0.7	1
90	Characterization of the <i>smtA</i> gene encoding an S-adenosylmethionine-dependent methyltransferase of <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 1995, 133, 59-63.	0.7	16

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91	New killing system controlled by two genes located immediately upstream of the mukB gene in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1994, 243, 136-147.	2.4	18
92	Multicopy suppressors, mssA and mssB, of an smbA mutation of <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1994, 243, 9-16.	2.4	36
93	Characterization of translucent segments observed in an smbA mutant of <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 1994, 116, 61-66.	0.7	0
94	Two mutant alleles of mukB, a gene essential for chromosome partition in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 1994, 123, 27-31.	0.7	21
95	Cloning, sequencing, and characterization of multicopy suppressors of a mukB mutation in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1994, 13, 301-312.	1.2	105
96	A defective non-LTR retrotransposon is dispersed throughout the genome of the silkworm, <i>Bombyx mori</i> . <i>Chromosoma</i> , 1994, 103, 311-323.	1.0	27
97	The <i>Escherichia coli</i> FtsH protein is a prokaryotic member of a protein family of putative ATPases involved in membrane functions, cell cycle control, and gene expression. <i>Journal of Bacteriology</i> , 1993, 175, 1344-1351.	1.0	241
98	Topology and subcellular localization of FtsH protein in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1993, 175, 1352-1357.	1.0	173
99	<i>Escherichia coli</i> mutant Y16 is a double mutant carrying thermosensitive ftsH and ftsI mutations. <i>Journal of Bacteriology</i> , 1992, 174, 2416-2417.	1.0	61
100	Characterization of high molecular weights of complexes and polymers of cytoplasmic proteins in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 1992, 143, 743-753.	1.0	12
101	Identification and characterization of the smbA gene, a suppressor of the mukB null mutant of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1992, 174, 7517-7526.	1.0	62
102	Mutants defective in chromosome partitioning in <i>E. coli</i> . <i>Research in Microbiology</i> , 1991, 142, 189-194.	1.0	44
103	Structure and function of the ftsH gene in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 1991, 142, 279-282.	1.0	100
104	Partitioning of a mini-F plasmid into anucleate cells of the mukB null mutant. <i>Journal of Bacteriology</i> , 1991, 173, 6643-6646.	1.0	31
105	Linear multimer formation of plasmid DNA in <i>Escherichia coli</i> hopE (recD) mutants. <i>Molecular Genetics and Genomics</i> , 1990, 224, 1-9.	2.4	36
106	Maintenance of plasmids in HU and IHF mutants of <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1990, 220, 197-203.	2.4	41
107	Possible involvement of the ugpA gene product in the stable maintenance of mini-F plasmid in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 1990, 223, 361-368.	2.4	8
108	Identification and characterization of gyrB mutants of <i>Escherichia coli</i> that are defective in partitioning of mini-F plasmids. <i>Journal of Bacteriology</i> , 1990, 172, 1562-1568.	1.0	29

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109	Positioning of replicated chromosomes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1990, 172, 31-39.	1.0	68
110	Nucleotide sequence of the <i>tolC</i> gene of <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 1990, 18, 5547-5547.	6.5	30
111	Penicillin-binding protein 2 is essential in wild-type <i>Escherichia coli</i> but not in <i>lov</i> or <i>cya</i> mutants. <i>Journal of Bacteriology</i> , 1989, 171, 3025-3030.	1.0	76
112	Molecular Cloning of a Human Apolipoprotein E Variant: E5 (Glu3 \rightarrow Lys)1. <i>Journal of Biochemistry</i> , 1989, 105, 491-493.	0.9	15
113	Identification of Human Apolipoprotein E Variant Gene: Apolipoprotein E7 (Glu244,245 \rightarrow Lys244,245)1. <i>Journal of Biochemistry</i> , 1989, 105, 51-54.	0.9	24
114	The complete cDNA sequence for the premature form of growth hormone of the flounder <i>Paralichthys olivaceus</i> . <i>Nucleic Acids Research</i> , 1989, 17, 3977-3977.	6.5	1
115	Involvement of DnaK protein in mini-F plasmid replication: Temperature-sensitive <i>seg</i> mutations are located in the <i>dnaK</i> gene. <i>Molecular Genetics and Genomics</i> , 1989, 218, 183-189.	2.4	47
116	Chromosome partitioning in <i>Escherichia coli</i> : novel mutants producing anucleate cells. <i>Journal of Bacteriology</i> , 1989, 171, 1496-1505.	1.0	373
117	Nucleolus organizers in the wild silkworm <i>Bombyx mandarina</i> and the domesticated silkworm <i>B. mori</i> . <i>Chromosoma</i> , 1988, 96, 263-269.	1.0	25
118	Structures and expression of mRNAs coding for major plasma proteins of <i>Bombyx mori</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1988, 949, 224-232.	2.4	73
119	Chromosomal genes essential for stable maintenance of the mini-F plasmid in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1988, 170, 5272-5278.	1.0	33
120	Structure and function of the F plasmid genes essential for partitioning. <i>Journal of Molecular Biology</i> , 1986, 192, 1-15.	2.0	177
121	The high molecular weight DNA prepared from the posterior silk gland of <i>Bombyx mori</i> by use of "Freezer-Mill". <i>Japanese Journal of Applied Entomology and Zoology</i> , 1985, 29, 83-85.	0.5	1
122	Mechanisms Essential for Stable Inheritance of Mini-F Plasmid. , 1985, 30, 469-487.		14
123	Introns and their flanking sequences of <i>Bombyx mori</i> rDNA. <i>Nucleic Acids Research</i> , 1984, 12, 6861-6869.	6.5	53
124	Prophage λ induction caused by mini-F plasmid genes. <i>Molecular Genetics and Genomics</i> , 1984, 196, 185-193.	2.4	24
125	Partition mechanism of F plasmid: Two plasmid gene-encoded products and a cis-acting region are involved in partition. <i>Cell</i> , 1983, 32, 351-360.	13.5	335