

Tetsuo Kobayashi

List of Publications by Year in descending order

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107
papers

5,448
citations

126708

33
h-index

82410

72
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109
all docs

109
docs citations

109
times ranked

4469
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of mitochondrial reactive oxygen species through a histidine kinase, HysA in <i>Aspergillus nidulans</i> . Journal of General and Applied Microbiology, 2022, .	0.4	0
2	Artificial AmyR::XlnR transcription factor induces α -amylase production in response to non-edible xylan-containing hemicellulosic biomass. Enzyme and Microbial Technology, 2021, 145, 109762.	1.6	5
3	Impact of nitrogen metabolism-associated culture pH changes on regulation of Fusarium trichothecene biosynthesis: revision of roles of polyamine agmatine and transcription factor AreA. Current Genetics, 2020, 66, 1179-1190.	0.8	4
4	Substrate specificities of Fusarium biosynthetic enzymes explain the genetic basis of a mixed chemotype producing both deoxynivalenol and nivalenol-type trichothecenes. International Journal of Food Microbiology, 2020, 320, 108532.	2.1	6
5	Synthetic liquid media for the study of trichothecene biosynthesis regulation in <i>Fusarium graminearum</i> . Mycotoxins, 2020, 70, 57-59.	0.2	0
6	CreA-independent carbon catabolite repression of cellulase genes by trimeric G-protein and protein kinase A in <i>Aspergillus nidulans</i> . Current Genetics, 2019, 65, 941-952.	0.8	23
7	Inhibition of Fusarium trichothecene biosynthesis by yeast extract components extractable with ethyl acetate. International Journal of Food Microbiology, 2019, 289, 24-29.	2.1	7
8	Comprehensive investigation of the gene expression system regulated by an <i>Aspergillus oryzae</i> transcription factor XlnR using integrated mining of gSELEX-Seq and microarray data. BMC Genomics, 2019, 20, 16.	1.2	11
9	Identification of amino acids negatively affecting Fusarium trichothecene biosynthesis. Antonie Van Leeuwenhoek, 2019, 112, 471-478.	0.7	10
10	Comparison of the paralogous transcription factors AraR and XlnR in <i>Aspergillus oryzae</i> . Current Genetics, 2018, 64, 1245-1260.	0.8	19
11	Identification and Characterization of Small Molecule Compounds That Modulate Trichothecene Production by <i>Fusarium graminearum</i> . ACS Chemical Biology, 2018, 13, 1260-1269.	1.6	5
12	Conservation and diversity of the regulators of cellulolytic enzyme genes in Ascomycete fungi. Current Genetics, 2017, 63, 951-958.	0.8	41
13	l-Threonine and its analogue added to autoclaved solid medium suppress trichothecene production by <i>Fusarium graminearum</i> . Archives of Microbiology, 2017, 199, 945-952.	1.0	12
14	Identification of a trichothecene production inhibitor by chemical array and library screening using trichodiene synthase as a target protein. Pesticide Biochemistry and Physiology, 2017, 138, 1-7.	1.6	7
15	Biochemical characterization of thermostable β -1,4-mannanase belonging to the glycoside hydrolase family 134 from <i>Aspergillus oryzae</i> . Applied Microbiology and Biotechnology, 2017, 101, 3237-3245.	1.7	40
16	Accumulation of an unusual trichothecene shunt metabolite in liquid culture of <i>Fusarium graminearum</i> with methionine as the sole nitrogen source. Mycotoxins, 2017, 67, 7-9.	0.2	1
17	Characterization of the acivicin effects on trichothecene production by <i>Fusarium graminearum</i> species complex. Journal of General and Applied Microbiology, 2016, 62, 272-276.	0.4	6
18	Spatial Abundance and Distribution of Potential Microbes and Functional Genes Associated with Anaerobic Mineralization of Pentachlorophenol in a Cylindrical Reactor. Scientific Reports, 2016, 6, 19015.	1.6	13

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19	McmA-dependent and -independent regulatory systems governing expression of C ₁ B-regulated cellulase and hemicellulase genes in <i>Aspergillus nidulans</i> . <i>Molecular Microbiology</i> , 2016, 102, 810-826.	1.2	15
20	Genome sequence of <i>Aspergillus luchuensis</i> NBRC 4314. <i>DNA Research</i> , 2016, 23, 507-515.	1.5	48
21	Oligosaccharides containing an α -(1 \rightarrow 2) (glucosyl/xylosyl)-fructosyl linkage as inducer molecules of trichothecene biosynthesis for <i>Fusarium graminearum</i> . <i>International Journal of Food Microbiology</i> , 2016, 238, 215-221.	2.1	11
22	Nuclear localization and relative stability of the zinc finger domain of TRI6 trichothecene regulator. <i>Mycotoxins</i> , 2016, 66, 13-15.	0.2	2
23	Trichothecene production in axenic liquid culture of <i>Fusarium graminearum</i> using xylose as a carbon source. <i>Mycotoxins</i> , 2016, 66, 17-19.	0.2	4
24	Regulation of plant biomass-degrading enzyme genes in filamentous fungi. <i>Mycotoxins</i> , 2016, 66, 85-96.	0.2	1
25	Introduction of a leptomycin-sensitive mutation into <i>Fusarium graminearum</i> . <i>Mycotoxins</i> , 2016, 66, 9-11.	0.2	0
26	Hydroxylations of trichothecene rings in the biosynthesis of <i>Fusarium</i> trichothecenes: evolution of alternative pathways in the nivalenol chemotype. <i>Environmental Microbiology</i> , 2016, 18, 3798-3811.	1.8	20
27	Involvement of an SRF-MADS protein McmA in regulation of extracellular enzyme production and asexual/sexual development in <i>Aspergillus nidulans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 1820-1828.	0.6	10
28	Regulation of genes encoding cellulolytic enzymes by Pal-PacC signaling in <i>Aspergillus nidulans</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3621-3635.	1.7	22
29	Re-examination of genetic and nutritional factors related to trichothecene biosynthesis in <i>Fusarium graminearum</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 414-417.	0.6	4
30	A Robust Analytical Pipeline for Genome-Wide Identification of the Genes Regulated by a Transcription Factor: Combinatorial Analysis Performed Using gSELEX-Seq and RNA-Seq. <i>PLoS ONE</i> , 2016, 11, e0159011.	1.1	11
31	Production of reactive oxygen species in <i>Aspergillus nidulans</i> through the function of His-Asp phosphorelay signal transduction system. <i>Mycotoxins</i> , 2015, 65, 49-56.	0.2	1
32	Effect of disrupting the trichothecene efflux pump encoded by <i>FgTri12</i> in the nivalenol chemotype of <i>Fusarium graminearum</i> . <i>Journal of General and Applied Microbiology</i> , 2015, 61, 93-96.	0.4	11
33	Deciphering the Combinatorial DNA-binding Code of the CCAAT-binding Complex and the Iron-regulatory Basic Region Leucine Zipper (bZIP) Transcription Factor HapX. <i>Journal of Biological Chemistry</i> , 2015, 290, 6058-6070.	1.6	36
34	Novel β -1,4-Mannanase Belonging to a New Glycoside Hydrolase Family in <i>Aspergillus nidulans</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 27914-27927.	1.6	53
35	A set of heterologous promoters useful for investigating gene functions in <i>Fusarium graminearum</i> . <i>Mycotoxins</i> , 2014, 64, 147-152.	0.2	21
36	Control of reactive oxygen species (ROS) production through histidine kinases in <i>Aspergillus nidulans</i> under different growth conditions. <i>FEBS Open Bio</i> , 2014, 4, 90-95.	1.0	13

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37	Complex regulation of hydrolytic enzyme genes for cellulosic biomass degradation in filamentous fungi. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4829-4837.	1.7	112
38	Regulation of cellulolytic genes by McmA, the SRF-MADS box protein in <i>Aspergillus nidulans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 777-782.	1.0	23
39	ManR, a Transcriptional Regulator of the \hat{I}^2 -Mannan Utilization System, Controls the Cellulose Utilization System in <i>Aspergillus oryzae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 426-429.	0.6	55
40	Identification and Characterization of an Inhibitor of Trichothecene 3-O-Acetyltransferase, TRI101, by the Chemical Array Approach. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 1958-1960.	0.6	11
41	ASYMMETRIC-LEAVES2 and an ortholog of eukaryotic NudC domain proteins repress expression of <i>AUXIN-RESPONSE-FACTOR</i> and class 1 <i>KNOX</i> homeobox genes for development of flat symmetric leaves in <i>Arabidopsis</i> . <i>Biology Open</i> , 2012, 1, 197-207.	0.6	28
42	Comprehensive Analysis of the DNA-Binding Specificity of an <i>Aspergillus nidulans</i> Transcription Factor, AmyR, Using a Bead Display System. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1128-1134.	0.6	11
43	Comparison and characterization of \hat{I}^{\pm} -amylase inducers in <i>Aspergillus nidulans</i> based on nuclear localization of AmyR. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1629-1635.	1.7	30
44	ManR, a novel Zn(II)2Cys6 transcriptional activator, controls the \hat{I}^2 -mannan utilization system in <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 987-995.	0.9	79
45	Xylose Triggers Reversible Phosphorylation of XlnR, the Fungal Transcriptional Activator of Xylanolytic and Cellulolytic Genes in <i>Aspergillus oryzae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 953-959.	0.6	45
46	Post-genomic approaches to understanding interactions between fungi and their environment. <i>IMA Fungus</i> , 2011, 2, 81-86.	1.7	11
47	High-throughput screening of DNA binding sites for transcription factor AmyR from <i>Aspergillus nidulans</i> using DNA beads display system. <i>Journal of Bioscience and Bioengineering</i> , 2010, 109, 519-525.	1.1	10
48	Enzymatic saccharification of Eucalyptus bark using hydrothermal pre-treatment with carbon dioxide. <i>Bioresource Technology</i> , 2010, 101, 4936-4939.	4.8	39
49	Inducer-Dependent Nuclear Localization of a Zn(II) ₂ Cys ₆ Transcriptional Activator, AmyR, in <i>Aspergillus nidulans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 391-399.	0.6	35
50	Genes regulated by AoXlnR, the xylanolytic and cellulolytic transcriptional regulator, in <i>Aspergillus oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 141-154.	1.7	104
51	Identification of specific binding sites for XYR1, a transcriptional activator of cellulolytic and xylanolytic genes in <i>Trichoderma reesei</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, 564-574.	0.9	117
52	æ€€fãã,%æf³ãfã¼CEãã-ã¼å%µéã. <i>Kagaku To Seibutsu</i> , 2009, 47, 665-665.	0.0	0
53	Title is missing!. <i>Kagaku To Seibutsu</i> , 2009, 47, 718-724.	0.0	0
54	Functional analysis of the egl3 upstream region in filamentous fungus <i>Trichoderma reesei</i> . <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 515-524.	1.7	20

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55	Identification of the cis-acting elements involved in regulation of xylanase III gene expression in <i>Trichoderma reesei</i> PC-3-7. <i>Fungal Genetics and Biology</i> , 2008, 45, 1094-1102.	0.9	27
56	Novel Promoter Sequence Required for Inductive Expression of the <i>Aspergillus nidulans</i> Endoglucanase Gene <i>eglA</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 312-320.	0.6	23
57	GFP-Tagged Expression Analysis Revealed That Some Histidine Kinases of <i>Aspergillus nidulans</i> Show Temporally and Spatially Different Expression during the Life Cycle. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 428-434.	0.6	16
58	Genomics of <i>Aspergillus oryzae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 646-670.	0.6	163
59	Analysis of Expressed Sequence Tags from the Fungus <i>Aspergillus oryzae</i> Cultured Under Different Conditions. <i>DNA Research</i> , 2007, 14, 47-57.	1.5	73
60	In Vitro Analysis of His-Asp Phosphorelays in <i>Aspergillus nidulans</i> : The First Direct Biochemical Evidence for the Existence of His-Asp Phosphotransfer Systems in Filamentous Fungi. <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 2493-2502.	0.6	25
61	The SskA and SrrA Response Regulators Are Implicated in Oxidative Stress Responses of Hyphae and Asexual Spores in the Phosphorelay Signaling Network of <i>Aspergillus nidulans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 1003-1014.	0.6	75
62	Characterization of the NikA Histidine Kinase Implicated in the Phosphorelay Signal Transduction of <i>Aspergillus nidulans</i> , with Special Reference to Fungicide Responses. <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 844-847.	0.6	73
63	Novel Reporter Gene Expression Systems for Monitoring Activation of the <i>Aspergillus nidulans</i> HOG Pathway. <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 1724-1730.	0.6	23
64	Expression Profile of Amylolytic Genes in <i>Aspergillus nidulans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2006, 70, 2363-2370.	0.6	43
65	The Region in a Subunit of the <i>Aspergillus</i> CCAAT-Binding Protein Similar to the HAP4p-Recruiting Domain of <i>Saccharomyces cerevisiae</i> Hap5p Is Not Essential for Transcriptional Enhancement. <i>Bioscience, Biotechnology and Biochemistry</i> , 2006, 70, 782-787.	0.6	4
66	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , 2005, 438, 1157-1161.	13.7	1,128
67	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
68	Nuclear translocation of the heterotrimeric CCAAT binding factor of <i>Aspergillus oryzae</i> is dependent on two redundant localising signals in a single subunit. <i>Archives of Microbiology</i> , 2005, 184, 93-100.	1.0	25
69	Construction of a Bacterial Artificial Chromosome Library for a Myxobacterium of the Genus <i>Cystobacter</i> and Characterization of an Antibiotic Biosynthetic Gene Cluster. <i>Bioscience, Biotechnology and Biochemistry</i> , 2005, 69, 1372-1380.	0.6	29
70	Mode of AmyR Binding to the CCGN8AGG Sequence in the <i>Aspergillus oryzae</i> <i>g2</i> Promoter. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004, 68, 1906-1911.	0.6	29
71	A Single Subunit of a Heterotrimeric CCAAT-binding Complex Carries a Nuclear Localization Signal: Piggy Back Transport of the Pre-assembled Complex to the Nucleus. <i>Journal of Molecular Biology</i> , 2004, 342, 515-524.	2.0	70
72	Upregulation of promoter activity of the <i>Aspergillus oryzae</i> xylanase gene by site-directed mutagenesis. <i>Biotechnology Letters</i> , 2003, 25, 371-374.	1.1	4

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73	Novel Î±-Glucosidase from <i>Aspergillus nidulans</i> with Strong Transglycosylation Activity. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1250-1256.	1.4	120
74	A Transcriptional Activator, AoXlnR, Controls the Expression of Genes Encoding Xylanolytic Enzymes in <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2002, 35, 157-169.	0.9	90
75	Transcriptional activator, AoXlnR, mediates cellulose-inductive expression of the xylanolytic and cellulolytic genes in <i>Aspergillus oryzae</i> . <i>FEBS Letters</i> , 2002, 528, 279-282.	1.3	65
76	Structural features of the glycogen branching enzyme encoding genes from aspergilli. <i>Microbiological Research</i> , 2002, 157, 337-344.	2.5	4
77	Isolation of genes encoding novel transcription factors which interact with the Hap complex from <i>Aspergillus</i> species. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1576, 176-182.	2.4	33
78	Upward shift of the pH optimum of <i>Acremonium</i> ascorbate oxidase. <i>BBA - Proteins and Proteomics</i> , 2002, 1596, 36-46.	2.1	9
79	Isomaltose formed by Î±-glucosidases triggers amylase induction in <i>Aspergillus nidulans</i> . <i>Current Genetics</i> , 2002, 42, 43-50.	0.8	35
80	Title is missing!. <i>Biotechnology Letters</i> , 2002, 24, 1089-1096.	1.1	10
81	In Vivo and in Vitro Analyses of the AmyR Binding Site of the <i>Aspergillus nidulans</i> agdA Promoter; Requirement of the CCG Direct Repeat for Induction and High Affinity Binding of AmyR. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 1568-1574.	0.6	34
82	Regulation of the amylolytic and (hemi-)cellulolytic genes in aspergilli. <i>Journal of General and Applied Microbiology</i> , 2001, 47, 1-19.	0.4	61
83	Characterization of the amyR gene encoding a transcriptional activator for the amylase genes in <i>Aspergillus nidulans</i> . <i>Current Genetics</i> , 2001, 39, 10-15.	0.8	81
84	AoHapB, AoHapC and AoHapE, subunits of the <i>Aspergillus oryzae</i> CCAAT-binding complex, are functionally interchangeable with the corresponding subunits in <i>Aspergillus nidulans</i> . <i>Current Genetics</i> , 2001, 39, 175-182.	0.8	17
85	No Factors Except for the Hap Complex increase the Taka-amylase A Gene Expression by Binding to the CCAAT Sequence in the Promoter Region. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 2340-2342.	0.6	9
86	An <i>Aspergillus oryzae</i> CCAAT-binding protein, AoCP, is involved in the high-level expression of the Taka-amylase A gene. <i>Current Genetics</i> , 2000, 37, 380-387.	0.8	25
87	A novel nuclear factor, SREB, binds to a cis-acting element, SRE, required for inducible expression of the <i>Aspergillus oryzae</i> Taka-amylase A gene in <i>A. nidulans</i> . <i>Molecular Genetics and Genomics</i> , 2000, 263, 232-238.	2.4	22
88	A Simple and Rapid Method for the Preparation of a Cell-free Extract with CCAAT-Binding Activity from Filamentous Fungi. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 455-457.	0.6	8
89	Structure and expression properties of the endo-1,4-glucanase A gene from the filamentous fungus <i>Aspergillus nidulans</i> . <i>FEMS Microbiology Letters</i> , 1999, 175, 239-245.	0.7	36
90	Molecular cloning, nucleotide sequence and expression in <i>Escherichia coli</i> of hyperthermophilic glutamate dehydrogenase gene from <i>Thermococcus profundus</i> . <i>Journal of Bioscience and Bioengineering</i> , 1997, 83, 405-411.	0.9	11

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91	Sequence analysis of the gene for and characterization of d-acetoin forming meso-2,3-butanediol dehydrogenase of <i>Klebsiella pneumoniae</i> expressed in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 1997, 83, 32-37.	0.9	36
92	Preparation of a chiral acetoinic compound using transgenic <i>Escherichia coli</i> expressing the 2,3-butanediol dehydrogenase gene. <i>Journal of Bioscience and Bioengineering</i> , 1996, 81, 386-389.	0.9	14
93	Cloning, nucleotide sequence, and hyperexpression of α -amylase gene from an archaeon, <i>Thermococcus profundus</i> . <i>Journal of Bioscience and Bioengineering</i> , 1996, 82, 432-438.	0.9	36
94	Molecular Cloning and Nucleotide Sequence of the groEL Gene from the Alkaliphilic <i>Bacillus</i> sp. Strain C-125 and Reactivation of Thermally Inactivated α -Glucosidase by Recombinant GroEL. <i>Bioscience, Biotechnology and Biochemistry</i> , 1996, 60, 1633-1636.	0.6	5
95	Properties of Glutamate Dehydrogenase and Its Involvement in Alanine Production in a Hyperthermophilic Archaeon, <i>Thermococcus profundus</i> . <i>Journal of Biochemistry</i> , 1995, 118, 587-592.	0.9	58
96	Metabolic Properties of Marine Hyperthermophiles, The Most Primitive Organisms on Earth.. <i>Kagaku To Seibutsu</i> , 1995, 33, 796-802.	0.0	0
97	A Hyperthermophilic Sulfur-reducing Archaeobacterium, <i>Thermococcus</i> sp. DT1331, Isolated from a Deep-sea Hydrothermal Vent. <i>Bioscience, Biotechnology and Biochemistry</i> , 1995, 59, 1666-1669.	0.6	9
98	<i>Thermococcus profundus</i> sp. nov., A New Hyperthermophilic Archaeon Isolated from a Deep-sea Hydrothermal Vent. <i>Systematic and Applied Microbiology</i> , 1994, 17, 232-236.	1.2	96
99	Location of F1ATPase-like Genes on the Physical Map of the <i>Bacillus subtilis</i> 168 Chromosome. <i>Bioscience, Biotechnology and Biochemistry</i> , 1993, 57, 1202-1203.	0.6	1
100	Molecular Cloning, Nucleotide Sequence, and Expression of the Structural Gene for Alkaline Serine Protease from Alkaliphilic <i>Bacillus</i> sp. 221. <i>Bioscience, Biotechnology and Biochemistry</i> , 1992, 56, 1455-1460.	0.6	17
101	Molecular cloning, nucleotide sequence and expression of the structural gene for a thermostable alkaline protease from <i>Bacillus</i> sp. no. AH-101. <i>Applied Microbiology and Biotechnology</i> , 1992, 38, 101-8.	1.7	22
102	A hypothetical protein (P20), homologous to Tn3 repressor is encoded downstream from the bla regulatory region in <i>Bacillus licheniformis</i> 749. <i>Nucleic Acids Research</i> , 1988, 16, 5691-5691.	6.5	2
103	Purification and biochemical characterization of streptothricin acetyltransferase coded by the cloned streptothricin-resistance gene of <i>Streptomyces lavendulae</i> .. <i>Journal of Antibiotics</i> , 1987, 40, 1016-1022.	1.0	14
104	Construction of an excretion vector and extracellular production of human growth hormone from <i>Escherichia coli</i> . <i>Gene</i> , 1987, 54, 197-202.	1.0	74
105	Cloning and characterization of the streptothricin-resistance gene which encodes streptothricin acetyltransferase from <i>Streptomyces lavendulae</i> .. <i>Journal of Antibiotics</i> , 1986, 39, 688-693.	1.0	17
106	Construction of an excretion vector: Extracellular production of <i>Aeromonas</i> xylanase and <i>Bacillus</i> cellulases by <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 1986, 36, 31-34.	0.7	30
107	Isolation and characterization of a pock-forming plasmid pTA4001 from <i>Streptomyces lavendulae</i> .. <i>Journal of Antibiotics</i> , 1984, 37, 368-375.	1.0	17