Katsuya Gomi

List of Publications by Year
in descending order

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127 papers	8,667 citations	41323 49 h-index	45285 90 g-index
132 all docs	132 docs citations	132 times ranked	5724 citing authors

#	Article	IF	Citations
1	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	13.7	1,272
2	Genome sequencing and analysis of Aspergillus oryzae. Nature, 2005, 438, 1157-1161.	13.7	1,128
3	Genomics of Aspergillus oryzae: Learning from the History of Koji Mold and Exploration of Its Future. DNA Research, 2008, 15, 173-183.	1.5	328
4	Integrative transformation of Aspergillus oryzae with a plasmid containing the Aspergillus nidulans argB gene.. Agricultural and Biological Chemistry, 1987, 51, 2549-2555.	0.3	239
5	Thiamine-regulated gene expression of Aspergillus oryzae thiA requires splicing of the intron containing a riboswitch-like domain in the 5â€²-UTR. FEBS Letters, 2003, 555, 516-520.	1.3	195
6	Purification and characterization of a biodegradable plastic-degrading enzyme from Aspergillus oryzae. Applied Microbiology and Biotechnology, 2005, 67, 778-788.	1.7	195
7	Reconstitution of Biosynthetic Machinery for Indole-Diterpene Paxilline in Aspergillus oryzae. Journal of the American Chemical Society, 2013, 135, 1260-1263.	6.6	170
8	ASPERGILLUS LUCHUENSIS, AN INDUSTRIALLY IMPORTANT BLACK ASPERGILLUS IN EAST ASIA. PLoS ONE, 2013, 8, e63769.	1.1	167
9	Genomics ofAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2007, 71, 646-670.	0.6	163
10	Identification of Ophiobolin F Synthase by a Genome Mining Approach: A Sesterterpene Synthase from Aspergillus clavatus. Organic Letters, 2013, 15, 594-597.	2.4	160
11	Genome Mining for Sesterterpenes Using Bifunctional Terpene Synthases Reveals a Unified Intermediate of Di/Sesterterpenes. Journal of the American Chemical Society, 2015, 137, 11846-11853.	6.6	141
12	A defect of LigD (human Lig4 homolog) for nonhomologous end joining significantly improves efficiency of gene-targeting in Aspergillus oryzae. Fungal Genetics and Biology, 2008, 45, 878-889.	0.9	132
13	Transformation System forAspergillus oryzaewith Double Auxotrophic Mutations,niaDandsC. Bioscience, Biotechnology and Biochemistry, 1997, 61, 1367-1369.	0.6	130
14	Integrative Transformation ofAspergillus oryzaewith a Plasmid Containing theAspergillus nidulans argBGene. Agricultural and Biological Chemistry, 1987, 51, 2549-2555.	0.3	118
15	Molecular Cloning and Characterization of a Transcriptional Activator Gene,amyR, Involved in the Amylolytic Gene Expression inAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2000, 64, 816-827.	0.6	114
16	A Novel Zn2-Cys6 Transcription Factor AtrR Plays a Key Role in an Azole Resistance Mechanism of Aspergillus fumigatus by Co-regulating cyp51A and cdr1B Expressions. PLoS Pathogens, 2017, 13, e1006096.	2.1	104
17	Reconstitution of Biosynthetic Machinery for the Synthesis of the Highly Elaborated Indole Diterpene Penitrem. Angewandte Chemie - International Edition, 2015, 54, 5748-5752.	7.2	101
18	High Level Secretion of Calf Chymosin Using a Glucoamylase-prochymosin Fusion Gene inAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1994, 58, 895-899.	0.6	99

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19	Cloning and Nucleotide Sequence of the Ribonuclease T₁Gene (rntA) fromAspergillus oryzaeand Its Expression inSaccharomyces cerevisiaeandAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1995, 59, 1869-1874.	0.6	92
20	Construction of a fusion gene comprising the Taka-amylase A promoter and the Escherichia coli Î²-glucuronidase gene and analysis of its expression in Aspergillus oryzae. Molecular Genetics and Genomics, 1991, 229, 301-306.	2.4	89
21	Deletion analysis of promoter elements of the Aspergillus oryzae agdA gene encoding Î± -glucosidase. Current Genetics, 1996, 30, 432-438.	0.8	87
22	Transcriptional analysis of genes for energy catabolism and hydrolytic enzymes in the filamentous fungus Aspergillus oryzae using cDNA microarrays and expressed sequence tags. Applied Microbiology and Biotechnology, 2004, 65, 74-83.	1.7	84
23	Novel Hydrophobic Surface Binding Protein, HsbA, Produced by Aspergillus oryzae. Applied and Environmental Microbiology, 2006, 72, 2407-2413.	1.4	82
24	Functional elements of the promoter region of the Aspergillus oryzae glaA gene encoding glucoamylase. Current Genetics, 1992, 22, 85-91.	0.8	81
25	Characterization of the amyR gene encoding a transcriptional activator for the amylase genes in Aspergillus nidulans. Current Genetics, 2001, 39, 10-15.	0.8	81
26	Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae.. Agricultural and Biological Chemistry, 1989, 53, 593-599.	0.3	81
27	Total Biosynthesis of Diterpene Aphidicolin, a Specific Inhibitor of DNA Polymerase Î±: Heterologous Expression of Four Biosynthetic Genes inAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2011, 75, 1813-1817.	0.6	79
28	Rapid Reconstitution of Biosynthetic Machinery for Fungal Metabolites in Aspergillus oryzae: Total Biosynthesis of Aflatrem. ChemBioChem, 2014, 15, 2076-2080.	1.3	76
29	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Postâ€translationally Modified Peptide Ustiloxin B in Filamentous Fungi. Angewandte Chemie - International Edition, 2016, 55, 8072-8075.	7.2	76
30	Use of a biosynthetic intermediate to explore the chemical diversity of pseudo-natural fungal polyketides. Nature Chemistry, 2015, 7, 737-743.	6.6	74
31	High level expression of the synthetic human lysozyme gene in Aspergillus oryzae. Applied Microbiology and Biotechnology, 1992, 38, 109-14.	1.7	73
32	Analysis of Expressed Sequence Tags from the Fungus Aspergillus oryzae Cultured Under Different Conditions. DNA Research, 2007, 14, 47-57.	1.5	73
33	The fungal hydrophobin RolA recruits polyesterase and laterally moves on hydrophobic surfaces. Molecular Microbiology, 2005, 57, 1780-1796.	1.2	71
34	Heterologous expression of highly reducing polyketide synthase involved in betaenone biosynthesis. Chemical Communications, 2015, 51, 1878-1881.	2.2	67
35	Molecular Cloning and Heterologous Expression of the Gene Encoding Dihydrogeodin Oxidase, a Multicopper Blue Enzyme from Aspergillus terreus. Journal of Biological Chemistry, 1995, 270, 21495-21502.	1.6	66
36	Modified Cre-loxPRecombination in Aspergillus oryzae by Direct Introduction of Cre Recombinase for Marker Gene Rescue. Applied and Environmental Microbiology, 2012, 78, 4126-4133.	1.4	66

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37	Aspergillus oryzae atfA controls conidial germination and stress tolerance. Fungal Genetics and Biology, 2009, 46, 887-897.	0.9	65
38	Signaling pathways for stress responses and adaptation in Aspergillus species: stress biology in the post-genomic era. Bioscience, Biotechnology and Biochemistry, 2016, 80, 1667-1680.	0.6	65
39	Transformation of Aspergillus oryzae through plasmid-mediated complementation of the methionine-auxotrophic mutation.. Agricultural and Biological Chemistry, 1987, 51, 323-328.	0.3	63
40	Aspergillus oryzae atfB encodes a transcription factor required for stress tolerance in conidia. Fungal Genetics and Biology, 2008, 45, 922-932.	0.9	62
41	Codon Optimization Increases Steady-State mRNA Levels in Aspergillus oryzae Heterologous Gene Expression. Applied and Environmental Microbiology, 2008, 74, 6538-6546.	1.4	61
42	Cloning and Nucleotide Sequence of the Acid Protease-encoding Gene (pepA) fromAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1993, 57, 1095-1100.	0.6	60
43	Cloning and functional analysis of the Aspergillus oryzae conidiation regulator gene brlA by its disruption and misscheduled expression. Journal of Bioscience and Bioengineering, 1999, 87, 424-429.	1.1	60
44	AtrR Is an Essential Determinant of Azole Resistance in Aspergillus fumigatus. MBio, 2019, 10, .	1.8	59
45	Subtractive cloning of cDNA from Aspergillus oryzae differentially regulated between solid-state culture and liquid (submerged) culture. Current Genetics, 2002, 41, 275-281.	0.8	58
46	Deletion Analysis of the Taka-amylase A Gene Promoter Using a Homologous Transformation System inAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1992, 56, 1849-1853.	0.6	57
47	Structurally Diverse Chaetophenol Productions Induced by Chemically Mediated Epigenetic Manipulation of Fungal Gene Expression. Organic Letters, 2013, 15, 3346-3349.	2.4	55
48	Improved Î±-amylase production by Aspergillus oryzae after a double deletion of genes involved in carbon catabolite repression. Applied Microbiology and Biotechnology, 2014, 98, 335-343.	1.7	55
49	chsZ , a gene for a novel class of chitin synthase from Aspergillus oryzae. Current Genetics, 2002, 41, 261-267.	0.8	54
50	Nucleotide Sequence and Expression ofÎ±-Glucosidase-encoding Gene (agdA) fromAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1995, 59, 1516-1521.	0.6	53
51	Self-excising Cre/mutant lox marker recycling system for multiple gene integrations and consecutive gene deletions in Aspergillus oryzae. Journal of Bioscience and Bioengineering, 2017, 123, 403-411.	1.1	49
52	Genome sequence ofAspergillus luchuensisNBRC 4314. DNA Research, 2016, 23, 507-515.	1.5	48
53	Secretion of calf chymosin from the filamentous fungus Aspergillus oryzae. Applied Microbiology and Biotechnology, 1993, 40, 327-32.	1.7	45
54	Regulatory mechanisms for amylolytic gene expression in the koji moldAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2019, 83, 1385-1401.	0.6	43

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55	Increased enzyme production under liquid culture conditions in the industrial fungus Aspergillus oryzae by disruption of the genes encoding cell wall Î±-1,3-glucan synthase. Bioscience, Biotechnology and Biochemistry, 2016, 80, 1853-1863.	0.6	42
56	Characterization and expression analysis of a maltose-utilizing (MAL) cluster in Aspergillus oryzae. Fungal Genetics and Biology, 2010, 47, 1-9.	0.9	40
57	Biosynthesis of Shearinine: Diversification of a Tandem Prenyl Moiety of Fungal Indole Diterpenes. Organic Letters, 2016, 18, 5026-5029.	2.4	39
58	Distinct mechanism of activation of two transcription factors, AmyR and MalR, involved in amylolytic enzyme production in Aspergillus oryzae. Applied Microbiology and Biotechnology, 2015, 99, 1805-1815.	1.7	38
59	Molecular and enzymic properties of recombinant 1,2-Î±-mannosidase from Aspergillus saitoi overexpressed in Aspergillus oryzae cells. Biochemical Journal, 1999, 339, 589-597.	1.7	37
60	Multiple Oxidative Modifications in the Ophiobolin Biosynthesis: P450 Oxidations Found in Genome Mining. Organic Letters, 2016, 18, 1980-1983.	2.4	36
61	Biosynthetic Machinery of Diterpene Pleuromutilin Isolated from Basidiomycete Fungi. ChemBioChem, 2017, 18, 2317-2322.	1.3	35
62	Biosynthetic Study on Antihypercholesterolemic Agent Phomoidride: General Biogenesis of Fungal Dimeric Anhydrides. Organic Letters, 2015, 17, 5658-5661.	2.4	34
63	Transformation of the industrial strain of Aspergillus oryzae with the homologous amdS gene as a dominant selectable marker. Journal of Bioscience and Bioengineering, 1992, 74, 389-391.	0.9	33
64	Deletion analysis of the enolase gene (enoA) promoter from the filamentous fungus Aspergillus oryzae. Current Genetics, 2001, 40, 260-267.	0.8	33
65	Crawler, a novel Tc1/mariner-type transposable element in Aspergillus oryzae transposes under stress conditions. Fungal Genetics and Biology, 2009, 46, 441-449.	0.9	31
66	Cell wall Î±-1,3-glucan prevents Î±-amylase adsorption onto fungal cell in submerged culture of Aspergillus oryzae. Journal of Bioscience and Bioengineering, 2017, 124, 47-53.	1.1	30
67	Insertion Analysis of Putative Functional Elements in the Promoter Region of theAspergillus oryzaeTaka-amylase A Gene (amyB) Using a HeterologousAspergillus nidulans amdS-lacZFusion Gene System. Bioscience, Biotechnology and Biochemistry, 1999, 63, 180-183.	0.6	28
68	Purification and enzymatic characterization of a novel Î²-1,6-glucosidase from Aspergillus oryzae. Journal of Bioscience and Bioengineering, 2016, 121, 259-264.	1.1	28
69	Molecular and enzymic properties of recombinant 1,2-Î±-mannosidase from Aspergillus saitoi overexpressed in Aspergillus oryzae cells. Biochemical Journal, 1999, 339, 589.	1.7	27
70	Identification of potential cell wall component that allows Taka-amylase A adsorption in submerged cultures of Aspergillus oryzae. Applied Microbiology and Biotechnology, 2011, 92, 961-969.	1.7	27
71	Effects of codon optimization on the mRNA levels of heterologous genes in filamentous fungi. Applied Microbiology and Biotechnology, 2014, 98, 3859-3867.	1.7	26
72	Purification and enzymatic characterization of secretory glycoside hydrolase family 3 (GH3) aryl Î²-glucosidases screened from Aspergillus oryzae genome. Journal of Bioscience and Bioengineering, 2015, 120, 614-623.	1.1	25

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73	Increased production of biomass-degrading enzymes by double deletion of creA and creB genes involved in carbon catabolite repression in Aspergillus oryzae. Journal of Bioscience and Bioengineering, 2018, 125, 141-147.	1.1	25
74	The Glucoamylase cDNA fromAspergillus oryzae: Its Cloning, Nucleotide Sequence, and Expression inSaccharomyces cerevisiae. Agricultural and Biological Chemistry, 1991, 55, 941-949.	0.3	24
75	Electrophoretic Karyotype and Gene Assignment to Chromosomes ofAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 1994, 58, 1467-1470.	0.6	24
76	Transcripts of a heterologous gene encoding mite allergen Der f 7 are stabilized by codon optimization in Aspergillus oryzae. Applied Microbiology and Biotechnology, 2012, 96, 1275-1282.	1.7	24
77	The C-terminal region of the yeast monocarboxylate transporter Jen1 acts as a glucose signalâ€“responding degron recognized by the Î±-arrestin Rod1. Journal of Biological Chemistry, 2018, 293, 10926-10936.	1.6	24
78	Functional analysis of FarA transcription factor in the regulation of the genes encoding lipolytic enzymes and hydrophobic surface binding protein for the degradation of biodegradable plastics in Aspergillus oryzae. Journal of Bioscience and Bioengineering, 2012, 113, 549-555.	1.1	23
79	Reconstitution of biosynthetic machinery of fungal polyketides: unexpected oxidations of biosynthetic intermediates by expression host. Bioscience, Biotechnology and Biochemistry, 2016, 80, 426-431.	0.6	23
80	The C2H2-type transcription factor, FlbC, is involved in the transcriptional regulation of Aspergillus oryzae glucoamylase and protease genes specifically expressed in solid-state culture. Applied Microbiology and Biotechnology, 2016, 100, 5859-5868.	1.7	23
81	Uniform culture in solid-state fermentation with fungi and its efficient enzyme production. Journal of Bioscience and Bioengineering, 2011, 111, 300-305.	1.1	21
82	Unfolded protein response is required for Aspergillus oryzae growth under conditions inducing secretory hydrolytic enzyme production. Fungal Genetics and Biology, 2015, 85, 1-6.	0.9	21
83	Endocytosis of a maltose permease is induced when amylolytic enzyme production is repressed in Aspergillus oryzae. Fungal Genetics and Biology, 2015, 82, 136-144.	0.9	21
84	Total Biosynthesis of Brassicicenes: Identification of a Key Enzyme for Skeletal Diversification. Organic Letters, 2018, 20, 6178-6182.	2.4	21
85	Induction and Repression of Hydrolase Genes in Aspergillus oryzae. Frontiers in Microbiology, 2021, 12, 677603.	1.5	21
86	Genomics of Economically Significant Aspergillus and Fusarium Species. Applied Mycology and Biotechnology, 2004, 4, 249-283.	0.3	19
87	Identification of the Promoter Region of the Taka-amylase A Gene Required for Starch Induction.. Agricultural and Biological Chemistry, 1991, 55, 1939-1941.	0.3	19
88	Cloning, nucleotide sequencing, and expression of the .BETA.-galactosidase-encoding gene (lacA) from Aspergillus oryzae.. Journal of General and Applied Microbiology, 2002, 48, 135-142.	0.4	18
89	Genome mining approach for harnessing the cryptic gene cluster in Alternaria solani: production of PKSâ€“NRPS hybrid metabolite, didymellamide B. Tetrahedron Letters, 2016, 57, 2793-2796.	0.7	18
90	Heterologous Biosynthesis of Fungal Indole Sesquiterpene Sespendole. ChemBioChem, 2018, 19, 1492-1497.	1.3	18

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91	Nuclear exportâ€dependent degradation of the carbon catabolite repressor CreA is regulated by a region located near the Câ€terminus in Aspergillus oryzae. Molecular Microbiology, 2018, 110, 176-190.	1.2	18
92	Studies on application of fungal cell wall lytic enzyme produced by Oerskovia sp. CK. (Part II) Estimation of mycelial weight in rice-koji with use of fungal cell wall lytic enzyme.. Journal of the Society of Brewing Japan, 1987, 82, 130-133.	0.0	17
93	Heterologous Production of a Novel Cyclic Peptide Compound, KK-1, in Aspergillus oryzae. Frontiers in Microbiology, 2018, 9, 690.	1.5	16
94	Regulation of gliotoxin biosynthesis and protection in Aspergillus species. PLoS Genetics, 2022, 18, e1009965.	1.5	16
95	Identification of the Promoter Region of the Taka-amylase A Gene Required for Starch Induction. Agricultural and Biological Chemistry, 1991, 55, 1939-1941.	0.3	15
96	Improved Î±-Amylase Production by Dephosphorylation Mutation of CreD, an Arrestin-Like Protein Required for Glucose-Induced Endocytosis of Maltose Permease and Carbon Catabolite Derepression in Aspergillusoryzae. Applied and Environmental Microbiology, 2017, 83, .	1.4	14
97	In silico Analysis of 3'-End-Processing Signals in Aspergillus oryzae Using Expressed Sequence Tags and Genomic Sequencing Data. DNA Research, 2011, 18, 189-200.	1.5	13
98	Cellular responses to the expression of unstable secretory proteins in the filamentous fungus Aspergillus oryzae. Applied Microbiology and Biotechnology, 2017, 101, 2437-2446.	1.7	13
99	Mapping haze-komi on rice koji grains using Î²-glucuronidase expressing Aspergillus oryzae and mass spectrometry imaging. Journal of Bioscience and Bioengineering, 2020, 129, 296-301.	1.1	13
100	Rapid enzyme production and mycelial growth in solid-state fermentation using the non-airflow box. Journal of Bioscience and Bioengineering, 2013, 116, 585-590.	1.1	12
101	Metaproteomics reveals protein composition of multiple saccharifying enzymes in nongxiangxing daqu and jiangxiangxing daqu under different thermophilic temperatures. International Journal of Food Science and Technology, 2022, 57, 5102-5113.	1.3	12
102	Analysis of fermentation control factors on volatile compounds of primary microorganisms in Jiangâ€flavor Daqu. Journal of Food Biochemistry, 2022, 46, .	1.2	12
103	Construction of a thiamine pyrophosphate high-producing strain of Aspergillus oryzae by overexpression of three genes involved in thiamine biosynthesis. Journal of Bioscience and Bioengineering, 2011, 111, 388-390.	1.1	11
104	Substantial decrease in cell wall Î±-1,3-glucan caused by disruption of the kexB gene encoding a subtilisin-like processing protease in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2016, 80, 1781-1791.	0.6	10
105	The PDR-type ABC transporters AtrA and AtrG are involved in azole drug resistance in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1840-1848.	0.6	10
106	Quantitative evaluation of haze formation of koji and progression of internal haze by drying of koji during koji making. Journal of Bioscience and Bioengineering, 2017, 124, 62-70.	1.1	9
107	Efficient production of recombinant tannase in Aspergillus oryzae using an improved glucoamylase gene promoter. Journal of Bioscience and Bioengineering, 2020, 129, 150-154.	1.1	9
108	A Novel Culture Method for High Level Production of Heterologous Protein inSaccharomyces cerevisiae. Bioscience, Biotechnology and Biochemistry, 1994, 58, 1292-1296.	0.6	8

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109	Identification and distinct regulation of three di/tripeptide transporters in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2021, 85, 452-463.	0.6	8
110	Alternative Processing of Proproteins in AspergillikexBGene Disruptants under Hyperosmotic Conditions. Bioscience, Biotechnology and Biochemistry, 2009, 73, 40-46.	0.6	7
111	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Postâ€translationally Modified Peptide Ustiloxin B in Filamentous Fungi. Angewandte Chemie, 2016, 128, 8204-8207.	1.6	7
112	Alternative transcription start sites of the enolase-encoding gene enoA are stringently used in glycolytic/gluconeogenic conditions in Aspergillus oryzae. Current Genetics, 2020, 66, 729-747.	0.8	7
113	Crucial role of the intracellular Î±-glucosidase MalT in the activation of the transcription factor AmyR essential for amylolytic gene expression in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2021, 85, 2076-2083.	0.6	6
114	Subcellular localization of aphidicolin biosynthetic enzymes heterologously expressed in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2018, 82, 139-147.	0.6	5
115	Enzymatic degradation of xyloglucans by Aspergillus species: a comparative view of this genus. Applied Microbiology and Biotechnology, 2021, 105, 2701-2711.	1.7	5
116	Change in enzyme production by gradually drying culture substrate during solid-state fermentation. Journal of Bioscience and Bioengineering, 2015, 119, 674-677.	1.1	4
117	Strategies for Increasing the Production Level of Heterologous Proteins in Aspergillus oryzae. , 2014, , 149-164.		4
118	Rapid detection of homologously integrated DNA fragments and accurate quantitation of their copy number in transgenic Aspergillus oryzae by PCR. Journal of Bioscience and Bioengineering, 2000, 90, 577-579.	1.1	3
119	Characterization of Cell Wall Î±-1,3-Glucanâ€“Deficient Mutants in Aspergillus oryzae Isolated by a Screening Method Based on Their Sensitivities to Congo Red or Lysing Enzymes. Journal of Applied Glycoscience (1999), 2017, 64, 65-73.	0.3	3
120	Chaperone complex formation of the transcription factor MalR involved in maltose utilization and amylolytic enzyme production in Aspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2018, 82, 827-835.	0.6	3
121	Visualization of dipeptidyl peptidase B enzymatic reaction in rice koji using mass spectrometry imaging. Journal of Bioscience and Bioengineering, 2022, 134, 133-137.	1.1	3
122	Transformation ofAspergillus oryzaethrough Plasmid-mediated Complementation of the Methionine-auxotrophic Mutation. Agricultural and Biological Chemistry, 1987, 51, 323-328.	0.3	2
123	3 Genetic Transfer Applied to Traditional Sake Brewing. Biotechnology and Genetic Engineering Reviews, 1991, 9, 89-125.	2.4	2
124	Expression profiles of amylolytic genes in AmyR and CreA transcription factor deletion mutants of the black koji mold Aspergillus luchuensis. Journal of Bioscience and Bioengineering, 2021, 132, 321-326.	1.1	2
125	Response and Adaptation to Cell Wall Stress and Osmotic Stress in Aspergillus Species. , 2015, , 199-218.		2
126	Visualization of polypeptides including fragmented Î±-amylase in rice koji grains using mass spectrometry imaging. Journal of Bioscience and Bioengineering, 2022, 134, 34-40.	1.1	1

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127	ç¨®ã„ã„ã•ã‹ã‰åºƒãŒã‚ç³¸çŠ¶èŒåˆ†ç”Ÿåœ°ã‚¤ãƒˆã‚¬¹è€æ€§æ©Ÿæ§‹. Kagaku To Seibutsu, 2009, 47, 684-689.	0.0	0