List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Administration of Aspergillus oryzae suppresses DSS-induced colitis. Food Chemistry Molecular Sciences, 2022, 4, 100063.	0.9	2
2	Enhanced Bioremediation of 4-Chlorophenol by Electrically Neutral Reactive Species Generated from Nonthermal Atmospheric-Pressure Plasma. ACS Omega, 2022, 7, 16197-16203.	1.6	1
3	Characterization of two 1,2,4-trihydroxybenzene 1,2-dioxygenases from Phanerochaete chrysosporium. Applied Microbiology and Biotechnology, 2022, 106, 4499-4509.	1.7	5
4	Biochemical Characterization of a Pectate Lyase AnPL9 from Aspergillus nidulans. Applied Biochemistry and Biotechnology, 2022, 194, 5627-5643.	1.4	6
5	The appeal of fermented foods in Aichi prefecture. Journal for the Integrated Study of Dietary Habits, 2021, 31, 195-199.	0.0	0
6	Artificial AmyR::XlnR transcription factor induces $\hat{l}\pm$ -amylase production in response to non-edible xylan-containing hemicellulosic biomass. Enzyme and Microbial Technology, 2021, 145, 109762.	1.6	5
7	Atomic oxygen radicalâ€induced intracellular oxidization of mould spore cells. Plasma Processes and Polymers, 2020, 17, 2000001.	1.6	4
8	Oxygen radical based on non-thermal atmospheric pressure plasma alleviates lignin-derived phenolic toxicity in yeast. Biotechnology for Biofuels, 2020, 13, 18.	6.2	11
9	Characterization of FsXEG12A from the cellulose-degrading ectosymbiotic fungus Fusarium spp. strain El cultured by the ambrosia beetle. AMB Express, 2020, 10, 96.	1.4	2
10	[Review] Isolation and Characterization of GH134 Family β-Mannanases. Bulletin of Applied Glycoscience, 2020, 10, 83-88.	0.0	0
11	Study on biomass degradation by filamentous fungi and its contribution to Sustainable Developement Goals (SDGs). Mycotoxins, 2020, 70, 83-94.	0.2	Ο
12	Promotion of Amylase Productions from Aspergillus Oryzae Spores Exposed to Oxygen Radicals. , 2020, , .		0
13	Ability of Saccharomyces cerevisiae MC87-46 to assimilate isomaltose and its effects on sake taste. Scientific Reports, 2019, 9, 13908.	1.6	9
14	A Study on Time Efficiency of CSMA/CA in Inter-Vehicle Communication Systems. , 2019, , .		1
15	Identification and characterization of a thermostable pectate lyase from Aspergillus luchuensis var. saitoi. Food Chemistry, 2019, 276, 503-510.	4.2	26
16	Comparison of the paralogous transcription factors AraR and XlnR in Aspergillus oryzae. Current Genetics, 2018, 64, 1245-1260.	0.8	19
17	Characterization of pH-tolerant and thermostable GH 134 β-1,4-mannanase SsGH134 possessing carbohydrate binding module 10 from Streptomyces sp. NRRL B-24484. Journal of Bioscience and Bioengineering, 2018, 125, 287-294.	1.1	10
18	Biochemical Characterization of CYP505D6, a Self-Sufficient Cytochrome P450 from the White-Rot Fungus Phanerochaete chrysosporium. Applied and Environmental Microbiology, 2018, 84, .	1.4	32

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19	Biochemical characterization of thermostable β-1,4-mannanase belonging to the glycoside hydrolase family 134 from Aspergillus oryzae. Applied Microbiology and Biotechnology, 2017, 101, 3237-3245.	1.7	40
20	Oxygen-radical pretreatment promotes cellulose degradation by cellulolytic enzymes. Biotechnology for Biofuels, 2017, 10, 290.	6.2	15
21	Novel 4-methyl-2-oxopentanoate reductase involved in synthesis of the Japanese sake flavor, ethyl leucate. Applied Microbiology and Biotechnology, 2016, 100, 3137-3145.	1.7	5
22	Thiamine synthesis regulates the fermentation mechanisms in the fungus <i>Aspergillus nidulans</i> . Bioscience, Biotechnology and Biochemistry, 2016, 80, 1768-1775.	0.6	15
23	Involvement of an SRF-MADS protein McmA in regulation of extracellular enzyme production and asexual/sexual development in <i>Aspergillus nidulans</i> . Bioscience, Biotechnology and Biochemistry, 2016, 80, 1820-1828.	0.6	10
24	Deciphering the Combinatorial DNA-binding Code of the CCAAT-binding Complex and the Iron-regulatory Basic Region Leucine Zipper (bZIP) Transcription Factor HapX. Journal of Biological Chemistry, 2015, 290, 6058-6070.	1.6	36
25	Novel β-1,4-Mannanase Belonging to a New Glycoside Hydrolase Family in Aspergillus nidulans. Journal of Biological Chemistry, 2015, 290, 27914-27927.	1.6	53
26	The <scp>J</scp> anus transcription factor <scp>H</scp> ap <scp>X</scp> controls fungal adaptation to both iron starvation and iron excess. EMBO Journal, 2014, 33, 2261-2276.	3.5	121
27	Control of reactive oxygen species (ROS) production through histidine kinases in <i>Aspergillus nidulans</i> under different growth conditions. FEBS Open Bio, 2014, 4, 90-95.	1.0	13
28	Characterization of Acid Phosphatase (AphC) from the Miso Koji Mold, Aspergillus oryzae KBN630: AphC is Mainly Responsible for Both Acid Phosphatase Activity and 5â€2-IMP Dephosphorylation Activity in Soybean-Koji Culture. Food Science and Technology Research, 2014, 20, 367-374.	0.3	3
29	Regulation of cellulolytic genes by McmA, the SRF-MADS box protein in Aspergillus nidulans. Biochemical and Biophysical Research Communications, 2013, 431, 777-782.	1.0	23
30	<scp>ProA</scp> , a transcriptional regulator of fungal fruiting body development, regulates leaf hyphal network development in the <i><scp>E</scp>pichloë festucae</i> – <i><scp>L</scp>olium perenne</i> symbiosis. Molecular Microbiology, 2013, 90, 551-568.	1.2	49
31	Molecular Analysis of AsamyR Gene Encoding Transcriptional Factor for Amylolytic Gene from Shoyu Koji Mold, Aspergillus sojae KBN1340. Food Science and Technology Research, 2013, 19, 505-511.	0.3	1
32	Molecular Analysis of the α-Amylase Gene, AstaaG1, from Shoyu Koji Mold, Aspergillus sojae KBN1340. Food Science and Technology Research, 2013, 19, 255-261.	0.3	6
33	Sequence Analysis and Heterologous Expression of Rhamnogalacturonan Lyase A Gene (AsrglA) from Shoyu Koji Mold, Aspergillus sojae KBN1340. Food Science and Technology Research, 2012, 18, 901-909.	0.3	12
34	Disruption and Overexpression of Acid Phosphatase Gene (aphA) from a Miso Koji Mold, Aspergillus oryzae KBN630, and Characterization of the Gene Product. Food Science and Technology Research, 2012, 18, 59-65.	0.3	7
35	Comparison and characterization of α-amylase inducers in Aspergillus nidulans based on nuclear localization of AmyR. Applied Microbiology and Biotechnology, 2012, 94, 1629-1635.	1.7	30
36	Development of a Highly Efficient Gene Replacement System for an Industrial Strain of Aspergillus oryzae Used in the Production of Miso, a Japanese Fermented Soybean Paste. Food Science and Technology Research, 2011, 17, 161-166.	0.3	12

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37	Sequence Analysis and Heterologous Expression of Polygalacturonase Gene (AspecA) from a Shoyu Koji Mold, Aspergillus sojae KBN1340. Food Science and Technology Research, 2011, 17, 579-584.	0.3	7
38	Xylose Triggers Reversible Phosphorylation of XlnR, the Fungal Transcriptional Activator of Xylanolytic and Cellulolytic Genes in <i>Aspergillus oryzae</i> . Bioscience, Biotechnology and Biochemistry, 2011, 75, 953-959.	0.6	45
39	High-throughput screening of DNA binding sites for transcription factor AmyR from Aspergillus nidulans using DNA beads display system. Journal of Bioscience and Bioengineering, 2010, 109, 519-525.	1.1	10
40	Enzymatic saccharification of Eucalyptus bark using hydrothermal pre-treatment with carbon dioxide. Bioresource Technology, 2010, 101, 4936-4939.	4.8	39
41	Regulation of the Violacein Biosynthetic Gene Cluster by Acylhomoserine Lactone-Mediated Quorum Sensing in <i>Chromobacterium violaceum</i> ATCC 12472. Bioscience, Biotechnology and Biochemistry, 2010, 74, 2116-2119.	0.6	37
42	Inducer-Dependent Nuclear Localization of a Zn(II) ₂ Cys ₆ Transcriptional Activator, AmyR, in <i>Aspergillus nidulans</i> . Bioscience, Biotechnology and Biochemistry, 2009, 73, 391-399.	0.6	35
43	Genes regulated by AoXInR, the xylanolytic and cellulolytic transcriptional regulator, in Aspergillus oryzae. Applied Microbiology and Biotechnology, 2009, 85, 141-154.	1.7	104
44	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99
45	Identification of specific binding sites for XYR1, a transcriptional activator of cellulolytic and xylanolytic genes in Trichoderma reesei. Fungal Genetics and Biology, 2009, 46, 564-574.	0.9	117
46	Title is missing!. Kagaku To Seibutsu, 2009, 47, 718-724.	0.0	0
47	Functional analysis of the egl3 upstream region in filamentous fungus Trichoderma reesei. Applied Microbiology and Biotechnology, 2008, 78, 515-524.	1.7	20
48	<i>N</i> -Acylhomoserine lactone regulates violacein production in <i>Chromobacterium violaceum</i> type strain ATCC 12472. FEMS Microbiology Letters, 2008, 279, 124-130.	0.7	203
49	Identification of the cis-acting elements involved in regulation of xylanase III gene expression in Trichoderma reesei PC-3-7. Fungal Genetics and Biology, 2008, 45, 1094-1102.	0.9	27
50	Novel Promoter Sequence Required for Inductive Expression of the <i>Aspergillus nidulans</i> Endoglucanase Gene <i>eglA</i> . Bioscience, Biotechnology and Biochemistry, 2008, 72, 312-320.	0.6	23
51	GFP-Tagged Expression Analysis Revealed That Some Histidine Kinases of <i>Aspergillus nidulans</i> Show Temporally and Spatially Different Expression during the Life Cycle. Bioscience, Biotechnology and Biochemistry, 2008, 72, 428-434.	0.6	16
52	Genomics ofAspergillus oryzae. Bioscience, Biotechnology and Biochemistry, 2007, 71, 646-670.	0.6	163
53	In VitroAnalysis of His-Asp Phosphorelays inAspergillus nidulans: The First Direct Biochemical Evidence for the Existence of His-Asp Phosphotransfer Systems in Filamentous Fungi. Bioscience, Biotechnology and Biochemistry, 2007, 71, 2493-2502.	0.6	25
54	The SskA and SrrA Response Regulators Are Implicated in Oxidative Stress Responses of Hyphae and Asexual Spores in the Phosphorelay Signaling Network ofAspergillus nidulans. Bioscience, Biotechnology and Biochemistry, 2007, 71, 1003-1014.	0.6	75

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55	Characterization of the NikA Histidine Kinase Implicated in the Phosphorelay Signal Transduction ofAspergillus nidulans, with Special Reference to Fungicide Responses. Bioscience, Biotechnology and Biochemistry, 2007, 71, 844-847.	0.6	73
56	Interaction of HapX with the CCAAT-binding complex—a novel mechanism of gene regulation by iron. EMBO Journal, 2007, 26, 3157-3168.	3.5	209
57	Expression Profile of Amylolytic Genes inAspergillus nidulans. Bioscience, Biotechnology and Biochemistry, 2006, 70, 2363-2370.	0.6	43
58	The Region in a Subunit of theAspergillusCCAAT-Binding Protein Similar to the HAP4p-Recruiting Domain ofSaccharomyces cerevisiaeHap5p Is Not Essential for Transcriptional Enhancement. Bioscience, Biotechnology and Biochemistry, 2006, 70, 782-787.	0.6	4
59	Genome sequencing and analysis of Aspergillus oryzae. Nature, 2005, 438, 1157-1161.	13.7	1,128
60	Nuclear translocation of the heterotrimeric CCAAT binding factor of Aspergillus oryzae is dependent on two redundant localising signals in a single subunit. Archives of Microbiology, 2005, 184, 93-100.	1.0	25
61	An Overview of the CCAAT-Box Binding Factor in Filamentous Fungi: Assembly, Nuclear Translocation, and Transcriptional Enhancement. Bioscience, Biotechnology and Biochemistry, 2005, 69, 663-672.	0.6	54
62	Mode of AmyR Binding to the CGGN8AGG Sequence in theAspergillus oryzaetaaG2Promoter. Bioscience, Biotechnology and Biochemistry, 2004, 68, 1906-1911.	0.6	29
63	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. Journal of Molecular Biology, 2004, 342, 515-524.	2.0	70
64	Upregulation of promoter activity of the Aspergillus oryzae xylanase gene by site-directed mutagenesis. Biotechnology Letters, 2003, 25, 371-374.	1.1	4
65	Characterization of AnRP-mediated negative regulation of the xylanase gene, cgxA, from Chaetomium gracile in Aspergillus nidulans. Letters in Applied Microbiology, 2003, 36, 59-63.	1.0	6
66	éº1èŒCCAAT-boxçµå•è¤å•ä¼2"ã®ã,¢ã,»ãf³ãƒ−ãfªã•転写äįƒé€2能ã«é−¢ã™ã,‹ç"ç©¶. Nippon Nogeikagakı	ı Kacischi, 20)0 3, 77, 960-
67	Novel α-Glucosidase from Aspergillus nidulans with Strong Transglycosylation Activity. Applied and Environmental Microbiology, 2002, 68, 1250-1256.	1.4	120
68	A Transcriptional Activator, AoXInR, Controls the Expression of Genes Encoding Xylanolytic Enzymes in Aspergillus oryzae. Fungal Genetics and Biology, 2002, 35, 157-169.	0.9	90
69	A quantity control mechanism regulating levels of the HapE subunit of the Hap complex inAspergillus nidulans: no accumulation of HapE inhapCdeletion mutants. FEBS Letters, 2002, 512, 227-229.	1.3	5
70	Transcriptional activator, AoXInR, mediates cellulose-inductive expression of the xylanolytic and cellulolytic genes inAspergillus oryzae. FEBS Letters, 2002, 528, 279-282.	1.3	65
71	Structural features of the glycogen branching enzyme encoding genes from aspergilli. Microbiological Research, 2002, 157, 337-344.	2.5	4
72	Isolation of genes encoding novel transcription factors which interact with the Hap complex from Aspergillus species. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1576, 176-182.	2.4	33

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73	Upward shift of the pH optimum of Acremonium ascorbate oxidase. BBA - Proteins and Proteomics, 2002, 1596, 36-46.	2.1	9
74	Isomaltose formed by α-glucosidases triggers amylase induction in Aspergillus nidulans. Current Genetics, 2002, 42, 43-50.	0.8	35
75	Title is missing!. Biotechnology Letters, 2002, 24, 1089-1096.	1.1	10
76	In Vivo and in Vitro Analyses of the AmyR Binding Site of the Aspergillus nidulans agdA Promoter; Requirement of the CGG Direct Repeat for Induction and High Affinity Binding of AmyR. Bioscience, Biotechnology and Biochemistry, 2001, 65, 1568-1574.	0.6	34
77	Regulation of the amylolytic and (hemi-)cellulolytic genes in aspergilli. Journal of General and Applied Microbiology, 2001, 47, 1-19.	0.4	61
78	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
79	AoHapB, AoHapC and AoHapE, subunits of the Aspergillus oryzae CCAAT-binding complex, are functionally interchangeable with the corresponding subunits in Aspergillus nidulans. Current Genetics, 2001, 39, 175-182.	0.8	17
80	No Factors Except for the Hap Complex increase the Taka-amylase A Gene Expression by Binding to the CCAAT Sequence in the Promoter Region. Bioscience, Biotechnology and Biochemistry, 2001, 65, 2340-2342.	0.6	9
81	An Aspergillus oryzae CCAAT-binding protein, AoCP, is involved in the high-level expression of the Taka-amylase A gene. Current Genetics, 2000, 37, 380-387.	0.8	25
82	A novel nuclear factor, SREB, binds to a cis-acting element, SRE, required for inducible expression of the Aspergillus oryzae Taka-amylase A gene in A. nidulans. Molecular Genetics and Genomics, 2000, 263, 232-238.	2.4	22
83	A Simple and Rapid Method for the Preparation of a Cell-free Extract with CCAAT-Binding Activity from Filamentous Fungi. Bioscience, Biotechnology and Biochemistry, 2000, 64, 455-457.	0.6	8
84	Structure and expression properties of the endo-β-1,4-glucanase A gene from the filamentous fungusAspergillus nidulans. FEMS Microbiology Letters, 1999, 175, 239-245.	0.7	36
85	Depression of the xylanase-encoding cgxA gene of Chaetomium gracile in Aspergillus nidulans. Microbiological Research, 1999, 153, 369-376.	2.5	10
86	Structure and expression properties of the endo-β-1,4-glucanase A gene from the filamentous fungus Aspergillus nidulans. FEMS Microbiology Letters, 1999, 175, 239-245.	0.7	26
87	HAP-Like CCAAT-Binding Complexes in Filamentous Fungi: Implications for Biotechnology. Fungal Genetics and Biology, 1999, 27, 243-252.	0.9	110
88	Cloning of a thermostable ascorbate oxidase gene from Acremonium sp. HI-25 and modification of the azide sensitivity of the enzyme by site-directed mutagenesis. BBA - Proteins and Proteomics, 1998, 1388, 444-456.	2.1	13
89	The Aspergillus nidulans CCAAT-binding factor AnCP/AnCF is a heteromeric protein analogous to the HAP complex of Saccharomyces cerevisiae. Molecular Genetics and Genomics, 1998, 257, 404-411.	2.4	39
90	Secretion of Human Interleukin-2 in Biologically Active Form byBacillus brevisDirectly into Cultute Medium. Bioscience, Biotechnology and Biochemistry, 1997, 61, 1858-1861.	0.6	36

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91	An Aspergillus nidulans nuclear protein, AnCP, involved in enhancement of Taka-amylase A gene expression, binds to the CCAAT-containing taaG2, amdS, and gatA promoters. Molecular Genetics and Genomics, 1997, 254, 119-126.	2.4	52
92	Sequence-specific Binding Sites in the Taka-amylase A G2 Promoter for the CreA Repressor Mediating Carbon Catabolite Repression. Bioscience, Biotechnology and Biochemistry, 1996, 60, 1776-1779.	0.6	43
93	Efficient Production of Casoxin D, a Bradykinin Agonist Peptide Derived from Human Casein, by <i>Bacillus brevis</i> . Bioscience, Biotechnology and Biochemistry, 1995, 59, 2056-2059.	0.6	11
94	Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans. Current Genetics, 1995, 29, 73-80.	0.8	24
95	Expression and Secretion of Recombinant Aspartic Proteinases by Bacillus Brevis. Advances in Experimental Medicine and Biology, 1995, 362, 589-596.	0.8	4
96	Chapter 6 Structural characteristics of presecretory proteins: their implication as to translocation competency. New Comprehensive Biochemistry, 1992, 22, 63-74.	0.1	0
97	Molecular Analysis by Deletion and Site-Directed Mutagenesis of the cis-Acting Upstream Sequence Involved in Activation of the ompF Promoter in Escherichia coli1. Journal of Biochemistry, 1989, 105, 341-347.	0.9	14
98	Location of phosphorylation site and DNA-binding site of a positive regulator, OmpR, involved in activation of the osmoregulatory genes ofEscherichia coli. FEBS Letters, 1989, 249, 168-172.	1.3	50
99	Insertion sequence IS5 contains a sharply curved DNA structure at its terminus. Molecular Genetics and Genomics, 1988, 214, 433-438.	2.4	28
100	Location of DNA-binding segment of a positive regulator, OmpR, involved in activation of theompFandompCgenes ofEscherichia coli. FEBS Letters, 1988, 242, 27-30.	1.3	45