Xyr1 (Xylanase Regulator 1) Regulates both the Hydroly Metabolism in Hypocrea jecorina

Eukaryotic Cell 5, 2128-2137

DOI: 10.1128/ec.00211-06

Citation Report

#	Article	IF	CITATIONS
1	Role of the Transcriptional Activator XInR of Fusarium oxysporum in Regulation of Xylanase Genes and Virulence. Molecular Plant-Microbe Interactions, 2007, 20, 977-985.	1.4	73
2	Xyr1 receives the lactose induction signal and regulates lactose metabolism in <i>Hypocrea jecorina</i> . FEBS Letters, 2007, 581, 3915-3920.	1.3	69
3	Lactose metabolism in filamentous fungi: how to deal with an unknown substrate. Fungal Biology Reviews, 2007, 21, 42-48.	1.9	48
4	The <scp>d</scp> â€xylose reductase of <i>Hypocrea jecorina</i> is the major aldose reductase in pentose and <scp>d</scp> â€galactose catabolism and necessary for βâ€galactosidase and cellulase induction by lactose. Molecular Microbiology, 2007, 66, 890-900.	1.2	96
5	Identification in the mould <i>Hypocrea jecorina</i> of a gene encoding an NADP ⁺ : d-xylose dehydrogenase. FEMS Microbiology Letters, 2007, 277, 249-253.	0.7	278
6	Xyr1 regulates xylanase but not cellulase formation in the head blight fungus Fusarium graminearum. Current Genetics, 2007, 52, 213-220.	0.8	47
7	Regulation of transcription of cellulases- and hemicellulases-encoding genes in Aspergillus niger and Hypocrea jecorina (Trichoderma reesei). Applied Microbiology and Biotechnology, 2008, 78, 211-220.	1.7	245
8	Functional analysis of the egl3 upstream region in filamentous fungus Trichoderma reesei. Applied Microbiology and Biotechnology, 2008, 78, 515-524.	1.7	20
9	Sulphur metabolism and cellulase gene expression are connected processes in the filamentous fungus Hypocrea jecorina (anamorph Trichoderma reesei). BMC Microbiology, 2008, 8, 174.	1.3	50
10	Role of Ace2 (Activator of Cellulases 2) within the xyn2 transcriptosome of Hypocrea jecorina. Fungal Genetics and Biology, 2008, 45, 436-445.	0.9	64
11	CreA mediates repression of the regulatory gene xlnR which controls the production of xylanolytic enzymes in Aspergillus nidulans. Fungal Genetics and Biology, 2008, 45, 984-993.	0.9	102
12	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
13	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
14	Transcriptional Regulation of <i>xyr1</i> , Encoding the Main Regulator of the Xylanolytic and Cellulolytic Enzyme System in <i>Hypocrea jecorina</i> . Applied and Environmental Microbiology, 2008, 74, 6554-6562.	1.4	192
15	Genetic Modification of Carbon Catabolite Repression in <i>Trichoderma reesei</i> for Improved Protein Production. Applied and Environmental Microbiology, 2009, 75, 4853-4860.	1.4	173
16	The G-Alpha Protein GNA3 of <i>Hypocrea jecorina</i> (Anamorph <i>Trichoderma reesei</i>) Regulates Cellulase Gene Expression in the Presence of Light. Eukaryotic Cell, 2009, 8, 410-420.	3.4	121
17	Molecular Regulation of Arabinan and <scp>l</scp> -Arabinose Metabolism in <i>Hypocrea jecorina</i> (<i>Trichoderma reesei</i>). Eukaryotic Cell, 2009, 8, 1837-1844.	3.4	69
18	An optimized microplate assay system for quantitative evaluation of plant cell wall–degrading enzyme activity of fungal culture extracts. Biotechnology and Bioengineering, 2009, 102, 1033-1044.	1.7	129

#	Article	IF	CITATIONS
19	Binding of two transcriptional factors, Xyr1 and ACEI, in the promoter region of cellulase cbh1 gene. Biotechnology Letters, 2009, 31, 227-231.	1.1	12
20	Transcriptional profiling of cellulase and expansin-related genes in a hypercellulolytic Trichoderma reesei. Biotechnology Letters, 2009, 31, 1399-1405.	1.1	27
21	Induction of cellulase gene transcription by a novel oligosaccharide: molasses alcohol stillage substance. World Journal of Microbiology and Biotechnology, 2009, 25, 1485-1489.	1.7	6
22	Xylose reductase from the thermophilic fungus Talaromyces emersonii: cloning and heterologous expression of the native gene (Texr) and a double mutant (Texr K271R + N273D) with altered coenzyme specificity. Journal of Biosciences, 2009, 34, 881-890.	0.5	14
23	Evaluation and characterization of Trichoderma reesei cellulase and xylanase promoters. Applied Microbiology and Biotechnology, 2009, 82, 899-908.	1.7	44
24	Genes regulated by AoXInR, the xylanolytic and cellulolytic transcriptional regulator, in Aspergillus oryzae. Applied Microbiology and Biotechnology, 2009, 85, 141-154.	1.7	104
25	Light-dependent roles of the G-protein Î \pm subunit GNA1 of Hypocrea jecorina (anamorph Trichoderma) Tj ETQqO	0 0 rgBT /0 1.7	Dverlock 10 T
26	Metabolic engineering strategies for the improvement of cellulase production by Hypocrea jecorina. Biotechnology for Biofuels, 2009, 2, 19.	6.2	353
27	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
28	Application ofTrichoderma reeseiCellulase and Xylanase Promoters through Homologous Recombination for Enhanced Production of Extracellular β-Glucosidase I. Bioscience, Biotechnology and Biochemistry, 2009, 73, 1083-1089.	0.6	73
29	From an electrophoretic mobility shift assay to isolated transcription factors: a fast genomic-proteomic approach. BMC Genomics, 2010, 11, 644.	1.2	16
30	An accurate normalization strategy for RT-qPCR in Hypocrea jecorina (Trichoderma reesei). Journal of Biotechnology, 2010, 145, 30-37.	1.9	102
31	<scp>d</scp> -Xylose as a Repressor or Inducer of Xylanase Expression in <i>Hypocrea jecorina</i> () Tj ETQq0 C	0 _{1.9} BT /O	verlock 10 Tf 72
32	Bimolecular Fluorescence Complementation. Journal of Visualized Experiments, 2011, , .	0.2	33
33	Antagonistic effect of Trichoderma harzianum VSL291 on phytopathogenic fungi isolated from cocoa (Theobroma cacao L.) fruits. African Journal of Biotechnology, 2011, 10, 10657-10663.	0.3	19
34	Fungal arabinan and l-arabinose metabolism. Applied Microbiology and Biotechnology, 2011, 89, 1665-1673.	1.7	115
35	Disruption of Trichoderma reesei cre2, encoding an ubiquitin C-terminal hydrolase, results in increased cellulase activity. BMC Biotechnology, 2011, 11, 103.	1.7	38

36	The effects of disruption of phosphoglucose isomerase gene on carbon utilisation and cellulase production in Trichoderma reesei Rut-C30. Microbial Cell Factories, 2011, 10, 40.	1	L . 9	14
----	--	---	--------------	----

#	Article	IF	CITATIONS
37	Transcriptome analysis of Aspergillus niger grown on sugarcane bagasse. Biotechnology for Biofuels, 2011, 4, 40.	6.2	122
38	Enhancement of β-xylosidase productivity in cellulase producing fungus Acremonium cellulolyticus. AMB Express, 2011, 1, 15.	1.4	24
39	A modified expression of the major hydrolase activator in Hypocrea jecorina (Trichoderma reesei) changes enzymatic catalysis of biopolymer degradation. Catalysis Today, 2011, 167, 122-128.	2.2	15
40	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
41	Expression of Biomass-Degrading Enzymes Is a Major Event during Conidium Development in Trichoderma reesei. Eukaryotic Cell, 2011, 10, 1527-1535.	3.4	68
42	Differential Regulation of the Cellulase Transcription Factors XYR1, ACE2, and ACE1 in Trichoderma reesei Strains Producing High and Low Levels of Cellulase. Eukaryotic Cell, 2011, 10, 262-271.	3.4	136
43	L -Arabitol Is the Actual Inducer of Xylanase Expression in Hypocrea jecorina (Trichoderma reesei). Applied and Environmental Microbiology, 2011, 77, 5988-5994.	1.4	24
44	Metabolic Engineering of Inducer Formation for Cellulase and Hemicellulase Gene Expression in Trichoderma reesei. Sub-Cellular Biochemistry, 2012, 64, 367-390.	1.0	42
45	<scp>d</scp> -Xylose Concentration-Dependent Hydrolase Expression Profiles and the Function of CreA and XInR in Aspergillus niger. Applied and Environmental Microbiology, 2012, 78, 3145-3155.	1.4	80
46	Functional Analysis of the Degradation of Cellulosic Substrates by a Chaetomium globosum Endophytic Isolate. Applied and Environmental Microbiology, 2012, 78, 3693-3705.	1.4	46
47	Cloning, Purification, and Characterization of a Heat- and Alkaline-Stable Endoglucanase B from Aspergillus niger BCRC31494. Molecules, 2012, 17, 9774-9789.	1.7	27
48	Roles of Protein Kinase A and Adenylate Cyclase in Light-Modulated Cellulase Regulation in Trichoderma reesei. Applied and Environmental Microbiology, 2012, 78, 2168-2178.	1.4	106
50	A new Zn(II)2Cys6-type transcription factor BglR regulates β-glucosidase expression in Trichoderma reesei. Fungal Genetics and Biology, 2012, 49, 388-397.	0.9	134
51	Unravelling the molecular basis for light modulated cellulase gene expression - the role of photoreceptors in Neurospora crassa. BMC Genomics, 2012, 13, 127.	1.2	70
52	Tracking dynamics of plant biomass composting by changes in substrate structure, microbial community, and enzyme activity. Biotechnology for Biofuels, 2012, 5, 20.	6.2	40
53	Heterologous Gene Expression in Filamentous Fungi. Advances in Applied Microbiology, 2012, 81, 1-61.	1.3	69
54	Reprogramming Microbial Metabolic Pathways. Sub-Cellular Biochemistry, 2012, , .	1.0	11
55	Ras GTPases Modulate Morphogenesis, Sporulation and Cellulase Gene Expression in the Cellulolytic Fungus Trichoderma reesei. PLoS ONE, 2012, 7, e48786.	1.1	39

#	Article	IF	Citations
56	Deciphering Transcriptional Regulatory Mechanisms Associated with Hemicellulose Degradation in Neurospora crassa. Eukaryotic Cell, 2012, 11, 482-493.	3.4	191
57	Conserved and essential transcription factors for cellulase gene expression in ascomycete fungi. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7397-7402.	3.3	326
58	XInR-independent signaling pathway regulates both cellulase and xylanase genes in response to cellobiose in Aspergillus aculeatus. Current Genetics, 2012, 58, 93-104.	0.8	31
59	The putative protein methyltransferase LAE1 controls cellulase gene expression in <i>Trichoderma reesei</i> . Molecular Microbiology, 2012, 84, 1150-1164.	1.2	232
60	A homologous production system for Trichoderma reesei secreted proteins in a cellulase-free background. Applied Microbiology and Biotechnology, 2012, 93, 1601-1608.	1.7	63
61	Mutation of the Xylanase regulator 1 causes a glucose blind hydrolase expressing phenotype in industrially used Trichoderma strains. Biotechnology for Biofuels, 2013, 6, 62.	6.2	108
62	Using a model filamentous fungus to unravel mechanisms of lignocellulose deconstruction. Biotechnology for Biofuels, 2013, 6, 6.	6.2	70
63	Enhancing cellulase production in <i>Trichoderma reesei</i> RUT C30 through combined manipulation of activating and repressing genes. Journal of Industrial Microbiology and Biotechnology, 2013, 40, 633-641.	1.4	85
64	<i>Trichoderma</i> Research in the Genome Era. Annual Review of Phytopathology, 2013, 51, 105-129.	3.5	370
65	Comparative transcriptomics reveals different strategies of Trichodermamycoparasitism. BMC Genomics, 2013, 14, 121.	1.2	260
66	Xlr1 is involved in the transcriptional control of the pentose catabolic pathway, but not hemi-cellulolytic enzymes in Magnaporthe oryzae. Fungal Genetics and Biology, 2013, 57, 76-84.	0.9	32
67	Genomics of Soil- and Plant-Associated Fungi. Soil Biology, 2013, , .	0.6	8
68	A novel transcriptional regulator, ClbR, controls the cellobiose- and cellulose-responsive induction of cellulase and xylanase genes regulated by two distinct signaling pathways in Aspergillus aculeatus. Applied Microbiology and Biotechnology, 2013, 97, 2017-2028.	1.7	47
69	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
70	Lignocellulose Conversion. , 2013, , .		17
71	Comparative analysis of the Trichoderma reeseitranscriptome during growth on the cellulase inducing substrates wheat straw and lactose. Biotechnology for Biofuels, 2013, 6, 127.	6.2	100
72	Analysis of a conserved cellulase transcriptional regulator reveals inducerâ€independent production of cellulolytic enzymes in <i>Neurospora crassa</i> . MicrobiologyOpen, 2013, 2, 595-609.	1.2	125
73	The Saccharification Step: Trichoderma Reesei Cellulase Hyper Producer Strains. , 2013, , 65-91.		1

#	Article	IF	Citations
74	Plant Cell Wall Deconstruction by Ascomycete Fungi. Annual Review of Microbiology, 2013, 67, 477-498.	2.9	328
75	RNA interference with carbon catabolite repression in Trichoderma koningii for enhancing cellulase production. Enzyme and Microbial Technology, 2013, 53, 104-109.	1.6	12
77	Two Major Facilitator Superfamily Sugar Transporters from Trichoderma reesei and Their Roles in Induction of Cellulase Biosynthesis. Journal of Biological Chemistry, 2013, 288, 32861-32872.	1.6	153
78	Xylanase Gene Transcription in Trichoderma reesei Is Triggered by Different Inducers Representing Different Hemicellulosic Pentose Polymers. Eukaryotic Cell, 2013, 12, 390-398.	3.4	69
79	Targets of light signalling in Trichoderma reesei. BMC Genomics, 2013, 14, 657.	1.2	81
80	Regulation of Plant Cell Wall Degrading Enzymes Formation in Filamentous Fungi. , 2013, , .		0
81	Enhancing cellulase and hemicellulase production by genetic modification of the carbon catabolite repressor gene, creA, in Acremonium cellulolyticus. AMB Express, 2013, 3, 73.	1.4	48
82	Evidence of a Critical Role for Cellodextrin Transporte 2 (CDT-2) in Both Cellulose and Hemicellulose Degradation and Utilization in Neurospora crassa. PLoS ONE, 2014, 9, e89330.	1.1	33
83	Deciphering the Cis-Regulatory Elements for XYR1 and CRE1 Regulators in Trichoderma reesei. PLoS ONE, 2014, 9, e99366.	1.1	44
84	Kinetic transcriptome analysis reveals an essentially intact induction system in a cellulase hyper-producer Trichoderma reesei strain. Biotechnology for Biofuels, 2014, 7, 173.	6.2	7
85	Insights into high-efficiency lignocellulolytic enzyme production by Penicillium oxalicum GZ-2 induced by a complex substrate. Biotechnology for Biofuels, 2014, 7, 162.	6.2	47
86	A truncated form of the Carbon catabolite repressor 1 increases cellulase production in Trichoderma reesei. Biotechnology for Biofuels, 2014, 7, 129.	6.2	75
87	Regulation of Glycoside Hydrolase Expression in Trichoderma. , 2014, , 291-308.		20
88	VIB1, a Link between Glucose Signaling and Carbon Catabolite Repression, Is Essential for Plant Cell Wall Degradation by Neurospora crassa. PLoS Genetics, 2014, 10, e1004500.	1.5	109
89	10 Genomics Analysis of Biocontrol biocontrol Species and Industrial Enzyme Producers from the Genus Trichoderma 0Trichoderma. , 2014, , 233-264.		7
90	Trichoderma atroviride Transcriptional Regulator Xyr1 Supports the Induction of Systemic Resistance in Plants. Applied and Environmental Microbiology, 2014, 80, 5274-5281.	1.4	32
91	A highly sensitive in vivo footprinting technique for condition-dependent identification of cis elements. Nucleic Acids Research, 2014, 42, e1-e1.	6.5	13
92	Genetic Transformation and Engineering of Trichoderma reesei for Enhanced Enzyme Production. , 2014, , 193-200.		4

	CITATION	Report	
#	Article	IF	CITATIONS
93	Applications of RNA Interference for Enhanced Cellulase Production in Trichoderma. , 2014, , 201-213.		3
94	Expression pattern of cellulolytic and xylanolytic genes regulated by transcriptional factors XYR1 and CRE1 are affected by carbon source in Trichoderma reesei. Gene Expression Patterns, 2014, 14, 88-95.	0.3	62
95	The role of CRE1 in nucleosome positioning within the cbh1 promoter and coding regions of Trichoderma reesei. Applied Microbiology and Biotechnology, 2014, 98, 749-762.	1.7	66
97	Screening of candidate regulators for cellulase and hemicellulase production in Trichoderma reesei and identification of a factor essential for cellulase production. Biotechnology for Biofuels, 2014, 7, 14.	6.2	215
98	Microbial cellulases: Engineering, production and applications. Renewable and Sustainable Energy Reviews, 2014, 33, 188-203.	8.2	340
99	Intracellular β-Glucosidases CEL1a and CEL1b Are Essential for Cellulase Induction on Lactose in Trichoderma reesei. Eukaryotic Cell, 2014, 13, 1001-1013.	3.4	39
100	Similar is not the same: Differences in the function of the (hemi-)cellulolytic regulator XInR (XIr1/Xyr1) in filamentous fungi. Fungal Genetics and Biology, 2014, 72, 73-81.	0.9	80
101	Nucleoâ€cytoplasmic shuttling dynamics of the transcriptional regulators <scp>XYR1</scp> and <scp>CRE1</scp> under conditions of cellulase and xylanase gene expression in <scp><i>T</i></scp> <i>i>richoderma reesei</i> . Molecular Microbiology, 2014, 94, 1162-1178.	1.2	90
102	Gluconolactone induces cellulase gene expression in cellulolytic filamentous fungus Trichoderma reesei. RSC Advances, 2014, 4, 36057-36063.	1.7	8
103	Trpac1, a pH response transcription regulator, is involved in cellulase gene expression in Trichoderma reesei. Enzyme and Microbial Technology, 2014, 67, 17-26.	1.6	79
104	Characterization of the xylanase regulator protein gene, xlnR, in Talaromyces cellulolyticus (formerly known as Acremonium cellulolyticus). Bioscience, Biotechnology and Biochemistry, 2014, 78, 1564-1567.	0.6	14
105	Regulation of Plant Biomass Utilization in Aspergillus. Advances in Applied Microbiology, 2014, 88, 31-56.	1.3	48
106	How nutritional status signalling coordinates metabolism and lignocellulolytic enzyme secretion. Fungal Genetics and Biology, 2014, 72, 48-63.	0.9	69
107	Complex regulation of hydrolytic enzyme genes for cellulosic biomass degradation in filamentous fungi. Applied Microbiology and Biotechnology, 2014, 98, 4829-4837.	1.7	112
108	Secretomic Survey of <i>Trichoderma harzianum</i> Grown on Plant Biomass Substrates. Journal of Proteome Research, 2014, 13, 1810-1822.	1.8	23
109	Enzymes for second generation ethanol: exploring new strategies for the use of xylose. RSC Advances, 2014, 4, 21361.	1.7	20
110	Transcriptional comparison of the filamentous fungus Neurospora crassagrowing on three major monosaccharides D-glucose, D-xylose and L-arabinose. Biotechnology for Biofuels, 2014, 7, 31.	6.2	80
111	Molecular Mechanism of Cellulase Production Systems in Trichoderma. , 2014, , 319-324.		8

#	Article	IF	CITATIONS
112	The transcriptional activators AraR and XlnR from Aspergillus niger regulate expression of pentose catabolic and pentose phosphate pathway genes. Research in Microbiology, 2014, 165, 531-540.	1.0	34
113	Ecophysiology of Trichoderma in Genomic Perspective. , 2014, , 25-40.		8
114	Effect of earlier unfolded protein response and efficient protein disposal system on cellulase production in Rut C30. World Journal of Microbiology and Biotechnology, 2014, 30, 2587-2595.	1.7	14
115	Biochemical characterization of a new β-glucosidase (Cel3E) from Penicillium piceum and its application in boosting lignocelluloses bioconversion and forming disaccharide inducers: New insights into the role of β-glucosidase. Process Biochemistry, 2014, 49, 768-774.	1.8	17
116	An endogenous promoter for conditional gene expression in Acremonium chrysogenum: The xylan and xylose inducible promoter xyl1P. Journal of Biotechnology, 2014, 169, 82-86.	1.9	15
117	Plant Cell Wall and Chitin Degradation. , 0, , 396-413.		6
118	Identification of the role of a MAP kinase Tmk2 in Hypocrea jecorina (Trichoderma reesei). Scientific Reports, 2014, 4, 6732.	1.6	49
119	Characterization of a copper responsive promoter and its mediated overexpression of the xylanase regulator 1 results in an induction-independent production of cellulases in Trichoderma reesei. Biotechnology for Biofuels, 2015, 8, 67.	6.2	95
120	The effects of extracellular pH and of the transcriptional regulator PACI on the transcriptome of Trichoderma reesei. Microbial Cell Factories, 2015, 14, 63.	1.9	42
121	The impact of a single-nucleotide mutation of bgl2 on cellulase induction in a Trichoderma reesei mutant. Biotechnology for Biofuels, 2015, 8, 230.	6.2	38
122	Identification of Genetic Targets to Improve Lignocellulosic Hydrocarbon Production in Trichoderma reesei Using Public Genomic and Transcriptomic Datasets. , 2015, , 177-195.		1
123	Genome sequencing of the Trichoderma reesei QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. BMC Genomics, 2015, 16, 326.	1.2	31
124	Decreased Cellulase and Xylanase Production in the Fungus Talaromyces cellulolyticus by Disruption of tacA and tctA Genes, Encoding Putative Zinc Finger Transcriptional Factors. Applied Biochemistry and Biotechnology, 2015, 175, 3218-3229.	1.4	19
125	Sugar Catabolism in Aspergillus and Other Fungi Related to the Utilization of Plant Biomass. Advances in Applied Microbiology, 2015, 90, 1-28.	1.3	46
126	Enhancing xylanase production in the thermophilic fungus <i>Myceliophthora thermophila</i> by homologous overexpression of <i>Mtxyr1</i> . Journal of Industrial Microbiology and Biotechnology, 2015, 42, 1233-1241.	1.4	36
127	An Ime2-like mitogen-activated protein kinase is involved in cellulase expression in the filamentous fungus Trichoderma reesei. Biotechnology Letters, 2015, 37, 2055-2062.	1.1	23
128	Secretomic Analysis Reveals Multi-Enzymatic Complexes in Trichoderma reesei Grown in Media Containing Lactose or Galactose. Bioenergy Research, 2015, 8, 1906-1911.	2.2	6
129	Heterologous Expression of an Alkali and Thermotolerant Lipase from Talaromyces thermophilus in Trichoderma reesei. Applied Biochemistry and Biotechnology, 2015, 176, 1722-1735.	1.4	18

#	Article	IF	CITATIONS
130	A novel major facilitator transporter TrSTR1 is essential for pentose utilization and involved in xylanase induction in Trichoderma reesei. Biochemical and Biophysical Research Communications, 2015, 460, 663-669.	1.0	44
131	The impact of chromatin remodelling on cellulase expression in Trichoderma reesei. BMC Genomics, 2015, 16, 588.	1.2	55
132	Direct Target Network of the Neurospora crassa Plant Cell Wall Deconstruction Regulators CLR-1, CLR-2, and XLR-1. MBio, 2015, 6, e01452-15.	1.8	109
133	The ßâ€importin <scp>KAP</scp> 8 (<scp>P</scp> se1/ <scp>K</scp> ap121) is required for nuclear import of the cellulase transcriptional regulator <scp>XYR</scp> 1, asexual sporulation and stress resistance in <scp><i>T</i></scp> <i>TT</i>	1.2	22
134	Xpp1 regulates the expression of xylanases, but not of cellulases in Trichoderma reesei. Biotechnology for Biofuels, 2015, 8, 112.	6.2	50
136	RNA Sequencing Reveals Xyr1 as a Transcription Factor Regulating Gene Expression beyond Carbohydrate Metabolism. BioMed Research International, 2016, 2016, 1-20.	0.9	33
137	Understanding the Role of the Master Regulator XYR1 in Trichoderma reesei by Global Transcriptional Analysis. Frontiers in Microbiology, 2016, 7, 175.	1.5	91
138	Characterization and Strain Improvement of a Hypercellulytic Variant, Trichoderma reesei SN1, by Genetic Engineering for Optimized Cellulase Production in Biomass Conversion Improvement. Frontiers in Microbiology, 2016, 7, 1349.	1.5	31
139	The Different Roles of Penicillium oxalicum LaeA in the Production of Extracellular Cellulase and β-xylosidase. Frontiers in Microbiology, 2016, 7, 2091.	1.5	50
140	Comparison of Nitrogen Depletion and Repletion on Lipid Production in Yeast and Fungal Species. Energies, 2016, 9, 685.	1.6	14
141	RNAseq reveals hydrophobins that are involved in the adaptation of Aspergillus nidulans to lignocellulose. Biotechnology for Biofuels, 2016, 9, 145.	6.2	43
142	Identification and functional characterization of novel xylose transporters from the cell factories Aspergillus niger and Trichoderma reesei. Biotechnology for Biofuels, 2016, 9, 148.	6.2	71
143	Characterization of the Ca ²⁺ â€responsive signaling pathway in regulating the expression and secretion of cellulases in <scp><i>T</i></scp> <i>richoderma reesei</i> Rut 30. Molecular Microbiology, 2016, 100, 560-575.	1.2	85
144	The <i>Fusarium graminearum</i> Xyr1 transcription factor regulates xylanase expression but is not essential for fungal virulence. Plant Pathology, 2016, 65, 713-722.	1.2	18
145	The Post-genomic Era of Trichoderma reesei : What's Next?. Trends in Biotechnology, 2016, 34, 970-982.	4.9	106
146	The ACEII recombinant Trichoderma reesei QM9414 strains with enhanced xylanase production and its applications in production of xylitol from tree barks. Microbial Cell Factories, 2016, 15, 215.	1.9	13
147	The Renaissance of Neurospora crassa: How a Classical Model System is Used for Applied Research. Fungal Biology, 2016, , 59-96.	0.3	11
149	Fungal Biotechnology for Industrial Enzyme Production: Focus on (Hemi)cellulase Production Strategies, Advances and Challenges. Fungal Biology, 2016, , 395-439.	0.3	8

#	Article	IF	CITATIONS
150	Deciphering the molecular mechanisms behind cellulase production in <i>Trichoderma reesei</i> , the hyper-cellulolytic filamentous fungus. Bioscience, Biotechnology and Biochemistry, 2016, 80, 1712-1729.	0.6	47
151	Understanding the Mechanism of Carbon Catabolite Repression to Increase Protein Production in Filamentous Fungi. Fungal Biology, 2016, , 275-288.	0.3	10
152	<scp>M</scp> cm <scp>A</scp> â€dependent and â€independent regulatory systems governing expression of <scp>C</scp> lr <scp>B</scp> â€regulated cellulase and hemicellulase genes in <scp><i>A</i></scp> <i>spergillus nidulans</i> . Molecular Microbiology, 2016, 102, 810-826.	1.2	15
153	Familiar Stranger. Advances in Applied Microbiology, 2016, 95, 69-147.	1.3	45
154	Triggering the Expression of Cellulolytic Genes Using a Recombinant Endoxylanase from Trichoderma harzianum IOC-3844. Bioenergy Research, 2016, 9, 931-941.	2.2	1
155	Enhanced cellulase production from <i>Trichoderma reesei</i> Rut 30 by engineering with an artificial zinc finger protein library. Biotechnology Journal, 2016, 11, 1282-1290.	1.8	42
156	Expression and chromatin structures of cellulolytic enzyme gene regulated by heterochromatin protein 1. Biotechnology for Biofuels, 2016, 9, 206.	6.2	29
157	Regulation of plant biomass-degrading enzyme genes in filamentous fungi. Mycotoxins, 2016, 66, 85-96.	0.2	1
158	Enhancing cellulase production by overexpression of xylanase regulator protein gene, <i>xlnR</i> , in <i>Talaromyces cellulolyticus</i> cellulase hyperproducing mutant strain. Bioscience, Biotechnology and Biochemistry, 2016, 80, 2065-2068.	0.6	13
159	A complete annotation of the chromosomes of the cellulase producer Trichoderma reesei provides insights in gene clusters, their expression and reveals genes required for fitness. Biotechnology for Biofuels, 2016, 9, 75.	6.2	54
160	Cellulases and beyond: the first 70Âyears of the enzyme producer Trichoderma reesei. Microbial Cell Factories, 2016, 15, 106.	1.9	412
161	The roles of the zinc finger transcription factors XInR, ClrA and ClrB in the breakdown of lignocellulose by Aspergillus niger. AMB Express, 2016, 6, 5.	1.4	51
162	Enhancing saccharification of wheat straw by mixing enzymes from genetically-modified Trichoderma reesei and Aspergillus niger. Biotechnology Letters, 2016, 38, 65-70.	1.1	24
163	The Genomes of Three Uneven Siblings: Footprints of the Lifestyles of Three Trichoderma Species. Microbiology and Molecular Biology Reviews, 2016, 80, 205-327.	2.9	194
164	Regulation of genes encoding cellulolytic enzymes by Pal-PacC signaling in Aspergillus nidulans. Applied Microbiology and Biotechnology, 2016, 100, 3621-3635.	1.7	22
165	Penicillium oxalicum PoFlbC regulates fungal asexual development and is important for cellulase gene expression. Fungal Genetics and Biology, 2016, 86, 91-102.	0.9	34
166	Regulation of cellulase expression, sporulation, and morphogenesis by velvet family proteins in Trichoderma reesei. Applied Microbiology and Biotechnology, 2016, 100, 769-779.	1.7	44
167	Transcriptomic responses of mixed cultures of ascomycete fungi to lignocellulose using dual RNA-seq reveal inter-species antagonism and limited beneficial effects on CAZyme expression. Fungal Genetics and Biology, 2017, 102, 4-21.	0.9	36

#	Article	IF	CITATIONS
168	Trichoderma reesei xylanase 5 is defective in the reference strain QM6a but functional alleles are present in other wild-type strains. Applied Microbiology and Biotechnology, 2017, 101, 4139-4149.	1.7	10
169	The relation between xyr1 overexpression in Trichoderma harzianum and sugarcane bagasse saccharification performance. Journal of Biotechnology, 2017, 246, 24-32.	1.9	39
170	Functional diversity for biomass deconstruction in family 5 subfamily 5 (GH5_5) of fungal endo-β1,4-glucanases. Applied Microbiology and Biotechnology, 2017, 101, 4093-4101.	1.7	9
171	Molecular and catalytic properties of fungal extracellular cellobiose dehydrogenase produced in prokaryotic and eukaryotic expression systems. Microbial Cell Factories, 2017, 16, 37.	1.9	32
172	Conservation and diversity of the regulators of cellulolytic enzyme genes in Ascomycete fungi. Current Genetics, 2017, 63, 951-958.	0.8	41
173	Regulators of plant biomass degradation in ascomycetous fungi. Biotechnology for Biofuels, 2017, 10, 152.	6.2	202
174	Deletion Analysis of GH7 Endoglucanase Gene (cel7B) Promoter Region in a Talaromyces cellulolyticus ligD-Disrupted Strain. Applied Biochemistry and Biotechnology, 2017, 183, 1516-1525.	1.4	5
175	Genetic engineering of <i>Trichoderma reesei</i> cellulases and their production. Microbial Biotechnology, 2017, 10, 1485-1499.	2.0	211
176	Rce1, a novel transcriptional repressor, regulates cellulase gene expression by antagonizing the transactivator Xyr1 in <i>Trichoderma reesei</i> . Molecular Microbiology, 2017, 105, 65-83.	1.2	93
177	The mating type locus protein MAT1-2-1 of Trichoderma reesei interacts with Xyr1 and regulates cellulase gene expression in response to light. Scientific Reports, 2017, 7, 17346.	1.6	37
178	Proteomic analysis reveals large amounts of decomposition enzymes and major metabolic pathways involved in algicidal process of Trametes versicolor F21a. Scientific Reports, 2017, 7, 3907.	1.6	25
179	Comparative transcriptome analysis reveals different strategies for degradation of steam-exploded sugarcane bagasse by Aspergillus niger and Trichoderma reesei. BMC Genomics, 2017, 18, 501.	1.2	79
180	Role of Trichoderma reesei mitogen-activated protein kinases (MAPKs) in cellulase formation. Biotechnology for Biofuels, 2017, 10, 99.	6.2	44
181	Role of carbon source in the shift from oxidative to hydrolytic wood decomposition by Postia placenta. Fungal Genetics and Biology, 2017, 106, 1-8.	0.9	40
182	Differences in the expression profile of endo-β-(1,6)- d -galactanase in pathogenic and non-pathogenic races of Colletotrichum lindemuthianum grown in the presence of arabinogalactan, xylan or Phaseolus vulgaris cell walls. Physiological and Molecular Plant Pathology, 2017, 99, 75-86.	1.3	1
183	Constitutive cellulase production from glucose using the recombinant Trichoderma reesei strain overexpressing an artificial transcription activator. Bioresource Technology, 2017, 223, 317-322.	4.8	97
184	Glucose Oxidase Production from Sustainable Substrates. Current Biotechnology, 2017, 6, .	0.2	6
185	Involvement of the Transcriptional Coactivator ThMBF1 in the Biocontrol Activity of Trichoderma harzianum. Frontiers in Microbiology, 2017, 8, 2273.	1.5	20

#	Article	IF	CITATIONS
186	Metadata Analysis of Phanerochaete chrysosporium Gene Expression Data Identified Common CAZymes Encoding Gene Expression Profiles Involved in Cellulose and Hemicellulose Degradation. International Journal of Biological Sciences, 2017, 13, 85-99.	2.6	16
187	A novel transcription factor specifically regulates GH11 xylanase genes in Trichoderma reesei. Biotechnology for Biofuels, 2017, 10, 194.	6.2	46
188	Network reconstruction and systems analysis of plant cell wall deconstruction by Neurospora crassa. Biotechnology for Biofuels, 2017, 10, 225.	6.2	42
189	Production of the versatile cellulase for cellulose bioconversion and cellulase inducer synthesis by genetic improvement of Trichoderma reesei. Biotechnology for Biofuels, 2017, 10, 272.	6.2	48
190	Engineering of the Trichoderma reesei xylanase3 promoter for efficient enzyme expression. Applied Microbiology and Biotechnology, 2018, 102, 2737-2752.	1.7	18
191	<scp>ARA</scp> 1 regulates not only <scp>l</scp> â€arabinose but also <scp>d</scp> â€galactose catabolism in <i>Trichoderma reesei</i> . FEBS Letters, 2018, 592, 60-70.	1.3	37
192	A copper-controlled RNA interference system for reversible silencing of target genes in Trichoderma reesei. Biotechnology for Biofuels, 2018, 11, 33.	6.2	18
193	Influence of cis Element Arrangement on Promoter Strength in Trichoderma reesei. Applied and Environmental Microbiology, 2018, 84, .	1.4	41
194	Improvement of cellulase production in Trichoderma reesei Rut-C30 by overexpression of a novel regulatory gene Trvib-1. Bioresource Technology, 2018, 247, 676-683.	4.8	116
195	Light, stress, sex and carbon – The photoreceptor ENVOY as a central checkpoint in the physiology of Trichoderma reesei. Fungal Biology, 2018, 122, 479-486.	1.1	44
196	Gene Co-expression Network Reveals Potential New Genes Related to Sugarcane Bagasse Degradation in Trichoderma reesei RUT-30. Frontiers in Bioengineering and Biotechnology, 2018, 6, 151.	2.0	36
197	The putative β-glucosidase BGL3I regulates cellulase induction in Trichoderma reesei. Biotechnology for Biofuels, 2018, 11, 314.	6.2	23
198	Truncation of the transcriptional repressor protein Cre1 in Trichoderma reesei Rut-C30 turns it into an activator. Fungal Biology and Biotechnology, 2018, 5, 15.	2.5	53
199	The Promoter Toolbox for Recombinant Gene Expression in Trichoderma reesei. Frontiers in Bioengineering and Biotechnology, 2018, 6, 135.	2.0	46
200	New Genomic Approaches to Enhance Biomass Degradation by the Industrial Fungus <i>Trichoderma reesei</i> . International Journal of Genomics, 2018, 2018, 1-17.	0.8	30
201	Regulation of the Cα-cAMP/PKA signaling pathway in cellulose utilization of Chaetomium globosum. Microbial Cell Factories, 2018, 17, 160.	1.9	13
202	Modulating Transcriptional Regulation of Plant Biomass Degrading Enzyme Networks for Rational Design of Industrial Fungal Strains. Frontiers in Bioengineering and Biotechnology, 2018, 6, 133.	2.0	33
203	Engineering Trichoderma reesei Rut-C30 with the overexpression of egl1 at the ace1 locus to relieve repression on cellulase production and to adjust the ratio of cellulolytic enzymes for more efficient hydrolysis of lignocellulosic biomass. Journal of Biotechnology, 2018, 285, 56-63.	1.9	47

ARTICLE

IF CITATIONS

Lignocellulase Formation, Regulation, and Secretion Mechanisms in Hypocrea jecorina (Trichoderma) Tj ETQq0 0 0 rgBT /Overjock 10 Tf

205	Metabolic Engineering of Fungal Strains for Efficient Production of Cellulolytic Enzymes. , 2018, , 27-41.		11
206	Fungal Cellulolytic Enzymes. , 2018, , .		7
207	A current view on long noncoding RNAs in yeast and filamentous fungi. Applied Microbiology and Biotechnology, 2018, 102, 7319-7331.	1.7	49
208	A long noncoding RNA promotes cellulase expression in Trichoderma reesei. Biotechnology for Biofuels, 2018, 11, 78.	6.2	38
209	Construction of enhanced transcriptional activators for improving cellulase production in Trichoderma reesei RUT C30. Bioresources and Bioprocessing, 2018, 5, 40.	2.0	23
210	Enhanced cellulase production by decreasing intercellular pH through H+-ATPase gene deletion in Trichoderma reesei RUT-C30. Biotechnology for Biofuels, 2019, 12, 195.	6.2	8
211	<i>Trichoderma reesei</i> XYR1 recruits SWI/SNF to facilitate cellulase gene expression. Molecular Microbiology, 2019, 112, 1145-1162.	1.2	47
212	Crosstalk of Cellulose and Mannan Perception Pathways Leads to Inhibition of Cellulase Production in Several Filamentous Fungi. MBio, 2019, 10, .	1.8	20
213	A Novel CreA-Mediated Regulation Mechanism of Cellulase Expression in the Thermophilic Fungus Humicola insolens. International Journal of Molecular Sciences, 2019, 20, 3693.	1.8	7
214	Protein phosphatases regulate growth, development, cellulases and secondary metabolism in Trichoderma reesei. Scientific Reports, 2019, 9, 10995.	1.6	30
215	Use of fusion transcription factors to reprogram cellulase transcription and enable efficient cellulase production in Trichoderma reesei. Biotechnology for Biofuels, 2019, 12, 244.	6.2	24
216	The influence of feedstock characteristics on enzyme production in Trichoderma reesei: a review on productivity, gene regulation and secretion profiles. Biotechnology for Biofuels, 2019, 12, 238.	6.2	68
217	The GATA-Type Transcriptional Factor Are1 Modulates the Expression of Extracellular Proteases and Cellulases in Trichoderma reesei. International Journal of Molecular Sciences, 2019, 20, 4100.	1.8	21
218	CLP1, a Novel Plant Homeo Domain Protein, Participates in Regulating Cellulase Gene Expression in the Filamentous Fungus Trichoderma reesei. Frontiers in Microbiology, 2019, 10, 1700.	1.5	13
219	The role of PKAc1 in gene regulation and trichodimerol production in Trichoderma reesei. Fungal Biology and Biotechnology, 2019, 6, 12.	2.5	28
220	The transcription factor ACE3 controls cellulase activities and lactose metabolism via two additional regulators in the fungus Trichoderma reesei. Journal of Biological Chemistry, 2019, 294, 18435-18450.	1.6	66
221	Fusion transcription factors for strong, constitutive expression of cellulases and xylanases in Trichoderma reesei. Biotechnology for Biofuels, 2019, 12, 231.	6.2	44

#	Article	IF	CITATIONS
222	A Novel Cys2His2 Zinc Finger Homolog of AZF1 Modulates Holocellulase Expression in <i>Trichoderma reesei</i> . MSystems, 2019, 4, .	1.7	32
223	Genetic Engineering Applications to Improve Cellulase Production and Efficiency: Part II. , 2019, , 227-260.		2
224	Regulation and production of lignocellulolytic enzymes from Trichoderma reesei for biofuels production. Advances in Bioenergy, 2019, 4, 79-119.	0.5	26
225	Enhancement of cellulase production in Trichoderma reesei RUT-C30 by comparative genomic screening. Microbial Cell Factories, 2019, 18, 81.	1.9	35
226	Deletion of either the regulatory gene ara1 or metabolic gene xki1 in Trichoderma reesei leads to increased CAZyme gene expression on crude plant biomass. Biotechnology for Biofuels, 2019, 12, 81.	6.2	10
227	A novel transcriptional regulator RXE1 modulates the essential transactivator XYR1 and cellulase gene expression in Trichoderma reesei. Applied Microbiology and Biotechnology, 2019, 103, 4511-4523.	1.7	38
228	Novel genetic tools that enable highly pure protein production in Trichoderma reesei. Scientific Reports, 2019, 9, 5032.	1.6	58
229	Introduction of heterologous transcription factors and their target genes into Penicillium oxalicum leads to increased lignocellulolytic enzyme production. Applied Microbiology and Biotechnology, 2019, 103, 2675-2687.	1.7	17
230	CLRâ€4, a novel conserved transcription factor for cellulase gene expression in ascomycete fungi. Molecular Microbiology, 2019, 111, 373-394.	1.2	38
231	Regulation of gene expression by the action of a fungal lncRNA on a transactivator. RNA Biology, 2020, 17, 47-61.	1.5	11
232	Promoting cellulase and hemicellulase production from Trichoderma orientalis EU7-22 by overexpression of transcription factors Xyr1 and Ace3. Bioresource Technology, 2020, 296, 122355.	4.8	32
233	The Putative Transcription Factor Gene thaB Regulates Cellulase and Xylanase Production at the Enzymatic and Transcriptional Level in the Fungus Talaromyces cellulolyticus. Applied Biochemistry and Biotechnology, 2020, 190, 1360-1370.	1.4	3
234	Development of genetic tools for the thermophilic filamentous fungus Thermoascus aurantiacus. Biotechnology for Biofuels, 2020, 13, 167.	6.2	8
235	Mini review: Advances in understanding regulation of cellulase enzyme in white-rot basidiomycetes. Microbial Pathogenesis, 2020, 147, 104410.	1.3	31
236	Constructing a novel expression system by specific activation of amylase expression pathway in Penicillium. Microbial Cell Factories, 2020, 19, 155.	1.9	5
237	Modification of transcriptional factor ACE3 enhances protein production in Trichoderma reesei in the absence of cellulase gene inducer. Biotechnology for Biofuels, 2020, 13, 137.	6.2	25
238	Trichoderma reesei XYR1 activates cellulase gene expression via interaction with the Mediator subunit TrGAL11 to recruit RNA polymerase II. PLoS Genetics, 2020, 16, e1008979.	1.5	18
239	Application of the human estrogen receptor within a synthetic transcription factor in Trichoderma reesei. Fungal Biology and Biotechnology, 2020, 7, 12.	2.5	3

#	Article	IF	CITATIONS
240	Studies on sugar transporter CRT1 reveal new characteristics that are critical for cellulase induction in Trichoderma reesei. Biotechnology for Biofuels, 2020, 13, 158.	6.2	32
241	Glucose-lactose mixture feeds in industry-like conditions: a gene regulatory network analysis on the hyperproducing Trichoderma reesei strain Rut-C30. BMC Genomics, 2020, 21, 885.	1.2	7
242	Engineering <i>Trichoderma reesei</i> for Hyperproduction of Cellulases on Glucose to Efficiently Saccharify Pretreated Corncobs. Journal of Agricultural and Food Chemistry, 2020, 68, 12671-12682.	2.4	28
243	Influence of spore morphology on spectrophotometric quantification of Trichoderma inocula. BioTechniques, 2020, 68, 279-282.	0.8	10
244	Studies of Cellulose and Starch Utilization and the Regulatory Mechanisms of Related Enzymes in Fungi. Polymers, 2020, 12, 530.	2.0	44
245	Identification of a novel repressor encoded by the putative gene <i>ctf1</i> for cellulase biosynthesis in <i>Trichoderma reesei</i> through artificial zinc finger engineering. Biotechnology and Bioengineering, 2020, 117, 1747-1760.	1.7	48
246	Engineering the Effector Domain of the Artificial Transcription Factor to Improve Cellulase Production by Trichoderma reesei. Frontiers in Bioengineering and Biotechnology, 2020, 8, 675.	2.0	9
247	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. Trends in Microbiology, 2020, 28, 487-499.	3.5	25
248	Involvement of Xyr1 and Are1 for Trichodermapepsin Gene Expression in Response to Cellulose and Galactose in Trichoderma reesei. Current Microbiology, 2020, 77, 1506-1517.	1.0	5
250	Secondary metabolites and lytic tool box of trichoderma and their role in plant health. , 2020, , 305-320.		7
251	Heterologous expression of Phanerochaete chrysosporium cellobiose dehydrogenase in Trichoderma reesei. Microbial Cell Factories, 2021, 20, 2.	1.9	11
252	Transcriptional Regulation: How Saprobic Fungi Tune the Production of Plant Cell Wall Degrading Enzymes. , 2021, , 528-535.		2
253	Strain Improvement and Genetic Engineering of Trichoderma for Industrial Applications. , 2021, , 505-517.		4
254	Interdependent recruitment of CYC8/TUP1 and the transcriptional activator XYR1 at target promoters is required for induced cellulase gene expression in Trichoderma reesei. PLoS Genetics, 2021, 17, e1009351.	1.5	16
255	Disruption of the <i>Trichoderma reesei gul1</i> gene stimulates hyphal branching and reduces broth viscosity in cellulase production. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	1.4	13
256	Effects of the Transcription Factor Ace2 from Trichoderma reesei on Cellulase and Hemicellulase Expression in Trichoderma orientalis EU7-22. Applied Biochemistry and Biotechnology, 2021, 193, 2098-2109.	1.4	1
257	Disruption of alpha-tubulin releases carbon catabolite repression and enhances enzyme production in Trichoderma reesei even in the presence of glucose. Biotechnology for Biofuels, 2021, 14, 39.	6.2	13
258	Comparative characterization of glyoxal oxidase from Phanerochaete chrysosporium expressed at high levels in Pichia pastoris and Trichoderma reesei. Enzyme and Microbial Technology, 2021, 145, 109748.	1.6	10

#	Article	IF	CITATIONS
260	Addressing challenges in production of cellulases for biomass hydrolysis: Targeted interventions into the genetics of cellulase producing fungi. Bioresource Technology, 2021, 329, 124746.	4.8	51
261	Genomic and transcriptomic analysis of the thermophilic lignocellulose-degrading fungus Thielavia terrestris LPH172. Biotechnology for Biofuels, 2021, 14, 131.	6.2	15
262	Understanding the Role of Trichoderma reesei Vib1 in Gene Expression during Cellulose Degradation. Journal of Fungi (Basel, Switzerland), 2021, 7, 613.	1.5	5
263	<i>Trichoderma reesei</i> ACE4, a Novel Transcriptional Activator Involved in the Regulation of Cellulase Genes during Growth on Cellulose. Applied and Environmental Microbiology, 2021, 87, e0059321.	1.4	20
264	Comparative transcriptome analysis of Trichoderma reesei reveals different gene regulatory networks induced by synthetic mixtures of glucose and β-disaccharide. Bioresources and Bioprocessing, 2021, 8, .	2.0	10
265	Serine–arginine protein kinase-like protein, SrpkF, stimulates both cellobiose-responsive and d-xylose-responsive signaling pathways in Aspergillus aculeatus. Current Genetics, 2022, 68, 143-152.	0.8	4
266	Functional expression and characterization of two laccases from the brown rot Fomitopsis pinicola. Enzyme and Microbial Technology, 2021, 148, 109801.	1.6	8
267	Functional analysis of the transcriptional activator XlnR of <i>Penicillium oxalicum</i> . Journal of Applied Microbiology, 2022, 132, 1112-1120.	1.4	7
268	The phenomenon of degeneration of industrial Trichoderma reesei strains. Biotechnology for Biofuels, 2021, 14, 193.	6.2	5
269	Microbial cellulases – An update towards its surface chemistry, genetic engineering and recovery for its biotechnological potential. Bioresource Technology, 2021, 340, 125710.	4.8	23
270	Trichoderma: Genomic Aspects of Mycoparasitism and Biomass Degradation. Soil Biology, 2013, , 127-156.	0.6	5
271	Enzymes for Bioenergy. , 2017, , 3-43.		1
272	A β-glucosidase Hyperproducing Strain, Pencillium piceum: Novel Characterization of Lignocellulolytic Enzyme Systems and Its Application in Biomass Bioconversion. , 2018, , 81-106.		2
273	Strain Improvement for Industrial Production of Lignocellulolytic Enzyme by Talaromyces cellulolyticus. , 2018, , 135-154.		3
275	Systems Analysis of Lactose Metabolism in Trichoderma reesei Identifies a Lactose Permease That Is Essential for Cellulase Induction. PLoS ONE, 2013, 8, e62631.	1.1	111
276	CRZ1 regulator and calcium cooperatively modulate holocellulases gene expression in Trichoderma reesei QM6a. Genetics and Molecular Biology, 2020, 43, e20190244.	0.6	18
277	Regulation of Cellulase and Hemicellulase Gene Expression in Fungi. Current Genomics, 2013, 14, 230-249.	0.7	212
278	The Relation Between Promoter Chromatin Status, Xyr1 and Cellulase Expression in Trichoderma reesei. Current Genomics, 2016, 17, 145-152.	0.7	47

ARTICLE IF CITATIONS Trichoderma reesei CRE1-mediated Carbon Catabolite Repression in Response to Sophorose Through 279 0.7 34 RNA Sequencing Analysis. Current Genomics, 2016, 17, 119-131. Molecular Characterization of Cold-Inducible ¥-Galactosidase from Arthrobacter sp. ON14 Isolated from Antarctica. Journal of Microbiology and Biotechnology, 2011, 21, 236-242. Improving Cellulase Production in Trichoderma koningii Through RNA Interference on ace1 Gene 281 0.9 22 Expression. Journal of Microbiology and Biotechnology, 2012, 22, 1133-1140. Impact of xylanase expression-inducing compounds on DNA accessibility in Trichoderma reesei. 1.9 Mycosphere, 2017, 8, 432-444. The novel repressor Rce2 competes with Ace3 to regulate cellulase gene expression in the filamentous 283 7 1.2 fungus <i>Trichoderma reesei</i>. Molecular Microbiology, 2021, 116, 1298-1314. CRISPR/Cas9-mediated genome editing directed by a 5S rRNA–tRNAGly hybrid promoter in the thermophilic filamentous fungus Humicola insolens. Biotechnology for Biofuels, 2021, 14, 206. 284 6.2 Trends in biological data integration for the selection of enzymes and transcription factors related 285 1.1 3 to cellulose and hemicellulose degradation in fungi. 3 Biotech, 2021, 11, 475. Induction and Repression of Carbohydrate Degrading Enzymes in Fungi with Special Reference to their 286 Coding Genes. , 2012, , 53-71. A truncated form of the Carbon catabolite repressor 1 increases cellulase production in Trichoderma 287 6.2 4 reesei. Biotechnology for Biofuels, 2014, 7, 129. A Carbohydrate Hydrolysis Enzymes encoding Genes in Neurospora crassa. Journal of Advances in 0.1 Biotechnology, 2016, 5, 711-727. Biorefinery of Lignocellulosics for Biofuels and Biochemicals. Green Chemistry and Sustainable 289 0.4 0 Technology, 2016, , 143-191. Integrated engineering of enzymes and microorganisms for improving the efficiency of industrial 294 2.2 34 lignocellulose deconstruction. Engineering Microbiology, 2021, 1, 100005. 10 Filamentous Fungi as Hosts for Heterologous Production of Proteins and Secondary Metabolites in 295 0 the Post-Genomic Era. , 2020, , 227-265. Hemicellulase in Degradation of Lignocellulosic Wastes., 2020, , 41-53. The complex <scp>Tup1 yc8</scp> bridges transcription factor <scp>ClrB</scp> and putative histone 298 methyltransferase <scp>LaeA</scp> to activate the expression of cellulolytic genes. Molecular 1.2 6 Micróbiology, 2022, 117, 1002-1022. Elimination of the Sugar Transporter GAT1 Increased Xylanase I Production in Trichoderma reesei. Frontiers in Microbiology, 2022, 13, 810066. Aptness of entomogenus fungi with diatomaceous earth against various stored grain insect pests. 300 0.8 8 Egyptian Journal of Biological Pest Control, 2022, 32, . Dual Regulatory Role of Chromatin Remodeler ISW1 in Coordinating Cellulase and Secondary 301 1.8 Metabolite Biosynthesis in Trichoderma reesei. MBio, 2022, 13, e0345621.

CITATION REPORT ARTICLE IF CITATIONS Network Analysis Reveals Different Cellulose Degradation Strategies Across Trichoderma harzianum 1.1 8 Strains Associated With XYR1 and CRE1. Frontiers in Genetics, 2022, 13, 807243. Simultaneous manipulation of multiple genes within a same regulatory stage for iterative evolution of Trichoderma reesei. , 2022, 15, 26. Factors regulating cellulolytic gene expression in filamentous fungi: an overview. Microbial Cell 1.9 20 Factories, 2022, 21, 44. Screening for genes involved in cellulase regulation by expression under the control of a novel 1.9 constitutive promoter in Trichoderma reesei. Current Research in Biotechnology, 2022, 4, 238-246. Reformulating the Hydrolytic Enzyme Cocktail of <i>Trichoderma reesei</i> by Combining XYR1 Overexpression and Elimination of Four Major Cellulases to Improve Saccharification of Corn Fiber. 12 2.4 Journal of Agricultural and Food Chemistry, 2022, 70, 211-222. Impairment of the cellulose degradation machinery enhances <i>Fusarium oxysporum</i> virulence 4.7 but limits its reproductive fitness. Science Advances, 2022, 8, eabl9734. The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying 1.8 10 Mushroom (i) Schizophyllum commune (i). MBio, 2022, 13, . Functional Characterization of Sugar Transporter CRT1 Reveals Differential Roles of Its C-Terminal Region in Sugar Transport and Cellulase Induction in Trichoderma reesei. Microbiology Spectrum, 1.2 <u>2022,</u>10,. Induction of cellulase production by Sr2+ in Trichoderma reesei via calcium signaling transduction. 2.0 9 Bioresources and Bioprocessing, 2022, 9, . MtTRC-1, a Novel Transcription Factor, Regulates Cellulase Production via Directly Modulating the Genes Expression of the <i>Mthac-1</i> and <i>Mtcbh-1</i> in <i>Myceliophthora thermophila</i>. 1.4 Applied and Environmental Microbiology, 0, , . Inducer-free cellulase production system based on the constitutive expression of mutated XYR1 and 8 1.6 ACE3 in the industrial fungus Trichoderma reesei. Scientific Reports, 2022, 12, . In Vitro Characterization of a Nuclear Receptor-like Domain of the Xylanase Regulator 1 from 1.5 Trichoderma reesei. Journal of Fungi (Basel, Switzerland), 2022, 8, 1254. Tailoring the expression of Xyr1 leads to efficient production of lignocellulolytic enzymes in 4 Trichoderma reesei for improved saccharification of corncob residues. , 2022, 15, . A novel fusion transcription factor drives high cellulase and xylanase production on glucose in 4.8 Trichoderma reesei. Bioresource Technology, 2023, 370, 128520. Botrytis cinerea Transcription Factor BcXyr1 Regulates (Hemi-)Cellulase Production and Fungal 1.7 5

330	Virulence. MSystems, 2022, 7, .	1.7	Э	
331	Role of the Nitrogen Metabolism Regulator TAM1 in Regulation of Cellulase Gene Expression in Trichoderma reesei. Applied and Environmental Microbiology, 0, , .	1.4	4	
332	Genetic Regulation Networks in Cellulase and Hemicellulase Production in an Industrially Applied Cellulase Producer Trichoderma reesei. , 2023, , 1-23.		1	
334	Genetic Engineering of Trichoderma reesei for Biomass Hydrolysis. , 2023, , 1-30.		0	

302

304

306

322

324

326

328

329

#	Article	IF	CITATIONS
335	The arabinose transporter MtLat-1 is involved in hemicellulase repression as a pentose transceptor in Myceliophthora thermophila. , 2023, 16, .		2
338	Regulation of nutrient utilization in filamentous fungi. Applied Microbiology and Biotechnology, 0, , .	1.7	0
342	Cellulose Degradation Enzymes in Filamentous Fungi, A Bioprocessing Approach Towards Biorefinery. Molecular Biotechnology, 0, , .	1.3	0
349	Degradation of lignocelluloses by microorganisms. , 2024, , 91-106.		0