

Bernhard Seiboth

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

4,794
citations

117453

34
h-index

174990

52
g-index

58
all docs

58
docs citations

58
times ranked

3740
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterologous expression of Phanerochaete chrysosporium cellobiose dehydrogenase in Trichoderma reesei. Microbial Cell Factories, 2021, 20, 2.	1.9	11
2	Replacement of the carbon catabolite regulator (cre1) and fed-batch cultivation as strategies to enhance cellulase production in Trichoderma harzianum. Bioresource Technology Reports, 2021, 13, 100634.	1.5	3
3	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
4	Functional expression and characterization of two laccases from the brown rot Fomitopsis pinicola. Enzyme and Microbial Technology, 2021, 148, 109801.	1.6	8
5	In Silico Gene Analysis and Oligonucleotide Design for the Construction of Expression Vectors. Methods in Molecular Biology, 2021, 2234, 297-309.	0.4	0
6	The impact of putative methyltransferase overexpression on the Trichoderma harzianum cellulolytic system for biomass conversion. Bioresource Technology, 2020, 313, 123616.	4.8	11
7	Deletion of the small GTPase rac1 in Trichoderma reesei provokes hyperbranching and impacts growth and cellulase production. Fungal Biology and Biotechnology, 2019, 6, 16.	2.5	18
8	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
9	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
10	<scp>ARA</scp>1 regulates not only <scp>l</scp>â€œarabinose but also <scp>d</scp>â€œgalactose catabolism in <i>Trichoderma reesei</i>. FEBS Letters, 2018, 592, 60-70.	1.3	37
11	The Promoter Toolbox for Recombinant Gene Expression in Trichoderma reesei. Frontiers in Bioengineering and Biotechnology, 2018, 6, 135.	2.0	46
12	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
13	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
14	The relation between xyr1 overexpression in Trichoderma harzianum and sugarcane bagasse saccharification performance. Journal of Biotechnology, 2017, 246, 24-32.	1.9	39
15	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
16	Regulators of plant biomass degradation in ascomycetous fungi. Biotechnology for Biofuels, 2017, 10, 152.	6.2	202
17	N -acetylglucosamine, the building block of chitin, inhibits growth of Neurospora crassa. Fungal Genetics and Biology, 2017, 107, 1-11.	0.9	29
18	Genome sequencing and transcriptome analysis of Trichoderma reesei QM9978 strain reveals a distal chromosome translocation to be responsible for loss of vib1 expression and loss of cellulase induction. Biotechnology for Biofuels, 2017, 10, 209.	6.2	43

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19	Gene Expression Systems in Industrial Ascomycetes: Advancements and Applications. <i>Fungal Biology</i> , 2016, , 3-22.	0.3	0
20	Functional characterization of the native swollenin from <i>Trichoderma reesei</i> : study of its possible role as C1 factor of enzymatic lignocellulose conversion. <i>Biotechnology for Biofuels</i> , 2016, 9, 178.	6.2	51
21	Cellulases and beyond: the first 70 years of the enzyme producer <i>Trichoderma reesei</i> . <i>Microbial Cell Factories</i> , 2016, 15, 106.	1.9	412
22	6 Degradation of Plant Cell Wall Polymers by Fungi. , 2016, , 127-148.		2
23	l-Methionine repressible promoters for tuneable gene expression in <i>Trichoderma reesei</i> . <i>Microbial Cell Factories</i> , 2015, 14, 120.	1.9	16
24	Restoration of female fertility in <i>Trichoderma reesei</i> QM6a provides the basis for inbreeding in this industrial cellulase producing fungus. <i>Biotechnology for Biofuels</i> , 2015, 8, 155.	6.2	37
25	Genome sequencing of the <i>Trichoderma reesei</i> QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. <i>BMC Genomics</i> , 2015, 16, 326.	1.2	31
26	The <i>Importin KAP8 (Pse1Kap121)</i> is required for nuclear import of the cellulase transcriptional regulator <i>XYR1</i> , asexual sporulation and stress resistance in <i>Trichoderma reesei</i> . <i>Molecular Microbiology</i> , 2015, 96, 405-418.	1.2	22
27	Kinetic transcriptome analysis reveals an essentially intact induction system in a cellulase hyper-producer <i>Trichoderma reesei</i> strain. <i>Biotechnology for Biofuels</i> , 2014, 7, 173.	6.2	7
28	Molecular Tools for Strain Improvement of <i>Trichoderma</i> spp. , 2014, , 179-191.		8
29	Nucleocytoplasmic shuttling dynamics of the transcriptional regulators <i>XYR1</i> and <i>CRE1</i> under conditions of cellulase and xylanase gene expression in <i>Trichoderma reesei</i> . <i>Molecular Microbiology</i> , 2014, 94, 1162-1178.	1.2	90
30	Comparative analysis of the <i>Trichoderma reesei</i> transcriptome during growth on the cellulase inducing substrates wheat straw and lactose. <i>Biotechnology for Biofuels</i> , 2013, 6, 127.	6.2	100
31	Xylitol Production by Genetically Engineered <i>Trichoderma reesei</i> Strains Using Barley Straw as Feedstock. <i>Applied Biochemistry and Biotechnology</i> , 2013, 169, 554-569.	1.4	23
32	Xylanase Gene Transcription in <i>Trichoderma reesei</i> Is Triggered by Different Inducers Representing Different Hemicellulosic Pentose Polymers. <i>Eukaryotic Cell</i> , 2013, 12, 390-398.	3.4	69
33	Systems Analysis of Lactose Metabolism in <i>Trichoderma reesei</i> Identifies a Lactose Permease That Is Essential for Cellulase Induction. <i>PLoS ONE</i> , 2013, 8, e62631.	1.1	111
34	Metabolic Engineering of Inducer Formation for Cellulase and Hemicellulase Gene Expression in <i>Trichoderma reesei</i> . <i>Sub-Cellular Biochemistry</i> , 2012, 64, 367-390.	1.0	42
35	A versatile toolkit for high throughput functional genomics with <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2012, 5, 1.	6.2	434
36	The putative protein methyltransferase LAE1 controls cellulase gene expression in <i>Trichoderma reesei</i> . <i>Molecular Microbiology</i> , 2012, 84, 1150-1164.	1.2	232

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37	A homologous production system for <i>Trichoderma reesei</i> secreted proteins in a cellulase-free background. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 1601-1608.	1.7	63
38	Fungal arabinan and l-arabinose metabolism. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1665-1673.	1.7	115
39	The CRE1 carbon catabolite repressor of the fungus <i>Trichoderma reesei</i> : a master regulator of carbon assimilation. <i>BMC Genomics</i> , 2011, 12, 269.	1.2	180
40	Expression of Biomass-Degrading Enzymes Is a Major Event during <i>Conidium</i> Development in <i>Trichoderma reesei</i> . <i>Eukaryotic Cell</i> , 2011, 10, 1527-1535.	3.4	68
41	Differential Regulation of the Cellulase Transcription Factors XYR1, ACE2, and ACE1 in <i>Trichoderma reesei</i> Strains Producing High and Low Levels of Cellulase. <i>Eukaryotic Cell</i> , 2011, 10, 262-271.	3.4	136
42	Tracking the roots of cellulase hyperproduction by the fungus <i>Trichoderma reesei</i> using massively parallel DNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16151-16156.	3.3	190
43	Molecular Regulation of Arabinan and <i>Trichoderma reesei</i> -Arabinose Metabolism in <i>Hypocrea jecorina</i> (<i>Trichoderma reesei</i>). <i>Eukaryotic Cell</i> , 2009, 8, 1837-1844.	3.4	69
44	Metabolic engineering strategies for the improvement of cellulase production by <i>Hypocrea jecorina</i> . <i>Biotechnology for Biofuels</i> , 2009, 2, 19.	6.2	353
45	Gene targeting in a nonhomologous end joining deficient <i>Hypocrea jecorina</i> . <i>Journal of Biotechnology</i> , 2009, 139, 146-151.	1.9	134
46	The <i>Hypocrea jecorina</i> (<i>Trichoderma reesei</i>) hypercellulolytic mutant RUT C30 lacks a 85 kb (29) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.2	132
47	Induction of the gal Pathway and Cellulase Genes Involves No Transcriptional Inducer Function of the Galactokinase in <i>Hypocrea jecorina</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 18654-18659.	1.6	38
48	Induction of extracellular β -galactosidase (Bga1) formation by d-galactose in <i>Hypocrea jecorina</i> is mediated by galactitol. <i>Microbiology (United Kingdom)</i> , 2007, 153, 507-512.	0.7	19
49	The β -xylose reductase of <i>Hypocrea jecorina</i> is the major aldose reductase in pentose and β -galactose catabolism and necessary for β -galactosidase and cellulase induction by lactose. <i>Molecular Microbiology</i> , 2007, 66, 890-900.	1.2	96
50	d-Galactose induces cellulase gene expression in <i>Hypocrea jecorina</i> at low growth rates. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1507-1514.	0.7	61
51	A complete survey of <i>Trichoderma</i> chitinases reveals three distinct subgroups of family 18 chitinases. <i>FEBS Journal</i> , 2005, 272, 5923-5939.	2.2	209
52	Role of the bga1 -Encoded Extracellular β -Galactosidase of <i>Hypocrea jecorina</i> in Cellulase Induction by Lactose. <i>Applied and Environmental Microbiology</i> , 2005, 71, 851-857.	1.4	59
53	The galactokinase of <i>Hypocrea jecorina</i> is essential for cellulase induction by lactose but dispensable for growth on d-galactose. <i>Molecular Microbiology</i> , 2004, 51, 1015-1025.	1.2	70
54	Glucose does not activate the plasma-membrane-bound H ⁺ -ATPase but affects pmaA transcript abundance in <i>Aspergillus nidulans</i> . <i>Archives of Microbiology</i> , 2000, 174, 340-345.	1.0	12

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55	The <i>bgl1</i> gene of <i>Trichoderma reesei</i> QM 9414 encodes an extracellular, cellulose-inducible β -glucosidase involved in cellulase induction by sophorose. <i>Molecular Microbiology</i> , 1995, 16, 687-697.	1.2	97
56	Plant Cell Wall and Chitin Degradation. , 0, , 396-413.		6