Marie FranÃ§oise Gorwa-Grauslund

List of Publications by Year
in descending order

85 papers	6,636 citations	101384 36 h-index	64668 79 g-index
87 all docs	87 docs citations	87 times ranked	5430 citing authors

#	Article	IF	Citations
1	Increased tolerance and conversion of inhibitors in lignocellulosic hydrolysates bySaccharomyces cerevisiae. Journal of Chemical Technology and Biotechnology, 2007, 82, 340-349.	1.6	816
2	Towards industrial pentose-fermenting yeast strains. Applied Microbiology and Biotechnology, 2007, 74, 937-953.	1.7	662
3	Kinetic modelling reveals current limitations in the production of ethanol from xylose by recombinant Saccharomyces cerevisiae. Metabolic Engineering, 2011, 13, 508-517.	3.6	316
4	Biological valorization of low molecular weight lignin. Biotechnology Advances, 2016, 34, 1318-1346.	6.0	304
5	Metabolic effects of furaldehydes and impacts on biotechnological processes. Applied Microbiology and Biotechnology, 2009, 82, 625-638.	1.7	267
6	Simultaneous saccharification and co-fermentation of glucose and xylose in steam-pretreated corn stover at high fiber content with Saccharomyces cerevisiae TMB3400. Journal of Biotechnology, 2006, 126, 488-498.	1.9	245
7	A 5-hydroxymethyl furfural reducing enzyme encoded by theSaccharomyces cerevisiae ADH6 gene conveys HMF tolerance. Yeast, 2006, 23, 455-464.	0.8	245
8	Investigation of limiting metabolic steps in the utilization of xylose by recombinantSaccharomyces cerevisiaeusing metabolic engineering. Yeast, 2005, 22, 359-368.	0.8	181
9	Role of cultivation media in the development of yeast strains for large scale industrial use. Microbial Cell Factories, 2005, 4, 31.	1.9	176
10	Reduced Oxidative Pentose Phosphate Pathway Flux in Recombinant Xylose-Utilizing Saccharomyces cerevisiae Strains Improves the Ethanol Yield from Xylose. Applied and Environmental Microbiology, 2002, 68, 1604-1609.	1.4	166
11	Metabolic Engineering for Pentose Utilization in Saccharomyces cerevisiae. , 2007, 108, 147-177.		161
12	Xylose reductase from Pichia stipitis with altered coenzyme preference improves ethanolic xylose fermentation by recombinant Saccharomyces cerevisiae. Biotechnology for Biofuels, 2009, 2, 9.	6.2	130
13	The expression of aPichia stipitis xylose reductase mutant with higherKM for NADPH increases ethanol production from xylose in recombinantSaccharomyces cerevisiae. Biotechnology and Bioengineering, 2006, 93, 665-673.	1.7	127
14	High activity of xylose reductase and xylitol dehydrogenase improves xylose fermentation by recombinant Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2007, 73, 1039-1046.	1.7	125
15	Adaptive evolution of an industrial strain of Saccharomyces cerevisiae for combined tolerance to inhibitors and temperature. Biotechnology for Biofuels, 2013, 6, 151.	6.2	125
16	NADH- vs NADPH-coupled reduction of 5-hydroxymethyl furfural (HMF) and its implications on product distribution in Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2008, 78, 939-945.	1.7	122
17	Improved xylose and arabinose utilization by an industrial recombinant Saccharomyces cerevisiae strain using evolutionary engineering. Biotechnology for Biofuels, 2010, 3, 13.	6.2	117
18	Arabinose and xylose fermentation by recombinant Saccharomyces cerevisiae expressing a fungal pentose utilization pathway. Microbial Cell Factories, 2009, 8, 40.	1.9	115

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19	Stressâ€related challenges in pentose fermentation to ethanol by the yeast <i>Saccharomyces cerevisiae</i>. Biotechnology Journal, 2011, 6, 286-299.	1.8	107
20	Conversion of lignin model compounds by Pseudomonas putida KT2440 and isolates from compost. Applied Microbiology and Biotechnology, 2017, 101, 5059-5070.	1.7	103
21	Cofactor Dependence in Furan Reduction by Saccharomyces cerevisiae in Fermentation of Acid-Hydrolyzed Lignocellulose. Applied and Environmental Microbiology, 2005, 71, 7866-7871.	1.4	88
22	The level of glucose-6-phosphate dehydrogenase activity strongly influences xylose fermentation and inhibitor sensitivity in recombinantSaccharomyces cerevisiaestrains. Yeast, 2003, 20, 1263-1272.	0.8	87
23	Identification of an NADHâ€dependent 5â€hydroxymethylfurfuralâ€reducing alcohol dehydrogenase in <i>Saccharomyces cerevisiae</i>. Yeast, 2008, 25, 191-198.	0.8	85
24	Mapping the diversity of microbial lignin catabolism: experiences from the eLignin database. Applied Microbiology and Biotechnology, 2019, 103, 3979-4002.	1.7	85
25	Effect of enhanced xylose reductase activity on xylose consumption and product distribution in xylose-fermenting recombinant. FEMS Yeast Research, 2003, 3, 167-175.	1.1	83
26	Control of xylose consumption by xylose transport in recombinant Saccharomyces cerevisiae. Biotechnology and Bioengineering, 2003, 82, 818-824.	1.7	80
27	Efficient anaerobic whole cell stereoselective bioreduction with recombinantsaccharomyces cerevisiae. Biotechnology and Bioengineering, 2003, 84, 573-582.	1.7	62
28	Comparing the xylose reductase/xylitol dehydrogenase and xylose isomerase pathways in arabinose and xylose fermenting Saccharomyces cerevisiae strains. Biotechnology for Biofuels, 2008, 1, 16.	6.2	61
29	Adaptation to low pH and lignocellulosic inhibitors resulting in ethanolic fermentation and growth of Saccharomyces cerevisiae. AMB Express, 2016, 6, 59.	1.4	55
30	Identification of common traits in improved xyloseâ€growing <i>Saccharomyces cerevisiae</i> for inverse metabolic engineering. Yeast, 2008, 25, 835-847.	0.8	49
31	Physiological requirements for growth and competitiveness of <i>Dekkera bruxellensis</i> under oxygenâ€limited or anaerobic conditions. Yeast, 2012, 29, 265-274.	0.8	48
32	Variability of the response of <i>Saccharomyces cerevisiae</i> strains to lignocellulose hydrolysate. Biotechnology and Bioengineering, 2008, 100, 423-429.	1.7	47
33	Carbon fluxes of xylose-consuming Saccharomyces cerevisiae strains are affected differently by NADH and NADPH usage in HMF reduction. Applied Microbiology and Biotechnology, 2009, 84, 751-761.	1.7	47
34	Isolation of xylose isomerases by sequence- and function-based screening from a soil metagenomic library. Biotechnology for Biofuels, 2011, 4, 9.	6.2	46
35	Endogenous NADPH-dependent aldose reductase activity influences product formation during xylose consumption in recombinantSaccharomyces cerevisiae. Yeast, 2004, 21, 141-150.	0.8	44
36	Strain engineering for stereoselective bioreduction of dicarbonyl compounds by yeast reductases. FEMS Yeast Research, 2005, 5, 513-525.	1.1	42

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37	Adaptation of Scheffersomyces stipitis to hardwood spent sulfite liquor by evolutionary engineering. Biotechnology for Biofuels, 2015, 8, 50.	6.2	38
38	Screening of two complementary collections of Saccharomyces cerevisiae to identify enzymes involved in stereo-selective reductions of specific carbonyl compounds: an alternative to protein purification. Enzyme and Microbial Technology, 2003, 33, 163-172.	1.6	37
39	Cell periphery-related proteins as major genomic targets behind the adaptive evolution of an industrial Saccharomyces cerevisiae strain to combined heat and hydrolysate stress. BMC Genomics, 2015, 16, 514.	1.2	36
40	Bacterial conversion of depolymerized Kraft lignin. Biotechnology for Biofuels, 2019, 12, 56.	6.2	36
41	Assessing the effect of d-xylose on the sugar signaling pathways of Saccharomyces cerevisiae in strains engineered for xylose transport and assimilation. FEMS Yeast Research, 2018, 18, .	1.1	35
42	Efficient bioreduction of bicyclo[2.2.2]octane-2,5-dione and bicyclo[2.2.2]oct-7-ene-2,5-dione by genetically engineered Saccharomyces cerevisiae. Organic and Biomolecular Chemistry, 2006, 4, 2304-2312.	1.5	31
43	Reaction and strain engineering for improved stereo-selective whole-cell reduction of a bicyclic diketone. Applied Microbiology and Biotechnology, 2008, 77, 1111-1118.	1.7	31
44	Proteome analysis of the xyloseâ€fermenting mutant yeast strain TMB 3400. Yeast, 2009, 26, 371-382.	0.8	31
45	Exploring the xylose paradox in Saccharomyces cerevisiae through in vivo sugar signalomics of targeted deletants. Microbial Cell Factories, 2019, 18, 88.	1.9	31
46	Muconic Acid Production Using Engineered <i>Pseudomonas putida</i> KT2440 and a Guaiacol-Rich Fraction Derived from Kraft Lignin. ACS Sustainable Chemistry and Engineering, 2021, 9, 8097-8106.	3.2	31
47	Flavonoids as inhibitors of human carbonyl reductase 1. Chemico-Biological Interactions, 2008, 174, 98-108.	1.7	30
48	PGM2 overexpression improves anaerobic galactose fermentation in Saccharomyces cerevisiae. Microbial Cell Factories, 2010, 9, 40.	1.9	30
49	Biocatalytic potential of vanillin aminotransferase from Capsicum chinense. BMC Biotechnology, 2014, 14, 25.	1.7	29
50	Engineering of Saccharomyces cerevisiae for the production of poly-3-d-hydroxybutyrate from xylose. AMB Express, 2015, 5, 14.	1.4	29
51	Identification of the two-component guaiacol demethylase system from Rhodococcus rhodochrous and expression in Pseudomonas putida EM42 for guaiacol assimilation. AMB Express, 2019, 9, 34.	1.4	29
52	Anaerobic poly-3-d-hydroxybutyrate production from xylose in recombinant Saccharomyces cerevisiae using a NADH-dependent acetoacetyl-CoA reductase. Microbial Cell Factories, 2016, 15, 197.	1.9	27
53	Identification of modifications procuring growth on xylose in recombinant Saccharomyces cerevisiae strains carrying the Weimberg pathway. Metabolic Engineering, 2019, 55, 1-11.	3.6	27
54	NADH-dependent biosensor in Saccharomyces cerevisiae: principle and validation at the single cell level. AMB Express, 2014, 4, 81.	1.4	26

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55	Engineering Yeast Hexokinase 2 for Improved Tolerance Toward Xylose-Induced Inactivation. PLoS ONE, 2013, 8, e75055.	1.1	24
56	Short-term adaptation improves the fermentation performance of Saccharomyces cerevisiae in the presence of acetic acid at low pH. Applied Microbiology and Biotechnology, 2013, 97, 7517-7525.	1.7	23
57	Biological conversion of aromatic monolignol compounds by a Pseudomonas isolate from sediments of the Baltic Sea. AMB Express, 2018, 8, 32.	1.4	23
58	Real-time monitoring of the sugar sensing in Saccharomyces cerevisiae indicates endogenous mechanisms for xylose signaling. Microbial Cell Factories, 2016, 15, 183.	1.9	22
59	Exploring d-xylose oxidation in Saccharomyces cerevisiae through the Weimberg pathway. AMB Express, 2018, 8, 33.	1.4	22
60	Exploiting cell metabolism for biocatalytic whole-cell transamination by recombinant Saccharomyces cerevisiae. Applied Microbiology and Biotechnology, 2014, 98, 4615-4624.	1.7	21
61	Saccharomyces cerevisiae: a potential host for carboxylic acid production from lignocellulosic feedstock?. Applied Microbiology and Biotechnology, 2014, 98, 7299-7318.	1.7	20
62	Effect of nitrogen availability on the poly-3-d-hydroxybutyrate accumulation by engineered Saccharomyces cerevisiae. AMB Express, 2017, 7, 35.	1.4	20
63	Increased lignocellulosic inhibitor tolerance of Saccharomyces cerevisiae cell populations in early stationary phase. Biotechnology for Biofuels, 2017, 10, 114.	6.2	20
64	Re-assessment of YAP1 and MCR1 contributions to inhibitor tolerance in robust engineered Saccharomyces cerevisiae fermenting undetoxified lignocellulosic hydrolysate. AMB Express, 2014, 4, 56.	1.4	19
65	Screening of yeast species for the stereo-selective reduction of bicyclo[2.2.2]octane-2,6-dione. Journal of the Chemical Society, Perkin Transactions 1, 2002, , 1111-1114.	1.3	17
66	Electrochemical Probing of in Vivo 5-Hydroxymethyl Furfural Reduction in <i>Saccharomyces cerevisiae</i>. Analytical Chemistry, 2009, 81, 9896-9901.	3.2	17
67	Cross-reactions between engineered xylose and galactose pathways in recombinant Saccharomyces cerevisiae. Biotechnology for Biofuels, 2010, 3, 19.	6.2	17
68	Vanillin Production in <i>Pseudomonas</i> : Whole-Genome Sequencing of <i>Pseudomonas</i> sp. Strain 9.1 and Reannotation of Pseudomonas putida CalA as a Vanillin Reductase. Applied and Environmental Microbiology, 2020, 86, .	1.4	17
69	D-Xylose Sensing in Saccharomyces cerevisiae: Insights from D-Glucose Signaling and Native D-Xylose Utilizers. International Journal of Molecular Sciences, 2021, 22, 12410.	1.8	17
70	Flotation as a tool for indirect DNA extraction from soil. Applied Microbiology and Biotechnology, 2010, 87, 1927-1933.	1.7	16
71	The deletion of <i>YLR042c</i> improves ethanolic xylose fermentation by recombinant <i>Saccharomyces cerevisiae</i>. Yeast, 2010, 27, 741-751.	0.8	15
72	Yeast Pathway Kit: A Method for Metabolic Pathway Assembly with Automatically Simulated Executable Documentation. ACS Synthetic Biology, 2016, 5, 386-394.	1.9	15

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73	Improvement of whole-cell transamination with Saccharomyces cerevisiae using metabolic engineering and cell pre-adaptation. Microbial Cell Factories, 2017, 16, 3.	1.9	14
74	Comparison of engineered Saccharomyces cerevisiae and engineered Escherichia coli for the production of an optically pure keto alcohol. Applied Microbiology and Biotechnology, 2009, 84, 487-497.	1.7	13
75	Isolation and characterization of a resident tolerant Saccharomyces cerevisiae strain from a spent sulfite liquor fermentation plant. AMB Express, 2012, 2, 68.	1.4	13
76	Physiological characterization and sequence analysis of a syringate-consuming Actinobacterium. Bioresource Technology, 2019, 285, 121327.	4.8	13
77	Mild detergent treatment ofCandida tropicalis reveals a NADPH-dependent reductase in the crude membrane fraction, which enables the production of pure bicyclic exo-alcohol. Yeast, 2004, 21, 1253-1267.	0.8	10
78	Genetically engineered Saccharomyces cerevisiae for kinetic resolution of racemic bicyclo[3.3.1]nonane-2,6-dione. Tetrahedron: Asymmetry, 2008, 19, 2293-2295.	1.8	9
79	Engineered bakerâ€™s yeast as whole-cell biocatalyst for one-pot stereo-selective conversion of amines to alcohols. Microbial Cell Factories, 2014, 13, 118.	1.9	9
80	Kinetic resolution of racemic 5,6-epoxy-bicyclo[2.2.1]heptane-2-one using genetically engineered Saccharomyces cerevisiae. Journal of Molecular Catalysis B: Enzymatic, 2009, 58, 98-102.	1.8	7
81	Furaldehyde substrate specificity and kinetics of Saccharomyces cerevisiae alcohol dehydrogenase 1 variants. Microbial Cell Factories, 2014, 13, 112.	1.9	6
82	Identification of a Candida sp. reductase behind bicyclic exo-alcohol production. Journal of Molecular Catalysis B: Enzymatic, 2009, 59, 286-291.	1.8	4
83	Physiological effects of over-expressing compartment-specific components of the protein folding machinery in xylose-fermenting Saccharomyces cerevisiae. BMC Biotechnology, 2014, 14, 28.	1.7	4
84	Rationalisation of the substrate concentration dependent diastereoselectivity of a Saccharomyces cerevisiae short-chain dehydrogenase. Tetrahedron: Asymmetry, 2007, 18, 2554-2556.	1.8	1
85	The Synthesis of Bicyclo[2.2.2]octan-2,6-dione Revisited. Synthesis, 2006, 2006, 3527-3530.	1.2	0