Isabel SÃ¡-correia

List of Publications by Year
in descending order

202 papers	10,271 citations	28128 55 h-index	49007 88 g-index
206 all docs	206 docs citations	206 times ranked	12669 citing authors

#	Article	IF	Citations
1	Lipopolysaccharide modification in Gram-negative bacteria during chronic infection. FEMS Microbiology Reviews, 2016, 40, 480-493.	8.9	471
2	The YEASTRACT database: a tool for the analysis of transcription regulatory associations in Saccharomyces cerevisiae. Nucleic Acids Research, 2006, 34, D446-D451.	14.0	427
3	Adaptive Response and Tolerance to Weak Acids in<i>Saccharomyces cerevisiae</i>: A Genome-Wide View. OMICS A Journal of Integrative Biology, 2010, 14, 525-540.	2.0	242
4	Occurrence, production, and applications of gellan: current state and perspectives. Applied Microbiology and Biotechnology, 2008, 79, 889-900.	3.7	224
5	Insights intoPseudomonas putida KT2440 response to phenol-induced stress by quantitative proteomics. Proteomics, 2004, 4, 2640-2652.	3.0	219
6	The YEASTRACT database: an upgraded information system for the analysis of gene and genomic transcription regulation in<i>Saccharomyces cerevisiae</i>. Nucleic Acids Research, 2014, 42, D161-D166.	14.0	216
7	Genome-wide identification of Saccharomyces cerevisiae genes required for tolerance to acetic acid. Microbial Cell Factories, 2010, 9, 79.	4.1	211
8	Genome-Wide Identification of <i>S</i> <i>accharomyces cerevisiae</i> Genes Required for Maximal Tolerance to Ethanol. Applied and Environmental Microbiology, 2009, 75, 5761-5772.	3.2	201
9	A Major Facilitator Superfamily Transporter Plays a Dual Role in Polar Auxin Transport and Drought Stress Tolerance in<i>Arabidopsis</i>Â. Plant Cell, 2013, 25, 901-926.	6.7	193
10	YEASTRACT: an upgraded database for the analysis of transcription regulatory networks in Saccharomyces cerevisiae. Nucleic Acids Research, 2018, 46, D348-D353.	14.0	179
11	YEASTRACT: providing a programmatic access to curated transcriptional regulatory associations in Saccharomyces cerevisiae through a web services interface. Nucleic Acids Research, 2011, 39, D136-D140.	14.0	172
12	YEASTRACT+: a portal for cross-species comparative genomics of transcription regulation in yeasts. Nucleic Acids Research, 2020, 48, D642-D649.	14.0	172
13	Effect of extracellular acidification on the activity of plasma membrane ATPase and on the cytosolic and vacuolar pH of Saccharomyces cerevisiae. Biochimica Et Biophysica Acta - Biomembranes, 1997, 1325, 63-70.	2.7	151
14	Drug:H+ antiporters in chemical stress response in yeast. Trends in Microbiology, 2009, 17, 22-31.	7.7	149
15	Inhibition of Yeast Growth by Octanoic and Decanoic Acids Produced during Ethanolic Fermentation. Applied and Environmental Microbiology, 1989, 55, 21-28.	3.2	146
16	YEASTRACT-DISCOVERER: new tools to improve the analysis of transcriptional regulatory associations in Saccharomyces cerevisiae. Nucleic Acids Research, 2007, 36, D132-D136.	14.0	140
17	Genomic Expression Program Involving the Haa1p-Regulon in<i>Saccharomyces cerevisiae</i>Response to Acetic Acid. OMICS A Journal of Integrative Biology, 2010, 14, 587-601.	2.0	128
18	Combined Bioaugmentation and Biostimulation To Cleanup Soil Contaminated with High Concentrations of Atrazine. Environmental Science & Technology, 2004, 38, 632-637.	10.5	124

#	ARTICLE	IF	CITATIONS
19	Studies on the Involvement of the Exopolysaccharide Produced by Cystic Fibrosis-Associated Isolates of the Burkholderia cepacia Complex in Biofilm Formation and in Persistence of Respiratory Infections. Journal of Clinical Microbiology, 2004, 42, 3052-3058.	4.4	119
20	Intron Retention in the 5â€²UTR of the Novel ZIF2 Transporter Enhances Translation to Promote Zinc Tolerance in Arabidopsis. PLoS Genetics, 2014, 10, e1004375.	3.4	118
21	Molecular and physiological basis of Saccharomyces cerevisiae tolerance to adverse lignocellulose-based process conditions. Applied Microbiology and Biotechnology, 2019, 103, 159-175.	3.7	112
22	Adaptive Response and Tolerance to Acetic Acid in Saccharomyces cerevisiae and Zygosaccharomyces bailii: A Physiological Genomics Perspective. Frontiers in Microbiology, 2018, 9, 274.	3.6	111
23	MFS multidrug transporters in pathogenic fungi: do they have real clinical impact?. Frontiers in Physiology, 2014, 5, 197.	2.8	104
24	Developing an international <i>Pseudomonas aeruginosa</i> reference panel. MicrobiologyOpen, 2013, 2, 1010-1023.	3.1	98
25	Environmental genomics: mechanistic insights into toxicity of and resistance to the herbicide 2,4-D. Trends in Biotechnology, 2007, 25, 363-370.	9.5	93
26	Expression of theAZR1 gene (ORF YGR224w), encoding a plasma membrane transporter of the major facilitator superfamily, is required for adaptation to acetic acid and resistance to azoles inSaccharomyces cerevisiae. Yeast, 2000, 16, 1469-1481.	1.8	92
27	Ethanol-Induced Leakage in <i>Saccharomyces cerevisiae</i> : Kinetics and Relationship to Yeast Ethanol Tolerance and Alcohol Fermentation Productivity. Applied and Environmental Microbiology, 1988, 54, 903-909.	3.2	88
28	Identification of Regulatory Modules in Time Series Gene Expression Data Using a Linear Time Biclustering Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 153-165.	3.2	87
29	<i>Burkholderia cepacia</i> Complex Bacteria: a Feared Contamination Risk in Water-Based Pharmaceutical Products. Clinical Microbiology Reviews, 2020, 33, .	14.4	87
30	The RIM101 pathway has a role in<i>Saccharomyces cerevisiae</i>adaptive response and resistance to propionic acid and other weak acids. FEMS Yeast Research, 2009, 9, 202-216.	2.3	82
31	FLR1 gene (ORF YBR008c) is required for benomyl and methotrexate resistance inSaccharomyces cerevisiae and its benomyl-induced expression is dependent on Pdr3 transcriptional regulator. Yeast, 1999, 15, 1595-1608.	1.8	80
32	Molecular Analysis of Burkholderia cepacia Complex Isolates from a Portuguese Cystic Fibrosis Center: a 7-Year Study. Journal of Clinical Microbiology, 2003, 41, 4113-4120.	4.4	77
33	Phenotypic characterization of an international Pseudomonas aeruginosa reference panel: strains of cystic fibrosis (CF) origin show less in vivo virulence than non-CF strains. Microbiology (United) Tj ETQq1 1 0.78431 rgBT /Overlock 10	1.8	77
34	Dtr1p, a Multidrug Resistance Transporter of the Major Facilitator Superfamily, Plays an Essential Role in Spore Wall Maturation in Saccharomyces cerevisiae. Eukaryotic Cell, 2002, 1, 799-810.	3.3	76
35	Identification and physical organization of the gene cluster involved in the biosynthesis of Burkholderia cepacia complex exopolysaccharide. Biochemical and Biophysical Research Communications, 2003, 312, 323-333.	2.2	76
36	MFS transporters required for multidrug/multixenobiotic (MD/MX) resistance in the model yeast: understanding their physiological function through post-genomic approaches. Frontiers in Physiology, 2014, 5, 180.	2.8	76

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37	Structural Study of the Exopolysaccharide Produced by a Clinical Isolate of Burkholderia cepacia. Biochemical and Biophysical Research Communications, 2000, 273, 1088-1094.	2.2	75
38	Saccharomyces cerevisiae Resistance to Chlorinated Phenoxyacetic Acid Herbicides Involves Pdr1p-Mediated Transcriptional Activation of TPO1 and PDR5 Genes. Biochemical and Biophysical Research Communications, 2002, 292, 530-537.	2.2	75
39	AQR1 Gene (ORF YNL065w) Encodes a Plasma Membrane Transporter of the Major Facilitator Superfamily That Confers Resistance to Short-Chain Monocarboxylic Acids and Quinidine in Saccharomyces cerevisiae. Biochemical and Biophysical Research Communications, 2002, 292, 741-748.	2.2	75
40	The SPI1 Gene, Encoding a Glycosylphosphatidylinositol-Anchored Cell Wall Protein, Plays a Prominent Role in the Development of Yeast Resistance to Lipophilic Weak-Acid Food Preservatives. Applied and Environmental Microbiology, 2006, 72, 7168-7175.	3.2	75
41	Insights into yeast adaptive response to the agricultural fungicide mancozeb: A toxicoproteomics approach. Proteomics, 2009, 9, 657-670.	3.0	75
42	Genomic Expression Analysis Reveals Strategies of Burkholderia cenocepacia to Adapt to Cystic Fibrosis Patients' Airways and Antimicrobial Therapy. PLoS ONE, 2011, 6, e28831.	2.5	75
43	Long-term colonization of the cystic fibrosis lung by Burkholderia cepacia complex bacteria: epidemiology, clonal variation, and genome-wide expression alterations. Frontiers in Cellular and Infection Microbiology, 2011, 1, 12.	4.0	68
44	Improvement of yeast tolerance to acetic acid through Haa1 transcription factor engineering: towards the underlying mechanisms. Microbial Cell Factories, 2017, 16, 7.	4.1	68
45	Yeast toxicogenomics: genome-wide responses to chemical stresses with impact in environmental health, pharmacology, and biotechnology. Frontiers in Genetics, 2012, 3, 63.	2.3	67
46	Candida glabrata Drug:H ⁺ Antiporter CgQdr2 Confers Imidazole Drug Resistance, Being Activated by Transcription Factor CgPdr1. Antimicrobial Agents and Chemotherapy, 2013, 57, 3159-3167.	3.4	67
47	Virulence of Burkholderia cepacia complex strains in gp91phoxâˆ’/âˆ’ mice. Cellular Microbiology, 2007, 9, 2817-2825.	2.3	66
48	The multidrug resistance transporters of the major facilitator superfamily, 6 years after disclosure of Saccharomyces cerevisiae genome sequence. Journal of Biotechnology, 2002, 98, 215-226.	3.9	65
49	A genome-wide perspective on the response and tolerance to food-relevant stresses in Saccharomyces cerevisiae. Current Opinion in Biotechnology, 2011, 22, 150-156.	6.8	65
50	Functional Analysis of Burkholderia cepacia Genes bceD and bceF, Encoding a Phosphotyrosine Phosphatase and a Tyrosine Autokinase, Respectively: Role in Exopolysaccharide Biosynthesis and Biofilm Formation. Applied and Environmental Microbiology, 2007, 73, 524-534.	3.2	63
51	The Genome Sequence of the Highly Acetic Acid-Tolerant Zygosaccharomyces bailii-Derived Interspecies Hybrid Strain ISA1307, Isolated From a Sparkling Wine Plant. DNA Research, 2014, 21, 299-313.	3.5	62
52	Temperature profiles of ethanol tolerance: Effects of ethanol on the minimum and the maximum temperatures for growth of the yeastsSaccharomyces cerevisiaeandKluyveromyces fragilis. Biotechnology and Bioengineering, 1983, 25, 1665-1667.	3.5	61
53	Yeast adaptation to mancozeb involves the up-regulation of FLR1 under the coordinate control of Yap1, Rpn4, Pdr3, and Yrr1. Biochemical and Biophysical Research Communications, 2008, 367, 249-255.	2.2	61
54	Ethanol tolerance and activity of plasma membrane ATPase in Kluyveromyces marxianus and Saccharomyces cerevisiae. Enzyme and Microbial Technology, 1992, 14, 23-27.	3.3	59

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55	The herbicide 2,4-dichlorophenoxyacetic acid induces the generation of free-radicals and associated oxidative stress responses in yeast. Biochemical and Biophysical Research Communications, 2004, 324, 1101-1107.	2.2	59
56	Adaptation of Saccharomyces cerevisiae to the Herbicide 2,4-Dichlorophenoxyacetic Acid, Mediated by Msn2p- and Msn4p-Regulated Genes: Important Role of SPI1. Applied and Environmental Microbiology, 2003, 69, 4019-4028.	3.2	58
57	Increased expression of the yeast multidrug resistance ABC transporter Pdr18 leads to increased ethanol tolerance and ethanol production in high gravity alcoholic fermentation. Microbial Cell Factories, 2012, 11, 98.	4.1	58
58	Early transcriptional response of Saccharomyces cerevisiae to stress imposed by the herbicide 2,4-dichlorophenoxyacetic acid. FEMS Yeast Research, 2006, 6, 230-248.	2.3	57
59	Influence of Calcium Ion on Ethanol Tolerance of <i>Saccharomyces bayanus</i> and Alcoholic Fermentation by Yeasts. Applied and Environmental Microbiology, 1988, 54, 2439-2446.	3.2	57
60	HAA1 and PRS3 overexpression boosts yeast tolerance towards acetic acid improving xylose or glucose consumption: unravelling the underlying mechanisms. Applied Microbiology and Biotechnology, 2018, 102, 4589-4600.	3.7	56
61	Response of Pseudomonas putida KT2440 to phenol at the level of membrane proteome. Journal of Proteomics, 2010, 73, 1461-1478.	2.5	55
62	Pdr18 is involved in yeast response to acetic acid stress counteracting the decrease of plasma membrane ergosterol content and order. Scientific Reports, 2018, 8, 7860.	3.4	55
63	Temperature profiles of cellular growth and exopolysaccharide synthesis by Botryococus braunii KÃ¼tz. UC 58. Journal of Applied Phycology, 1991, 3, 35-42.	2.9	54
64	Identification of a DNA-binding site for the transcription factor Haa1, required for Saccharomyces cerevisiae response to acetic acid stress. Nucleic Acids Research, 2011, 39, 6896-6907.	14.0	54
65	The yeast ABC transporter Pdr18 (ORF <i>YNR070w</i>) controls plasma membrane sterol composition, playing a role in multidrug resistance. Biochemical Journal, 2011, 440, 195-202.	3.8	53
66	Synergistic effects of ethanol, octanoic, and decanoic acids on the kinetics and the activation parameters of thermal death in Saccharomyces bayanus. Biotechnology and Bioengineering, 1986, 28, 761-763.	3.5	52
67	Human Mesenchymal Stem Cell Expression Program upon Extended Ex-Vivo Cultivation, as Revealed by 2-DE-Based Quantitative Proteomics. PLoS ONE, 2012, 7, e43523.	2.5	51
68	Mechanistic Insights Into the Global Response to Phenol in the Phenol-biodegrading Strain<i>Pseudomonas</i>sp. M1 Revealed by Quantitative Proteomics. OMICS A Journal of Integrative Biology, 2007, 11, 233-251.	2.0	50
69	The Major Facilitator Superfamily Transporter ZIFL2 Modulates Cesium and Potassium Homeostasis in Arabidopsis. Plant and Cell Physiology, 2015, 56, 148-162.	3.2	50
70	A proteome analysis of the yeast response to the herbicide 2,4-dichlorophenoxyacetic acid. Proteomics, 2005, 5, 1889-1901.	3.0	49
71	Yeast adaptation to 2,4-dichlorophenoxyacetic acid involves increased membrane fatty acid saturation degree and decreased OLE1 transcription. Biochemical and Biophysical Research Communications, 2005, 330, 271-278.	2.2	48
72	Saccharomyces cerevisiae Multidrug Resistance Transporter Qdr2 Is Implicated in Potassium Uptake, Providing a Physiological Advantage to Quinidine-Stressed Cells. Eukaryotic Cell, 2007, 6, 134-142.	3.3	48

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73	Burkholderia cenocepacia Phenotypic Clonal Variation during a 3.5-Year Colonization in the Lungs of a Cystic Fibrosis Patient. Infection and Immunity, 2011, 79, 2950-2960.	2.4	48
74	Effect of cinnamic acid on the growth and on plasma membrane H+â€"ATPase activity of Saccharomyces cerevisiae. International Journal of Food Microbiology, 1999, 50, 173-179.	4.8	47
75	Toxicity of octanoic acid in Saccharomyces cerevisiae at temperatures between 8.5 and 30Â°C. Enzyme and Microbial Technology, 1995, 17, 826-831.	3.3	45
76	Saccharomyces cerevisiae Multidrug Transporter Qdr2p (Yil121wp): Localization and Function as a Quinidine Resistance Determinant. Antimicrobial Agents and Chemotherapy, 2004, 48, 2531-2537.	3.4	45
77	Insights into the Mechanisms of Toxicity and Tolerance to the Agricultural Fungicide Mancozeb in Yeast, as Suggested by a Chemogenomic Approach. OMICS A Journal of Integrative Biology, 2010, 14, 211-227.	2.0	45
78	Quantitative proteomics (2â€Đ DIGE) reveals molecular strategies employed by <i>Burkholderia cenocepacia</i> to adapt to the airways of cystic fibrosis patients under antimicrobial therapy. Proteomics, 2011, 11, 1313-1328.	3.0	45
79	Exceptionally High Representation of Burkholderia cepacia among B. cepacia Complex Isolates Recovered from the Major Portuguese Cystic Fibrosis Center. Journal of Clinical Microbiology, 2007, 45, 1628-1633.	4.4	44
80	Identification of candidate genes for yeast engineering to improve bioethanol production in very high gravity and lignocellulosic biomass industrial fermentations. Biotechnology for Biofuels, 2011, 4, 57.	6.3	44
81	COMPARISON OF TWO SCREENING BIOASSAYS, BASED ON THE FROG SCIATIC NERVE AND YEAST CELLS, FOR THE ASSESSMENT OF HERBICIDE TOXICITY. Environmental Toxicology and Chemistry, 2004, 23, 1211.	4.4	43
82	The yeast multidrug transporter Qdr3 (Ybr043c): localization and role as a determinant of resistance to quinidine, barban, cisplatin, and bleomycin. Biochemical and Biophysical Research Communications, 2005, 327, 952-959.	2.2	43
83	Yeast toxicogenomics: lessons from a eukaryotic cell model and cell factory. Current Opinion in Biotechnology, 2015, 33, 183-191.	6.8	43
84	Valorisation of pectin-rich agro-industrial residues by yeasts: potential and challenges. Applied Microbiology and Biotechnology, 2020, 104, 6527-6547.	3.7	41
85	Transcriptional Activation of FLR1 Gene during Saccharomyces cerevisiae Adaptation to Growth with Benomyl: Role of Yap1p and Pdr3p. Biochemical and Biophysical Research Communications, 2001, 280, 216-222.	2.2	40
86	Sphingomonas paucimobilis beta-glucosidase Bgl1: a member of a new bacterial subfamily in glycoside hydrolase family 1. Biochemical Journal, 2003, 370, 793-804.	3.8	40
87	Sphingolipid biosynthesis upregulation by TOR complex 2â€"Ypk1 signaling during yeast adaptive response to acetic acid stress. Biochemical Journal, 2016, 473, 4311-4325.	3.8	40
88	The dual role of candida glabrata drug:H+ antiporter CgAqr1 (ORF CAGL0J09944g) in antifungal drug and acetic acid resistance. Frontiers in Microbiology, 2013, 4, 170.	3.6	39
89	Macromolecular and solution properties of Cepacian: the exopolysaccharide produced by a strain of Burkholderia cepacia isolated from a cystic fibrosis patient. Carbohydrate Research, 2003, 338, 1861-1867.	2.4	38
90	Adaptive response to the antimalarial drug artesunate in yeast involves Pdr1p/Pdr3p-mediated transcriptional activation of the resistance determinantsTPO1andPDR5. FEMS Yeast Research, 2006, 6, 1130-1139.	2.3	38

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91	Temperature profiles of gellan gum synthesis and activities of biosynthetic enzymes¹. Biotechnology and Applied Biochemistry, 1994, 20, 385-395.	3.1	38
92	The drug:H+ antiporters of family 2 (DHA2), siderophore transporters (ARN) and glutathione:H+ antiporters (GEX) have a common evolutionary origin in hemiascomycete yeasts. BMC Genomics, 2013, 14, 901.	2.9	37
93	Transcription patterns ofPMA1andPMA2genes and activity of plasma membrane H+-ATPase inSaccharomyces cerevisiaeduring diauxic growth and stationary phase. Yeast, 2003, 20, 207-219.	1.8	36
94	Heterologous expression of a Tpo1 homolog from Arabidopsis thaliana confers resistance to the herbicide 2,4-D and other chemical stresses in yeast. Applied Microbiology and Biotechnology, 2009, 84, 927-936.	3.7	36
95	Yeast response and tolerance to polyamine toxicity involving the drugâ€Š:â€ŠH+ antiporter Qdr3 and the transcription factors Yap1 and Gcn4. Microbiology (United Kingdom), 2011, 157, 945-956.	1.8	36
96	The PathoYeastract database: an information system for the analysis of gene and genomic transcription regulation in pathogenic yeasts. Nucleic Acids Research, 2017, 45, D597-D603.	14.0	35
97	Regulation of the expression of the H+-ATPase genes PMA1 and PMA2 during growth and effects of octanoic acid in Saccharomyces cerevisiae. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1217, 65-73.	2.3	34
98	Adaptive response to acetic acid in the highly resistant yeast species <i><scp>Z</scp>ygosaccharomyces bailii</i> revealed by quantitative proteomics. Proteomics, 2012, 12, 2303-2318.	3.0	34
99	Incidence of Burkholderia contaminans at a cystic fibrosis centre with an unusually high representation of Burkholderia cepacia during 15 years of epidemiological surveillance. Journal of Medical Microbiology, 2015, 64, 927-935.	1.8	34
100	Use of Hanseniaspora guilliermondii and Hanseniaspora opuntiae to enhance the aromatic profile of beer in mixed-culture fermentation with Saccharomyces cerevisiae. Food Microbiology, 2021, 95, 103678.	4.2	34
101	Proteomic Profiling of Burkholderia cenocepacia Clonal Isolates with Different Virulence Potential Retrieved from a Cystic Fibrosis Patient during Chronic Lung Infection. PLoS ONE, 2013, 8, e83065.	2.5	34
102	Mechanisms underlying the acquisition of resistance to octanoic-acid-induced-death following exposure of Saccharomyces cerevisiae to mild stress imposed by octanoic acid or ethanol. Archives of Microbiology, 2001, 175, 301-307.	2.2	33
103	Roles of Mn2+, Mg2+ and Ca2+ on alginate biosynthesis by Pseudomonas aeruginosa. Enzyme and Microbial Technology, 1990, 12, 794-799.	3.3	31
104	Genome-wide screening of <i>Saccharomyces cerevisiae</i> genes required to foster tolerance towards industrial wheat straw hydrolysates. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 1753-1761.	3.0	31
105	Structural analysis of gellans produced by Sphingomonas elodea strains by electrospray tandem mass spectrometry. Carbohydrate Polymers, 2009, 77, 10-19.	10.5	30
106	The Zygosaccharomyces bailii transcription factor Haa1 is required for acetic acid and copper stress responses suggesting subfunctionalization of the ancestral bifunctional protein Haa1/Cup2. BMC Genomics, 2017, 18, 75.	2.9	30
107	Yeast adaptive response to acetic acid stress involves structural alterations and increased stiffness of the cell wall. Scientific Reports, 2021, 11, 12652.	3.4	30
108	The activity of plasma membrane H+-ATPase is strongly stimulated duringSaccharomyces cerevisiaeadaptation to growth under high copper stress, accompanying intracellular acidification. Yeast, 2001, 18, 511-521.	1.8	29

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109	The Complex of Sphingomonas elodea ATCC 31461 Glucose-1-Phosphate Uridylyltransferase with Glucose-1-Phosphate Reveals a Novel Quaternary Structure, Unique among Nucleoside Diphosphate-Sugar Pyrophosphorylase Members. Journal of Bacteriology, 2007, 189, 4520-4528.	2.4	28
110	In vivo activation of yeast plasma membrane H+-ATPase by ethanol: effect on the kinetic parameters and involvement of the carboxyl-terminus regulatory domain. Biochimica Et Biophysica Acta - Biomembranes, 1998, 1370, 310-316.	2.7	27
111	The Burkholderia cepacia bceA gene encodes a protein with phosphomannose isomerase and GDP-d-mannose pyrophosphorylase activities. Biochemical and Biophysical Research Communications, 2007, 353, 200-206.	2.2	27
112	Characterization of the unique organization and co-regulation of a gene cluster required for phenol and benzene catabolism in Pseudomonas sp. M1. Journal of Biotechnology, 2007, 131, 371-378.	3.9	27
113	2D electrophoresis-based expression proteomics: a microbiologistâ€™s perspective. Expert Review of Proteomics, 2010, 7, 943-953.	3.0	27
114	MUSA: a parameter free algorithm for the identification of biologically significant motifs. Bioinformatics, 2006, 22, 2996-3002.	4.2	26
115	Identification of Genes Required for Maximal Tolerance to High-Glucose Concentrations, as Those Present in Industrial Alcoholic Fermentation Media, Through a Chemogenomics Approach. OMICS A Journal of Integrative Biology, 2010, 14, 201-210.	2.0	26
116	Structure of Burkholderia cepacia UDP-Glucose Dehydrogenase (UGD) BceC and Role of Tyr10 in Final Hydrolysis of UGD Thioester Intermediate. Journal of Bacteriology, 2011, 193, 3978-3987.	2.4	26
117	Enzymes Leading to the Nucleotide Sugar Precursors for Exopolysaccharide Synthesis in Burkholderia cepacia. Biochemical and Biophysical Research Communications, 2000, 276, 71-76.	2.2	25
118	Proteins Encoded by Sphingomonas elodea ATCC 31461 rmlA and ugpG Genes, Involved in Gellan Gum Biosynthesis, Exhibit both dTDP- and UDP-Glucose Pyrophosphorylase Activities. Applied and Environmental Microbiology, 2005, 71, 4703-4712.	3.2	25
119	Chemistry and Biology of the Potent Endotoxin from a <i>Burkholderia dolosa</i> Clinical Isolate from a Cystic Fibrosis Patient. ChemBioChem, 2013, 14, 1105-1115.	2.8	25
120	The CgHaa1-Regulon Mediates Response and Tolerance to Acetic Acid Stress in the Human Pathogen <i>Candida glabrata</i>. G3: Genes, Genomes, Genetics, 2017, 7, 1-18.	1.9	25
121	Genome-wide search for candidate genes for yeast robustness improvement against formic acid reveals novel susceptibility (Trk1 and positive regulators) and resistance (Haa1-regulon) determinants. Biotechnology for Biofuels, 2017, 10, 96.	6.3	24
122	Quantitative 1H-NMR-Metabolomics Reveals Extensive Metabolic Reprogramming and the Effect of the Aquaglyceroporin FPS1 in Ethanol-Stressed Yeast Cells. PLoS ONE, 2013, 8, e55439.	2.5	23
123	Modification of plasma membrane lipid order and H + -ATPase activity as part of the response of Saccharomyces cerevisiae to cultivation under mild and high copper stress. Archives of Microbiology, 2000, 173, 262-268.	2.2	22
124	Transcriptomic Profiling of the<i>Saccharomyces cerevisiae</i>Response to Quinine Reveals a Glucose Limitation Response Attributable to Drug-Induced Inhibition of Glucose Uptake. Antimicrobial Agents and Chemotherapy, 2009, 53, 5213-5223.	3.4	22
125	Biochemical characterization and phylogenetic analysis of UDP-glucose dehydrogenase from the gellan gum producer Sphingomonas elodea ATCC 31461. Applied Microbiology and Biotechnology, 2007, 76, 1319-1327.	3.7	21
126	Search for genes responsible for the remarkably high acetic acid tolerance of a Zygosaccharomyces bailii-derived interspecies hybrid strain. BMC Genomics, 2015, 16, 1070.	2.9	21

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127	Structure of O-Antigen and Hybrid Biosynthetic Locus in Burkholderia cenocepacia Clonal Variants Recovered from a Cystic Fibrosis Patient. Frontiers in Microbiology, 2017, 8, 1027.	3.6	21
128	Exploring Yeast Diversity to Produce Lipid-Based Biofuels from Agro-Forestry and Industrial Organic Residues. Journal of Fungi (Basel, Switzerland), 2022, 8, 687.	3.6	21
129	Bacterial Removal of Quinolizidine Alkaloids and Other Carbon Sources from aLupinus albusAqueous Extract. Journal of Agricultural and Food Chemistry, 2002, 50, 2318-2323.	5.3	20
130	Genome-Wide Identification of Genes Required for Yeast Growth Under Imatinib Stress: Vacuolar H+-ATPase Function Is an Important Target of This Anticancer Drug. OMICS A Journal of Integrative Biology, 2009, 13, 185-198.	2.0	20
131	Use of Fourier transform infrared spectroscopy and chemometrics to discriminate clinical isolates of bacteria of the Burkholderia cepacia complex from different species and ribopatterns. Analytical and Bioanalytical Chemistry, 2009, 394, 2161-2171.	3.9	20
132	Genome sequence of the highly weak-acid-tolerant Zygosaccharomyces bailii IST302, amenable to genetic manipulations and physiological studies. FEMS Yeast Research, 2017, 17, .	2.3	20
133	Variation ofBurkholderia cenocepaciavirulence potential during cystic fibrosis chronic lung infection. Virulence, 2017, 8, 782-796.	4.5	20
134	Burkholderia cepacia Complex Species Differ in the Frequency of Variation of the Lipopolysaccharide O-Antigen Expression During Cystic Fibrosis Chronic Respiratory Infection. Frontiers in Cellular and Infection Microbiology, 2019, 9, 273.	4.0	20
135	Complete Utilization of the Major Carbon Sources Present in Sugar Beet Pulp Hydrolysates by the Oleaginous Red Yeasts Rhodotorula toruloides and R. mucilaginosa. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rg BT /Overlock 10 Tf	3.6	20
136	TFRank: network-based prioritization of regulatory associations underlying transcriptional responses. Bioinformatics, 2011, 27, 3149-3157.	4.2	19
137	Synthesis and Structure of Copper Complexes of a N6O4 Macrocyclic Ligand and Catalytic Application in Alcohol Oxidation. Catalysts, 2019, 9, 424.	3.6	19
138	Metabolic insights into the yeast response to propionic acid based on high resolution 1H NMR spectroscopy. Metabolomics, 2011, 7, 457-468.	3.1	18
139	Impact of assimilable nitrogen availability in glucose uptake kinetics in Saccharomyces cerevisiae during alcoholic fermentation. Microbial Cell Factories, 2012, 11, 99.	4.1	18
140	Modification of Saccharomyces cerevisiae thermotolerance following rapid exposure to acid stress. International Journal of Food Microbiology, 1998, 42, 225-230.	4.8	17
141	Conformation of the exopolysaccharide of Burkholderia cepacia predicted with molecular mechanics (MM3) using genetic algorithm search. Carbohydrate Research, 2005, 340, 1019-1024.	2.4	17
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