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	The role of ion homeostasis in adaptation and tolerance to acetic acid stress in yeasts. FEMS Yeast Research, 2024, 24, .	2.3	0
2	Candida boidinii isolates from olive curation water: a promising platform for methanol-based biomanufacturing. AMB Express, 2024, 14, .	3.1	0
3	An Evolved Strain of the Oleaginous Yeast Rhodotorula toruloides, Multi-Tolerant to the Major Inhibitors Present in Lignocellulosic Hydrolysates, Exhibits an Altered Cell Envelope. Journal of Fungi (Basel, Switzerland), 2023, 9, 1073.	3.6	1
4	The Hrk1 kinase is a determinant of acetic acid tolerance in yeast by modulating H+ and K+ homeostasis. Microbial Cell, 2023, 10, 261-276.	3.1	3
5	Towards valorization of pectin-rich agro-industrial residues: Engineering of Saccharomyces cerevisiae for co-fermentation of d-galacturonic acid and glycerol. Metabolic Engineering, 2022, 69, 1-14.	7.1	11
6	Exploring the biological function of efflux pumps for the development of superior industrial yeasts. Current Opinion in Biotechnology, 2022, 74, 32-41.	6.8	10
7	Crosstalk between Yeast Cell Plasma Membrane Ergosterol Content and Cell Wall Stiffness under Acetic Acid Stress Involving Pdr18. Journal of Fungi (Basel, Switzerland), 2022, 8, 103.	3.6	17
8	Genome Sequence and Analysis of the Flavinogenic Yeast Candida membranifaciens IST 626. Journal of Fungi (Basel, Switzerland), 2022, 8, 254.	3.6	1
9	Prediction of Gene and Genomic Regulation in Candida Species, Using the PathoYeastract Database: A Comparative Genomics Approach. Methods in Molecular Biology, 2022, 2477, 419-437.	0.0	0
10	Characterization of a new Blastobotrys navarrensis strain indicates that it is not a later synonym of Blastobotrys proliferans. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.8	2
11	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
12	The <scp>ABC</scp> transporter Pdr18 is required for yeast thermotolerance due to its role in ergosterol transport and plasma membrane properties. Environmental Microbiology, 2021, 23, 69-80.	3.9	11
13	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
14	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 ETQq0 0 0 rgBT /Overlock 10 Tf 50 217 T	3.6	20
15	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
16	From a genome assembly to full regulatory network prediction: the case study of Rhodotorula toruloides putative Haa1-regulon. BMC Bioinformatics, 2021, 22, 399.	2.7	4
17	The N.C.Yeastract and CommunityYeastract databases to study gene and genomic transcription regulation in non-conventional yeasts. FEMS Yeast Research, 2021, 21, .	2.3	8
18	The Identification of Genetic Determinants of Methanol Tolerance in Yeast Suggests Differences in Methanol and Ethanol Toxicity Mechanisms and Candidates for Improved Methanol Tolerance Engineering. Journal of Fungi (Basel, Switzerland), 2021, 7, 90.	3.6	17

#	ARTICLE	IF	CITATIONS
19	YEASTRACT+: a portal for cross-species comparative genomics of transcription regulation in yeasts. Nucleic Acids Research, 2020, 48, D642-D649.	14.0	172
20	Comparative Evolutionary Patterns of Burkholderia cenocepacia and B. multivorans During Chronic Co-infection of a Cystic Fibrosis Patient Lung. Frontiers in Microbiology, 2020, 11, 574626.	3.6	9
21	Valorisation of pectin-rich agro-industrial residues by yeasts: potential and challenges. Applied Microbiology and Biotechnology, 2020, 104, 6527-6547.	3.7	41
22	Adaptation and Survival of Burkholderia cepacia and B. contaminans During Long-Term Incubation in Saline Solutions Containing Benzalkonium Chloride. Frontiers in Bioengineering and Biotechnology, 2020, 8, 630.	4.2	14
23	<i>Burkholderia cepacia</i> Complex Bacteria: a Feared Contamination Risk in Water-Based Pharmaceutical Products. Clinical Microbiology Reviews, 2020, 33, .	14.4	87
24	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
25	Variation of Burkholderia cenocepacia cell wall morphology and mechanical properties during cystic fibrosis lung infection, assessed by atomic force microscopy. Scientific Reports, 2019, 9, 16118.	3.4	13
26	Synthesis and Structure of Copper Complexes of a N6O4 Macrocyclic Ligand and Catalytic Application in Alcohol Oxidation. Catalysts, 2019, 9, 424.	3.6	19
27	Physiological Genomics of Multistress Resistance in the Yeast Cell Model and Factory: Focus on MDR/MXR Transporters. Progress in Molecular and Subcellular Biology, 2019, 58, 1-35.	0.0	4
28	Physiological Genomics of the Highly Weak-Acid-Tolerant Food Spoilage Yeasts of Zygosaccharomyces bailii sensu lato. Progress in Molecular and Subcellular Biology, 2019, 58, 85-109.	0.0	11
29	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
30	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
31	YEASTRACT: an upgraded database for the analysis of transcription regulatory networks in Saccharomyces cerevisiae. Nucleic Acids Research, 2018, 46, D348-D353.	14.0	179
32	The Paralogous Genes PDR18 and SNQ2, Encoding Multidrug Resistance ABC Transporters, Derive From a Recent Duplication Event, PDR18 Being Specific to the Saccharomyces Genus. Frontiers in Genetics, 2018, 9, 476.	2.3	15
33	Transcriptional profiling of Zygosaccharomyces bailii early response to acetic acid or copper stress mediated by ZbHaa1. Scientific Reports, 2018, 8, 14122.	3.4	16
34	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
35	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
36	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

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37	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
38	Yeast response and tolerance to benzoic acid involves the Gcn4- and Stp1-regulated multidrug/multixenobiotic resistance transporter Tpo1. Applied Microbiology and Biotechnology, 2017, 101, 5005-5018.	3.7	8
39	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
40	Using dendritic cells to evaluate how Burkholderia cenocepacia clonal isolates from a chronically infected cystic fibrosis patient subvert immune functions. Medical Microbiology and Immunology, 2017, 206, 111-123.	4.9	17
41	Heterologous expression of the yeast Tpo1p or Pdr5p membrane transporters in Arabidopsis confers plant xenobiotic tolerance. Scientific Reports, 2017, 7, 4529.	3.4	11
42	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
43	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
44	Variation ofBurkholderia cenocepaciavirulence potential during cystic fibrosis chronic lung infection. Virulence, 2017, 8, 782-796.	4.5	20
45	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
46	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
47	Membrane Phosphoproteomics of Yeast Early Response to Acetic Acid: Role of Hrk1 Kinase and Lipid Biosynthetic Pathways, in Particular Sphingolipids. Frontiers in Microbiology, 2017, 8, 1302.	3.6	15
48	1H-NMR-Based Endometabolome Profiles of Burkholderia cenocepacia Clonal Variants Retrieved from a Cystic Fibrosis Patient during Chronic Infection. Frontiers in Microbiology, 2016, 7, 2024.	3.6	3
49	Lipopolysaccharide modification in Gram-negative bacteria during chronic infection. FEMS Microbiology Reviews, 2016, 40, 480-493.	8.9	471
50	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
51	SNaPBceBcon : a Practical Tool for Identification and Genotyping of Burkholderia cepacia and Burkholderia contaminans. Journal of Clinical Microbiology, 2016, 54, 483-488.	4.4	1
52	Mitochondrial proteomics of the acetic acid - induced programmed cell death response in a highly tolerant Zygosaccharomyces bailii - derived hybrid strain. Microbial Cell, 2016, 3, 65-78.	3.1	11
53	Predicting Gene and Genomic Regulation in Saccharomyces cerevisiae, using the YEASTRACT Database: A Step-by-Step Guided Analysis. Methods in Molecular Biology, 2016, 1361, 391-404.	0.0	1
54	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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55	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
56	Yeast toxicogenomics: lessons from a eukaryotic cell model and cell factory. Current Opinion in Biotechnology, 2015, 33, 183-191.	6.8	43
57	The Major Facilitator Superfamily Transporter ZIFL2 Modulates Cesium and Potassium Homeostasis in Arabidopsis. Plant and Cell Physiology, 2015, 56, 148-162.	3.2	50
58	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 ETQq0 0 0 rgBT /Overlock 10 Tf 50 61	1.8	17
59	MFS multidrug transporters in pathogenic fungi: do they have real clinical impact?. Frontiers in Physiology, 2014, 5, 197.	2.8	104
60	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
61	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
62	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
63	Conformational and mechanical changes of DNA upon transcription factor binding detected by a QCM and transmission line model. Analyst, The, 2014, 139, 1847-1855.	3.5	10
64	Transmission line model analysis of transcription factors binding to oligoduplexes â€“ differentiation of the effect of single nucleotide modifications. Analyst, The, 2014, 139, 3871-3874.	3.5	2
65	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
66	Burkholderia dolosa phenotypic variation during the decline in lung function of a cystic fibrosis patient during 5.5 years of chronic colonization. Journal of Medical Microbiology, 2014, 63, 594-601.	1.8	17
67	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
68	Phylogenetic and syntenic analyses of the 12-spanner drug:H + antiporter family 1 (DHA1) in pathogenic Candida species: evolution of MDR1 and FLU1 genes. Genomics, 2014, 104, 45-57.	2.9	11
69	Developing an international <i>Pseudomonas aeruginosa</i> reference panel. MicrobiologyOpen, 2013, 2, 1010-1023.	3.1	98
70	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
71	<i>SNaPBcen</i> : a Novel and Practical Tool for Genotyping Burkholderia cenocepacia. Journal of Clinical Microbiology, 2013, 51, 2646-2653.	4.4	9
72	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

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73	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
74	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
75	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
76	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
77	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
78	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
79	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
80	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
81	Impact of assimilable nitrogen availability in glucose uptake kinetics in Saccharomyces cerevisiae during alcoholic fermentation. Microbial Cell Factories, 2012, 11, 99.	4.1	18
82	Quantitative- and Phospho-Proteomic Analysis of the Yeast Response to the Tyrosine Kinase Inhibitor Imatinib to Pharmacoproteomics-Guided Drug Line Extension. OMICS A Journal of Integrative Biology, 2012, 16, 537-551.	2.0	9
83	Characterization of Complex Regulatory Networks and Identification of Promoter Regulatory Elements in Yeast: â€œIn Silicoâ€•and â€œWet-Labâ€•Approaches. Methods in Molecular Biology, 2012, 809, 27-48.	0.0	4
84	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
85	Identification of targets and mechanisms of resistance to imatinib and quinine using a molecular systems biology approach. , 2011, , .		0
86	Using systems biology approaches to study a multidrug resistance network. , 2011, , .		0
87	Response and resistance to drugs and chemical stress in the yeast model: A genome-wide view. , 2011, , .		0
88	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
89	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
90	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

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91	Metabolic insights into the yeast response to propionic acid based on high resolution 1H NMR spectroscopy. Metabolomics, 2011, 7, 457-468.	3.1	18
92	A genome-wide screen identifies yeast genes required for protection against or enhanced cytotoxicity of the antimalarial drug quinine. Molecular Genetics and Genomics, 2011, 286, 333-346.	2.1	15
93	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
94	Quantitative proteomics (2â€Ð 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
95	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
96	Reconstruction of the evolutionary history of the DHA1 family of yeast multidrug resistance transporters of the major facilitator superfamily. , 2011, , .		0
97	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
98	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
99	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
100	OMICS approaches to reveal Burkholderia cenocepacia adaptive strategies to long-term residence in the lungs of cystic fibrosis patients under antibiotic therapy. , 2011, , .		0
101	TFRank: network-based prioritization of regulatory associations underlying transcriptional responses. Bioinformatics, 2011, 27, 3149-3157.	4.2	19
102	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
103	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
104	Response of Pseudomonas putida KT2440 to phenol at the level of membrane proteome. Journal of Proteomics, 2010, 73, 1461-1478.	2.5	55
105	Cloning, expression, purification, crystallization and preliminary crystallographic studies of UgdG, an UDP-glucose dehydrogenase fromSphingomonas elodeaATCC 31461. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 69-72.	0.7	8
106	Cloning, expression, purification, crystallization and preliminary crystallographic studies of BceC, aÂUDP-glucose dehydrogenase fromBurkholderia cepaciaIST408. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 269-271.	0.7	3
107	Genome-wide identification of Saccharomyces cerevisiae genes required for tolerance to acetic acid. Microbial Cell Factories, 2010, 9, 79.	4.1	211
108	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

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109	2D electrophoresis-based expression proteomics: a microbiologistâ€™s perspective. Expert Review of Proteomics, 2010, 7, 943-953.	3.0	27
110	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
111	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
112	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
113	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
114	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
115	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
116	Teaching expression proteomics: From the wetâ€lab to the laptop. Biochemistry and Molecular Biology Education, 2009, 37, 279-286.	1.2	8
117	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
118	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
119	Insights into yeast adaptive response to the agricultural fungicide mancozeb: A toxicoproteomics approach. Proteomics, 2009, 9, 657-670.	3.0	75
120	Adaptation to Î²â€myrcene catabolism in <i>Pseudomonas</i> sp. M1: An expression proteomics analysis. Proteomics, 2009, 9, 5101-5111.	3.0	13
121	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
122	Structural analysis of gellans produced by Sphingomonas elodea strains by electrospray tandem mass spectrometry. Carbohydrate Polymers, 2009, 77, 10-19.	10.5	30
123	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
124	Drug:H+ antiporters in chemical stress response in yeast. Trends in Microbiology, 2009, 17, 22-31.	7.7	149
125	Occurrence, production, and applications of gellan: current state and perspectives. Applied Microbiology and Biotechnology, 2008, 79, 889-900.	3.7	224
126	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

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127	The clinical course of Burkholderia cepacia complex bacteria respiratory infection in cystic fibrosis patients. Revista Portuguesa De Pneumologia, 2008, 14, 5-26.	0.7	9
128	InfecÃ§Ã£o respiratÃ³ria por bactÃ©rias do complexo Burkholderia cepacia: EvoluÃ§Ã£o clÃnica em doentes com fibrose quÃstica. Revista Portuguesa De Pneumologia, 2008, 14, 5-26.	0.7	15
129	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
130	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
131	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
132	Biotechnology of the Bacterial Gellan Gum: Genes and Enzymes of the Biosynthetic Pathway. , 2007, , 233-250.		4
133	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
134	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
135	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
136	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
137	Virulence of Burkholderia cepacia complex strains in gp91phoxâˆ’/âˆ’ mice. Cellular Microbiology, 2007, 9, 2817-2825.	2.3	66
138	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
139	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
140	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
141	Bioinformatics: A New Approach for the Challenges of Molecular Biology. , 2007, , 295-309.		0
142	HySP26 gene transcription is strongly induced during Saccharomyces cerevisiae growth at low pH. FEMS Microbiology Letters, 2006, 149, 85-88.	1.8	16
143	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
144	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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145	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
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