

Raquel M Silva

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

1,174
citations

331670

21
h-index

414414

32
g-index

55
all docs

55
docs citations

55
times ranked

2015
citing authors

#	ARTICLE	IF	CITATIONS
1	A genetic code alteration generates a proteome of high diversity in the human pathogen <i>Candida albicans</i> . <i>Genome Biology</i> , 2007, 8, R206.	9.6	99
2	Comparative context analysis of codon pairs on an ORFeome scale. <i>Genome Biology</i> , 2005, 6, R28.	9.6	85
3	Transcriptional Profiling of Azole-Resistant <i>Candida parapsilosis</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 3546-3556.	3.2	78
4	Evolution of the genetic code in yeasts. <i>Yeast</i> , 2006, 23, 203-213.	1.7	67
5	Gains, Losses and Changes of Function after Gene Duplication: Study of the Metallothionein Family. <i>PLoS ONE</i> , 2011, 6, e18487.	2.5	67
6	Extensive regulation of nicotinate phosphoribosyltransferase (NAPRT) expression in human tissues and tumors. <i>Oncotarget</i> , 2016, 7, 1973-1983.	1.8	54
7	Critical roles for a genetic code alteration in the evolution of the genus <i>Candida</i> . <i>EMBO Journal</i> , 2007, 26, 4555-4565.	7.8	43
8	Impact of ERG3 mutations and expression of ergosterol genes controlled by UPC2 and NDT80 in <i>Candida parapsilosis</i> azole resistance. <i>Clinical Microbiology and Infection</i> , 2017, 23, 575.e1-575.e8.	6.0	42
9	Essential genetic findings in neurodevelopmental disorders. <i>Human Genomics</i> , 2019, 13, 31.	2.9	41
10	Three minimal sequences found in Ebola virus genomes and absent from human DNA. <i>Bioinformatics</i> , 2015, 31, 2421-2425.	4.1	38
11	Fluconazole and Voriconazole Resistance in <i>Candida parapsilosis</i> Is Conferred by Gain-of-Function Mutations in MRR1 Transcription Factor Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6629-6633.	3.2	38
12	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
13	<i>In Vivo</i> and <i>In Vitro</i> Acquisition of Resistance to Voriconazole by <i>Candida krusei</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4604-4611.	3.2	33
14	<i>FKS2</i> Mutations Associated with Decreased Echinocandin Susceptibility of <i>Candida glabrata</i> following Anidulafungin Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1312-1314.	3.2	32
15	Medical Emergency Team: How do we play when we stay? Characterization of MET actions at the scene. <i>Scandinavian Journal of Trauma, Resuscitation and Emergency Medicine</i> , 2016, 24, 33.	2.6	31
16	A Transcriptomics Approach To Unveiling the Mechanisms of <i>In Vitro</i> Evolution towards Fluconazole Resistance of a <i>Candida glabrata</i> Clinical Isolate. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	31
17	An alignment-free method to find and visualise rearrangements between pairs of DNA sequences. <i>Scientific Reports</i> , 2015, 5, 10203.	3.3	27
18	Improving the in silico assessment of pathogenicity for compensated variants. <i>European Journal of Human Genetics</i> , 2017, 25, 2-7.	2.8	24

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19	Environmental azole fungicide, prochloraz, can induce cross-resistance to medical triazoles in <i>Candida glabrata</i> . <i>FEMS Yeast Research</i> , 2014, 14, n/a-n/a.	2.3	22
20	The exceptional genomic word symmetry along DNA sequences. <i>BMC Bioinformatics</i> , 2016, 17, 59.	2.6	22
21	NAMPT and NAPRT1: novel polymorphisms and distribution of variants between normal tissues and tumor samples. <i>Scientific Reports</i> , 2014, 4, 6311.	3.3	21
22	Evolution of the NET (NocA, Nlz, Elbow, TLP-1) protein family in metazoans: insights from expression data and phylogenetic analysis. <i>Scientific Reports</i> , 2016, 6, 38383.	3.3	17
23	Yeast proteome map (update 2006). <i>Proteomics</i> , 2007, 7, 1117-1120.	2.2	16
24	The Yeast PNC1 Longevity Gene Is Up-Regulated by mRNA Mistranslation. <i>PLoS ONE</i> , 2009, 4, e5212.	2.5	15
25	Population wide testing pooling strategy for SARS-CoV-2 detection using saliva. <i>PLoS ONE</i> , 2022, 17, e0263033.	2.5	15
26	DNA word analysis based on the distribution of the distances between symmetric words. <i>Scientific Reports</i> , 2017, 7, 728.	3.3	14
27	Metagenomic Composition Analysis of an Ancient Sequenced Polar Bear Jawbone from Svalbard. <i>Genes</i> , 2018, 9, 445.	2.4	13
28	Yeast as a model organism for studying the evolution of nonstandard genetic codes. <i>Briefings in Functional Genomics & Proteomics</i> , 2004, 3, 35-46.	3.8	12
29	Exosomal A β -Binding Proteins Identified by α -Silico Analysis Represent Putative Blood-Derived Biomarker Candidates for Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3933.	4.1	12
30	Epidemiology and susceptibility profile to classic antifungals and over-the-counter products of <i>Malassezia</i> clinical isolates from a Portuguese University Hospital: a prospective study. <i>Journal of Medical Microbiology</i> , 2019, 68, 778-784.	1.8	10
31	Merging microarray studies to identify a common gene expression signature to several structural heart diseases. <i>BioData Mining</i> , 2020, 13, 8.	4.0	9
32	Codon-triplet context unveils unique features of the <i>Candida albicans</i> protein coding genome. <i>BMC Genomics</i> , 2007, 8, 444.	2.8	8
33	The Evolutionary Portrait of Metazoan NAD Salvage. <i>PLoS ONE</i> , 2013, 8, e64674.	2.5	8
34	Influence of saliva interaction on surface properties manufactured for rapid osseointegration in dental implants. <i>Biofouling</i> , 2021, 37, 757-766.	2.2	8
35	A proteomic analysis of the interactions between poly(L-lactic acid) nanofibers and SH-SY5Y neuronal-like cells. <i>AIMS Molecular Science</i> , 2016, 3, 661-682.	0.5	8
36	<i>Malassezia</i> species retrieved from skin with pityriasis versicolor, seborrhoeic dermatitis and skin free of lesions: a comparison of two sampling methods. <i>British Journal of Dermatology</i> , 2018, 179, 526-527.	1.5	7

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37	Tracking the functional meaning of the human oral-microbiome protein-protein interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 199-235.	2.3	7
38	The Role of Recombination in the Origin and Evolution of Alu Subfamilies. <i>PLoS ONE</i> , 2013, 8, e64884.	2.5	7
39	Prognostic value of plasma D-dimer level in adults with community-acquired pneumonia: A prospective study. <i>Revista Portuguesa De Pneumologia</i> , 2015, 21, 218-219.	0.7	6
40	Mining clinical attributes of genomic variants through assisted literature curation in Egas. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw096.	3.0	6
41	FKS1 mutation associated with decreased echinocandin susceptibility of <i>Aspergillus fumigatus</i> following anidulafungin exposure. <i>Scientific Reports</i> , 2020, 10, 11976.	3.3	6
42	Mechanisms of Acquired In Vivo and In Vitro Resistance to Voriconazole by <i>Candida krusei</i> following Exposure to Suboptimal Drug Concentration. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	6
43	The transcription factor Ndt80 is a repressor of <i>Candida parapsilosis</i> virulence attributes. <i>Virulence</i> , 2021, 12, 601-614.	4.4	6
44	Comparison of Compression-Based Measures with Application to the Evolution of Primate Genomes. <i>Entropy</i> , 2018, 20, 393.	2.2	5
45	Exceptional Symmetry by Genomic Word. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 14-23.	3.6	4
46	The role of NAD metabolism in neuronal differentiation. <i>Neurochemistry International</i> , 2022, 159, 105402.	3.8	3
47	The mitochondrial genome of the pinewood nematode (<i>Bursaphelenchus xylophilus</i>) lineage introduced in Europe. <i>Mitochondrial DNA</i> , 2014, 25, 420-421.	0.6	2
48	Identification of DNA CpG Islands Using Inter-dinucleotide Distances. <i>Communications in Computer and Information Science</i> , 2015, , 162-172.	0.5	2
49	Distribution of Distances Between Symmetric Words in the Human Genome: Analysis of Regular Peaks. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 367-372.	3.6	2
50	Visualization of Distinct DNA Regions of the Modern Human Relatively to a Neanderthal Genome. <i>Lecture Notes in Computer Science</i> , 2017, , 235-242.	1.3	2
51	Comparing Reverse Complementary Genomic Words Based on Their Distance Distributions and Frequencies. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 1-11.	3.6	1
52	Exceptional Symmetry Profile: A Genomic Word Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2016, , 151-159.	0.6	1
53	Mutation Analysis in PARK2 Gene Uncovers Patterns of Associated Genetic Variants. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 145-152.	0.6	0
54	Dissimilar Symmetric Word Pairs in the Human Genome. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 248-256.	0.6	0