

Juan Lucas Argueso

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

33
papers

1,357
citations

20
h-index

36
g-index

42
ext. papers

1,626
ext. citations

5.3
avg, IF

4.03
L-index

#	Paper	IF	Citations
33	Systemic and rapid restructuring of the genome: a new perspective on punctuated equilibrium. <i>Current Genetics</i> , 2021 , 67, 57-63	2.9	4
32	Genome-Wide Analysis of Mitotic Recombination in Budding Yeast. <i>Methods in Molecular Biology</i> , 2021 , 2153, 201-219	1.4	1
31	Hundreds of thousands of cell generations reveal a treasure chest of genome alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 31567-31569 ^{11.5}	11.5	
30	Mutagenicity assessment downstream of oil and gas produced water discharges intended for agricultural beneficial reuse. <i>Science of the Total Environment</i> , 2020 , 715, 136944	10.2	18
29	Characterization of systemic genomic instability in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28221-28231	11.5	6
28	Punctuated Aneuploidization of the Budding Yeast Genome. <i>Genetics</i> , 2020 , 216, 43-50	4	3
27	Controlled Reduction of Genomic Heterozygosity in an Industrial Yeast Strain Reveals Wide Cryptic Phenotypic Variation. <i>Frontiers in Genetics</i> , 2019 , 10, 782	4.5	6
26	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019 , 6, 1-64	3.9	27
25	A Case Study of Genomic Instability in an Industrial Strain of. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3703-3713	3.7	9
24	Genome Instability Is Promoted by the Chromatin-Binding Protein Spn1 in. <i>Genetics</i> , 2018 , 210, 1227-1237	4	4
23	Both R-loop removal and ribonucleotide excision repair activities of RNase H2 contribute substantially to chromosome stability. <i>DNA Repair</i> , 2017 , 52, 110-114	4.3	23
22	Contrasting mechanisms of de novo copy number mutagenesis suggest the existence of different classes of environmental copy number mutagens. <i>Environmental and Molecular Mutagenesis</i> , 2016 , 57, 3-9	3.2	6
21	Unraveling the genetic basis of xylose consumption in engineered <i>Saccharomyces cerevisiae</i> strains. <i>Scientific Reports</i> , 2016 , 6, 38676	4.9	42
20	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. <i>Microbial Cell Factories</i> , 2015 , 14, 13	6.4	42
19	Stimulation of Chromosomal Rearrangements by Ribonucleotides. <i>Genetics</i> , 2015 , 201, 951-61	4	34
18	The sister chromatid cohesion pathway suppresses multiple chromosome gain and chromosome amplification. <i>Genetics</i> , 2014 , 196, 373-84	4	26
17	Higher-order septin assembly is driven by GTP-promoted conformational changes: evidence from unbiased mutational analysis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014 , 196, 711-27	4	27

16	Cascades of genetic instability resulting from compromised break-induced replication. <i>PLoS Genetics</i> , 2014 , 10, e1004119	6	26
15	Topoisomerase I plays a critical role in suppressing genome instability at a highly transcribed G-quadruplex-forming sequence. <i>PLoS Genetics</i> , 2014 , 10, e1004839	6	35
14	Gene copy-number variation in haploid and diploid strains of the yeast <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013 , 193, 785-801	4	52
13	A simple and effective set of PCR-based molecular markers for the monitoring of the <i>Saccharomyces cerevisiae</i> cell population during bioethanol fermentation. <i>Journal of Biotechnology</i> , 2013 , 168, 701-9	3.7	12
12	Harnessing genomics to identify environmental determinants of heritable disease. <i>Mutation Research - Reviews in Mutation Research</i> , 2013 , 752, 6-9	7	25
11	The baker's yeast diploid genome is remarkably stable in vegetative growth and meiosis. <i>PLoS Genetics</i> , 2010 , 6, e1001109	6	79
10	Genome structure of a <i>Saccharomyces cerevisiae</i> strain widely used in bioethanol production. <i>Genome Research</i> , 2009 , 19, 2258-70	9.7	186
9	Double-strand breaks associated with repetitive DNA can reshape the genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 11845-50	11.5	183
8	Negative epistasis between natural variants of the <i>Saccharomyces cerevisiae</i> MLH1 and PMS1 genes results in a defect in mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3256-61	11.5	64
7	Competing crossover pathways act during meiosis in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2004 , 168, 1805-16	7.1	122
6	Mismatch repair proteins: key regulators of genetic recombination. <i>Cytogenetic and Genome Research</i> , 2004 , 107, 146-59	1.9	125
5	Systematic mutagenesis of the <i>Saccharomyces cerevisiae</i> MLH1 gene reveals distinct roles for Mlh1p in meiotic crossing over and in vegetative and meiotic mismatch repair. <i>Molecular and Cellular Biology</i> , 2003 , 23, 873-86	4.8	66
4	Analysis of conditional mutations in the <i>Saccharomyces cerevisiae</i> MLH1 gene in mismatch repair and in meiotic crossing over. <i>Genetics</i> , 2002 , 160, 909-21	4	31
3	Identification of rad27 mutations that confer differential defects in mutation avoidance, repeat tract instability, and flap cleavage. <i>Molecular and Cellular Biology</i> , 2001 , 21, 4889-99	4.8	56
2	Methods for yeast characterization from industrial products. <i>Food Microbiology</i> , 2000 , 17, 217-223	6	15
1	Mitotic systemic genomic instability in yeast		2