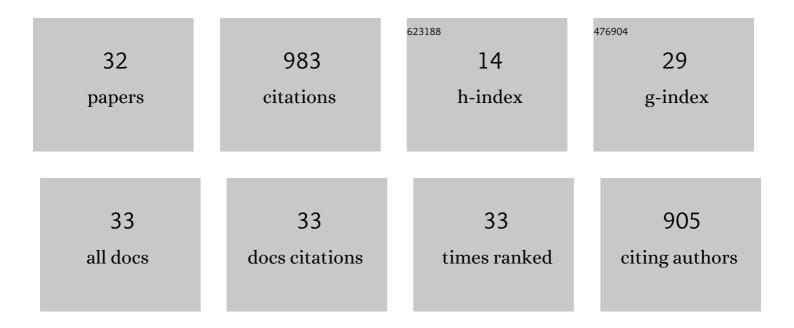
Juan Jimenez Martinez

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	twine, a cdc25 homolog that functions in the male and female germline of drosophila. Cell, 1992, 69, 977-988.	13.5	219
2	Adaptive evolution by mutations in the FLO11 gene. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11228-11233.	3.3	197
3	Yeast cell viability under conditions of high temperature and ethanol concentrations depends on the mitochondrial genome. Current Genetics, 1988, 13, 461-469.	0.8	67
4	Identification of Novel Activation Mechanisms for <i>FLO11</i> Regulation in <i>Saccharomyces cerevisiae</i> . Genetics, 2008, 178, 145-156.	1.2	64
5	Coding repeat instability in the <i>FLO11</i> gene of <i>Saccharomyces</i> yeasts. Yeast, 2008, 25, 879-889.	0.8	63
6	Chromatin Modulation at the FLO11 Promoter of <i>Saccharomyces cerevisiae</i> by HDAC and Swi/Snf Complexes. Genetics, 2012, 191, 791-803.	1.2	35
7	A Drosophila homologue of oxysterol binding protein (OSBP) – implications for the role of OSBP. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1395, 159-164.	2.4	34
8	Selection of Ethanol-Tolerant Yeast Hybrids in pH-Regulated Continuous Culture. Applied and Environmental Microbiology, 1988, 54, 917-922.	1.4	31
9	Antagonistic Roles of PP2A-Pab1 and Etd1 in the Control of Cytokinesis in Fission Yeast. Genetics, 2010, 186, 1261-1270.	1.2	27
10	Ethanol-hypersensitive and ethanol-dependent cdc â^' mutants in Schizosaccharomyces pombe. Molecular Genetics and Genomics, 1994, 245, 86-95.	2.4	26
11	Etd1p is a novel protein that links the SIN cascade with cytokinesis. EMBO Journal, 2005, 24, 2436-2446.	3.5	26
12	Feedback Regulation of SIN by Etd1 and Rho1 in Fission Yeast. Genetics, 2014, 196, 455-470.	1.2	24
13	Genome-wide search ofSchizosaccharomyces pombegenes causing overexpression-mediated cell cycle defects. Yeast, 2002, 19, 1139-1151.	0.8	23
14	Search for ancient patterns in protein sequences. Journal of Molecular Evolution, 1996, 42, 224-233.	0.8	18
15	Nucleocytoplasmic transport in the midzone membrane domain controls yeast mitotic spindle disassembly. Journal of Cell Biology, 2015, 209, 387-402.	2.3	18
16	Importin α and vNEBD Control Meiotic Spindle Disassembly in Fission Yeast. Cell Reports, 2018, 23, 933-941.	2.9	16
17	RNA metabolism is the primary target of formamide in vivo. Scientific Reports, 2017, 7, 15895.	1.6	14
18	Electrophoretic Karyotype of budding yeasts with intact cell Wall. Nucleic Acids Research, 1993, 21, 3902-3902.	6.5	13

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19	Ethanol inhibition of Saccharomyces and Candida enzymes. Current Genetics, 1989, 15, 7-16.	0.8	12
20	AnABlast: a new <i>in silico</i> strategy for the genome-wide search of novel genes and fossil regions. DNA Research, 2015, 22, 439-449.	1.5	11
21	A G2-Phase Microtubule-Damage Response in Fission Yeast. Genetics, 2008, 180, 2073-2080.	1.2	10
22	Proteomeâ€wide search for PP2A substrates in fission yeast. Proteomics, 2014, 14, 1367-1380.	1.3	9
23	Using AnABlast for intergenic sORF prediction in the <i>Caenorhabditis elegans</i> genome. Bioinformatics, 2020, 36, 4827-4832.	1.8	6
24	Hsp90 interaction with Cdc2 and Plo1 kinases contributes to actomyosin ring condensation in fission yeast. Current Genetics, 2012, 58, 191-203.	0.8	4
25	AnABlast: Re-searching for Protein-Coding Sequences in Genomic Regions. Methods in Molecular Biology, 2019, 1962, 207-214.	0.4	4
26	CRISPR sequences are sometimes erroneously translated and can contaminate public databases with spurious proteins containing spaced repeats. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	4
27	Ancient evolutionary signals of protein-coding sequences allow the discovery of new genes in the Drosophila melanogaster genome. BMC Genomics, 2020, 21, 210.	1.2	3
28	A Simple Multiplex Reverse Transcription-PCR Method for the Diagnosis of L-A and M Totiviruses in Saccharomyces cerevisiae. Applied and Environmental Microbiology, 2022, 88, AEM0221321.	1.4	3
29	Some comments on the variance of heterozygosity in finite populations. Journal of Theoretical Biology, 1986, 119, 103-106.	0.8	1
30	Assessment of selection pressure exerted on genes from complete pangenomes helps to improve the accuracy in the prediction of new genes. Briefings in Bioinformatics, 2022, 23, .	3.2	1
31	Mutational Analysis of N-Ethyl-N-Nitrosourea (ENU) in the Fission Yeast <i>Schizosaccharomyces pombe</i> . G3: Genes, Genomes, Genetics, 2020, 10, 917-923.	0.8	0
32	Protein-coding tRNA sequences?. Gene, 2022, 814, 146154.	1.0	0