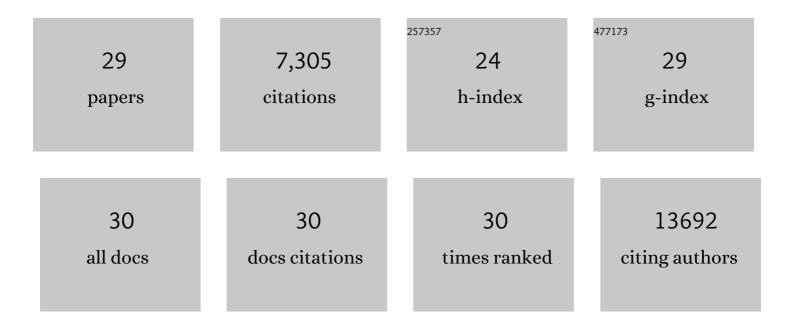
Javier Santoyo-Lopez

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	13.7	4,232
2	Statistical methods for analysis of high-throughput RNA interference screens. Nature Methods, 2009, 6, 569-575.	9.0	532
3	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	9.4	506
4	Initial Genomics of the Human Nucleolus. PLoS Genetics, 2010, 6, e1000889.	1.5	324
5	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Nucleic Acids Research, 2010, 38, W210-W213.	6.5	283
6	Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase. FEBS Journal, 1999, 265, 754-762.	0.2	239
7	GEPAS: a web-based resource for microarray gene expression data analysis. Nucleic Acids Research, 2003, 31, 3461-3467.	6.5	161
8	Mutational landscape of a chemically-induced mouse model of liver cancer. Journal of Hepatology, 2018, 69, 840-850.	1.8	97
9	Discrete Clusters of Virus-Encoded MicroRNAs Are Associated with Complementary Strands of the Genome and the 7.2-Kilobase Stable Intron in Murine Cytomegalovirus. Journal of Virology, 2007, 81, 13761-13770.	1.5	81
10	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	3.5	78
11	A Dominantly Inherited 5′ UTR Variant Causing Methylation-Associated Silencing of BRCA1 as a Cause of Breast and Ovarian Cancer. American Journal of Human Genetics, 2018, 103, 213-220.	2.6	78
12	Cloning and Characterization of a cDNA Encoding a Protein Synthesis Initiation Factor-2α (eIF-2α) Kinase fromDrosophila melanogaster. Journal of Biological Chemistry, 1997, 272, 12544-12550.	1.6	74
13	Phylogenomics and the number of characters required for obtaining an accurate phylogeny of eukaryote model species. Bioinformatics, 2004, 20, i116-i121.	1.8	71
14	DNA Polymerase Epsilon Deficiency Causes IMAGe Syndrome with Variable Immunodeficiency. American Journal of Human Genetics, 2018, 103, 1038-1044.	2.6	71
15	Mutation spectrum of EYS in Spanish patients with autosomal recessive retinitis pigmentosa. Human Mutation, 2010, 31, E1772-E1800.	1.1	69
16	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). Nature Communications, 2016, 7, 12339.	5.8	69
17	Highly specific and accurate selection of siRNAs for high-throughput functional assays. Bioinformatics, 2005, 21, 1376-1382.	1.8	49
18	Mutation Screening of Multiple Genes in Spanish Patients with Autosomal Recessive Retinitis Pigmentosa by Targeted Resequencing. PLoS ONE, 2011, 6, e27894.	1.1	36

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#	Article	IF	CITATIONS
19	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
20	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
21	PAX4 preserves endoplasmic reticulum integrity preventing beta cell degeneration in a mouse model of type 1 diabetes mellitus. Diabetologia, 2016, 59, 755-765.	2.9	33
22	Extensive Translatome Remodeling during ER Stress Response in Mammalian Cells. PLoS ONE, 2012, 7, e35915.	1.1	32
23	A map of human microRNA variation uncovers unexpectedly high levels of variability. Genome Medicine, 2012, 4, 62.	3.6	28
24	The role of the interactome in the maintenance of deleterious variability in human populations. Molecular Systems Biology, 2014, 10, 752.	3.2	28
25	Localization, structure and expression of the gene for translation initiation factor eIF-4E from Drosophila melanogaster. Molecular Genetics and Genomics, 1997, 253, 624-633.	2.4	24
26	Whole-exome sequencing identifies novel compound heterozygous mutations in USH2A in Spanish patients with autosomal recessive retinitis pigmentosa. Molecular Vision, 2013, 19, 2187-95.	1.1	17
27	Deciphering intrafamilial phenotypic variability by exome sequencing in a Bardet–Biedl family. Molecular Genetics & Genomic Medicine, 2014, 2, 124-133.	0.6	13
28	Modeling and Managing Experimental Data Using FuGE. OMICS A Journal of Integrative Biology, 2009, 13, 239-251.	1.0	8
29	Assessing Differential Expression Measurements by Highly Parallel Pyrosequencing and DNA Microarrays: A Comparative Study. OMICS A Journal of Integrative Biology, 2013, 17, 53-59.	1.0	2