Javier Santoyo-Lopez

List of Publications by Year
in descending order

29 papers	7,305 citations	257357 24 h-index	477173 29 g-index
30 all docs	30 docs citations	30 times ranked	13692 citing authors

#	Article	IF	Citations
1	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
2	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
3	DNA Polymerase Epsilon Deficiency Causes IMAGe Syndrome with Variable Immunodeficiency. American Journal of Human Genetics, 2018, 103, 1038-1044.	2.6	71
4	Mutational landscape of a chemically-induced mouse model of liver cancer. Journal of Hepatology, 2018, 69, 840-850.	1.8	97
5	A Dominantly Inherited 5â€² 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
6	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). Nature Communications, 2016, 7, 12339.	5.8	69
7	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	3.5	78
8	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
9	The role of the interactome in the maintenance of deleterious variability in human populations. Molecular Systems Biology, 2014, 10, 752.	3.2	28
10	Deciphering intrafamilial phenotypic variability by exome sequencing in a Bardetâ€“Biedl family. Molecular Genetics & Genomic Medicine, 2014, 2, 124-133.	0.6	13
11	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
12	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
13	Extensive Translatome Remodeling during ER Stress Response in Mammalian Cells. PLoS ONE, 2012, 7, e35915.	1.1	32
14	A map of human microRNA variation uncovers unexpectedly high levels of variability. Genome Medicine, 2012, 4, 62.	3.6	28
15	Mutation Screening of Multiple Genes in Spanish Patients with Autosomal Recessive Retinitis Pigmentosa by Targeted Resequencing. PLoS ONE, 2011, 6, e27894.	1.1	36
16	Mutation spectrum of EYS in Spanish patients with autosomal recessive retinitis pigmentosa. Human Mutation, 2010, 31, E1772-E1800.	1.1	69
17	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
18	Initial Genomics of the Human Nucleolus. PLoS Genetics, 2010, 6, e1000889.	1.5	324

#	Article	IF	Citations
19	Modeling and Managing Experimental Data Using FuGE. OMICS A Journal of Integrative Biology, 2009, 13, 239-251.	1.0	8
20	Statistical methods for analysis of high-throughput RNA interference screens. Nature Methods, 2009, 6, 569-575.	9.0	532
21	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	9.4	506
22	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
23	Highly specific and accurate selection of siRNAs for high-throughput functional assays. Bioinformatics, 2005, 21, 1376-1382.	1.8	49
24	Phylogenomics and the number of characters required for obtaining an accurate phylogeny of eukaryote model species. Bioinformatics, 2004, 20, i116-i121.	1.8	71
25	Finishing the euchromatic sequence of the human genome. Nature, 2004, 431, 931-945.	13.7	4,232
26	GEPAS: a web-based resource for microarray gene expression data analysis. Nucleic Acids Research, 2003, 31, 3461-3467.	6.5	161
27	Characterization of a mammalian homolog of the GCN2 eukaryotic initiation factor 2alpha kinase. FEBS Journal, 1999, 265, 754-762.	0.2	239
28	Cloning and Characterization of a cDNA Encoding a Protein Synthesis Initiation Factor-2Î± (eIF-2Î±) Kinase fromDrosophila melanogaster. Journal of Biological Chemistry, 1997, 272, 12544-12550.	1.6	74
29	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