

Javier Santoyo-Lopez

List of Publications by Year in descending order

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Version: 2024-02-01

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

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