

# Josep F. Abril

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

39,880  
citations

172457

29  
h-index

182427

51  
g-index

63  
all docs

63  
docs citations

63  
times ranked

38959  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
2	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
3	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	12.6	5,566
4	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
5	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	27.8	2,421
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
7	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	12.6	1,859
8	The Diploid Genome Sequence of an Individual Human. <i>PLoS Biology</i> , 2007, 5, e254.	5.6	1,491
9	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
10	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , 2006, 7, S2.	9.6	228
11	Comparative Gene Prediction in Human and Mouse. <i>Genome Research</i> , 2003, 13, 108-117.	5.5	183
12	An Assessment of Gene Prediction Accuracy in Large DNA Sequences. <i>Genome Research</i> , 2000, 10, 1631-1642.	5.5	179
13	Sequence and analysis of chromosome 2 of <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2002, 418, 79-85.	27.8	176
14	Genome Annotation Assessment in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2000, 10, 483-501.	5.5	172
15	Metagenomics for the study of viruses in urban sewage as a tool for public health surveillance. <i>Science of the Total Environment</i> , 2018, 618, 870-880.	8.0	116
16	Evaluation of Methods for the Concentration and Extraction of Viruses from Sewage in the Context of Metagenomic Sequencing. <i>PLoS ONE</i> , 2017, 12, e0170199.	2.5	107
17	Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1140-1145.	7.1	106
18	Planarian regeneration: achievements and future directions after 20 years of research. <i>International Journal of Developmental Biology</i> , 2009, 53, 1317-1327.	0.6	99

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19	Fusion of the Human Gene for the Polyubiquitination Coeffector UEV1 with Kua, a Newly Identified Gene. <i>Genome Research</i> , 2000, 10, 1743-1756.	5.5	91
20	Comparison of splice sites in mammals and chicken. <i>Genome Research</i> , 2005, 15, 111-119.	5.5	88
21	Characterisation of the sewage virome: comparison of NGS tools and occurrence of significant pathogens. <i>Science of the Total Environment</i> , 2020, 713, 136604.	8.0	58
22	gff2ps: visualizing genomic annotations. <i>Bioinformatics</i> , 2000, 16, 743-744.	4.1	55
23	Evidence of viral dissemination and seasonality in a Mediterranean river catchment: Implications for water pollution management. <i>Journal of Environmental Management</i> , 2015, 159, 58-67.	7.8	51
24	<i>GGPS1</i> Mutation and Atypical Femoral Fractures with Bisphosphonates. <i>New England Journal of Medicine</i> , 2017, 376, 1794-1795.	27.0	50
25	Smed454 dataset: unravelling the transcriptome of <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2010, 11, 731.	2.8	48
26	Planarians as a Model to Assess In Vivo the Role of Matrix Metalloproteinase Genes during Homeostasis and Regeneration. <i>PLoS ONE</i> , 2013, 8, e55649.	2.5	38
27	Ask1 and Akt act synergistically to promote ROS-dependent regeneration in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007926.	3.5	37
28	The nervous system of Xenacoelomorpha: a genomic perspective. <i>Journal of Experimental Biology</i> , 2015, 218, 618-628.	1.7	36
29	A proteomics approach to decipher the molecular nature of planarian stem cells. <i>BMC Genomics</i> , 2011, 12, 133.	2.8	33
30	A metagenomic assessment of viral contamination on fresh parsley plants irrigated with fecally tainted river water. <i>International Journal of Food Microbiology</i> , 2017, 257, 80-90.	4.7	31
31	High Transcriptional Complexity of the Retinitis Pigmentosa <i>CERKL</i> Gene in Human and Mouse. , 2011, 52, 5202.		30
32	Metagenomic analysis of viruses, bacteria and protozoa in irrigation water. <i>International Journal of Hygiene and Environmental Health</i> , 2020, 224, 113440.	4.3	29
33	Computational Gene Annotation in New Genome Assemblies Using GeneD. <i>Methods in Molecular Biology</i> , 2009, 537, 243-261.	0.9	28
34	Complex selection on 5â€² splice sites in intron-rich organisms. <i>Genome Research</i> , 2009, 19, 2021-2027.	5.5	25
35	The Deubiquitinating Enzyme Ataxin-3 Regulates Ciliogenesis and Phagocytosis in the Retina. <i>Cell Reports</i> , 2020, 33, 108360.	6.4	23
36	Functional Characterization of a GGPPS Variant Identified in Atypical Femoral Fracture Patients and Delineation of the Role of GGPPS in Bone-Relevant Cell Types. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 2091-2098.	2.8	21

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37	PlanNET: homology-based predicted interactome for multiple planarian transcriptomes. <i>Bioinformatics</i> , 2018, 34, 1016-1023.	4.1	19
38	Digital gene expression approach over multiple RNA-Seq data sets to detect neoblast transcriptional changes in <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2015, 16, 361.	2.8	17
39	Exploring the diversity of coronavirus in sewage during COVID-19 pandemic: Don't miss the forest for the trees. <i>Science of the Total Environment</i> , 2021, 800, 149562.	8.0	14
40	Host-dependent editing of SARS-CoV-2 in COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2021, 10, 1777-1789.	6.5	13
41	PlanExp: intuitive integration of complex RNA-seq datasets with planarian omics resources. <i>Bioinformatics</i> , 2020, 36, 1889-1895.	4.1	12
42	Identification of sapovirus GV.2, astrovirus VA3 and novel anelloviruses in serum from patients with acute hepatitis of unknown aetiology. <i>PLoS ONE</i> , 2017, 12, e0185911.	2.5	10
43	gff2aplot: Plotting sequence comparisons. <i>Bioinformatics</i> , 2003, 19, 2477-2479.	4.1	9
44	The coelomic epithelium transcriptome from a clonal sea star, <i>Coscinasterias muricata</i> . <i>Marine Genomics</i> , 2015, 24, 245-248.	1.1	9
45	ECCB//BI 2005. <i>Bioinformatics</i> , 2005, 21, ii1-ii2.	4.1	4
46	Genome Annotation. , 2019, , 195-209.		3
47	Distilling a Visual Network of Retinitis Pigmentosa Gene-Protein Interactions to Uncover New Disease Candidates. <i>PLoS ONE</i> , 2015, 10, e0135307.	2.5	3
48	Gene Network of Susceptibility to Atypical Femoral Fractures Related to Bisphosphonate Treatment. <i>Genes</i> , 2022, 13, 146.	2.4	3
49	SiNoPsis: Single Nucleotide Polymorphisms selection and promoter profiling. <i>Bioinformatics</i> , 2018, 34, 303-305.	4.1	2
50	RPGeNet v2.0: expanding the universe of retinal disease gene interactions network. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	2
51	PPaxe: easy extraction of protein occurrence and interactions from the scientific literature. <i>Bioinformatics</i> , 2019, 35, 2523-2524.	4.1	2
52	Viral populations of SARS-CoV-2 in upper respiratory tract, placenta, amniotic fluid and umbilical cord blood support viral replication in placenta. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1542-1544.	6.0	2
53	Sequence Similarity Based Gene Prediction. , 2002, , 95-106.		1