

Josep F. Abril

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54
papers

33,838
citations

26
h-index

63
g-index

63
ext. papers

37,449
ext. citations

14
avg, IF

6.05
L-index

#	Paper	IF	Citations
54	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	9.5	2
53	Host-dependent editing of SARS-CoV-2 in COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1777-1789	18.9	4
52	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	10.2	3
51	Characterisation of the sewage virome: comparison of NGS tools and occurrence of significant pathogens. <i>Science of the Total Environment</i> , 2020 , 713, 136604	10.2	34
50	PlanExp: intuitive integration of complex RNA-seq datasets with planarian omics resources. <i>Bioinformatics</i> , 2020 , 36, 1889-1895	7.2	5
49	Metagenomic analysis of viruses, bacteria and protozoa in irrigation water. <i>International Journal of Hygiene and Environmental Health</i> , 2020 , 224, 113440	6.9	9
48	The Deubiquitinating Enzyme Ataxin-3 Regulates Ciliogenesis and Phagocytosis in the Retina. <i>Cell Reports</i> , 2020 , 33, 108360	10.6	7
47	Ask1 and Akt act synergistically to promote ROS-dependent regeneration in Drosophila. <i>PLoS Genetics</i> , 2019 , 15, e1007926	6	15
46	Genome Annotation 2019 , 195-209		2
45	RPGeNet v2.0: expanding the universe of retinal disease gene interactions network. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	2
44	PPaxe: easy extraction of protein occurrence and interactions from the scientific literature. <i>Bioinformatics</i> , 2019 , 35, 2523-2524	7.2	1
43	SiNoPsis: Single Nucleotide Polymorphisms selection and promoter profiling. <i>Bioinformatics</i> , 2018 , 34, 303-305	7.2	1
42	PlanNET: homology-based predicted interactome for multiple planarian transcriptomes. <i>Bioinformatics</i> , 2018 , 34, 1016-1023	7.2	12
41	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	10.2	70
40	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	6.3	12
39	GGPS1 Mutation and Atypical Femoral Fractures with Bisphosphonates. <i>New England Journal of Medicine</i> , 2017 , 376, 1794-1795	59.2	32
38	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	5.8	23

37	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	3.7	73
36	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	3.7	9
35	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	7.9	40
34	The nervous system of Xenacoelomorpha: a genomic perspective. <i>Journal of Experimental Biology</i> , 2015 , 218, 618-28	3	25
33	The coelomic epithelium transcriptome from a clonal sea star, <i>Coscinasterias muricata</i> . <i>Marine Genomics</i> , 2015 , 24 Pt 3, 245-8	1.9	6
32	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	4.5	15
31	Distilling a Visual Network of Retinitis Pigmentosa Gene-Protein Interactions to Uncover New Disease Candidates. <i>PLoS ONE</i> , 2015 , 10, e0135307	3.7	3
30	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
29	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	3.7	24
28	High transcriptional complexity of the retinitis pigmentosa CERKL gene in human and mouse 2011 , 52, 5202-14		21
27	A proteomics approach to decipher the molecular nature of planarian stem cells. <i>BMC Genomics</i> , 2011 , 12, 133	4.5	26
26	Smed454 dataset: unravelling the transcriptome of <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2010 , 11, 731	4.5	37
25	Planarian regeneration: achievements and future directions after 20 years of research. <i>International Journal of Developmental Biology</i> , 2009 , 53, 1317-27	1.9	78
24	Complex selection on 5Vsplice sites in intron-rich organisms. <i>Genome Research</i> , 2009 , 19, 2021-7	9.7	18
23	Computational gene annotation in new genome assemblies using GeneID. <i>Methods in Molecular Biology</i> , 2009 , 537, 243-61	1.4	21
22	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
21	The diploid genome sequence of an individual human. <i>PLoS Biology</i> , 2007 , 5, e254	9.7	1249
20	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S2.1-31	18.3	187

19	ECCB/JBI 2005. <i>Bioinformatics</i> , 2005 , 21, ii1-ii2	7.2	3
18	Comparison of splice sites in mammals and chicken. <i>Genome Research</i> , 2005 , 15, 111-9	9.7	64
17	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
16	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004 , 432, 695-716	50.4	2143
15	GENEID 2004 ,		1
14	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, 1140-5	11.5	95
13	Comparative gene prediction in human and mouse. <i>Genome Research</i> , 2003 , 13, 108-17	9.7	144
12	gff2aplot: Plotting sequence comparisons. <i>Bioinformatics</i> , 2003 , 19, 2477-9	7.2	7
11	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. <i>Nature</i> , 2002 , 418, 79-85	50.4	158
10	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
9	The genome sequence of the malaria mosquito Anopheles gambiae. <i>Science</i> , 2002 , 298, 129-49	33.3	1622
8	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609
7	Sequence Similarity Based Gene Prediction 2000 , 95-106		1
6	The genome sequence of Drosophila melanogaster. <i>Science</i> , 2000 , 287, 2185-95	33.3	4857
5	gff2ps: visualizing genomic annotations. <i>Bioinformatics</i> , 2000 , 16, 743-4	7.2	51
4	An assessment of gene prediction accuracy in large DNA sequences. <i>Genome Research</i> , 2000 , 10, 1631-42	9.7	140
3	Fusion of the human gene for the polyubiquitination coeffecter UEV1 with Kua, a newly identified gene. <i>Genome Research</i> , 2000 , 10, 1743-56	9.7	73
2	Genome annotation assessment in Drosophila melanogaster. <i>Genome Research</i> , 2000 , 10, 483-501	9.7	139

- 1 Genomic analyses reveal FoxG as an upstream regulator of wnt1 required for posterior identity specification in planarians