Josep F. Abril

List of Publications by Year
in descending order

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	Gene Network of Susceptibility to Atypical Femoral Fractures Related to Bisphosphonate Treatment. Genes, 2022, 13, 146.	2.4	3
2	Host-dependent editing of SARS-CoV-2 in COVID-19 patients. Emerging Microbes and Infections, 2021, 10, 1777-1789.	6.5	13
3	Viral populations of SARS-CoV-2 in upper respiratory tract, placenta, amniotic fluid and umbilical cord blood support viral replication in placenta. Clinical Microbiology and Infection, 2021, 27, 1542-1544.	6.0	2
4	Exploring the diversity of coronavirus in sewage during COVID-19 pandemic: Don't miss the forest for the trees. Science of the Total Environment, 2021, 800, 149562.	8.0	14
5	PlanExp: intuitive integration of complex RNA-seq datasets with planarian omics resources. Bioinformatics, 2020, 36, 1889-1895.	4.1	12
6	Metagenomic analysis of viruses, bacteria and protozoa in irrigation water. International Journal of Hygiene and Environmental Health, 2020, 224, 113440.	4.3	29
7	The Deubiquitinating Enzyme Ataxin-3 Regulates Ciliogenesis and Phagocytosis in the Retina. Cell Reports, 2020, 33, 108360.	6.4	23
8	Characterisation of the sewage virome: comparison of NGS tools and occurrence of significant pathogens. Science of the Total Environment, 2020, 713, 136604.	8.0	58
9	Genome Annotation. , 2019, , 195-209.		3
10	RPGeNet v2.0: expanding the universe of retinal disease gene interactions network. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	2
11	Ask1 and Akt act synergistically to promote ROS-dependent regeneration in Drosophila. PLoS Genetics, 2019, 15, e1007926.	3.5	37
12	PPaxe: easy extraction of protein occurrence and interactions from the scientific literature. Bioinformatics, 2019, 35, 2523-2524.	4.1	2
13	SiNoPsis: Single Nucleotide Polymorphisms selection and promoter profiling. Bioinformatics, 2018, 34, 303-305.	4.1	2
14	PlanNET: homology-based predicted interactome for multiple planarian transcriptomes. Bioinformatics, 2018, 34, 1016-1023.	4.1	19
15	Metagenomics for the study of viruses in urban sewage as a tool for public health surveillance. Science of the Total Environment, 2018, 618, 870-880.	8.0	116
16	Functional Characterization of a GGPPS Variant Identified in Atypical Femoral Fracture Patients and Delineation of the Role of GGPPS in Bone-Relevant Cell Types. Journal of Bone and Mineral Research, 2018, 33, 2091-2098.	2.8	21
17	<i>GGPS1</i> Mutation and Atypical Femoral Fractures with Bisphosphonates. New England Journal of Medicine, 2017, 376, 1794-1795.	27.0	50
18	A metagenomic assessment of viral contamination on fresh parsley plants irrigated with fecally tainted river water. International Journal of Food Microbiology, 2017, 257, 80-90.	4.7	31

#	ARTICLE	IF	CITATIONS
19	Evaluation of Methods for the Concentration and Extraction of Viruses from Sewage in the Context of Metagenomic Sequencing. PLoS ONE, 2017, 12, e0170199.	2.5	107
20	Identification of sapovirus GV.2, astrovirus VA3 and novel anelloviruses in serum from patients with acute hepatitis of unknown aetiology. PLoS ONE, 2017, 12, e0185911.	2.5	10
21	Evidence of viral dissemination and seasonality in a Mediterranean river catchment: Implications for water pollution management. Journal of Environmental Management, 2015, 159, 58-67.	7.8	51
22	The nervous system of Xenacoelomorpha: a genomic perspective. Journal of Experimental Biology, 2015, 218, 618-628.	1.7	36
23	The coelomic epithelium transcriptome from a clonal sea star, Coscinasterias muricata. Marine Genomics, 2015, 24, 245-248.	1.1	9
24	Digital gene expression approach over multiple RNA-Seq data sets to detect neoblast transcriptional changes in Schmidtea mediterranea. BMC Genomics, 2015, 16, 361.	2.8	17
25	Distilling a Visual Network of Retinitis Pigmentosa Gene-Protein Interactions to Uncover New Disease Candidates. PLoS ONE, 2015, 10, e0135307.	2.5	3
26	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
27	Planarians as a Model to Assess In Vivo the Role of Matrix Metalloproteinase Genes during Homeostasis and Regeneration. PLoS ONE, 2013, 8, e55649.	2.5	38
28	High Transcriptional Complexity of the Retinitis Pigmentosa *CERKL* Gene in Human and Mouse. , 2011, 52, 5202.		30
29	A proteomics approach to decipher the molecular nature of planarian stem cells. BMC Genomics, 2011, 12, 133.	2.8	33
30	Smed454 dataset: unravelling the transcriptome of Schmidtea mediterranea. BMC Genomics, 2010, 11, 731.	2.8	48
31	Planarian regeneration: achievements and future directions after 20 years of research. International Journal of Developmental Biology, 2009, 53, 1317-1327.	0.6	99
32	Complex selection on 5â€² splice sites in intron-rich organisms. Genome Research, 2009, 19, 2021-2027.	5.5	25
33	Computational Gene Annotation in New Genome Assemblies Using GeneID. Methods in Molecular Biology, 2009, 537, 243-261.	0.9	28
34	The Diploid Genome Sequence of an Individual Human. PLoS Biology, 2007, 5, e254.	5.6	1,491
35	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
36	EGASP: the human ENCODE Genome Annotation Assessment Project. Genome Biology, 2006, 7, S2.	9.6	228

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37	ECCB/JBI 2005. Bioinformatics, 2005, 21, ii1-ii2.	4.1	4
38	Comparison of splice sites in mammals and chicken. Genome Research, 2005, 15, 111-119.	5.5	88
39	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
40	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
41	gff2aplot: Plotting sequence comparisons. Bioinformatics, 2003, 19, 2477-2479.	4.1	9
42	Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1140-1145.	7.1	106
43	Comparative Gene Prediction in Human and Mouse. Genome Research, 2003, 13, 108-117.	5.5	183
44	Sequence Similarity Based Gene Prediction. , 2002, , 95-106.		1
45	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i>. Science, 2002, 298, 129-149.	12.6	1,859
46	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. Nature, 2002, 418, 79-85.	27.8	176
47	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
48	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
49	The Genome Sequence of <i>Drosophila melanogaster</i>. Science, 2000, 287, 2185-2195.	12.6	5,566
50	gff2ps: visualizing genomic annotations. Bioinformatics, 2000, 16, 743-744.	4.1	55
51	An Assessment of Gene Prediction Accuracy in Large DNA Sequences. Genome Research, 2000, 10, 1631-1642.	5.5	179
52	Fusion of the Human Gene for the Polyubiquitination Coeffector UEV1 with Kua, a Newly Identified Gene. Genome Research, 2000, 10, 1743-1756.	5.5	91
53	Genome Annotation Assessment in Drosophila melanogaster. Genome Research, 2000, 10, 483-501.	5.5	172