

Vicente Arnau

List of Publications by Year in descending order

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29
papers

1,100
citations

1040056

9
h-index

642732

23
g-index

33
all docs

33
docs citations

33
times ranked

2057
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring the universal healthy human gut microbiota around the World. Computational and Structural Biotechnology Journal, 2022, 20, 421-433.	4.1	14
2	DVGfinder: A Metasearch Tool for Identifying Defective Viral Genomes in RNA-Seq Data. Viruses, 2022, 14, 1114.	3.3	8
3	Deep viral blood metagenomics reveals extensive anellovirus diversity in healthy humans. Scientific Reports, 2021, 11, 6921.	3.3	31
4	Transcriptional changes through menstrual cycle reveal a global transcriptional derepression underlying the molecular mechanism involved in the window of implantation. Molecular Human Reproduction, 2021, 27, .	2.8	5
5	Reverse-Transcribing Viruses (Belpaoviridae, Metaviridae, and Pseudoviridae). , 2021, , 653-666.		0
6	Driven progressive evolution of genome sequence complexity in Cyanobacteria. Scientific Reports, 2020, 10, 19073.	3.3	7
7	Uterine disorders affecting female fertility: what are the molecular functions altered in endometrium?. Fertility and Sterility, 2020, 113, 1261-1274.	1.0	26
8	Metatranscriptomic dynamics after Verticillium dahliae infection and root damage in Olea europaea. BMC Plant Biology, 2020, 20, 79.	3.6	5
9	Reactome pathway analysis: a high-performance in-memory approach. BMC Bioinformatics, 2017, 18, 142.	2.6	600
10	VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. BMC Bioinformatics, 2017, 18, 421.	2.6	1
11	HPG pore: an efficient and scalable framework for nanopore sequencing data. BMC Bioinformatics, 2016, 17, 107.	2.6	9
12	A web application for the unspecific detection of differentially expressed DNA regions in strand-specific expression data: Fig. 1.. Bioinformatics, 2015, 31, 3228-3230.	4.1	0
13	Acceleration of short and long DNA read mapping without loss of accuracy using suffix array. Bioinformatics, 2014, 30, 3396-3398.	4.1	16
14	mRNASTabâ€”a web application for mRNA stability analysis. Bioinformatics, 2013, 29, 813-814.	4.1	1
15	A sequence motif enriched in regions bound by the Drosophila dosage compensation complex. BMC Genomics, 2010, 11, 169.	2.8	8
16	Fast comparison of DNA sequences by oligonucleotide profiling. BMC Research Notes, 2008, 1, 5.	1.4	7
17	Global patterns of sequence evolution in Drosophila. BMC Genomics, 2007, 8, 408.	2.8	17
18	THE SPANISH MELON GENOMICS INITIATIVE. Acta Horticulturae, 2007, , 47-54.	0.2	3

#	ARTICLE	IF	CITATIONS
19	Comparative Genomics and Protein Domain Graph Analyses Link Ubiquitination and RNA Metabolism. Journal of Molecular Biology, 2006, 357, 9-17.	4.2	33
20	LIVPAR: fast detection of functional shifts in duplicate genes. BMC Bioinformatics, 2006, 7, 174.	2.6	5
21	Iterative Cluster Analysis of Protein Interaction Data. Bioinformatics, 2005, 21, 364-378.	4.1	199
22	A Clustering Approach for Improving Network Performance in Heterogeneous Systems. Lecture Notes in Computer Science, 2000, , 1206-1209.	1.3	1
23	Reproducibility of Digital Image Analysis for Measuring Corneal Haze After Myopic Photorefractive Keratectomy. American Journal of Ophthalmology, 1997, 123, 31-41.	3.3	31
24	Direct Objective Quantification of Corneal Haze after Excimer Laser Photorefractive Keratectomy for High Myopia. Ophthalmology, 1996, 103, 1970-1978.	5.2	41
25	A new chromatic encoding for machine vision invariant to the change of illuminant. Journal of Optics, 1996, 27, 171-181.	0.3	2
26	An application of neural networks to natural scene segmentation. , 1991, , 333-339.		0
27	Characterization of communications between processes in message-passing applications. , 0, , .		10
28	On the design of communication-aware task scheduling strategies for heterogeneous systems. , 0, , .		10
29	A fast algorithm for the exhaustive analysis of 12-nucleotide-long DNA sequences. Applications to human genomics. , 0, , .		1