

Ignacio Medina

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

3,702
citations

304368

22
h-index

276539

41
g-index

42
all docs

42
docs citations

42
times ranked

8646
citing authors

#	ARTICLE	IF	CITATIONS
1	PyCellBase, an efficient python package for easy retrieval of biological data from heterogeneous sources. BMC Bioinformatics, 2019, 20, 159.	1.2	0
2	HGVA: the Human Genome Variation Archive. Nucleic Acids Research, 2017, 45, W189-W194.	6.5	6
3	VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. BMC Bioinformatics, 2017, 18, 421.	1.2	1
4	Web-based network analysis and visualization using CellMaps. Bioinformatics, 2016, 32, 3041-3043.	1.8	15
5	Actionable pathways: interactive discovery of therapeutic targets using signaling pathway models. Nucleic Acids Research, 2016, 44, W212-W216.	6.5	27
6	HPG pore: an efficient and scalable framework for nanopore sequencing data. BMC Bioinformatics, 2016, 17, 107.	1.2	9
7	Pair-End Inexact Mapping on Hybrid GPU Environments and Out-Of-Core Indexes. Current Bioinformatics, 2016, 11, 459-469.	0.7	1
8	Identification of epistatic interactions through genome-wide association studies in sporadic medullary and juvenile papillary thyroid carcinomas. BMC Medical Genomics, 2015, 8, 83.	0.7	15
9	Assessing the impact of mutations found in next generation sequencing data over human signaling pathways. Nucleic Acids Research, 2015, 43, W270-W275.	6.5	16
10	Babelomics 5.0: functional interpretation for new generations of genomic data. Nucleic Acids Research, 2015, 43, W117-W121.	6.5	114
11	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	9.4	338
12	Acceleration of short and long DNA read mapping without loss of accuracy using suffix array. Bioinformatics, 2014, 30, 3396-3398.	1.8	16
13	A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. Nucleic Acids Research, 2014, 42, W88-W93.	6.5	39
14	A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Nucleic Acids Research, 2014, 42, W83-W87.	6.5	6
15	Inferring the functional effect of gene expression changes in signaling pathways. Nucleic Acids Research, 2013, 41, W213-W217.	6.5	23
16	Genome Maps, a new generation genome browser. Nucleic Acids Research, 2013, 41, W41-W46.	6.5	27
17	Multicore and Cloud-Based Solutions for Genomic Variant Analysis. Lecture Notes in Computer Science, 2013, , 273-284.	1.0	2
18	Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. Nucleic Acids Research, 2012, 40, e158-e158.	6.5	22

#	ARTICLE	IF	CITATIONS
19	VARIANT: Command Line, Web service and Web interface for fast and accurate functional characterization of variants found by Next-Generation Sequencing. <i>Nucleic Acids Research</i> , 2012, 40, W54-W58.	6.5	37
20	Inferring the regulatory network behind a gene expression experiment. <i>Nucleic Acids Research</i> , 2012, 40, W168-W172.	6.5	10
21	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , 2012, 7, 542-550.	1.3	68
22	CellBase, a comprehensive collection of RESTful web services for retrieving relevant biological information from heterogeneous sources. <i>Nucleic Acids Research</i> , 2012, 40, W609-W614.	6.5	31
23	Select Your SNPs (SYSNPs): a web tool for automatic and massive selection of SNPs. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 324.	0.1	20
24	Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprung's disease. <i>Orphanet Journal of Rare Diseases</i> , 2012, 7, 103.	1.2	7
25	A map of human microRNA variation uncovers unexpectedly high levels of variability. <i>Genome Medicine</i> , 2012, 4, 62.	3.6	28
26	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011, 39, W470-W474.	6.5	182
27	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795
28	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
29	Initial Genomics of the Human Nucleolus. <i>PLoS Genetics</i> , 2010, 6, e1000889.	1.5	324
30	Serial Expression Analysis: a web tool for the analysis of serial gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, W239-W245.	6.5	12
31	Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies. <i>Nucleic Acids Research</i> , 2009, 37, W340-W344.	6.5	64
32	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. <i>BMC Medical Genomics</i> , 2008, 1, 62.	0.7	13
33	SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , 2008, 40, 560-566.	9.4	172
34	Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeff and PupaSuite databases. <i>Nucleic Acids Research</i> , 2008, 36, D825-D829.	6.5	60
35	GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008, 36, W308-W314.	6.5	67
36	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. <i>Nucleic Acids Research</i> , 2008, 36, W341-W346.	6.5	73

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37	FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. <i>Nucleic Acids Research</i> , 2007, 35, W91-W96.	6.5	248
38	Prophet, a web-based tool for class prediction using microarray data. <i>Bioinformatics</i> , 2007, 23, 390-391.	1.8	36
39	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , 2007, 35, W38-W42.	6.5	47
40	ISACGH: a web-based environment for the analysis of Array CGH and gene expression which includes functional profiling. <i>Nucleic Acids Research</i> , 2007, 35, W81-W85.	6.5	29
41	Inhibition of cancer growth by resveratrol is related to its low bioavailability. <i>Free Radical Biology and Medicine</i> , 2002, 33, 387-398.	1.3	338
42	Î³-Glutamyl transpeptidase overexpression increases metastatic growth of B16 melanoma cells in the mouse liver. <i>Hepatology</i> , 2002, 35, 74-81.	3.6	81