Ignacio Medina

List of Publications by Year
in descending order

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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	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	9.4	795
2	Inhibition of cancer growth by resveratrol is related to its low bioavailability. Free Radical Biology and Medicine, 2002, 33, 387-398.	1.3	338
3	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	9.4	338
4	Initial Genomics of the Human Nucleolus. PLoS Genetics, 2010, 6, e1000889.	1.5	324
5	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Nucleic Acids Research, 2010, 38, W210-W213.	6.5	283
6	FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. Nucleic Acids Research, 2007, 35, W91-W96.	6.5	248
7	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	6.5	182
8	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
9	Babelomics 5.0: functional interpretation for new generations of genomic data. Nucleic Acids Research, 2015, 43, W117-W121.	6.5	114
10	Î³-Glutamyl transpeptidase overexpression increases metastatic growth of B16 melanoma cells in the mouse liver. Hepatology, 2002, 35, 74-81.	3.6	81
11	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. Nucleic Acids Research, 2008, 36, W341-W346.	6.5	73
12	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. Epigenetics, 2012, 7, 542-550.	1.3	68
13	GEPAS, a web-based tool for microarray data analysis and interpretation. Nucleic Acids Research, 2008, 36, W308-W314.	6.5	67
14	Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies. Nucleic Acids Research, 2009, 37, W340-W344.	6.5	64
15	Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeffect and PupaSuite databases. Nucleic Acids Research, 2008, 36, D825-D829.	6.5	60
16	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. Nucleic Acids Research, 2007, 35, W38-W42.	6.5	47
17	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
18	VARIANT: Command Line, Web service and Web interface for fast and accurate functional characterization of variants found by Next-Generation Sequencing. Nucleic Acids Research, 2012, 40, W54-W58.	6.5	37

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19	Prophet, a web-based tool for class prediction using microarray data. Bioinformatics, 2007, 23, 390-391.	1.8	36
20	CellBase, a comprehensive collection of RESTful web services for retrieving relevant biological information from heterogeneous sources. Nucleic Acids Research, 2012, 40, W609-W614.	6.5	31
21	ISACGH: a web-based environment for the analysis of Array CGH and gene expression which includes functional profiling. Nucleic Acids Research, 2007, 35, W81-W85.	6.5	29
22	A map of human microRNA variation uncovers unexpectedly high levels of variability. Genome Medicine, 2012, 4, 62.	3.6	28
23	Genome Maps, a new generation genome browser. Nucleic Acids Research, 2013, 41, W41-W46.	6.5	27
24	Actionable pathways: interactive discovery of therapeutic targets using signaling pathway models. Nucleic Acids Research, 2016, 44, W212-W216.	6.5	27
25	Inferring the functional effect of gene expression changes in signaling pathways. Nucleic Acids Research, 2013, 41, W213-W217.	6.5	23
26	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
27	Select Your SNPs (SYSNPs): a web tool for automatic and massive selection of SNPs. International Journal of Data Mining and Bioinformatics, 2012, 6, 324.	0.1	20
28	Acceleration of short and long DNA read mapping without loss of accuracy using suffix array. Bioinformatics, 2014, 30, 3396-3398.	1.8	16
29	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
30	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
31	Web-based network analysis and visualization using CellMaps. Bioinformatics, 2016, 32, 3041-3043.	1.8	15
32	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. BMC Medical Genomics, 2008, 1, 62.	0.7	13
33	Serial Expression Analysis: a web tool for the analysis of serial gene expression data. Nucleic Acids Research, 2010, 38, W239-W245.	6.5	12
34	Inferring the regulatory network behind a gene expression experiment. Nucleic Acids Research, 2012, 40, W168-W172.	6.5	10
35	HPG pore: an efficient and scalable framework for nanopore sequencing data. BMC Bioinformatics, 2016, 17, 107.	1.2	9
36	Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprungâ€™s disease. Orphanet Journal of Rare Diseases, 2012, 7, 103.	1.2	7

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37	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
38	HGVA: the Human Genome Variation Archive. Nucleic Acids Research, 2017, 45, W189-W194.	6.5	6
39	Multicore and Cloud-Based Solutions for Genomic Variant Analysis. Lecture Notes in Computer Science, 2013, , 273-284.	1.0	2
40	VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. BMC Bioinformatics, 2017, 18, 421.	1.2	1
41	Pair-End Inexact Mapping on Hybrid GPU Environments and Out-Of-Core Indexes. Current Bioinformatics, 2016, 11, 459-469.	0.7	1
42	PyCellBase, an efficient python package for easy retrieval of biological data from heterogeneous sources. BMC Bioinformatics, 2019, 20, 159.	1.2	0