

MarÃ-a del Mar Abad-Grau

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1663022/publications.pdf>

Version: 2024-02-01

26
papers

568
citations

933447

10
h-index

642732

23
g-index

28
all docs

28
docs citations

28
times ranked

1114
citing authors

#	ARTICLE	IF	CITATIONS
1	A network model to predict the risk of death in sickle cell disease. <i>Blood</i> , 2007, 110, 2727-2735.	1.4	159
2	Multiple Sclerosis Risk Variant HLA-DRB1*1501 Associates with High Expression of DRB1 Gene in Different Human Populations. <i>PLoS ONE</i> , 2012, 7, e29819.	2.5	100
3	IL2RA/CD25 Gene Polymorphisms: Uneven Association with Multiple Sclerosis (MS) and Type 1 Diabetes (T1D). <i>PLoS ONE</i> , 2009, 4, e4137.	2.5	65
4	Identification of a functional variant in the <i>KIF5A-CYP27B1-METTL1-FAM119B</i> locus associated with multiple sclerosis. <i>Journal of Medical Genetics</i> , 2013, 50, 25-33.	3.2	59
5	A functional variant that affects exon-skipping and protein expression of <i>SP140</i> as genetic mechanism predisposing to multiple sclerosis. <i>Human Molecular Genetics</i> , 2015, 24, 5619-5627.	2.9	43
6	A hierarchical and modular approach to the discovery of robust associations in genome-wide association studies from pooled DNA samples. <i>BMC Genetics</i> , 2008, 9, 6.	2.7	26
7	Operations strategy and flexibility: modeling with Bayesian classifiers. <i>Industrial Management and Data Systems</i> , 2006, 106, 460-484.	3.7	22
8	Robust Transmission/Disequilibrium Test for Incomplete Family Genotypes. <i>Genetics</i> , 2004, 168, 2329-2337.	2.9	18
9	Evolution and challenges in the design of computational systems for triage assistance. <i>Journal of Biomedical Informatics</i> , 2008, 41, 432-441.	4.3	15
10	Members 6B and 14 of the TNF receptor superfamily in multiple sclerosis predisposition. <i>Genes and Immunity</i> , 2011, 12, 145-148.	4.1	14
11	Building chromosome-wide LD maps. <i>Bioinformatics</i> , 2006, 22, 1933-1934.	4.1	8
12	Variant alleles of the mannose binding lectin 2 gene (<i>MBL2</i>) confer heterozygote advantage within Crohn's families. <i>Scandinavian Journal of Gastroenterology</i> , 2010, 45, 1129-1130.	1.5	6
13	Bayesian estimates of linkage disequilibrium. <i>BMC Genetics</i> , 2007, 8, 36.	2.7	5
14	Genome-wide association filtering using a highly locus-specific transmission/disequilibrium test. <i>Human Genetics</i> , 2010, 128, 325-344.	3.8	5
15	INCREASING POWER BY USING HAPLOTYPE SIMILARITY IN A MULTIMARKER TRANSMISSION/DISEQUILIBRIUM TEST. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1250014.	0.8	5
16	Sample Reproducibility of Genetic Association Using Different Multimarker TDTs in Genome-Wide Association Studies: Characterization and a New Approach. <i>PLoS ONE</i> , 2012, 7, e29613.	2.5	5
17	A comparison of genomic profiles of complex diseases under different models. <i>BMC Medical Genomics</i> , 2015, 9, 3.	1.5	4
18	GeneOnEarth: Fitting Genetic PC Plots on the Globe. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1009-1016.	3.0	2

#	ARTICLE	IF	CITATIONS
19	Riskoweb: Web-Based Genetic Profiling to Complex Disease Using Genome-Wide SNP Markers. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 1-8.	0.2	2
20	Bayesian Correction for SNP Ascertainment Bias. <i>Lecture Notes in Computer Science</i> , 2006, , 262-273.	1.3	1
21	HAPLOTYPE-BASED CLASSIFIERS TO PREDICT INDIVIDUAL SUSCEPTIBILITY TO COMPLEX DISEASES - An Example for Multiple Sclerosis. , 2012, , .		1
22	Discretization of Expression Quantitative Trait Loci in Association Analysis Between Genotypes and Expression Data. <i>Current Bioinformatics</i> , 2015, 10, 144-164.	1.5	1
23	Fetal Hemoglobin (HbF) in Sickle Cell Anemia: Genome-Wide Association Studies Using Pooled DNA Samples Can Reveal Genetic Associations with HbF Concentration.. <i>Blood</i> , 2006, 108, 1221-1221.	1.4	0
24	3D VISUALIZATION OF HAPLOTYPE RISK MAPS. , 2012, , .		0
25	Homogenizing Access to Highly Time-Consuming Biomedical Applications through a Web-Based Interface. <i>Lecture Notes in Computer Science</i> , 2012, , 33-42.	1.3	0
26	Multivariate Imputation of Genotype Data Using Short and Long Range Disequilibrium. , 2007, , 187-194.		0