# MarÃ-a del Mar Abad-Grau

List of Publications by Year
in descending order

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

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|---|---|---|---|
| 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 comparison of genomic profiles of complex diseases under different models. BMC Medical Genomics, 2015, 9, 3. | 1.5 | 4 |
| 2 | A functional variant that affects exon-skipping and protein expression ofSP140as genetic mechanism predisposing to multiple sclerosis. Human Molecular Genetics, 2015, 24, 5619-5627. | 2.9 | 43 |
| 3 | Discretization of Expression Quantitative Trait Loci in Association Analysis Between Genotypes and Expression Data<sup>Â§</sup>. Current Bioinformatics, 2015, 10, 144-164. | 1.5 | 1 |
| 4 | GeneOnEarth: Fitting Genetic PC Plots on the Globe. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1009-1016. | 3.0 | 2 |
| 5 | Identification of a functional variant in theKIF5A-CYP27B1-METTL1-FAM119Blocus associated with multiple sclerosis. Journal of Medical Genetics, 2013, 50, 25-33. | 3.2 | 59 |
| 6 | INCREASING POWER BY USING HAPLOTYPE SIMILARITY IN A MULTIMARKER TRANSMISSION/DISEQUILIBRIUM TEST. Journal of Bioinformatics and Computational Biology, 2013, 11, 1250014. | 0.8 | 5 |
| 7 | Multiple Sclerosis Risk Variant HLA-DRB1*1501 Associates with High Expression of DRB1 Gene in Different Human Populations. PLoS ONE, 2012, 7, e29819. | 2.5 | 100 |
| 8 | Sample Reproducibility of Genetic Association Using Different Multimarker TDTs in Genome-Wide Association Studies: Characterization and a New Approach. PLoS ONE, 2012, 7, e29613. | 2.5 | 5 |
| 9 | HAPLOTYPE-BASED CLASSIFIERS TO PREDICT INDIVIDUAL SUSCEPTIBILITY TO COMPLEX DISEASES - An Example for Multiple Sclerosis. , 2012, , . | | 1 |
| 10 | 3D VISUALIZATION OF HAPLOTYPE RISK MAPS. , 2012, , . | | 0 |
| 11 | Homogenizing Access to Highly Time-Consuming Biomedical Applications through a Web-Based Interface. Lecture Notes in Computer Science, 2012, , 33-42. | 1.3 | 0 |
| 12 | Members 6B and 14 of the TNF receptor superfamily in multiple sclerosis predisposition. Genes and Immunity, 2011, 12, 145-148. | 4.1 | 14 |
| 13 | Riskoweb: Web-Based Genetic Profiling to Complex Disease Using Genome-Wide SNP Markers. Advances in Intelligent and Soft Computing, 2011, , 1-8. | 0.2 | 2 |
| 14 | Genome-wide association filtering using a highly locus-specific transmission/disequilibrium test. Human Genetics, 2010, 128, 325-344. | 3.8 | 5 |
| 15 | Variant alleles of the mannose binding lectin 2 gene (MBL2) confer heterozygote advantage within Crohn's families. Scandinavian Journal of Gastroenterology, 2010, 45, 1129-1130. | 1.5 | 6 |
| 16 | IL2RA/CD25 Gene Polymorphisms: Uneven Association with Multiple Sclerosis (MS) and Type 1 Diabetes (T1D). PLoS ONE, 2009, 4, e4137. | 2.5 | 65 |
| 17 | A hierarchical and modular approach to the discovery of robust associations in genome-wide association studies from pooled DNA samples. BMC Genetics, 2008, 9, 6. | 2.7 | 26 |
| 18 | Evolution and challenges in the design of computational systems for triage assistance. Journal of Biomedical Informatics, 2008, 41, 432-441. | 4.3 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A network model to predict the risk of death in sickle cell disease. Blood, 2007, 110, 2727-2735. | 1.4 | 159 |
| 20 | Bayesian estimates of linkage disequilibrium. BMC Genetics, 2007, 8, 36. | 2.7 | 5 |
| 21 | Multivariate Imputation of Genotype Data Using Short and Long Range Disequilibrium. , 2007, , 187-194. | | 0 |
| 22 | Operations strategy and flexibility: modeling with Bayesian classifiers. Industrial Management and Data Systems, 2006, 106, 460-484. | 3.7 | 22 |
| 23 | Building chromosome-wide LD maps. Bioinformatics, 2006, 22, 1933-1934. | 4.1 | 8 |
| 24 | Bayesian Correction for SNP Ascertainment Bias. Lecture Notes in Computer Science, 2006, , 262-273. | 1.3 | 1 |
| 25 | Fetal Hemoglobin (HbF) in Sickle Cell Anemia: Genome-Wide Association Studies Using Pooled DNA Samples Can Reveal Genetic Associations with HbF Concentration.. Blood, 2006, 108, 1221-1221. | 1.4 | 0 |
| 26 | Robust Transmission/Disequilibrium Test for Incomplete Family Genotypes. Genetics, 2004, 168, 2329-2337. | 2.9 | 18 |