Jorge Amigo

List of Publications by Year
in descending order

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47 papers	1,476 citations	331538 21 h-index	330025 37 g-index
48 all docs	48 docs citations	48 times ranked	2732 citing authors

#	Article	IF	Citations
1	Trio-based exome sequencing reveals a high rate of the de novo variants in intellectual disability. European Journal of Human Genetics, 2022, 30, 938-945.	1.4	7
2	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
3	Normalization of DNA encoded library affinity selection results driven by high throughput sequencing and HPLC purification. Bioorganic and Medicinal Chemistry, 2021, 40, 116178.	1.4	6
4	Building a custom large-scale panel of novel microhaplotypes for forensic identification using MiSeq and Ion S5 massively parallel sequencing systems. Forensic Science International: Genetics, 2020, 45, 102213.	1.6	70
5	Longitudinal analysis on parasite diversity in honeybee colonies: new taxa, high frequency of mixed infections and seasonal patterns of variation. Scientific Reports, 2020, 10, 10454.	1.6	18
6	Broadening the Applicability of a Custom Multi-Platform Panel of Microhaplotypes: Bio-Geographical Ancestry Inference and Expanded Reference Data. Frontiers in Genetics, 2020, 11, 581041.	1.1	17
7	A compilation of tri-allelic SNPs from 1000 Genomes and use of the most polymorphic loci for a large-scale human identification panel. Forensic Science International: Genetics, 2020, 46, 102232.	1.6	34
8	Early Colorectal Cancers Provide New Evidence for a Lynch Syndrome-to-CMMRD Phenotypic Continuum. Cancers, 2019, 11, 1081.	1.7	8
9	tagFinder: A Novel Tag Analysis Methodology That Enables Detection of Molecules from DNA-Encoded Chemical Libraries. SLAS Discovery, 2018, 23, 397-404.	1.4	10
10	Identification of putative second genetic hits in schizophrenia carriers of high-risk copy number variants and resequencing in additional samples. European Archives of Psychiatry and Clinical Neuroscience, 2018, 268, 585-592.	1.8	6
11	Identification of genes carrying rare variants of moderate to large effect in schizophrenia: A replication study. Schizophrenia Research, 2018, 197, 577-578.	1.1	0
12	Whole Exome Sequencing Identifies New Host Genomic Susceptibility Factors in Empyema Caused by Streptococcus pneumoniae in Children: A Pilot Study. Genes, 2018, 9, 240.	1.0	9
13	Postmortem genetic testing should be recommended in sudden cardiac death cases due to thoracic aortic dissection. International Journal of Legal Medicine, 2017, 131, 1211-1219.	1.2	13
14	Evaluating the Calling Performance of a Rare Disease NGS Panel for Single Nucleotide and Copy Number Variants. Molecular Diagnosis and Therapy, 2017, 21, 303-313.	1.6	7
15	Whole Exome Sequencing reveals new candidate genes in host genomic susceptibility to Respiratory Syncytial Virus Disease. Scientific Reports, 2017, 7, 15888.	1.6	29
16	SparkBWA: Speeding Up the Alignment of High-Throughput DNA Sequencing Data. PLoS ONE, 2016, 11, e0155461.	1.1	72
17	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. Forensic Science International: Genetics, 2016, 23, 19-24.	1.6	21
18	Targeted resequencing of regulatory regions at schizophrenia risk loci: Role of rare functional variants at chromatin repressive states. Schizophrenia Research, 2016, 174, 10-16.	1.1	6

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19	Comprehensive molecular testing in patients with high functioning autism spectrum disorder. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2016, 784-785, 46-52.	0.4	24
20	Targeted NGS meets expert clinical characterization: Efficient diagnosis of spastic paraplegia type 11. Applied & Translational Genomics, 2015, 5, 33-36.	2.1	3
21	Genetic Analysis of Arrhythmogenic Diseases in the Era of NGS: The Complexity of Clinical Decision-Making in Brugada Syndrome. PLoS ONE, 2015, 10, e0133037.	1.1	46
22	Resequencing and association analysis of coding regions at twenty candidate genes suggest a role for rare risk variation at AKAP9 and protective variation at NRXN1 in schizophrenia susceptibility. Journal of Psychiatric Research, 2015, 66-67, 38-44.	1.5	18
23	Tetra-allelic SNPs: Informative forensic markers compiled from public whole-genome sequence data. Forensic Science International: Genetics, 2015, 19, 100-106.	1.6	44
24	An efficient screening method for simultaneous detection of recurrent copy number variants associated with psychiatric disorders. Clinica Chimica Acta, 2015, 445, 34-40.	0.5	7
25	Completion of a worldwide reference panel of samples for an ancestry informative Indel assay. Forensic Science International: Genetics, 2015, 17, 75-80.	1.6	30
26	BigBWA: approaching the Burrowsâ€“Wheeler aligner to Big Data technologies. Bioinformatics, 2015, 31, 4003-4005.	1.8	107
27	Mitogenomes from The 1000 Genome Project Reveal New Near Eastern Features in Present-Day Tuscans. PLoS ONE, 2015, 10, e0119242.	1.1	15
28	A novel stop mutation in the vascular endothelial growth factor-C gene (VEGFC) results in Milroy-like disease. Journal of Medical Genetics, 2014, 51, 475-478.	1.5	43
29	Whole exome sequencing for the identification of a new mutation in TGFB2 involved in a familial case of non-syndromic aortic disease. Clinica Chimica Acta, 2014, 437, 88-92.	0.5	19
30	Next generation sequencing challenges in the analysis of cardiac sudden death due to arrhythmogenic disorders. Electrophoresis, 2014, 35, 3111-3116.	1.3	24
31	Global population variability in Qiagen Investigator HDplex STRs. Forensic Science International: Genetics, 2014, 8, 36-43.	1.6	19
32	A Genome-Wide Study of Modern-Day Tuscans: Revisiting Herodotus's Theory on the Origin of the Etruscans. PLoS ONE, 2014, 9, e105920.	1.1	23
33	A Generalized Model to Estimate the Statistical Power in Mitochondrial Disease Studies Involving 2Ã—k Tables. PLoS ONE, 2013, 8, e73567.	1.1	11
34	GDF: Dealing with High-throughput Genotyping Multiplatform Data for Medical and Population Genetic Applications. Journal of Proteomics and Bioinformatics, 2012, 05, .	0.4	2
35	The impact of modern migrations on present-day multi-ethnic Argentina as recorded on the mitochondrial DNA genome. BMC Genetics, 2011, 12, 77.	2.7	63
36	Analysis of global variability in 15 established and 5 new European Standard Set (ESS) STRs using the CEPH human genome diversity panel. Forensic Science International: Genetics, 2011, 5, 155-169.	1.6	103

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37	Call for participation in the neurogenetics consortium within the Human Variome Project. Neurogenetics, 2011, 12, 169-173.	0.7	5
38	ENGINES: exploring single nucleotide variation in entire human genomes. BMC Bioinformatics, 2011, 12, 105.	1.2	34
39	Adaptive selection of an incretin gene in Eurasian populations. Genome Research, 2011, 21, 21-32.	2.4	19
40	A Reduced Number of mtSNPs Saturates Mitochondrial DNA Haplotype Diversity of Worldwide Population Groups. PLoS ONE, 2010, 5, e10218.	1.1	13
41	Genome-wide identification of hypoxia-inducible factor binding sites and target genes by a probabilistic model integrating transcription-profiling data and in silico binding site prediction. Nucleic Acids Research, 2010, 38, 2332-2345.	6.5	179
42	Viability of in-house datamarting approaches for population genetics analysis of SNP genotypes. BMC Bioinformatics, 2009, 10, S5.	1.2	17
43	pop.STRâ€"An online population frequency browser for established and new forensic STRs. Forensic Science International: Genetics Supplement Series, 2009, 2, 361-362.	0.1	38
44	The SNPforID browser: an online tool for query and display of frequency data from the SNPforID project. International Journal of Legal Medicine, 2008, 122, 435-440.	1.2	47
45	SPSmart: adapting population based SNP genotype databases for fast and comprehensive web access. BMC Bioinformatics, 2008, 9, 428.	1.2	95
46	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. Bioinformatics, 2008, 24, 1643-1644.	1.8	61
47	Viability of in-house datamarting approaches for population genetics analysis of snp genotypes. , 2008, , .		0