Arcadi Navarro

List of Publications by Year
in descending order

126 papers	8,691 citations	61857 43 h-index	51492 86 g-index
138 all docs	138 docs citations	138 times ranked	14794 citing authors

#	Article	IF	Citations
1	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
2	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
3	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
4	Chromosomal speciation revisited: rearranging theory with pieces of evidence. Trends in Ecology and Evolution, 2010, 25, 660-669.	4.2	388
5	Chromosomal Speciation and Molecular Divergence--Accelerated Evolution in Rearranged Chromosomes. Science, 2003, 300, 321-324.	6.0	384
6	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	9.4	338
7	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
8	ACCUMULATING POSTZYGOTIC ISOLATION GENES IN PARAPATRY: A NEW TWIST ON CHROMOSOMAL SPECIATION. Evolution; International Journal of Organic Evolution, 2003, 57, 447-459.	1.1	324
9	Statistical Power Analysis of Neutrality Tests Under Demographic Expansions, Contractions and Bottlenecks With Recombination. Genetics, 2008, 179, 555-567.	1.2	242
10	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	6.0	230
11	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	13.7	222
12	Signatures of Positive Selection in Genes Associated with Human Skin Pigmentation as Revealed from Analyses of Single Nucleotide Polymorphisms. Annals of Human Genetics, 2007, 71, 354-369.	0.3	212
13	High Trans-ethnic Replicability of GWAS Results Implies Common Causal Variants. PLoS Genetics, 2013, 9, e1003566.	1.5	207
14	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173
15	Genetic and Clinical Factors Associated with Chronic Postsurgical Pain after Hernia Repair, Hysterectomy, and Thoracotomy. Anesthesiology, 2015, 122, 1123-1141.	1.3	148
16	Replicability and Prediction: Lessons and Challenges from GWAS. Trends in Genetics, 2018, 34, 504-517.	2.9	138
17	Inversion polymorphisms and nucleotide variability in Drosophila. Genetical Research, 2001, 77, 1-8.	0.3	136
18	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. PLoS Genetics, 2013, 9, e1003763.	1.5	118

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19	Genome-wide Scan of 500Â000 Single-Nucleotide Polymorphisms Among Responders and Nonresponders to Interferon Beta Therapy in Multiple Sclerosis. Archives of Neurology, 2009, 66, 972-8.	4.9	104
20	Identification of a Novel Risk Locus for Multiple Sclerosis at 13q31.3 by a Pooled Genome-Wide Scan of 500,000 Single Nucleotide Polymorphisms. PLoS ONE, 2008, 3, e3490.	1.1	99
21	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
22	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	2.4	82
23	Antagonistic pleiotropy and mutation accumulation influence human senescence and disease. Nature Ecology and Evolution, 2017, 1, 55.	3.4	82
24	Patterns and rates of intron divergence between humans and chimpanzees. Genome Biology, 2007, 8, R21.	13.9	81
25	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	3.5	78
26	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	3.3	75
27	Genome-Wide Analysis of Wild-Type Epsteinâ€“Barr Virus Genomes Derived from Healthy Individuals of the 1000 Genomes Project. Genome Biology and Evolution, 2014, 6, 846-860.	1.1	74
28	ACCUMULATING POSTZYGOTIC ISOLATION GENES IN PARAPATRY: A NEW TWIST ON CHROMOSOMAL SPECIATION. Evolution; International Journal of Organic Evolution, 2003, 57, 447.	1.1	73
29	Dynamics of a Human Interparalog Gene Conversion Hotspot. Genome Research, 2004, 14, 835-844.	2.4	70
30	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	3.5	70
31	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
32	Chromosomal rearrangements and the genomic distribution of gene-expression divergence in humans and chimpanzees. Trends in Genetics, 2004, 20, 524-529.	2.9	66
33	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. Genome Research, 2011, 21, 1626-1639.	2.4	66
34	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	2.4	65
35	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
36	The measurement of the lactonase activity of paraoxonase-1 in the clinical evaluation of patients with chronic liver impairment. Clinical Biochemistry, 2009, 42, 91-98.	0.8	59

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37	Identification of a functional variant in theKIF5A-CYP27B1-METTL1-FAM119Blocus associated with multiple sclerosis. Journal of Medical Genetics, 2013, 50, 25-33.	1.5	59
38	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. Molecular Biology and Evolution, 2018, 35, 1990-2004.	3.5	58
39	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	6.5	55
40	Chitinase 3-like 1 plasma levels are increased in patients with progressive forms of multiple sclerosis. Multiple Sclerosis Journal, 2012, 18, 983-990.	1.4	54
41	Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. PLoS Computational Biology, 2010, 6, e1000953.	1.5	53
42	Combining Multiple Hypothesis Testing with Machine Learning Increases the Statistical Power of Genome-wide Association Studies. Scientific Reports, 2016, 6, 36671.	1.6	53
43	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
44	Frequent appearance of novel protein-coding sequences by frameshift translation. Genomics, 2006, 88, 690-697.	1.3	47
45	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the diseaseâ€. Human Molecular Genetics, 2015, 24, 2023-2034.	1.4	45
46	Allele-Specific Gene Expression Is Widespread Across the Genome and Biological Processes. PLoS ONE, 2009, 4, e4150.	1.1	44
47	Assessing statistical significance in multivariable genome wide association analysis. Bioinformatics, 2016, 32, 1990-2000.	1.8	39
48	Properties of human disease genes and the role of genes linked to Mendelian disorders in complex disease aetiology. Human Molecular Genetics, 2017, 26, ddw405.	1.4	38
49	Positive selection in MAOA gene is human exclusive: determination of the putative amino acid change selected in the human lineage. Human Genetics, 2004, 115, 377-86.	1.8	36
50	New Subtype of Spinocerebellar Ataxia With Altered Vertical Eye Movements Mapping to Chromosome 1p32. JAMA Neurology, 2013, 70, 764.	4.5	36
51	A genomic screen of Spanish multiple sclerosis patients reveals multiple loci associated with the disease. Journal of Neuroimmunology, 2003, 143, 124-128.	1.1	35
52	Transcriptional network analysis in frontal cortex in <scp>L</scp>ewy body diseases with focus on dementia with <scp>L</scp>ewy bodies. Brain Pathology, 2018, 28, 315-333.	2.1	35
53	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. Molecular Ecology Resources, 2018, 18, 319-333.	2.2	33
54	Roles of the ubiquitin peptidase <scp>USP</scp>18 in multiple sclerosis and the response to interferonâ€Î² treatment. European Journal of Neurology, 2013, 20, 1390-1397.	1.7	32

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55	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. Genome Research, 2005, 16, 231-239.	2.4	29
56	Murine segmental duplications are hot spots for chromosome and gene evolution. Genomics, 2005, 86, 692-700.	1.3	28
57	Gender-Associated Differences of Perforin Polymorphisms in the Susceptibility to Multiple Sclerosis. Journal of Immunology, 2010, 185, 5392-5404.	0.4	27
58	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	1.2	27
59	Genetic association between polymorphisms in the ADAMTS14 gene and multiple sclerosis. Journal of Neuroimmunology, 2005, 164, 140-147.	1.1	26
60	Whole genome diversity of inherited chromosomally integrated HHV-6 derived from healthy individuals of diverse geographic origin. Scientific Reports, 2018, 8, 3472.	1.6	26
61	Extending the coalescent to multilocus systems: the case of balancing selection. Genetical Research, 2002, 79, 129-140.	0.3	25
62	On the association between chromosomal rearrangements and genic evolution in humans and chimpanzees. Genome Biology, 2007, 8, R230.	13.9	24
63	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC Genomics, 2017, 18, 977.	1.2	24
64	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	1.8	24
65	The Presence of Human Herpesvirus 6 in the Brain in Health and Disease. Biomolecules, 2020, 10, 1520.	1.8	24
66	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. Human Genetics, 2007, 121, 759-762.	1.8	23
67	Chromosomal rearrangements are associated with higher rates of molecular evolution in mammals. Gene, 2005, 353, 147-154.	1.0	22
68	Genetic factors affecting EBV copy number in lymphoblastoid cell lines derived from the 1000 Genome Project samples. PLoS ONE, 2017, 12, e0179446.	1.1	22
69	International federation of genomic medicine databases using GA4GH standards. Cell Genomics, 2021, 1, 100032.	3.0	22
70	Application of Multi-SNP Approaches Bayesian LASSO and AUC-RF to Detect Main Effects of Inflammatory-Gene Variants Associated with Bladder Cancer Risk. PLoS ONE, 2013, 8, e83745.	1.1	21
71	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	3.5	20
72	Genetic association between polymorphisms in the BTG1 gene and multiple sclerosis. Journal of Neuroimmunology, 2009, 213, 142-147.	1.1	20

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73	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
74	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. BMC Genomics, 2009, 10, 338.	1.2	19
75	Accelerated exon evolution within primate segmental duplications. Genome Biology, 2013, 14, R9.	13.9	19
76	Pharmacogenomic study in patients with multiple sclerosis. Neurology: Neuroimmunology and NeuroInflammation, 2015, 2, e154.	3.1	19
77	Demographic History of the GenusPanInferred from Whole Mitochondrial Genome Reconstructions. Genome Biology and Evolution, 2016, 8, 2020-2030.	1.1	19
78	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	5.8	19
79	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
80	IL28B polymorphisms are not associated with the response to interferon-beta in multiple sclerosis. Journal of Neuroimmunology, 2011, 239, 101-104.	1.1	18
81	Genetic Variation in the TP53 Pathway and Bladder Cancer Risk. A Comprehensive Analysis. PLoS ONE, 2014, 9, e89952.	1.1	18
82	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6.	3.3	17
83	Genomic analysis of the blood attributed to Louis XVI (1754â€“1793), king of France. Scientific Reports, 2015, 4, 4666.	1.6	16
84	The shared genetic architecture of schizophrenia, bipolar disorder and lifespan. Human Genetics, 2021, 140, 441-455.	1.8	16
85	Effect of Collapsed Duplications on Diversity Estimates: What to Expect. Genome Biology and Evolution, 2018, 10, 2899-2905.	1.1	15
86	Comparative Analysis of Mammal Genomes Unveils Key Genomic Variability for Human Life Span. Molecular Biology and Evolution, 2021, 38, 4948-4961.	3.5	15
87	Interplay of Interlocus Gene Conversion and Crossover in Segmental Duplications Under a Neutral Scenario. G3: Genes, Genomes, Genetics, 2014, 4, 1479-1489.	0.8	14
88	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. Human Genomics, 2004, 1, 399.	1.4	13
89	Differences in molecular evolutionary rates among microRNAs in the human and chimpanzee genomes. BMC Genomics, 2016, 17, 528.	1.2	13
90	Genetic association of CASP8 polymorphisms with primary progressive multiple sclerosis. Journal of Neuroimmunology, 2010, 222, 70-75.	1.1	12

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91	Structure of Linkage Disequilibrium in Humans: Genome Factors and Population Stratification. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 79-88.	2.0	12
92	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
93	Dynamics of gametic disequilibria between loci linked to chromosome inversions: the recombination-redistributing effect of inversions. Genetical Research, 1996, 67, 67-76.	0.3	11
94	Single-cell Transcriptional Changes in Neurodegenerative Diseases. Neuroscience, 2021, 479, 192-205.	1.1	11
95	Chromosomal evolution: Inversions: the chicken or the egg?. Heredity, 2007, 99, 479-480.	1.2	10
96	Integrating genomics into evolutionary medicine. Current Opinion in Genetics and Development, 2014, 29, 97-102.	1.5	10
97	Expanding the Geographic Characterisation of Epsteinâ€“Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686.	1.6	10
98	Copy number variantsÂand fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS Genetics, 2020, 16, e1008742.	1.5	10
99	Coexpression of the discoidin domain receptor 1 gene with oligodendrocyteâ€related and schizophrenia risk genes in the developing and adult human brain. Brain and Behavior, 2021, 11, e2309.	1.0	10
100	Beacon v2 and Beacon networks: A â€œlingua francaâ€•for federated data discovery in biomedical genomics, and beyond. Human Mutation, 2022, , .	1.1	10
101	Extreme differences between human germline and tumor mutation densities are driven by ancestral human-specific deviations. Nature Communications, 2020, 11, 2512.	5.8	9
102	Genoeconomics: Promises and Caveats for a New Field. Annals of the New York Academy of Sciences, 2009, 1167, 57-65.	1.8	8
103	Genome-wide association studies pipeline (GWASpi): a desktop application for genome-wide SNP analysis and management. Bioinformatics, 2011, 27, 1871-1872.	1.8	8
104	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	0.8	7
105	Inversions and genomic differentiation after secondary contact: When drift contributes to maintenance, not loss, of differentiation. Evolution; International Journal of Organic Evolution, 2021, 75, 1288-1303.	1.1	7
106	Inversions with classical style and trendy lines. Nature Genetics, 2005, 37, 115-116.	9.4	6
107	Association Cluster Detector: a tool for heuristic detection of significance clusters in whole-genome scans. Bioinformatics, 2005, 21, ii180-ii181.	1.8	6
108	The genomic distribution of intraspecific and interspecific sequence divergence of human segmental duplications relative to human/chimpanzee chromosomal rearrangements. BMC Genomics, 2008, 9, 384.	1.2	6

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109	Potential damaging mutation in LRP5 from genome sequencing of the first reported chimpanzee with the Chiari malformation. Scientific Reports, 2017, 7, 15224.	1.6	6
110	FaST-LMM for Two-Way Epistasis Tests on High-Performance Clusters. Journal of Computational Biology, 2018, 25, 862-870.	0.8	6
111	Pool and conquer: new tricks for (c)old problems. Molecular Ecology, 2014, 23, 1653-1655.	2.0	5
112	A pharmacogenetic study implicates NINJ2 in the response to Interferon-Î² in multiple sclerosis. Multiple Sclerosis Journal, 2020, 26, 1074-1082.	1.4	5
113	A New Risk Variant for Multiple Sclerosis at 11q23.3 Locus Is Associated with Expansion of CXCR5+ Circulating Regulatory T Cells. Journal of Clinical Medicine, 2020, 9, 625.	1.0	5
114	Positive Selection and Gene Conversion Drive the Evolution of a Brain-Expressed snoRNAs Cluster. Molecular Biology and Evolution, 2009, 26, 2563-2571.	3.5	4
115	SeDuS: segmental duplication simulator. Bioinformatics, 2016, 32, 148-150.	1.8	4
116	Reply to: Retesting the influences of mutation accumulation and antagonistic pleiotropy on human senescence and disease. Nature Ecology and Evolution, 2019, 3, 994-995.	3.4	4
117	Genome-phenome explorer (GePhEx): a tool for the visualization and interpretation of phenotypic relationships supported by genetic evidence. Bioinformatics, 2019, 36, 890-896.	1.8	3
118	HeT-A_pi1, a piRNA Target Sequence in the Drosophila Telomeric Retrotransposon HeT-A, Is Extremely Conserved across Copies and Species. PLoS ONE, 2012, 7, e37405.	1.1	3
119	Human herpesvirus diversity is altered in HLA class I binding peptides. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123248119.	3.3	3
120	The genetic impact of an Ebola outbreak on a wild gorilla population. BMC Genomics, 2021, 22, 735.	1.2	2
121	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. Genome Biology and Evolution, 2015, 7, 1490-1505.	1.1	1
122	GWAS: a milestone in the road from genotypes to phenotypes. , 2016, , 12-25.		1
123	Targeted resequencing reveals rare variants enrichment in multiple sclerosis susceptibility genes. Human Mutation, 2020, 41, 1308-1320.	1.1	1
124	Re: CASP8 in MS. Journal of Neuroimmunology, 2011, 230, 193-193.	1.1	0
125	Association between telomere length and cognitive function among cognitively unimpaired individuals at risk of Alzheimerâ€™s disease. Alzheimer's and Dementia, 2021, 17, .	0.4	0
126	Sex differences in genetic susceptibility of hippocampal subfields: A polygenic association study. Alzheimer's and Dementia, 2021, 17, .	0.4	0