Antonio Salas

List of Publications by Year
in descending order

318 papers	18,108 citations	18482 62 h-index	18647 119 g-index
337 all docs	337 docs citations	337 times ranked	15880 citing authors

#	Article	IF	Citations
1	CovidPhy: A tool for phylogeographic analysis of SARS-CoV-2 variation. Environmental Research, 2022, 204, 111909.	7.5	5
2	Evaluation of BNT162b2 Vaccine Effectiveness in Galicia, Northwest Spain. International Journal of Environmental Research and Public Health, 2022, 19, 4039.	2.6	4
3	A multi-tissue study of immune gene expression profiling highlights the key role of the nasal epithelium in COVID-19 severity. Environmental Research, 2022, 210, 112890.	7.5	23
4	Role and Diagnostic Performance of Host Epigenome in Respiratory Morbidity after RSV Infection: The EPIRESVi Study. Frontiers in Immunology, 2022, 13, .	4.8	5
5	Recognising the asymptomatic enemy. Lancet Infectious Diseases, The, 2021, 21, 305-306.	9.1	2
6	Pitfalls of barcodes in the study of worldwide SARS-CoV-2 variation and phylodynamics. Zoological Research, 2021, 42, 87-93.	2.1	7
7	Contamination detection in sequencing studies using the mitochondrial phylogeny. Genome Research, 2021, 31, 309-316.	5.5	44
8	Changes in epigenetic profiles throughout early childhood and their relationship to the response to pneumococcal vaccination. Clinical Epigenetics, 2021, 13, 29.	4.1	4
9	Association of Rare CYP39A1 Variants With Exfoliation Syndrome Involving the Anterior Chamber of the Eye. JAMA - Journal of the American Medical Association, 2021, 325, 753.	7.4	16
10	Identification of a Minimal 3-Transcript Signature to Differentiate Viral from Bacterial Infection from Best Genome-Wide Host RNA Biomarkers: A Multi-Cohort Analysis. International Journal of Molecular Sciences, 2021, 22, 3148.	4.1	6
11	Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell, 2021, 184, 1706-1723.e24.	28.9	30
12	Case Report: Two Monochorionic Twins With a Critically Different Course of Progressive Osseous Heteroplasia. Frontiers in Pediatrics, 2021, 9, 662669.	1.9	3
13	Superspreading in the emergence of COVID-19 variants. Trends in Genetics, 2021, 37, 1069-1080.	6.7	31
14	Sensogenomics and the Biological Background Underlying Musical Stimuli: Perspectives for a New Era of Musical Research. Genes, 2021, 12, 1454.	2.4	7
15	Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. Scientific Reports, 2021, 11, 18121.	3.3	8
16	TIPICO XI: report of the first series and podcast on infectious diseases and vaccines (aTIPICO). Human Vaccines and Immunotherapeutics, 2021, 17, 4299-4327.	3.3	0
17	PIMA: A population informative multiplex for the Americas. Forensic Science International: Genetics, 2020, 44, 102200.	3.1	7
18	Routine infant vaccination of pneumococcal conjugate vaccines has decreased pneumonia across all age groups in Northern Spain. Human Vaccines and Immunotherapeutics, 2020, 16, 1446-1453.	3.3	5

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19	Seroprevalence of SARS-CoV-2 Among Pediatric Healthcare Workers in Spain. Frontiers in Pediatrics, 2020, 8, 547.	1.9	19
20	Increased Serum Levels of sCD14 and sCD163 Indicate a Preponderant Role for Monocytes in COVID-19 Immunopathology. Frontiers in Immunology, 2020, 11, 560381.	4.8	59
21	Predicting haplogroups using a versatile machine learning program (PredYMaLe) on a new mutationally balanced 32 Y-STR multiplex (CombYplex): Unlocking the full potential of the human STR mutation rate spectrum to estimate forensic parameters. Forensic Science International: Genetics, 2020, 48, 102342.	3.1	7
22	Role of Monocytes/Macrophages in Covid-19 Pathogenesis: Implications for Therapy . Infection and Drug Resistance, 2020, Volume 13, 2485-2493.	2.7	93
23	Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders. Genome Research, 2020, 30, 1434-1448.	5.5	91
24	Identification of novel risk loci and causal insights for sporadic Creutzfeldt-Jakob disease: a genome-wide association study. Lancet Neurology, The, 2020, 19, 840-848.	10.2	42
25	Rotavirus and autoimmunity. Journal of Infection, 2020, 81, 183-189.	3.3	41
26	Extraordinary claims require extraordinary evidence in asserted mtDNA biparental inheritance. Forensic Science International: Genetics, 2020, 47, 102274.	3.1	23
27	A Meta-Analysis of Multiple Whole Blood Gene Expression Data Unveils a Diagnostic Host-Response Transcript Signature for Respiratory Syncytial Virus. International Journal of Molecular Sciences, 2020, 21, 1831.	4.1	19
28	RNA-Seq Data-Mining Allows the Discovery of Two Long Non-Coding RNA Biomarkers of Viral Infection in Humans. International Journal of Molecular Sciences, 2020, 21, 2748.	4.1	7
29	Host Transcriptomic Response Following Administration of Rotavirus Vaccine in Infantsâ€™ Mimics Wild Type Infection. Frontiers in Immunology, 2020, 11, 580219.	4.8	4
30	Phylogeography of SARS-CoV-2 pandemic in Spain: a story of multiple introductions, micro-geographic stratification, founder effects, and super-spreaders. Zoological Research, 2020, 41, 605-620.	2.1	34
31	Rotavirus infection beyond the gut. Infection and Drug Resistance, 2019, Volume 12, 55-64.	2.7	32
32	A qPCR expression assay of IFI44L gene differentiates viral from bacterial infections in febrile children. Scientific Reports, 2019, 9, 11780.	3.3	27
33	Biogeographical informativeness of Y-STR haplotypes. Science Bulletin, 2019, 64, 1381-1384.	9.0	2
34	Further considerations on rotavirus vaccination and seizure-related hospitalization rates . Infection and Drug Resistance, 2019, Volume 12, 989-991.	2.7	5
35	Identification of regulatory variants associated with genetic susceptibility to meningococcal disease. Scientific Reports, 2019, 9, 6966.	3.3	3
36	Impact of rotavirus vaccination on childhood hospitalizations for seizures: Heterologous or unforeseen direct vaccine effects?. Vaccine, 2019, 37, 3362-3368.	3.8	11

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37	Biogeographical origin and timing of the founder ichthyosis TGM1 c.1187Gâ€‰>â€‰A mutation in an isolated Ecuadorian population. Scientific Reports, 2019, 9, 7175.	3.3	7
38	Ancestry patterns inferred from massive RNA-seq data. Rna, 2019, 25, 857-868.	3.5	16
39	A western route of prehistoric human migration from Africa into the Iberian Peninsula. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182288.	2.6	47
40	Plasma lipid profiles discriminate bacterial from viral infection in febrile children. Scientific Reports, 2019, 9, 17714.	3.3	15
41	The natural selection that shapes our genomes. Forensic Science International: Genetics, 2019, 39, 57-60.	3.1	6
42	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	7.1	64
43	The Paleo-Indian Entry into South America According to Mitogenomes. Molecular Biology and Evolution, 2018, 35, 299-311.	8.9	54
44	The geographic mosaic of Ecuadorian Y-chromosome ancestry. Forensic Science International: Genetics, 2018, 33, 59-65.	3.1	19
45	Early human dispersals within the Americas. Science, 2018, 362, .	12.6	230
46	Whole Exome Sequencing Identifies New Host Genomic Susceptibility Factors in Empyema Caused by Streptococcus pneumoniae in Children: A Pilot Study. Genes, 2018, 9, 240.	2.4	9
47	Rotavirus intestinal infection induces an oral mucosa cytokine response. PLoS ONE, 2018, 13, e0195314.	2.5	5
48	A 2-transcript host cell signature distinguishes viral from bacterial diarrhea and it is influenced by the severity of symptoms. Scientific Reports, 2018, 8, 8043.	3.3	20
49	Life-threatening infections in children in Europe (the EUCLIDS Project): a prospective cohort study. The Lancet Child and Adolescent Health, 2018, 2, 404-414.	5.6	69
50	The peopling of South America and the trans-Andean gene flow of the first settlers. Genome Research, 2018, 28, 767-779.	5.5	59
51	Y-chromosome Peruvian origin of the 500-year-old Inca child mummy sacrificed in Cerro Aconcagua (Argentina). Science Bulletin, 2018, 63, 1457-1459.	9.0	5
52	Colitis microscÃ³pica: avances para una mejor identificaciÃ³n en los pacientes con diarrea crÃ³nica. GastroenterologÃa Y HepatologÃa, 2017, 40, 107-116.	0.5	4
53	Advances for improved diagnosis of microscopic colitis in patients with chronic diarrhoea. GastroenterologÃa Y HepatologÃa (English Edition), 2017, 40, 107-116.	0.1	2
54	Phylogenetic and population-based approaches to mitogenome variation do not support association with male infertility. Journal of Human Genetics, 2017, 62, 361-371.	2.3	3

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55	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
56	Updating the African human mitochondrial DNA tree: Relevance to forensic and population genetics. Forensic Science International: Genetics, 2017, 27, 156-159.	3.1	18
57	Phylogeographic and genome-wide investigations of Vietnam ethnic groups reveal signatures of complex historical demographic movements. Scientific Reports, 2017, 7, 12630.	3.3	17
58	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. American Journal of Human Genetics, 2017, 101, 725-736.	6.2	50
59	Whole Exome Sequencing reveals new candidate genes in host genomic susceptibility to Respiratory Syncytial Virus Disease. Scientific Reports, 2017, 7, 15888.	3.3	29
60	Salivary epidermal growth factor correlates with hospitalization length in rotavirus infection. BMC Infectious Diseases, 2017, 17, 370.	2.9	4
61	Bacteremia in Children Hospitalized with Respiratory Syncytial Virus Infection. PLoS ONE, 2016, 11, e0146599.	2.5	36
62	Development and Validation of a New Clinical Scale for Infants with Acute Respiratory Infection: The ReSVinet Scale. PLoS ONE, 2016, 11, e0157665.	2.5	41
63	Meta-Analysis of Mitochondrial DNA Variation in the Iberian Peninsula. PLoS ONE, 2016, 11, e0159735.	2.5	17
64	Role of Vitamin D in Hospitalized Children With Lower Tract Acute Respiratory Infections. Journal of Pediatric Gastroenterology and Nutrition, 2016, 62, 479-485.	1.8	12
65	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. Scientific Reports, 2016, 6, 35842.	3.3	33
66	Whole mitochondrial DNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman. Scientific Reports, 2016, 6, 18932.	3.3	18
67	HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. Nucleic Acids Research, 2016, 44, W58-W63.	14.5	688
68	â€˜Infertileâ€™ studies on mitochondrial DNA variation in asthenozoospermic Tunisian men. Biochemistry and Biophysics Reports, 2016, 8, 114-119.	1.3	4
69	Strong down-regulation of glycophorin genes: A host defense mechanism against rotavirus infection. Infection, Genetics and Evolution, 2016, 44, 403-411.	2.3	10
70	Analysis of uni and bi-parental markers in mixture samples: Lessons from the 22nd GHEP-ISFG Intercomparison Exercise. Forensic Science International: Genetics, 2016, 25, 63-72.	3.1	7
71	Diagnostic Test Accuracy of a 2-Transcript Host RNA Signature for Discriminating Bacterial vs Viral Infection in Febrile Children. JAMA - Journal of the American Medical Association, 2016, 316, 835.	7.4	263
72	Mapping human dispersals into the Horn of Africa from Arabian Ice Age refugia using mitogenomes. Scientific Reports, 2016, 6, 25472.	3.3	40

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73	Genomic continuity of Argentinean Mennonites. Scientific Reports, 2016, 6, 36392.	3.3	4
74	Mapping the genomic mosaic of two â€˜Afro-Boliviansâ€™ from the isolated Yungas valleys. BMC Genomics, 2016, 17, 207.	2.8	9
75	Regional Specialisation of T Cell Subsets and Apoptosis in the Human Gut Mucosa: Differences Between Ileum and Colon in Healthy Intestine and Inflammatory Bowel Diseases. Journal of Crohn's and Colitis, 2016, 10, 1042-1054.	1.3	14
76	Charting the Y-chromosome ancestry of present-day Argentinean Mennonites. Journal of Human Genetics, 2016, 61, 507-513.	2.3	10
77	Prevalence and Natural History of Microscopic Colitis: A Population-Based Study With Long-term Clinical Follow-up in Terrassa, Spain. Journal of Crohn's and Colitis, 2016, 10, 805-811.	1.3	20
78	Analysis of Y-chromosome STRs in Chile confirms an extensive introgression of European male lineages in urban populations. Forensic Science International: Genetics, 2016, 21, 76-80.	3.1	12
79	Comprehensive Analysis of Pan-African Mitochondrial DNA Variation Provides New Insights into Continental Variation and Demography. Journal of Genetics and Genomics, 2016, 43, 133-143.	3.9	10
80	Revealing latitudinal patterns of mitochondrial DNA diversity in Chileans. Forensic Science International: Genetics, 2016, 20, 81-88.	3.1	20
81	A comprehensive Y-STR portrait of Argentinean populations. Forensic Science International: Genetics, 2016, 20, 1-5.	3.1	9
82	The relationship between surname frequency and Y chromosome variation in Spain. European Journal of Human Genetics, 2016, 24, 120-128.	2.8	24
83	Does Viral Co-Infection Influence the Severity of Acute Respiratory Infection in Children?. PLoS ONE, 2016, 11, e0152481.	2.5	46
84	The complete mitogenome of a 500-year-old Inca child mummy. Scientific Reports, 2015, 5, 16462.	3.3	31
85	Impact of Rotavirus Vaccination on Childhood Hospitalization for Seizures. Pediatric Infectious Disease Journal, 2015, 34, 769-773.	2.0	40
86	Genomic insights on the ethno-history of the Maya and the â€˜Ladinosâ€™ from Guatemala. BMC Genomics, 2015, 16, 131.	2.8	32
87	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	7.1	110
88	A reference frequency database of 15 autosomal STRs in Chile. Forensic Science International: Genetics, 2015, 19, 35-36.	3.1	5
89	Mosaic maternal ancestry in the Great Lakes region of East Africa. Human Genetics, 2015, 134, 1013-1027.	3.8	18
90	Mitochondrial DNA as a Risk Factor for False Positives in Case-Control Association Studies. Journal of Genetics and Genomics, 2015, 42, 169-172.	3.9	30

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91	A parametric approach to kinship hypothesis testing using identity-by-descent parameters. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 465-79.	0.6	5
92	No evidence of association between common European mitochondrial DNA variants in Alzheimer, Parkinson, and migraine in the Spanish population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 54-65.	1.7	37
93	The multiethnic ancestry of Bolivians as revealed by the analysis of Y-chromosome markers. Forensic Science International: Genetics, 2015, 14, 210-218.	3.1	18
94	Mitogenomes from The 1000 Genome Project Reveal New Near Eastern Features in Present-Day Tuscans. PLoS ONE, 2015, 10, e0119242.	2.5	15
95	The Genomic Legacy of the Transatlantic Slave Trade in the Yungas Valley of Bolivia. PLoS ONE, 2015, 10, e0134129.	2.5	8
96	Viral Co-Infections in Pediatric Patients Hospitalized with Lower Tract Acute Respiratory Infections. PLoS ONE, 2015, 10, e0136526.	2.5	67
97	Intestinal Intraepithelial Lymphocyte Cytometric Pattern Is More Accurate than Subepithelial Deposits of Anti-Tissue Transglutaminase IgA for the Diagnosis of Celiac Disease in Lymphocytic Enteritis. PLoS ONE, 2014, 9, e101249.	2.5	40
98	Cuba: Exploring the History of Admixture and the Genetic Basis of Pigmentation Using Autosomal and Uniparental Markers. PLoS Genetics, 2014, 10, e1004488.	3.5	57
99	The saga of the many studies wrongly associating mitochondrial DNA with breast cancer. BMC Cancer, 2014, 14, 659.	2.6	36
100	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	3.1	214
101	Evaluating the role of mitochondrial DNA variation to the genetic predisposition to radiation-induced toxicity. Radiotherapy and Oncology, 2014, 111, 199-205.	0.6	8
102	No association between typical European mitochondrial variation and prostate cancer risk in a Spanish cohort. Journal of Human Genetics, 2014, 59, 411-414.	2.3	5
103	DNA Commission of the International Society for Forensic Genetics: Revised and extended guidelines for mitochondrial DNA typing. Forensic Science International: Genetics, 2014, 13, 134-142.	3.1	243
104	Evaluating the accuracy of AIM panels at quantifying genome ancestry. BMC Genomics, 2014, 15, 543.	2.8	29
105	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
106	Mitochondrial DNA (mtDNA) variants in the European haplogroups HV, JT, and U do not have a major role in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 607-617.	1.7	8
107	A Genome-Wide Study of Modern-Day Tuscans: Revisiting Herodotus's Theory on the Origin of the Etruscans. PLoS ONE, 2014, 9, e105920.	2.5	23
108	Ancestry analysis reveals a predominant Native American component with moderate European admixture in Bolivians. Forensic Science International: Genetics, 2013, 7, 537-542.	3.1	26

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109	The West African Ethnicity of the Enslaved in Jamaica. Slavery and Abolition, 2013, 34, 376-400.	0.3	5
110	Human Mitochondrial Genetics and Evolution. , 2013, , 555-557.		0
111	Impact of Current Smoking on the Clinical Course of Microscopic Colitis. Inflammatory Bowel Diseases, 2013, 19, 1470-1476.	1.9	54
112	Indian Signatures in the Westernmost Edge of the European Romani Diaspora: New Insight from Mitogenomes. PLoS ONE, 2013, 8, e75397.	2.5	24
113	The Genetic Legacy of the Pre-Colonial Period in Contemporary Bolivians. PLoS ONE, 2013, 8, e58980.	2.5	42
114	A Generalized Model to Estimate the Statistical Power in Mitochondrial Disease Studies Involving 2Ã—k Tables. PLoS ONE, 2013, 8, e73567.	2.5	11
115	Development of a Panel of Genome-Wide Ancestry Informative Markers to Study Admixture Throughout the Americas. PLoS Genetics, 2012, 8, e1002554.	3.5	212
116	Raising Doubts about the Pathogenicity of Mitochondrial DNA Mutation m.3308T>C in Left Ventricular Hypertraveculation/Noncompaction. Cardiology, 2012, 122, 113-115.	1.4	6
117	Differentiation of African Components of Ancestry to Stratify Groups in a Caseâ€“Control Study of a Brazilian Urban Population. Genetic Testing and Molecular Biomarkers, 2012, 16, 524-530.	0.7	5
118	The maintenance of mitochondrial genetic stability is crucial during the oncogenic process. Communicative and Integrative Biology, 2012, 5, 34-38.	1.4	5
119	A cautionary note on switching mitochondrial DNA reference sequences in forensic genetics. Forensic Science International: Genetics, 2012, 6, e182-e184.	3.1	24
120	Uniparental Markers of Contemporary Italian Population Reveals Details on Its Pre-Roman Heritage. PLoS ONE, 2012, 7, e50794.	2.5	36
121	Current Next Generation Sequencing technology may not meet forensic standards. Forensic Science International: Genetics, 2012, 6, 143-145.	3.1	60
122	Analysis of a claimed distant relationship in a deficient pedigree using high density SNP data. Forensic Science International: Genetics, 2012, 6, 350-353.	3.1	22
123	Patterns of Y-STR variation in Italy. Forensic Science International: Genetics, 2012, 6, 834-839.	3.1	14
124	Haplogrouping mitochondrial DNA sequences in Legal Medicine/Forensic Genetics. International Journal of Legal Medicine, 2012, 126, 901-916.	2.2	58
125	SNPs as Supplements in Simple Kinship Analysis or as Core Markers in Distant Pairwise Relationship Tests: When Do SNPs Add Value or Replace Well-Established and Powerful STR Tests?. Transfusion Medicine and Hemotherapy, 2012, 39, 202-210.	1.6	52
126	Genetic Continuity in the Franco-Cantabrian Region: New Clues from Autochthonous Mitogenomes. PLoS ONE, 2012, 7, e32851.	2.5	19

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127	Prevalence and clinical relevance of enteropathy associated with systemic autoimmune diseases. Digestive and Liver Disease, 2012, 44, 636-642.	0.9	11
128	Arrival of Paleo-Indians to the Southern Cone of South America: New Clues from Mitogenomes. PLoS ONE, 2012, 7, e51311.	2.5	57
129	Reconstructing ancient mitochondrial DNA links between Africa and Europe. Genome Research, 2012, 22, 821-826.	5.5	57
130	Rapid coastal spread of First Americans: Novel insights from South America's Southern Cone mitochondrial genomes. Genome Research, 2012, 22, 811-820.	5.5	167
131	Toward a mtDNA locus-specific mutation database using the LOVD platform. Human Mutation, 2012, 33, 1352-1358.	2.5	8
132	No evidence that major mtDNA European haplogroups confer risk to schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 414-421.	1.7	25
133	Reconstructing Native American population history. Nature, 2012, 488, 370-374.	27.8	699
134	Interdisciplinary approach to the demography of Jamaica. BMC Evolutionary Biology, 2012, 12, 24.	3.2	26
135	A melting pot of multicontinental mtDNA lineages in admixed Venezuelans. American Journal of Physical Anthropology, 2012, 147, 78-87.	2.1	29
136	Multiple Local and Recent Founder Effects of TGM1 in Spanish Families. PLoS ONE, 2012, 7, e33580.	2.5	15
137	Evaluating Methods to Correct for Population Stratification when Estimating Paternity Indexes. PLoS ONE, 2012, 7, e49832.	2.5	12
138	GDF: Dealing with High-throughput Genotyping Multiplatform Data for Medical and Population Genetic Applications. Journal of Proteomics and Bioinformatics, 2012, 05, .	0.4	2
139	Efficacy of anti-TNF therapies in refractory severe microscopic colitis. Journal of Crohn's and Colitis, 2011, 5, 612-618.	1.3	120
140	Mild enteropathy as a cause of iron-deficiency anaemia of previously unknown origin. Digestive and Liver Disease, 2011, 43, 448-453.	0.9	20
141	New Insights into the Lake Chad Basin Population Structure Revealed by High-Throughput Genotyping of Mitochondrial DNA Coding SNPs. PLoS ONE, 2011, 6, e18682.	2.5	26
142	A Statistical Framework for the Interpretation of mtDNA Mixtures: Forensic and Medical Applications. PLoS ONE, 2011, 6, e26723.	2.5	11
143	P2-171 Pain among older people and its impact on disability: a 10/66 cross-sectional population-based surveys in Latin America, India and China. Journal of Epidemiology and Community Health, 2011, 65, A268-A268.	3.7	2
144	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

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145	Call for participation in the neurogenetics consortium within the Human Variome Project. Neurogenetics, 2011, 12, 169-173.	1.4	5
146	Reassessing the role of mitochondrial DNA mutations in autism spectrum disorder. BMC Medical Genetics, 2011, 12, 50.	2.1	20
147	ENGINES: exploring single nucleotide variation in entire human genomes. BMC Bioinformatics, 2011, 12, 105.	2.6	34
148	Male lineages in South American native groups: Evidence of M19 traveling south. American Journal of Physical Anthropology, 2011, 146, 188-196.	2.1	22
149	A putative â€œhepitypeâ€•in the ATM gene associated with chronic lymphocytic leukemia risk. Genes Chromosomes and Cancer, 2011, 50, 887-895.	2.8	5
150	Evolution of the incidence of collagenous colitis and lymphocytic colitis in Terrassa, Spain: A population-based study. Inflammatory Bowel Diseases, 2011, 17, 1015-1020.	1.9	53
151	Pharmacogenetics of OATP Transporters Reveals That SLCO1B1 c.388A>G Variant Is Determinant of Increased Atorvastatin Response. International Journal of Molecular Sciences, 2011, 12, 5815-5827.	4.1	49
152	Evolutionary Analyses of Entire Genomes Do Not Support the Association of mtDNA Mutations with Ras/MAPK Pathway Syndromes. PLoS ONE, 2011, 6, e18348.	2.5	8
153	The Mitochondrial Genome Is a â€œGenetic Sanctuaryâ€•during the Oncogenic Process. PLoS ONE, 2011, 6, e23327.	2.5	26
154	Mitochondrial DNA Haplogroup Background Affects LHON, but Not Suspected LHON, in Chinese Patients. PLoS ONE, 2011, 6, e27750.	2.5	39
155	The initial peopling of the Americas: A growing number of founding mitochondrial genomes from Beringia. Genome Research, 2010, 20, 1174-1179.	5.5	147
156	Population stratification in Argentina strongly influences likelihood ratio estimates in paternity testing as revealed by a simulation-based approach. International Journal of Legal Medicine, 2010, 124, 63-69.	2.2	11
157	Colorectal Cancer OncoGuia: surgical pathology report guidelines. Clinical and Translational Oncology, 2010, 12, 211-213.	2.4	4
158	Linking the sub-Saharan and West Eurasian gene pools: maternal and paternal heritage of the Tuareg nomads from the African Sahel. European Journal of Human Genetics, 2010, 18, 915-923.	2.8	47
159	Genome-wide association study identifies variants in the CFH region associated with host susceptibility to meningococcal disease. Nature Genetics, 2010, 42, 772-776.	21.4	275
160	A Reduced Number of mtSNPs Saturates Mitochondrial DNA Haplotype Diversity of Worldwide Population Groups. PLoS ONE, 2010, 5, e10218.	2.5	13
161	Problemas y retos de futuro de la genÃ©tica forense en el siglo XXI. Cuadernos De Medicina Forense, 2010, 16, .	0.0	3
162	New Population and Phylogenetic Features of the Internal Variation within Mitochondrial DNA Macro-Haplogroup R0. PLoS ONE, 2009, 4, e5112.	2.5	75

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163	Ancestry Analysis in the 11-M Madrid Bomb Attack Investigation. PLoS ONE, 2009, 4, e6583.	2.5	110
164	Mitochondrial Echoes of First Settlement and Genetic Continuity in El Salvador. PLoS ONE, 2009, 4, e6882.	2.5	23
165	High Mitochondrial DNA Stability in B-Cell Chronic Lymphocytic Leukemia. PLoS ONE, 2009, 4, e7902.	2.5	22
166	Median network analysis of defectively sequenced entire mitochondrial genomes from early and contemporary disease studies. Journal of Human Genetics, 2009, 54, 174-181.	2.3	32
167	Inferring the Demographic History of African Farmers and Pygmy Hunterâ€"Gatherers Using a Multilocus Resequencing Data Set. PLoS Genetics, 2009, 5, e1000448.	3.5	142
168	Contamination and sample mix-up can best explain some patterns of mtDNA instabilities in buccal cells and oral squamous cell carcinoma. BMC Cancer, 2009, 9, 113.	2.6	44
169	Evaluating new candidate SNPs as low penetrance risk factors in sporadic breast cancer: A two-stage Spanish caseâ€"control study. Gynecologic Oncology, 2009, 112, 210-214.	1.4	13
170	Exaggerated status of â€œnovelâ€•and â€œpathogenicâ€•mtDNA sequence variants due to inadequate database searches. Human Mutation, 2009, 30, 191-196.	2.5	79
171	Applications of MALDIâ€TOF MS to largeâ€scale human mtDNA populationâ€based studies. Electrophoresis, 2009, 30, 3665-3673.	2.4	26
172	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. Human Genetics, 2009, 126, 521-531.	3.8	40
173	The Etruscan timeline: a recent Anatolian connection. European Journal of Human Genetics, 2009, 17, 693-696.	2.8	32
174	Evaluating the Ability of Treeâ€Based Methods and Logistic Regression for the Detection of SNPâ€SNP Interaction. Annals of Human Genetics, 2009, 73, 360-369.	0.8	66
175	Viability of in-house datamarting approaches for population genetics analysis of SNP genotypes. BMC Bioinformatics, 2009, 10, S5.	2.6	17
176	Distinctive Paleo-Indian Migration Routes from Beringia Marked by Two Rare mtDNA Haplogroups. Current Biology, 2009, 19, 1-8.	3.9	738
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