Angel Carracedo

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7700969/publications.pdf

Version: 2024-02-01

724 papers	42,578 citations	3721 89 h-index	4323 173 g-index
763 all docs	763 docs citations	763 times ranked	48763 citing authors

#	Article	IF	Citations
1	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
2	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates Aî², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
3	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
4	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
5	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
6	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
8	Reconstructing Native American population history. Nature, 2012, 488, 370-374.	13.7	699
9	Supercomplex Assembly Determines Electron Flux in the Mitochondrial Electron Transport Chain. Science, 2013, 340, 1567-1570.	6.0	687
10	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
11	The contribution of cannabis use to variation in the incidence of psychotic disorder across Europe (EU-GEI): a multicentre case-control study. Lancet Psychiatry,the, 2019, 6, 427-436.	3.7	528
12	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	9.4	514
13	Genetic variants near TIMP3 and high-density lipoproteinâ€“associated loci influence susceptibility to age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7401-7406.	3.3	475
14	A multiplex assay with 52 single nucleotide polymorphisms for human identification. Electrophoresis, 2006, 27, 1713-1724.	1.3	462
15	The Making of the African mtDNA Landscape. American Journal of Human Genetics, 2002, 71, 1082-1111.	2.6	451
16	An overview of STRUCTURE: applications, parameter settings, and supporting software. Frontiers in Genetics, 2013, 4, 98.	1.1	432
17	DNA Commission of the International Society of Forensic Genetics (ISFG): An update of the recommendations on the use of Y-STRs in forensic analysis. Forensic Science International, 2006, 157, 187-197.	1.3	366
18	SNPs in forensic genetics: a review on SNP typing methodologies. Forensic Science International, 2005, 154, 181-194.	1.3	364

#	Article	IF	Citations
19	Mitochondrial and nuclear DNA matching shapes metabolism and healthy ageing. Nature, 2016, 535, 561-565.	13.7	333
20	Inferring ancestral origin using a single multiplex assay of ancestry-informative marker SNPs. Forensic Science International: Genetics, 2007, 1, 273-280.	1.6	332
21	DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. Forensic Science International, 2006, 160, 90-101.	1.3	329
22	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	2.6	305
23	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
24	DNA Commission of the International Society for Forensic Genetics (ISFG): Recommendations regarding the role of forensic genetics for disaster victim identification (DVI). Forensic Science International: Genetics, 2007, 1, 3-12.	1.6	285
25	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
26	The Human Early-Life Exposome (HELIX): Project Rationale and Design. Environmental Health Perspectives, 2014, 122, 535-544.	2.8	280
27	Mutations in the gene encoding PDGF-B cause brain calcifications in humans and mice. Nature Genetics, 2013, 45, 1077-1082.	9.4	273
28	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
29	Mutations in XPR1 cause primary familial brain calcification associated with altered phosphate export. Nature Genetics, 2015, 47, 579-581.	9.4	237
30	ISFG: Recommendations on biostatistics in paternity testing. Forensic Science International: Genetics, 2007, 1, 223-231.	1.6	229
31	Identifying Gene-Environment Interactions in Schizophrenia: Contemporary Challenges for Integrated, Large-scale Investigations. Schizophrenia Bulletin, 2014, 40, 729-736.	2.3	229
32	Common variants at 2q37.3, 8q24.21, 15q21.3 and 16q24.1 influence chronic lymphocytic leukemia risk. Nature Genetics, 2010, 42, 132-136.	9.4	223
33	The African Diaspora: Mitochondrial DNA and the Atlantic Slave Trade. American Journal of Human Genetics, 2004, 74, 454-465.	2.6	213
34	Development of a Panel of Genome-Wide Ancestry Informative Markers to Study Admixture Throughout the Americas. PLoS Genetics, 2012, 8, e1002554.	1.5	212
35	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. Nature Neuroscience, 2017, 20, 1217-1224.	7.1	212
36	Straightforward Inference of Ancestry and Admixture Proportions through Ancestry-Informative Insertion Deletion Multiplexing. PLoS ONE, 2012, 7, e29684.	1.1	211

#	Article	IF	Citations
37	Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. Forensic Science International, 2001, 118, 106-113.	1.3	198
38	A new multiplex for human identification using insertion/deletion polymorphisms. Electrophoresis, 2009, 30, 3682-3690.	1.3	197
39	Publication of population data for forensic purposes. Forensic Science International: Genetics, 2010, 4, 145-147.	1.6	195
40	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	1.4	193
41	Risk of Cancer in Cases of Suspected Lynch Syndrome Without Germline Mutation. Gastroenterology, 2013, 144, 926-932.e1.	0.6	189
42	A Critical Reassessment of the Role of Mitochondria in Tumorigenesis. PLoS Medicine, 2005, 2, e296.	3.9	188
43	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	1.5	188
44	DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. Forensic Science International, 2001, 124, 5-10.	1.3	179
45	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179
46	The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. American Journal of Human Genetics, 2008, 83, 725-736.	2.6	174
47	Comparison between universal molecular screening for Lynch syndrome and revised Bethesda guidelines in a large population-based cohort of patients with colorectal cancer. Gut, 2012, 61, 865-872.	6.1	172
48	DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis. International Journal of Legal Medicine, 2006, 120, 191-200.	1.2	171
49	Typing of mitochondrial DNA coding region SNPs of forensic and anthropological interest using SNaPshot minisequencing. Forensic Science International, 2004, 140, 251-257.	1.3	161
50	Human Early Life Exposome (HELIX) study: a European population-based exposome cohort. BMJ Open, 2018, 8, e021311.	0.8	161
51	Analysis ofBRCA1andBRCA2genes in Spanish breast/ovarian cancer patients: A high proportion of mutations unique to Spain and evidence of founder effects. Human Mutation, 2003, 22, 301-312.	1.1	154
52	AMPA receptor GluA2 subunit defects are a cause of neurodevelopmental disorders. Nature Communications, 2019, 10, 3094.	5.8	150
53	Update of the guidelines for the publication of genetic population data. Forensic Science International: Genetics, 2014, 10, A1-A2.	1.6	144
54	New guidelines for the publication of genetic population data. Forensic Science International: Genetics, 2013, 7, 217-220.	1.6	142

#	Article	IF	Citations
55	mtDNA analysis of the Galician population: a genetic edge of European variation. European Journal of Human Genetics, 1998, 6, 365-375.	1.4	141
56	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140
57	Considerations by the European DNA profiling (EDNAP) group on the working practices, nomenclature and interpretation of mitochondrial DNA profiles. Forensic Science International, 2001, 124, 83-91.	1.3	139
58	A practical guide to mitochondrial DNA error prevention in clinical, forensic, and population genetics. Biochemical and Biophysical Research Communications, 2005, 335, 891-899.	1.0	138
59	Revised guidelines for the publication of genetic population data. Forensic Science International: Genetics, 2017, 30, 160-163.	1.6	135
60	Mutation rates at Y chromosome specific microsatellites. Human Mutation, 2005, 26, 520-528.	1.1	133
61	The genetic legacy of western Bantu migrations. Human Genetics, 2005, 117, 366-375.	1.8	131
62	Development of a methylation marker set for forensic age estimation using analysis of public methylation data and the Agena Bioscience EpiTYPER system. Forensic Science International: Genetics, 2016, 24, 65-74.	1.6	127
63	Examining the independent and joint effects of molecular genetic liability and environmental exposures in schizophrenia: results from the EUGEI study. World Psychiatry, 2019, 18, 173-182.	4.8	127
64	Analysis of artificially degraded DNA using STRs and SNPsâ€”results of a collaborative European (EDNAP) exercise. Forensic Science International, 2006, 164, 33-44.	1.3	124
65	DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. International Journal of Legal Medicine, 2001, 114, 305-309.	1.2	119
66	Further development of forensic eye color predictive tests. Forensic Science International: Genetics, 2013, 7, 28-40.	1.6	119
67	Human Spermatogenic Failure Purges Deleterious Mutation Load from the Autosomes and Both Sex Chromosomes, including the Gene DMRT1. PLoS Genetics, 2013, 9, e1003349.	1.5	118
68	Building a forensic ancestry panel from the ground up: The EUROFORGEN Global AIM-SNP set. Forensic Science International: Genetics, 2014, 11, 13-25.	1.6	116
69	A three-stage genome-wide association study identifies a susceptibility locus for late radiotherapy toxicity at 2q24.1. Nature Genetics, 2014, 46, 891-894.	9.4	114
70	Considerations from the European DNA profiling group (EDNAP) concerning STR nomenclature. Forensic Science International, 1997, 87, 185-192.	1.3	113
71	A Pentanucleotide ATTTC Repeat Insertion in the Non-coding Region of DAB1, Mapping to SCA37, Causes Spinocerebellar Ataxia. American Journal of Human Genetics, 2017, 101, 87-103.	2.6	112
72	Genomeâ€wide association analysis of dementia and its clinical endophenotypes reveal novel loci associated with Alzheimer's disease and three causality networks: The GR@ACE project. Alzheimer's and Dementia, 2019, 15, 1333-1347.	0.4	111

#	Article	IF	Citations
73	Ancestry Analysis in the 11-M Madrid Bomb Attack Investigation. PLoS ONE, 2009, 4, e6583.	1.1	110
74	Charting the Ancestry of African Americans. American Journal of Human Genetics, 2005, 77, 676-680.	2.6	109
75	Association of PDCD1 with susceptibility to systemic lupus erythematosus. Arthritis and Rheumatism, 2004, 50, 2590-2597.	6.7	106
76	The EDNAP mitochondrial DNA population database (EMPOP) collaborative exercises: organisation, results and perspectives. Forensic Science International, 2004, 139, 215-226.	1.3	105
77	Inter-laboratory evaluation of SNP-based forensic identification by massively parallel sequencing using the Ion PGMâ„¢. Forensic Science International: Genetics, 2015, 17, 110-121.	1.6	105
78	The R71GBRCA1is a founder Spanish mutation and leads to aberrant splicing of the transcript. Human Mutation, 2001, 17, 520-521.	1.1	103
79	A GEP-ISFG collaborative study on the optimization of an X-STR decaplex: data on 15 Iberian and Latin American populations. International Journal of Legal Medicine, 2009, 123, 227-234.	1.2	103
80	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
81	Revision of the SNPforID 34-plex forensic ancestry test: Assay enhancements, standard reference sample genotypes and extended population studies. Forensic Science International: Genetics, 2013, 7, 63-74.	1.6	102
82	Eurasiaplex: A forensic SNP assay for differentiating European and South Asian ancestries. Forensic Science International: Genetics, 2013, 7, 359-366.	1.6	102
83	Resolving relationship tests that show ambiguous STR results using autosomal SNPs as supplementary markers. Forensic Science International: Genetics, 2008, 2, 198-204.	1.6	100
84	Identification of new putative susceptibility genes for several psychiatric disorders by association analysis of regulatory and nonâ€synonymous SNPs of 306 genes involved in neurotransmission and neurodevelopment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 808-816.	1.1	98
85	RNA/DNA co-analysis from human saliva and semen stains â€“ Results of a third collaborative EDNAP exercise. Forensic Science International: Genetics, 2013, 7, 230-239.	1.6	97
86	A European Spectrum of Pharmacogenomic Biomarkers: Implications for Clinical Pharmacogenomics. PLoS ONE, 2016, 11, e0162866.	1.1	96
87	SPSmart: adapting population based SNP genotype databases for fast and comprehensive web access. BMC Bioinformatics, 2008, 9, 428.	1.2	95
88	mRNA profiling for the identification of bloodâ€"Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2011, 5, 21-26.	1.6	93
89	A candidate gene study of capecitabine-related toxicity in colorectal cancer identifies new toxicity variants atDPYDand a putative role forENOSF1rather thanTYMS. Gut, 2015, 64, 111-120.	6.1	93
90	Effect of environmental factors on PCR-DNA analysis from dental pulp. International Journal of Legal Medicine, 1996, 109, 125-129.	1.2	92

#	Article	IF	Citations
91	Hierarchical analysis of 30 Y-chromosome SNPs in European populations. International Journal of Legal Medicine, 2005, 119, 10-15.	1.2	92
92	Evaluating HapMap SNP data transferability in a large-scale genotyping project involving 175 cancer-associated genes. Human Genetics, 2006, 118, 669-679.	1.8	92
93	RNA/DNA co-analysis from blood stainsâ€"Results of a second collaborative EDNAP exercise. Forensic Science International: Genetics, 2012, 6, 70-80.	1.6	92
94	Paternity Testing Commission of the International Society of Forensic Genetics: recommendations on genetic investigations in paternity cases. Forensic Science International, 2002, 129, 148-157.	1.3	85
95	Evaluation of the Genplex SNP typing system and a 49plex forensic marker panel. Forensic Science International: Genetics, 2007, 1, 180-185.	1.6	85
96	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
97	A SNaPshot of next generation sequencing for forensic SNP analysis. Forensic Science International: Genetics, 2015, 14, 50-60.	1.6	85
98	Genetic admixture in three mexican mestizo populations based on D1S80 and HLA-DQA1 Loci. American Journal of Human Biology, 2002, 14, 257-263.	0.8	82
99	A new SNP assay for identification of highly degraded human DNA. Forensic Science International: Genetics, 2012, 6, 341-349.	1.6	82
100	Whole-exome sequencing identifies rare pathogenic variants in new predisposition genes for familial colorectal cancer. Genetics in Medicine, 2015, 17, 131-142.	1.1	82
101	Association of schizophrenia with DTNBP1 but not with DAO, DAOA, NRG1 and RGS4 nor their genetic interaction. Journal of Psychiatric Research, 2008, 42, 278-288.	1.5	80
102	Coding region mitochondrial DNA SNPs: Targeting East Asian and Native American haplogroups. Forensic Science International: Genetics, 2007, 1, 44-55.	1.6	78
103	Association Study of Nonsynonymous Single Nucleotide Polymorphisms in Schizophrenia. Biological Psychiatry, 2012, 71, 169-177.	0.7	78
104	â€˜Costa da Morteâ€™ ataxia is spinocerebellar ataxia 36: clinical and genetic characterization. Brain, 2012, 135, 1423-1435.	3.7	78
105	Molecular genetics of sudden cardiac death. Forensic Science International, 2008, 182, 1-12.	1.3	77
106	Micro-Phylogeographic and Demographic History of Portuguese Male Lineages. Annals of Human Genetics, 2006, 70, 181-194.	0.3	76
107	Heteroplasmy in mtDNA and the weight of evidence in forensic mtDNA analysis: a case report. International Journal of Legal Medicine, 2001, 114, 186-190.	1.2	75
108	New Population and Phylogenetic Features of the Internal Variation within Mitochondrial DNA Macro-Haplogroup R0. PLoS ONE, 2009, 4, e5112.	1.1	75

#	Article	IF	Citations
109	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
110	A highly variable STR at the D12S391 locus. International Journal of Legal Medicine, 1996, 109, 134-138.	1.2	74
111	Forensic validation of the SNPforID 52-plex assay. Forensic Science International: Genetics, 2007, 1, 186-190.	1.6	74
112	Association of common copy number variants at the glutathione S-transferase genes and rare novel genomic changes with schizophrenia. Molecular Psychiatry, 2010, 15, 1023-1033.	4.1	74
113	Introduction of an single nucleodite polymorphism-based â€œMajor Y-chromosome haplogroup typing kitâ€•suitable for predicting the geographical origin of male lineages. Electrophoresis, 2005, 26, 4411-4420.	1.3	73
114	The recombination landscape around forensic STRs: Accurate measurement of genetic distances between syntenic STR pairs using HapMap high density SNP data. Forensic Science International: Genetics, 2012, 6, 354-365.	1.6	73
115	A collaborative European exercise on mRNA-based body fluid/skin typing and interpretation of DNA and RNA results. Forensic Science International: Genetics, 2014, 10, 40-48.	1.6	71
116	Forensic genetics and genomics: Much more than just a human affair. PLoS Genetics, 2017, 13, e1006960.	1.5	71
117	Investigation of the STR locus HUMTH01 using PCR and two electrophoresis formats: UK and Galician Caucasian population surveys and usefulness in paternity investigations. Forensic Science International, 1994, 66, 41-52.	1.3	70
118	Robustness of the Y STRs DYS19, DYS389 I and II, DYS390 and DYS393: optimization of a PCR pentaplex. Forensic Science International, 1999, 106, 163-172.	1.3	70
119	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. Human Genetics, 2004, 115, 439-47.	1.8	70
120	Dissection of mitochondrial superhaplogroup H using coding region SNPs. Electrophoresis, 2006, 27, 2541-2550.	1.3	70
121	Forensic performance of two insertionâ€“deletion marker assays. International Journal of Legal Medicine, 2012, 126, 725-737.	1.2	70
122	Association study of 44 candidate genes with depressive and anxiety symptoms in post-partum women. Journal of Psychiatric Research, 2010, 44, 717-724.	1.5	69
123	Development of a forensic skin colour predictive test. Forensic Science International: Genetics, 2014, 13, 34-44.	1.6	69
124	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. EBioMedicine, 2016, 10, 150-163.	2.7	69
125	Case report: Identification of skeletal remains using short-amplicon marker analysis of severely degraded DNA extracted from a decomposed and charred femur. Forensic Science International: Genetics, 2008, 2, 212-218.	1.6	66
126	Inter-laboratory evaluation of the EUROFORGEN Global ancestry-informative SNP panel by massively parallel sequencing using the Ion PGMâ„¢. Forensic Science International: Genetics, 2016, 23, 178-189.	1.6	65

#	Article	IF	Citations
127	Social Camouflaging in Females with Autism Spectrum Disorder: A Systematic Review. Journal of Autism and Developmental Disorders, 2021, 51, 2190-2199.	1.7	65
128	Sequence variation of a hypervariable short tandem repeat at the D1S1656 locus. International Journal of Legal Medicine, 1998, 111, 244-247.	1.2	63
129	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
130	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	5.8	63
131	Gender bias in the multiethnic genetic composition of central Argentina. Journal of Human Genetics, 2008, 53, 662-674.	1.1	62
132	Refinement of the basis and impact of common 11q23.1 variation to the risk of developing colorectal cancer. Human Molecular Genetics, 2008, 17, 3720-3727.	1.4	61
133	Genomic Rearrangements at the BRCA1 Locus in Spanish Families with Breast/Ovarian Cancer. Clinical Chemistry, 2006, 52, 1480-1485.	1.5	60
134	Genetic analysis of three US population groups using an X-chromosomal STR decaplex. International Journal of Legal Medicine, 2007, 121, 198-203.	1.2	60
135	Typing short amplicon binary polymorphisms: Supplementary SNP and Indel genetic information in the analysis of highly degraded skeletal remains. Forensic Science International: Genetics, 2012, 6, 469-476.	1.6	60
136	Pacifiplex : an ancestry-informative SNP panel centred on Australia and the Pacific region. Forensic Science International: Genetics, 2016, 20, 71-80.	1.6	60
137	A C-terminal mutation of ATP1A3 underscores the crucial role of sodium affinity in the pathophysiology of rapid-onset dystonia-parkinsonism. Human Molecular Genetics, 2009, 18, 2370-2377.	1.4	59
138	Ethical-legal problems of DNA databases in criminal investigation. Journal of Medical Ethics, 2000, 26, 266-271.	1.0	57
139	A Strong Genetic Association between the Tumor Necrosis Factor Locus and Proliferative Vitreoretinopathy: The Retina 4 Project. Ophthalmology, 2010, 117, 2417-2423.e2.	2.5	57
140	Reconstructing ancient mitochondrial DNA links between Africa and Europe. Genome Research, 2012, 22, 821-826.	2.4	57
141	Cuba: Exploring the History of Admixture and the Genetic Basis of Pigmentation Using Autosomal and Uniparental Markers. PLoS Genetics, 2014, 10, e1004488.	1.5	57
142	The Global AIMs Nano set: A 31-plex SNaPshot assay of ancestry-informative SNPs. Forensic Science International: Genetics, 2016, 22, 81-88.	1.6	57
143	Rapid Real-Time Fluorescent PCR Gene Dosage Test for the Diagnosis of DNA Duplications and Deletions. Clinical Chemistry, 2000, 46, 1574-1582.	1.5	55
144	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. Translational Psychiatry, 2020, 10, 398.	2.4	54

#	Article	IF	Citations
145	Forensic typing of autosomal SNPs with a 29 SNP-multiplexâ€"Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2008, 2, 176-183.	1.6	53
146	RNA/DNA co-analysis from human skin and contact traces â€“ results of a sixth collaborative EDNAP exercise. Forensic Science International: Genetics, 2015, 16, 139-147.	1.6	53
147	Shipwrecks and founder effects: Divergent demographic histories reflected in Caribbean mtDNA. American Journal of Physical Anthropology, 2005, 128, 855-860.	2.1	52
148	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.	0.7	52
149	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
150	The use of the STRs HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS, HUMLPL in forensic application: Validation studies and population data for Galicia (NW Spain). International Journal of Legal Medicine, 1995, 107, 283-290.	1.2	51
151	Mutation spectra ofABCC8 gene in Spanish patients with hyperinsulinism of infancy (HI). Human Mutation, 2006, 27, 214-214.	1.1	51
152	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. PLoS ONE, 2015, 10, e0127852.	1.1	51
153	Prevalence of somatic mutl homolog 1 promoter hypermethylation in Lynch syndrome colorectal cancer. Cancer, 2015, 121, 1395-1404.	2.0	51
154	Global patterns of STR sequence variation: Sequencing the CEPH human genome diversity panel for 58 forensic STRs using the Illumina ForenSeq DNA Signature Prep Kit. Electrophoresis, 2018, 39, 2708-2724.	1.3	51
155	Chimpanzee homologous of human Y specific STRs. Forensic Science International, 2002, 126, 129-136.	1.3	50
156	The discoidin domain receptor 1 as a novel susceptibility gene for schizophrenia. Molecular Psychiatry, 2007, 12, 833-841.	4.1	50
157	Insertion/deletion polymorphisms: A multiplex assay and forensic applications. Forensic Science International: Genetics Supplement Series, 2009, 2, 513-515.	0.1	50
158	Detection of a large rearrangement in PALB2 in Spanish breast cancer families with male breast cancer. Breast Cancer Research and Treatment, 2012, 132, 307-315.	1.1	50
159	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
160	Analysis of the CODIS autosomal STR loci in four main Colombian regions. Forensic Science International, 2003, 137, 67-73.	1.3	49
161	17 STR data (AmpF/STR Identifiler and Powerplex 16 System) from Cabinda (Angola). Forensic Science International, 2004, 141, 193-196.	1.3	49
162	Digging deeper into East African human Y chromosome lineages. Human Genetics, 2010, 127, 603-613.	1.8	49

#	Article	IF	Citations
163	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.	1.8	49
164	Molecular analysis of the APC and MUTYH genes in Galician and Catalonian FAP families: a different spectrum of mutations?. BMC Medical Genetics, 2009, 10, 57.	2.1	48
165	High frequency and founder effect of the CYP3A4*20 loss-of-function allele in the Spanish population classifies CYP3A4 as a polymorphic enzyme. Pharmacogenomics Journal, 2015, 15, 288-292.	0.9	48
166	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
167	Susceptibility Genetic Variants Associated With Colorectal Cancer Risk Correlate With Cancer Phenotype. Gastroenterology, 2010, 139, 788-796.e6.	0.6	47
168	A novel MYH7 mutation links congenital fiber type disproportion and myosin storage myopathy. Neuromuscular Disorders, 2011, 21, 254-262.	0.3	47
169	The early-life exposome and epigenetic age acceleration in children. Environment International, 2021, 155, 106683.	4.8	47
170	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
171	Estimating Exposome Score for Schizophrenia Using Predictive Modeling Approach in Two Independent Samples: The Results From the EUGEI Study. Schizophrenia Bulletin, 2019, 45, 960-965.	2.3	46
172	DNA mixtures in forensic casework: a 4-year retrospective study. Forensic Science International, 2003, 134, 180-186.	1.3	45
173	Analysis of TGM1, ALOX12B, ALOXE3, NIPAL4 and CYP4F22 in autosomal recessive congenital ichthyosis from Galicia (NW Spain): evidence of founder effects. British Journal of Dermatology, 2011, 165, 906-911.	1.4	45
174	A method for the analysis of 32 X chromosome insertion deletion polymorphisms in a single PCR. International Journal of Legal Medicine, 2012, 126, 97-105.	1.2	45
175	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
176	Identification of Mycobacterium marinum in sea-urchin granulomas. British Journal of Dermatology, 2001, 145, 114-116.	1.4	44
177	The mtDNA ancestry of admixed Colombian populations. American Journal of Human Biology, 2008, 20, 584-591.	0.8	44
178	Sarcomeric gene mutations in sudden infant death syndrome (SIDS). Forensic Science International, 2012, 219, 278-281.	1.3	44
179	Analysis of PALB2 Gene in BRCA1/BRCA2 Negative Spanish Hereditary Breast/Ovarian Cancer Families with Pancreatic Cancer Cases. PLoS ONE, 2013, 8, e67538.	1.1	44
180	Thyroid cancer <scp>GWAS</scp> identifies 10q26.12 and 6q14.1 as novel susceptibility loci and reveals genetic heterogeneity among populations. International Journal of Cancer, 2015, 137, 1870-1878.	2.3	44

#	Article	IF	Citations
181	Tetra-allelic SNPs: Informative forensic markers compiled from public whole-genome sequence data. Forensic Science International: Genetics, 2015, 19, 100-106.	1.6	44
182	Distribution of Y-chromosome STR defined haplotypes in Iberia. Forensic Science International, 2000, 110, 117-126.	1.3	43
183	Human genome-wide screen of haplotype-like blocks of reduced diversity. Gene, 2005, 349, 219-225.	1.0	43
184	RAS gene polymorphisms, classical risk factors and the advent of coronary artery disease in the Portuguese population. BMC Cardiovascular Disorders, 2008, 8, 15.	0.7	43
185	COGENT (COlorectal cancer GENeTics): an international consortium to study the role of polymorphic variation on the risk of colorectal cancer. British Journal of Cancer, 2010, 102, 447-454.	2.9	43
186	A Genetic Case-Control Study Confirms the Implication ofSMAD7andTNF Locusin the Development of Proliferative Vitreoretinopathy. , 2013, 54, 1665.		43
187	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
188	Is Mitochondrial DNA Variation Associated with Sporadic Breast Cancer Risk?. Cancer Research, 2008, 68, 623-625.	0.4	42
189	BDNF genetic variants and methylation: effects on cognition in major depressive disorder. Translational Psychiatry, 2019, 9, 265.	2.4	42
190	The Genetic Legacy of the Pre-Colonial Period in Contemporary Bolivians. PLoS ONE, 2013, 8, e58980.	1.1	42
191	Results of a collaborative study of the EDNAP group regarding the reproducibility and robustness of the Y-chromosome STRs DYS19, DYS389 I and II, DYS390 and DYS393 in a PCR pentaplex format. Forensic Science International, 2001, 119, 28-41.	1.3	41
192	mtDNA mutations in tumors of the central nervous system reflect the neutral evolution of mtDNA in populations. Oncogene, 2004, 23, 1314-1320.	2.6	41
193	Exon-focused genome-wide association study of obsessive-compulsive disorder and shared polygenic risk with schizophrenia. Translational Psychiatry, 2016, 6, e768-e768.	2.4	41
194	Use of a comprehensive panel of biomarkers to predict response to a fluorouracilâ€“oxaliplatin regimen in patients with metastatic colorectal cancer. Pharmacogenomics, 2011, 12, 433-442.	0.6	40
195	Genome-wide study links MTMR7 gene to variant Creutzfeldt-Jakob risk. Neurobiology of Aging, 2012, 33, 1487.e21-1487.e28.	1.5	40
196	Novel genes detected by transcriptional profiling from whole-blood cells in patients with early onset of acute coronary syndrome. Clinica Chimica Acta, 2013, 421, 184-190.	0.5	40
197	De novo Mutations (DNMs) in Autism Spectrum Disorder (ASD): Pathway and Network Analysis. Frontiers in Genetics, 2018, 9, 406.	1.1	40
198	Y chromosome STR haplotypes: genetic and sequencing data of the Galician population (NW Spain). International Journal of Legal Medicine, 1998, 112, 15-21.	1.2	39

#	Article	IF	Citations
199	The 1998â€“1999 collaborative exercises and proficiency testing program on DNA typing of the Spanish and Portuguese Working Group of the International Society for Forensic Genetics (GEP-ISFG). Forensic Science International, 2000, 114, 21-30.	1.3	39
200	SNP Typing in Forensic Genetics: A Review. , 2005, 297, 107-126.		39
201	Breast Feeding, Parity and Breast Cancer Subtypes in a Spanish Cohort. PLoS ONE, 2012, 7, e40543.	1.1	39
202	Population genetics of three VNTR polymorphisms in two different Spanish populations. International Journal of Legal Medicine, 1993, 105, 251-256.	1.2	38
203	Micro-geographical differentiation in Northern Iberia revealed by Y-chromosomal DNA analysis. Gene, 2004, 329, 17-25.	1.0	38
204	Challenging DNA: Assessment of a range of genotyping approaches for highly degraded forensic samples. Forensic Science International: Genetics Supplement Series, 2008, 1, 26-28.	0.1	38
205	Naturalistic pharmacogenetic study of treatment resistance to typical neuroleptics in Europeanâ€“Brazilian schizophrenics. Pharmacogenetics and Genomics, 2008, 18, 599-609.	0.7	38
206	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
207	Case-control study for colorectal cancer genetic susceptibility in EPICOLON: previously identified variants and mucins. BMC Cancer, 2011, 11, 339.	1.1	38
208	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. Forensic Science International: Genetics, 2018, 37, 241-251.	1.6	38
209	A report of an international collaborative experiment to demonstrate the uniformity obtainable using DNA profiling techniques. Forensic Science International, 1992, 53, 29-43.	1.3	37
210	Pharmacogenomics in colorectal cancer: a genome-wide association study to predict toxicity after 5-fluorouracil or FOLFOX administration. Pharmacogenomics Journal, 2013, 13, 209-217.	0.9	37
211	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	1.1	37
212	Massive parallel sequencing applied to the molecular autopsy in sudden cardiac death in the young. Forensic Science International: Genetics, 2015, 18, 160-170.	1.6	37
213	Cognitive and emotional impairments in obsessiveâ€“compulsive disorder: Evidence from functional brain alterations. Porto Biomedical Journal, 2016, 1, 92-105.	0.4	37
214	Reproducibility of mtDNA analysis between laboratories: a report of the European DNA profiling group (EDNAP). Forensic Science International, 1998, 97, 165-170.	1.3	36
215	Association Study of 69 Genes in the Ret Pathway Identifies Low-penetrance Loci in Sporadic Medullary Thyroid Carcinoma. Cancer Research, 2007, 67, 9561-9567.	0.4	36
216	Extensive linkage disequilibrium mapping at HTR2A and DRD3 for schizophrenia susceptibility genes in the Galician population. Schizophrenia Research, 2007, 90, 123-129.	1.1	36

#	Article	IF	Citations
217	Timing and deciphering mitochondrial DNA macro-haplogroup R0 variability in Central Europe and Middle East. BMC Evolutionary Biology, 2008, 8, 191.	3.2	36
218	Prediction of Postpartum Depression Using Multilayer Perceptrons and Pruning. Methods of Information in Medicine, 2009, 48, 291-298.	0.7	36
219	Uniparental Markers of Contemporary Italian Population Reveals Details on Its Pre-Roman Heritage. PLoS ONE, 2012, 7, e50794.	1.1	36
220	A colorectal cancer genome-wide association study in a Spanish cohort identifies two variants associated with colorectal cancer risk at 1p33 and 8p12. BMC Genomics, 2013, 14, 55.	1.2	36
221	Replication of previous genome-wide association studies of psychiatric diseases in a large schizophrenia caseâ€“control sample from Spain. Schizophrenia Research, 2014, 159, 107-113.	1.1	36
222	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. Forensic Science International: Genetics, 2015, 19, 280-288.	1.6	36
223	Multiplex SNaPshot for detection of BRCA1/2 common mutations in Spanish and Spanish related breast/ovarian cancer families. BMC Medical Genetics, 2007, 8, 40.	2.1	35
224	Pharmacogenetic analysis in neoadjuvant chemoradiation for rectal cancer: high incidence of somatic mutations and their relation with response. Pharmacogenomics, 2010, 11, 747-761.	0.6	35
225	Susceptibility genetic variants associated with early-onset colorectal cancer. Carcinogenesis, 2012, 33, 613-619.	1.3	35
226	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	1.6	35
227	Population and segregation data on 17 Y-STRs: results of a GEP-ISFG collaborative study. International Journal of Legal Medicine, 2008, 122, 529-533.	1.2	34
228	Development of Predictive Models of Proliferative Vitreoretinopathy Based on Genetic Variables: The Retina 4 Project. , 2009, 50, 2384.		34
229	Verification that common variation at 2q37.1, 6p25.3, 11q24.1, 15q23, and 19q13.32 influences chronic lymphocytic leukaemia risk. British Journal of Haematology, 2010, 150, 473-479.	1.2	34
230	Development of a novel forensic STR multiplex for ancestry analysis and extended identity testing. Electrophoresis, 2013, 34, 1151-1162.	1.3	34
231	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	2.3	34
232	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
233	New genes emerging for colorectal cancer predisposition. World Journal of Gastroenterology, 2014, 20, 1961.	1.4	34
234	Y-chromosome variation in a Norwegian population sample. Forensic Science International, 2001, 117, 163-173.	1.3	33

#	Article	IF	Citations
235	Sequence structure of 12 novel Y chromosome microsatellites and PCR amplification strategies. Forensic Science International, 2001, 122, 19-26.	1.3	33
236	Genetic association study of age-related macular degeneration in the Spanish population. Acta Ophthalmologica, 2011, 89, e12-e22.	0.6	33
237	Association of a XRCC3 polymorphism and rectum mean dose with the risk of acute radio-induced gastrointestinal toxicity in prostate cancer patients. Radiotherapy and Oncology, 2012, 105, 321-328.	0.3	33
238	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. Scientific Reports, 2016, 6, 35842.	1.6	33
239	Evaluation of the Qiagen 140-SNP forensic identification multiplex for massively parallel sequencing. Forensic Science International: Genetics, 2017, 28, 35-43.	1.6	33
240	Patterns of Default Mode Network Deactivation in Obsessive Compulsive Disorder. Scientific Reports, 2017, 7, 44468.	1.6	33
241	The Etruscan timeline: a recent Anatolian connection. European Journal of Human Genetics, 2009, 17, 693-696.	1.4	32
242	Medical genomics: The intricate path from genetic variant identification to clinical interpretation. Applied & Translational Genomics, 2014, 3, 60-67.	2.1	32
243	Exploring iris colour prediction and ancestry inference in admixed populations of South America. Forensic Science International: Genetics, 2014, 13, 3-9.	1.6	32
244	Neutrophil to lymphocyte ratio and breast cancer risk: analysis by subtype and potential interactions. Scientific Reports, 2020, 10, 13203.	1.6	32
245	The three most common CARD15 mutations associated with Crohn's disease and the chromosome 16 susceptibility locus for systemic lupus erythematosus. British Journal of Rheumatology, 2003, 42, 570-574.	2.5	31
246	Deletion of LCE3C and LCE3B is a susceptibility factor for psoriatic arthritis: A study in Spanish and Italian populations and meta-analysis. Arthritis and Rheumatism, 2011, 63, 1860-1865.	6.7	31
247	Enhanced Localization of Genetic Samples through Linkage-Disequilibrium Correction. American Journal of Human Genetics, 2013, 92, 882-894.	2.6	31
248	â€œNew turns from old STaRsâ€• Enhancing the capabilities of forensic short tandem repeat analysis. Electrophoresis, 2014, 35, 3173-3187.	1.3	31
249	Exploration of SNP variants affecting hair colour prediction in Europeans. International Journal of Legal Medicine, 2015, 129, 963-975.	1.2	31
250	Executive Functioning: A Mediator Between Sensory Processing and Behaviour in Autism Spectrum Disorder. Journal of Autism and Developmental Disorders, 2021, 51, 2091-2103.	1.7	31
251	Alternative primers for DYS391 typing: advantages of their application to forensic genetics. Forensic Science International, 2000, 112, 49-57.	1.3	30
252	Analysis of BRCA1 and BRCA2 in breast and breast/ovarian cancer families shows population substructure in the Iberian peninsula. Annals of Human Genetics, 2002, 66, 29-36.	0.3	30

#	Article	IF	Citations
253	Insights into Iberian population origins through the construction of highly informative Y-chromosome haplotypes using biallelic markers, STRs, and the MSY1 minisatellite. American Journal of Physical Anthropology, 2003, 122, 147-161.	2.1	30
254	Novel high-throughput SNP genotyping cosegregation analysis for genetic diagnosis of autosomal recessive retinitis pigmentosa and Leber congenital amaurosis. Human Mutation, 2007, 28, 511-516.	1.1	30
255	Novel splice donor site mutation in MERTK gene associated with retinitis pigmentosa. British Journal of Ophthalmology, 2008, 92, 1419-1423.	2.1	30
256	Molecular diversity at the CYP2D6 locus in healthy and schizophrenic southern Brazilians. Pharmacogenomics, 2009, 10, 1457-1466.	0.6	30
257	Recent adaptive selection at MAOB and ancestral susceptibility to schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 369-374.	1.1	30
258	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
259	Report on the third EDNAP collaborative STR exercise. Forensic Science International, 1996, 78, 83-93.	1.3	29
260	Rapid and enhanced detection of mitochondrial DNA variation using single-strand conformation analysis of superposed restriction enzyme fragments from polymerase chain reaction-amplified products. Electrophoresis, 1997, 18, 52-54.	1.3	29
261	The use of the LightCycler for the detection of Y chromosome SNPs. Forensic Science International, 2001, 118, 163-168.	1.3	29
262	Y chromosome microsatellite genetic variation in two Native American populations from Argentina: Population stratification and mutation data. Forensic Science International: Genetics, 2008, 2, 274-280.	1.6	29
263	X-Ray Cross-Complementing Group 1 and Thymidylate Synthase Polymorphisms Might Predict Response to Chemoradiotherapy in Rectal Cancer Patients. International Journal of Radiation Oncology Biology Physics, 2012, 82, 138-144.	0.4	29
264	A melting pot of multicontinental mtDNA lineages in admixed Venezuelans. American Journal of Physical Anthropology, 2012, 147, 78-87.	2.1	29
265	RAD51C germline mutations found in Spanish site-specific breast cancer and breast-ovarian cancer families. Breast Cancer Research and Treatment, 2014, 147, 133-143.	1.1	29
266	A pathwayâ€based association study reveals variants from Wnt signalling genes contributing to asthma susceptibility. Clinical and Experimental Allergy, 2017, 47, 618-626.	1.4	29
267	Prevalence of CYP2C9 polymorphisms in the south of Europe. Pharmacogenomics Journal, 2009, 9, 306-310.	0.9	28
268	A Genome Wide Association Study Links Glutamate Receptor Pathway to Sporadic Creutzfeldt-Jakob Disease Risk. PLoS ONE, 2015, 10, e0123654.	1.1	28
269	Association between SNPs of Metalloproteinases and Prostaglandin F2Î± Receptor Genes and Latanoprost Response in Open-Angle Glaucoma. Ophthalmology, 2015, 122, 1040-1048.e4.	2.5	28
270	Prevalence ofMLH1constitutional epimutations as a cause of Lynch syndrome in unselected versus selected consecutive series of patients with colorectal cancer. Journal of Medical Genetics, 2015, 52, 498-502.	1.5	28

#	Article	IF	Citations
271	Replicated evidence that endophenotypic expression of schizophrenia polygenic risk is greater in healthy siblings of patients compared to controls, suggesting geneâ€“environment interaction. The EUGEI study. Psychological Medicine, 2020, 50, 1884-1897.	2.7	28
272	Identification of autosomal cis expression quantitative trait methylation (cis eQTMs) in childrenâ€™s blood. ELife, 2022, 11, .	2.8	28
273	mtDNA hypervariable region II (HVII) sequences in human evolution studies. European Journal of Human Genetics, 2000, 8, 964-974.	1.4	27
274	Grouping of Y-STR haplotypes discloses European geographic clines. Forensic Science International, 2003, 134, 172-179.	1.3	27
275	Distinct phenotypic features and gender-specific disease manifestations in a Spanish family with desmin L370P mutation. Neuromuscular Disorders, 2006, 16, 498-503.	0.3	27
276	Analysis of 10 X-STRs in three African populations. Forensic Science International: Genetics, 2007, 1, 208-211.	1.6	27
277	Genetic data of 10 X-STRs in a Spanish population sample. Forensic Science International, 2007, 173, 193-196.	1.3	27
278	Allele frequencies of fifteen STRs in a representative sample of the Italian population. Forensic Science International: Genetics, 2009, 3, e29-e30.	1.6	27
279	Genetic variants in genes related to lipid metabolism and atherosclerosis, dyslipidemia and atorvastatin response. Clinica Chimica Acta, 2013, 417, 8-11.	0.5	27
280	Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2015, 19, 56-67.	1.6	27
281	Inference of Ancestry in Forensic Analysis II: Analysis of Genetic Data. Methods in Molecular Biology, 2016, 1420, 255-285.	0.4	27
282	Analysis of the R1b-DF27 haplogroup shows that a large fraction of Iberian Y-chromosome lineages originated recently in situ. Scientific Reports, 2017, 7, 7341.	1.6	27
283	Systematic meta-analyses, field synopsis and global assessment of the evidence of genetic association studies in colorectal cancer. Gut, 2020, 69, 1460-1471.	6.1	27
284	Sequence variation of a hypervariable short tandem repeat at the D12S391 locus. Gene, 1996, 182, 151-153.	1.0	26
285	Failed PCR amplifications of MBP-STR alleles due to polymorphism in the primer annealing region. International Journal of Legal Medicine, 1996, 108, 313-315.	1.2	26
286	The variant E233G of theRAD51Dgene could be a low-penetrance allele in high-risk breast cancer families withoutBRCA1/2mutations. International Journal of Cancer, 2004, 110, 845-849.	2.3	26
287	Applications of MALDIâ€TOF MS to largeâ€scale human mtDNA populationâ€based studies. Electrophoresis, 2009, 30, 3665-3673.	1.3	26
288	New Insights into the Lake Chad Basin Population Structure Revealed by High-Throughput Genotyping of Mitochondrial DNA Coding SNPs. PLoS ONE, 2011, 6, e18682.	1.1	26

#	Article	IF	Citations
289	Ancestry analysis reveals a predominant Native American component with moderate European admixture in Bolivians. Forensic Science International: Genetics, 2013, 7, 537-542.	1.6	26
290	A Colorectal Cancer Susceptibility New Variant at 4q26 in the Spanish Population Identified by Genome-Wide Association Analysis. PLoS ONE, 2014, 9, e101178.	1.1	26
291	A Comparison of Forensic Age Prediction Models Using Data From Four DNA Methylation Technologies. Frontiers in Genetics, 2020, 11, 932.	1.1	26
292	The distribution of HLA DQA1 and D1S80 (pMCT118) alleles and genotypes in the populations of Galicia and Central Portugal. International Journal of Legal Medicine, 1993, 106, 124-128.	1.2	25
293	Testing for genetic structure in different urban Argentinian populations. Forensic Science International, 2007, 165, 35-40.	1.3	25
294	D9S1120, a simple STR with a common Native American-specific allele: Forensic optimization, locus characterization and allele frequency studies. Forensic Science International: Genetics, 2008, 3, 7-13.	1.6	25
295	Prevalence of HCM and long QT syndrome mutations in young sudden cardiac death-related cases. International Journal of Legal Medicine, 2011, 125, 565-572.	1.2	25
296	Touch Processing and Social Behavior in ASD. Journal of Autism and Developmental Disorders, 2017, 47, 2425-2433.	1.7	25
297	Novel Gene-Based Analysis of ASD GWAS: Insight Into the Biological Role of Associated Genes. Frontiers in Genetics, 2019, 10, 733.	1.1	25
298	Mutation analysis of the adenomatous polyposis coli (APC) gene in northwest Spanish patients with familial adenomatous polyposis (FAP) and sporadic colorectal cancer. Human Mutation, 2001, 18, 355-355.	1.1	24
299	Duplications of the Y-chromosome specific loci P25 and 92R7 and forensic implications. Forensic Science International, 2004, 140, 241-250.	1.3	24
300	Population data defined by 15 autosomal STR loci in Karamoja population (Uganda) using AmpF/STR Identifiler kit. Forensic Science International: Genetics, 2009, 3, e55-e58.	1.6	24
301	BRCA1 mutations do not increase prostate cancer risk: Results from a metaâ€analysis including new data. Prostate, 2011, 71, 1768-1779.	1.2	24
302	The CYP1A2 â€“163C>A polymorphism is associated with clozapine-induced generalized tonic-clonic seizures in Brazilian schizophrenia patients. Psychiatry Research, 2013, 209, 242-245.	1.7	24
303	Next generation sequencing challenges in the analysis of cardiac sudden death due to arrhythmogenic disorders. Electrophoresis, 2014, 35, 3111-3116.	1.3	24
304	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	1.6	24
305	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
306	The relationship between surname frequency and Y chromosome variation in Spain. European Journal of Human Genetics, 2016, 24, 120-128.	1.4	24

#	Article	IF	Citations
307	Single Nucleotide Polymorphisms in the Wnt and BMP Pathways and Colorectal Cancer Risk in a Spanish Cohort. PLoS ONE, 2010, 5, e12673.	1.1	24
308	Analyses of variants located in estrogen metabolism genes (ESR1, ESR2, COMT and APOE) and schizophrenia. Schizophrenia Research, 2008, 100, 308-315.	1.1	23
309	Mitochondrial Echoes of First Settlement and Genetic Continuity in El Salvador. PLoS ONE, 2009, 4, e6882.	1.1	23
310	Y-chromosome lineages in native South American population. Forensic Science International: Genetics, 2010, 4, 187-193.	1.6	23
311	How executive functions are related to intelligence in Williams syndrome. Research in Developmental Disabilities, 2012, 33, 1169-1175.	1.2	23
312	Cognitive functioning in children and adults with Smith-Magenis syndrome. European Journal of Medical Genetics, 2012, 55, 394-399.	0.7	23
313	Broad-based molecular autopsy: a potential tool to investigate the involvement of subtle cardiac conditions in sudden unexpected death in infancy and early childhood. Archives of Disease in Childhood, 2015, 100, 952-956.	1.0	23
314	Variability of multi-omics profiles in a population-based child cohort. BMC Medicine, 2021, 19, 166.	2.3	23
315	Cognitive functioning throughout adulthood and illness stages in individuals with psychotic disorders and their unaffected siblings. Molecular Psychiatry, 2021, 26, 4529-4543.	4.1	23
316	Guidelines for Mitochondrial DNA Typing. Vox Sanguinis, 2000, 79, 121-125.	0.7	22
317	Allele frequencies for 13 STRâ€™s from two Colombian populations: BogotÃ¡ and BoyacÃ¡. Forensic Science International, 2003, 136, 83-85.	1.3	22
318	High Mitochondrial DNA Stability in B-Cell Chronic Lymphocytic Leukemia. PLoS ONE, 2009, 4, e7902.	1.1	22
319	Testing the performance of mtSNP minisequencing in forensic samples. Forensic Science International: Genetics, 2009, 3, 261-264.	1.6	22
320	Analysis of a claimed distant relationship in a deficient pedigree using high density SNP data. Forensic Science International: Genetics, 2012, 6, 350-353.	1.6	22
321	The value of genetic polymorphisms to predict toxicity in metastatic colorectal patients with irinotecan-based regimens. Cancer Chemotherapy and Pharmacology, 2012, 69, 1591-1599.	1.1	22
322	Comparison of the genetic background of different Colombian populations using the SNPforID 52plex identification panel. International Journal of Legal Medicine, 2014, 128, 19-25.	1.2	22
323	Identification of a novelPNPLA1mutation in a Spanish family with autosomal recessive congenital ichthyosis. British Journal of Dermatology, 2014, 170, 980-982.	1.4	22
324	In utero and childhood exposure to tobacco smoke and multi-layer molecular signatures in children. BMC Medicine, 2020, 18, 243.	2.3	22

#	Article	IF	Citations
325	Using methylome data to inform exposome-health association studies: An application to the identification of environmental drivers of child body mass index. Environment International, 2020, 138, 105622.	4.8	22
326	Genetic variants of uncertain significance: How to match scientific rigour and standard of proof in sudden cardiac death?. Legal Medicine, 2020, 45, 101712.	0.6	22
327	Low frequency of replication errors in primary nervous system tumours. Journal of Neurology, Neurosurgery and Psychiatry, 2000, 69, 369-375.	0.9	21
328	Nonbinary single-nucleotide polymorphism markers. International Congress Series, 2004, 1261, 27-29.	0.2	21
329	The Karimojong from Uganda: Genetic characterization using an X-STR decaplex system. Forensic Science International: Genetics, 2009, 3, e127-e128.	1.6	21
330	Identification of a novel mutation in the human PDE6A gene in autosomal recessive retinitis pigmentosa: homology with the nmf28/nmf28 mice model. Clinical Genetics, 2010, 78, 495-498.	1.0	21
331	TGFÎ²1 SNPs and radio-induced toxicity in prostate cancer patients. Radiotherapy and Oncology, 2012, 103, 206-209.	0.3	21
332	Association of thromboxane A1 synthase (TBXAS1) gene polymorphism with acute urticaria induced by nonsteroidal anti-inflammatory drugs. Journal of Allergy and Clinical Immunology, 2013, 132, 989-991.	1.5	21
333	Predicting proliferative vitreoretinopathy: temporal and external validation of models based on genetic and clinical variables. British Journal of Ophthalmology, 2015, 99, 41-48.	2.1	21
334	<scp>PRKG</scp>1 and genetic diagnosis of earlyâ€onset thoracic aortic disease. European Journal of Clinical Investigation, 2016, 46, 787-794.	1.7	21
335	Medico-legal perspectives on sudden cardiac death in young athletes. International Journal of Legal Medicine, 2017, 131, 393-409.	1.2	21
336	Pleomorphism and drug resistant cancer stem cells are characteristic of aggressive primary meningioma cell lines. Cancer Cell International, 2017, 17, 72.	1.8	21
337	Ethical publication of research on genetics and genomics of biological material: guidelines and recommendations. Forensic Science International: Genetics, 2020, 48, 102299.	1.6	21
338	Purification and partial characterization of tomentine. An N-acetylglucosamine-specific lectin from the green alga Codium tomentosum (Huds.) Stackh.. Journal of Experimental Marine Biology and Ecology, 1988, 124, 21-30.	0.7	20
339	Genetic Differentiation of the Cabo Verde Archipelago Population Analysed by STR Polymorphisms. Annals of Human Genetics, 2003, 67, 340-347.	0.3	20
340	Methylenetetrahydrofolate reductase gene, homocysteine and coronary artery disease: The A1298C polymorphism does matter. Inferences from a case study (Madeira, Portugal). Thrombosis Research, 2008, 122, 648-656.	0.8	20
341	Results of the GEP-ISFG collaborative study on an X-STR Decaplex. Forensic Science International: Genetics Supplement Series, 2008, 1, 677-679.	0.1	20
342	Reassessing the role of mitochondrial DNA mutations in autism spectrum disorder. BMC Medical Genetics, 2011, 12, 50.	2.1	20

#	Article	IF	Citations
343	A two-phase caseâ€“control study for colorectal cancer genetic susceptibility: candidate genes from chromosomal regions 9q22 and 3q22. British Journal of Cancer, 2011, 105, 870-875.	2.9	20
344	Hypothesized role of pregnancy hormones on HER2+ breast tumor development. Breast Cancer Research and Treatment, 2013, 137, 237-246.	1.1	20
345	New genetic associations in thiopurine-related bone marrow toxicity among inflammatory bowel disease patients. Pharmacogenomics, 2013, 14, 631-640.	0.6	20
346	A genome-wide association study on copy-number variation identifies a 11q11 loss as a candidate susceptibility variant for colorectal cancer. Human Genetics, 2014, 133, 525-534.	1.8	20
347	Involvement of LCA5 in Leber Congenital Amaurosis and Retinitis Pigmentosa in the Spanish Population. Ophthalmology, 2014, 121, 399-407.	2.5	20
348	Inference of Ancestry in Forensic Analysis I: Autosomal Ancestry-Informative Marker Sets. Methods in Molecular Biology, 2016, 1420, 233-253.	0.4	20
349	Copy number variation analysis of patients with intellectual disability from North-West Spain. Gene, 2017, 626, 189-199.	1.0	20
350	Whole exome sequencing approach to analysis of the origin of cancer stem cells in patients with head and neck squamous cell carcinoma. Journal of Oral Pathology and Medicine, 2018, 47, 938-944.	1.4	20
351	Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. Genes, 2021, 12, 1284.	1.0	20
352	Electrophoretic human leukocyte antigenHLA-DQA1 DNA typing after polymerase chain reaction amplification. Electrophoresis, 1991, 12, 1041-1045.	1.3	19
353	Y-chromosome STR haplotypes from a Western Mediterranean population sample. Forensic Science International, 2001, 119, 254-257.	1.3	19
354	Testing for kinship in a subdivided population. Forensic Science International, 2003, 135, 105-109.	1.3	19
355	Finding genes that underlie physical traits of forensic interest using genetic tools. Forensic Science International: Genetics, 2007, 1, 100-104.	1.6	19
356	Clinical and molecular characterization of Wilson disease in Spanish patients. Hepatology Research, 2007, 37, 18-26.	1.8	19
357	New technologies in the genetic approach to sudden cardiac death in the young. Forensic Science International, 2010, 203, 15-24.	1.3	19
358	Refinement of the associations between risk of colorectal cancer and polymorphisms on chromosomes 1q41 and 12q13.13. Human Molecular Genetics, 2012, 21, 934-946.	1.4	19
359	Characterization of CYP1A2, CYP2C19, CYP3A4 and CYP3A5 polymorphisms in South Brazilians. Molecular Biology Reports, 2014, 41, 1453-1460.	1.0	19
360	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

#	Article	IF	Citations
361	Global population variability in Qiagen Investigator HDplex STRs. Forensic Science International: Genetics, 2014, 8, 36-43.	1.6	19
362	Cerebral and cerebellar MRI volumes in Williams syndrome. Research in Developmental Disabilities, 2014, 35, 922-928.	1.2	19
363	High-resolution copy number analysis of paired normal-tumor samples from diffuse large B cell lymphoma. Annals of Hematology, 2016, 95, 253-262.	0.8	19
364	FKBP5 polymorphisms and hypothalamic-pituitary-adrenal axis negative feedback in major depression and obsessive-compulsive disorder. Journal of Psychiatric Research, 2018, 104, 227-234.	1.5	19
365	Do polygenic risk and stressful life events predict pharmacological treatment response in obsessive compulsive disorder? A geneâ€“environment interaction approach. Translational Psychiatry, 2019, 9, 70.	2.4	19
366	Family History and Breast Cancer Hormone Receptor Status in a Spanish Cohort. PLoS ONE, 2012, 7, e29459.	1.1	19
367	Meta-Analysis of Mismatch Repair Polymorphisms within the Cogent Consortium for Colorectal Cancer Susceptibility. PLoS ONE, 2013, 8, e72091.	1.1	19
368	A silver staining method for the detection of polymorphic proteins in minute bloodstains after isoelectric focusing. Forensic Science International, 1983, 23, 241-248.	1.3	18
369	Allele frequency distribution of four PCR-amplified loci in the Spanish population. Forensic Science International, 1995, 71, 153-164.	1.3	18
370	Autosomal STR genetic variation in negroid ChocÃ³ and BogotÃ¡ populations. International Journal of Legal Medicine, 2001, 115, 102-104.	1.2	18
371	CYP2D6 genotyping by liquid chromatography-electrospray ionization mass spectrometry. Analytical and Bioanalytical Chemistry, 2011, 400, 2361-2370.	1.9	18
372	Genetic susceptibility variants associated with colorectal cancer prognosis. Carcinogenesis, 2013, 34, 2286-2291.	1.3	18
373	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
374	Mosaic maternal ancestry in the Great Lakes region of East Africa. Human Genetics, 2015, 134, 1013-1027.	1.8	18
375	The multiethnic ancestry of Bolivians as revealed by the analysis of Y-chromosome markers. Forensic Science International: Genetics, 2015, 14, 210-218.	1.6	18
376	Sequenom MassARRAY approach in the arrhythmogenic right ventricular cardiomyopathy post-mortem setting: clinical and forensic implications. International Journal of Legal Medicine, 2015, 129, 1-10.	1.2	18
377	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
378	Experimental Models to Study Autism Spectrum Disorders: hiPSCs, Rodents and Zebrafish. Genes, 2020, 11, 1376.	1.0	18

#	Article	IF	Citations
379	Looking into the genetic bases of OCD dimensions: a pilot genome-wide association study. Translational Psychiatry, 2020, 10, 151.	2.4	18
380	Examining the association between exposome score for schizophrenia and functioning in schizophrenia, siblings, and healthy controls: Results from the EUGEI study. European Psychiatry, 2021, 64, e25.	0.1	18
381	TWEAK Signaling Pathway Blockade Slows Cyst Growth and Disease Progression in Autosomal Dominant Polycystic Kidney Disease. Journal of the American Society of Nephrology: JASN, 2021, 32, 1913-1932.	3.0	18
382	Large Genomic Rearrangements of BRCA1 and BRCA2 among Patients Referred for Genetic Analysis in Galicia (NW Spain): Delimitation and Mechanism of Three Novel BRCA1 Rearrangements. PLoS ONE, 2014, 9, e93306.	1.1	18
383	Association of BDNF, HTR2A, TPH1, SLC6A4, and COMT polymorphisms with tDCS and escitalopram efficacy: ancillary analysis of a double-blind, placebo-controlled trial. Revista Brasileira De Psiquiatria, 2020, 42, 128-135.	0.9	18
384	PGM₁ Subtypes in Galicia (NW Spain). Human Heredity, 1982, 32, 133-135.	0.4	17
385	Comparison between isoelectric focusing methods for the detection of orosomucoid phenotypes. Electrophoresis, 1988, 9, 268-272.	1.3	17
386	Y chromosome specific polymorphisms in forensic analysis. Legal Medicine, 1999, 1, 55-60.	0.6	17
387	Genetic diversity of nine STRs in two northwest Iberian populations: Galicia and northern Portugal. International Journal of Legal Medicine, 2000, 114, 109-113.	1.2	17
388	Results of the GEP-ISFG collaborative study on the Y chromosome STRs GATA A10, GATA C4, GATA H4, DYS437, DYS438, DYS439, DYS460 and DYS461: population data. Forensic Science International, 2003, 135, 150-157.	1.3	17
389	CARD15/NOD2 analysis in rheumatoid arthritis susceptibility. British Journal of Rheumatology, 2003, 42, 1380-1382.	2.5	17
390	Whole genome amplificationâ€"the solution for a common problem in forensic casework?. International Congress Series, 2004, 1261, 24-26.	0.2	17
391	Cognitive functioning in Williams Syndrome: A study in Portuguese and Spanish patients. European Journal of Paediatric Neurology, 2009, 13, 337-342.	0.7	17
392	Viability of in-house datamarting approaches for population genetics analysis of SNP genotypes. BMC Bioinformatics, 2009, 10, S5.	1.2	17
393	Genetic Variations in SMAD7 Are Associated with Colorectal Cancer Risk in the Colon Cancer Family Registry. PLoS ONE, 2013, 8, e60464.	1.1	17
394	Synaptotagmin XI in Parkinson's disease: New evidence from an association study in Spain and Mexico. Journal of the Neurological Sciences, 2016, 362, 321-325.	0.3	17
395	Inference of biogeographical ancestry across central regions of Eurasia. International Journal of Legal Medicine, 2016, 130, 73-79.	1.2	17
396	Gene-based analysis of ADHD using PASCAL: a biological insight into the novel associated genes. BMC Medical Genomics, 2019, 12, 143.	0.7	17

#	Article	IF	Citations
397	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
398	Y-chromosome STR haplotypes in CÃ³rdoba (Argentina). Forensic Science International, 2003, 137, 217-220.	1.3	16
399	Results of the GEP-ISFG collaborative study on two Y-STRs tetraplexes: GEPY I (DYS461, GATA C4, DYS437) Tj ETQq1 1 0.784314 rgBT /O 135, 158-162.	1.3	16
400	Over-representation of two specific haplotypes among chromosomes harbouring BRCA1 mutations. European Journal of Human Genetics, 2003, 11, 489-492.	1.4	16
401	Association of the ARLTS1 Cys148Arg variant with sporadic and familial colorectal cancer. Carcinogenesis, 2007, 28, 1687-1691.	1.3	16
402	Minisequencing mitochondrial DNA pathogenic mutations. BMC Medical Genetics, 2008, 9, 26.	2.1	16
403	Association of MUTYH and MSH6 germline mutations in colorectal cancer patients. Familial Cancer, 2009, 8, 525-531.	0.9	16
404	Beyond BRCA1 and BRCA2 wildâ€type breast and/or ovarian cancer families: germline mutations in TP53 and PTEN. Clinical Genetics, 2010, 77, 193-196.	1.0	16
405	Association of a let-7 miRNA binding region ofTGFBR1with hereditary mismatch repair proficient colorectal cancer (MSS HNPCC). Carcinogenesis, 2016, 37, 751-758.	1.3	16
406	The genetic component of bicuspid aortic valve and aortic dilation. An exome-wide association study. Journal of Molecular and Cellular Cardiology, 2017, 102, 3-9.	0.9	16
407	UTMOST, a single and cross-tissue TWAS (Transcriptome Wide Association Study), reveals new ASD (Autism Spectrum Disorder) associated genes. Translational Psychiatry, 2021, 11, 256.	2.4	16
408	Distribution of the Pi, TfC, and Gc subtypes in Galicia (North West Spain). Zeitschrift Fur Rechtsmedizin Journal of Legal Medicine, 1983, 90, 153-158.	0.2	15
409	Genetic Markers: Association Study in Migraine. Cephalalgia, 1995, 15, 200-204.	1.8	15
410	Band shift analysis of three base-pair repeat alleles in the short tandem repeat locus D12S391. Forensic Science International, 1998, 93, 79-88.	1.3	15
411	Fluorescent SSCP of overlapping fragments (FSSCP-OF): a highly sensitive method for the screening of mitochondrial DNA variation. Forensic Science International, 2001, 124, 97-103.	1.3	15
412	A Novel Loss-of-Function Mutation (N48K) in the PTEN Gene in a Spanish Patient with Cowden Disease. Journal of Investigative Dermatology, 2003, 121, 1356-1359.	0.3	15
413	The genetic male legacy from El Salvador. Forensic Science International, 2007, 171, 198-203.	1.3	15
414	A common haplotype of DRD3 affected by recent positive selection is associated with protection from schizophrenia. Human Genetics, 2009, 124, 607-613.	1.8	15

#	Article	IF	Citations
415	X-chromosome STR sequence variation, repeat structure, and nomenclature in humans and chimpanzees. International Journal of Legal Medicine, 2009, 123, 143-149.	1.2	15
416	Genetic variability of the SNPforID 52-plex identification-SNP panel in Central West Colombia. Forensic Science International: Genetics, 2009, 4, e9-e10.	1.6	15
417	FAS system deregulation in T-cell lymphoblastic lymphoma. Cell Death and Disease, 2014, 5, e1110-e1110.	2.7	15
418	Y-chromosomal DNA analysis in French male lineages. Forensic Science International: Genetics, 2014, 9, 162-168.	1.6	15
419	A maternally inherited 16p13.11â€p12.3 duplication concomitant with a de novo SOX5 deletion in a male patient with global developmental delay, disruptive and obsessive behaviors and minor dysmorphic features. American Journal of Medical Genetics, Part A, 2015, 167, 1315-1322.	0.7	15
420	Brain activation of the defensive and appetitive survival systems in obsessive compulsive disorder. Brain Imaging and Behavior, 2015, 9, 255-263.	1.1	15
421	Genome-wide association study in Spanish identifies ADAM metallopeptidase with thrombospondin type 1 motif, 9 (ADAMTS9), as a novel asthma susceptibility gene. Journal of Allergy and Clinical Immunology, 2016, 137, 964-966.	1.5	15
422	In situ characterization of stem cells-like biomarkers in meningiomas. Cancer Cell International, 2018, 18, 77.	1.8	15
423	The search process: Integrating the investigation and identification of missing and unidentified persons. Forensic Science International (Online), 2021, 3, 100154.	0.6	15
424	Genetic Associations in the Vitamin D Receptor and Colorectal Cancer in African Americans and Caucasians. PLoS ONE, 2011, 6, e26123.	1.1	15
425	Normal and anomalous electrophoretic behavior of polymerase chain reaction-based DNA polymorphisms in polyacrylamide gels. Electrophoresis, 1998, 19, 1566-1572.	1.3	14
426	Low Incidence of Microsatellite Instability in Patients With Cervical Carcinomas. Diagnostic Molecular Pathology, 1998, 7, 276-282.	2.1	14
427	Population data on the D1S1656 and D12S391 STR loci in Andalusia (South Spain) and the Maghreb (North Africa). Forensic Science International, 1999, 104, 33-36.	1.3	14
428	Point mutations in the flanking regions of the Y-chromosome specific STRs DYS391, DYS437 and DYS438. International Journal of Legal Medicine, 2002, 116, 322-326.	1.2	14
429	DNA typing of short tandem repeat. Forensic Science International, 2002, 126, 261-264.	1.3	14
430	The GarÃfuna (Black Carib) people of the Atlantic coasts of Honduras: Population dynamics, structure, and phylogenetic relations inferred from genetic data, migration matrices, and isonymy. American Journal of Human Biology, 2010, 22, 36-44.	0.8	14
431	Patterns of Y-STR variation in Italy. Forensic Science International: Genetics, 2012, 6, 834-839.	1.6	14
432	Increased clopidogrel response is associated with ABCC3 expression: A pilot study. Clinica Chimica Acta, 2012, 413, 417-421.	0.5	14

#	Article	IF	Citations
433	The genetic landscape of Equatorial Guinea and the origin and migration routes of the Y chromosome haplogroup R-V88. European Journal of Human Genetics, 2013, 21, 324-331.	1.4	14
434	BMP2 / BMP4 colorectal cancer susceptibility loci in northern and southern European populations. Carcinogenesis, 2013, 34, 314-318.	1.3	14
435	High-throughput genotyping assay for the large-scale genetic characterization ofCryptosporidiumparasites from human and bovine samples. Parasitology, 2014, 141, 491-500.	0.7	14
436	Premorbid Adjustment and IQ in Patients With First-Episode Psychosis: A Multisite Case-Control Study of Their Relationship With Cannabis Use. Schizophrenia Bulletin, 2020, 46, 517-529.	2.3	14
437	Impact of CYP2C19 Genotype and Drug Interactions on Voriconazole Plasma Concentrations: A Spain Pharmacogeneticâ€Pharmacokinetic Prospective Multicenter Study. Pharmacotherapy, 2020, 40, 17-25.	1.2	14
438	Evidence, and replication thereof, that molecular-genetic and environmental risks for psychosis impact through an affective pathway. Psychological Medicine, 2022, 52, 1910-1922.	2.7	14
439	Review of Pharmacokinetics and Pharmacogenetics in Atypical Long-Acting Injectable Antipsychotics. Pharmaceutics, 2021, 13, 935.	2.0	14
440	The isoelectric focusing of keratins in hair followed by silver staining. Forensic Science International, 1985, 29, 83-89.	1.3	13
441	Detection of polymorphisms of human DNA after polymerase chain reaction by miniaturized SDS-PAGE. Forensic Science International, 1992, 55, 27-36.	1.3	13
442	Reply to Bortolini et al.. American Journal of Human Genetics, 2004, 75, 524-526.	2.6	13
443	Duplication and deletion analysis by fluorescent real-time PCR-based genotyping. Clinica Chimica Acta, 2006, 363, 138-146.	0.5	13
444	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006â€“2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	1.6	13
445	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.	0.6	13
446	Nucleotide variation in central nervous system genes among male suicide attempters. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 208-213.	1.1	13
447	Involvement of hypertrophic cardiomyopathy genes in sudden infant death syndrome (SIDS). Forensic Science International: Genetics Supplement Series, 2009, 2, 495-496.	0.1	13
448	A new approach to long QT syndrome mutation detection by Sequenom MassARRAY^{Â®} system. Electrophoresis, 2010, 31, 1648-1655.	1.3	13
449	A study of East Timor variability using the SNPforID 52-plex SNP panel. Forensic Science International: Genetics, 2011, 5, e25-e26.	1.6	13
450	Focus issueâ€”Analysis and biostatistical interpretation of complex and low template DNA samples. Forensic Science International: Genetics, 2012, 6, 677-678.	1.6	13

#	Article	IF	Citations
451	Allele frequencies of the five new European Standard Set (ESS) STRs and 15 established STRs in a Turkish population. Forensic Science International: Genetics, 2014, 9, e26.	1.6	13
452	Alcohol and breast cancer tumor subtypes in a Spanish Cohort. SpringerPlus, 2016, 5, 39.	1.2	13
453	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
454	Native American gene continuity to the modern admixed population from the Colombian Andes: Implication for biomedical, population and forensic studies. Forensic Science International: Genetics, 2018, 36, e1-e7.	1.6	13
455	A multicentre prospective study evaluating the impact of protonâ€pump inhibitors omeprazole and pantoprazole on voriconazole plasma concentrations. British Journal of Clinical Pharmacology, 2020, 86, 1661-1666.	1.1	13
456	Schuursâ€“Hoeijmakers Syndrome (PACS1 Neurodevelopmental Disorder): Seven Novel Patients and a Review. Genes, 2021, 12, 738.	1.0	13
457	Population study of the STRs HUMTH01 (including a new variant) and HUMVWA31A in Catalonia (northeast Spain). International Journal of Legal Medicine, 1996, 108, 318-320.	1.2	12
458	A review of the collaborative exercises on DNA typing of the Spanish and Portuguese ISFH working group. International Journal of Legal Medicine, 1997, 110, 273-277.	1.2	12
459	Catalonian population study of the tetranucleotide repeat loci D3S1358, D8S1179, D18S51 and D19S253. International Journal of Legal Medicine, 1998, 112, 75-77.	1.2	12
460	Evaluation of DXS9902, DXS7132, DXS6809, DXS7133, and DXS7423 in humans and chimpanzees: sequence variation, repeat structure, and nomenclature. International Journal of Legal Medicine, 2009, 123, 403-412.	1.2	12
461	Genetic profile characterization of 10 X-STRs in four populations of the southeastern region of Brazil. International Journal of Legal Medicine, 2010, 124, 427-432.	1.2	12
462	Colorectal Cancer Susceptibility Quantitative Trait Loci in Mice as a Novel Approach to Detect Low-Penetrance Variants in Humans: A Two-Stage Case-Control Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 619-623.	1.1	12
463	Population genetics of 17 Y-STR markers in West Libya (Tripoli region). Forensic Science International: Genetics, 2013, 7, e59-e61.	1.6	12
464	The molecular characterization of a depurinated trial DNA sample can be a model to understand the reliability of the results in forensic genetics. Electrophoresis, 2014, 35, 3134-3144.	1.3	12
465	Inferior frontal gyrus white matter abnormalities in obsessiveâ€“compulsive disorder. NeuroReport, 2015, 26, 495-500.	0.6	12
466	Interstitial microdeletions including the chromosome band 4q13.2 and the UBA6 gene as possible causes of intellectual disability and behavior disorder. American Journal of Medical Genetics, Part A, 2015, 167, 3113-3120.	0.7	12
467	Paternal lineages in <scp>L</scp>ibya inferred from Yâ€chromosome haplogroups. American Journal of Physical Anthropology, 2015, 157, 242-251.	2.1	12
468	Genetic structure of the <scp>K</scp>uwaiti population revealed by paternal lineages. American Journal of Human Biology, 2016, 28, 203-212.	0.8	12

#	Article	IF	Citations
469	Progress in pharmacogenetics: consortiums and new strategies. Drug Metabolism and Personalized Therapy, 2016, 31, 17-23.	0.3	12
470	Novel truncating variants expand the phenotypic spectrum of KAT6Bâ€related disorders. American Journal of Medical Genetics, Part A, 2019, 179, 290-294.	0.7	12
471	Psychiatric comorbidities in Asperger syndrome are related with polygenic overlap and differ from other Autism subtypes. Translational Psychiatry, 2020, 10, 258.	2.4	12
472	The continuity of effect of schizophrenia polygenic risk score and patterns of cannabis use on transdiagnostic symptom dimensions at first-episode psychosis: findings from the EU-GEI study. Translational Psychiatry, 2021, 11, 423.	2.4	12
473	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. SSRN Electronic Journal, 0, , .	0.4	12
474	Anti-VEGF Treatment and Response in Age-related Macular Degeneration: Diseaseâ€™s Susceptibility, Pharmacogenetics and Pharmacokinetics. Current Medicinal Chemistry, 2020, 27, 549-569.	1.2	12
475	Orosomucoid (ORM1 and ORM2) types in the Spanish Basque Country, Galicia and Northern Portugal. Human Heredity, 1990, 40, 330-334.	0.4	11
476	Double- and single-strand conformation polymorphism analysis of point mutations and short tandem repeats. Electrophoresis, 1994, 15, 566-571.	1.3	11
477	Genetic variability at nine STR loci in the Chueta (Majorcan Jews) and the Balearic populations investigated by a single multiplex reaction. International Journal of Legal Medicine, 2000, 113, 263-267.	1.2	11
478	Genetic diversity of Y-specific STRs in chimpanzees (Pan troglodytes). American Journal of Primatology, 2002, 57, 21-29.	0.8	11
479	Spanish population data and forensic usefulness of a novel Y-STR set (DYS437, DYS438, DYS439, DYS460,) Tj ETQq1 1 0.784314 rgB	1.2	11
480	STR-CODIS typing in Greece. Forensic Science International, 2003, 137, 104-106.	1.3	11
481	Y-chromosome STR-haplotype typing in El Salvador. Forensic Science International, 2004, 142, 45-49.	1.3	11
482	Selecting single nucleotide polymorphisms for forensic applications. International Congress Series, 2004, 1261, 18-20.	0.2	11
483	The genetic male component of two South-Western Colombian populations. Forensic Science International: Genetics, 2009, 3, e59-e61.	1.6	11
484	Population data on 15 autosomal STRs in a sample from Colombia. Forensic Science International: Genetics, 2009, 3, e81-e82.	1.6	11
485	Nilotes from Karamoja, Uganda: Haplotype data defined by 17 Y-chromosome STRs. Forensic Science International: Genetics, 2010, 4, e83-e86.	1.6	11
486	Forensic performance of insertionâ€“deletion marker systems. Forensic Science International: Genetics Supplement Series, 2011, 3, e443-e444.	0.1	11

#	Article	IF	Citations
487	Characterization of TGM1 c.984+1G>A mutation identified in a homozygous carrier of lamellar ichthyosis. International Journal of Dermatology, 2012, 51, 427-430.	0.5	11
488	Global population variability in Promega PowerPlex CS7, D6S1043, and Penta B STRs. International Journal of Legal Medicine, 2013, 127, 901-906.	1.2	11
489	<scp>BMPR1A</scp> mutations in early‐onset colorectal cancer with mismatch repair proficiency. Clinical Genetics, 2013, 84, 94-96.	1.0	11
490	Gene–gene interactions between DRD3, MRP4 and CYP2B6 polymorphisms and its influence on the pharmacokinetic parametersÂof efavirenz in HIV infected patients. Drug Metabolism and Pharmacokinetics, 2016, 31, 349-355.	1.1	11
491	Association of GSTP1 and ERCC1 polymorphisms with toxicity in locally advanced head and neck cancer platinum‐based chemoradiotherapy treatment. Head and Neck, 2019, 41, 2704-2715.	0.9	11
492	SDCBP Modulates Stemness and Chemoresistance in Head and Neck Squamous Cell Carcinoma through Src Activation. Cancers, 2021, 13, 4952.	1.7	11
493	Population Data on the Loci LDLR, GYPA, HBGG, D7S8, and GC in Three Southwest European Populations. Journal of Forensic Sciences, 1996, 41, 291-296.	0.9	11
494	Sequence variation of a variable short tandem repeat at the D18S535 locus. International Journal of Legal Medicine, 1998, 111, 337-339.	1.2	10
495	RareHRAS1 alleles are a risk factor for the development of brain tumors. Cancer, 2001, 92, 2920-2926.	2.0	10
496	STR data for the AmpFlSTR profiler plus loci from Macau (China). Forensic Science International, 2001, 123, 74-75.	1.3	10
497	Genetic data on eight STRs (D5S818, D7S820, F13B, LPL, TH01, TPOX, VWA31, CSF1PO) from a Colombian population. Forensic Science International, 2002, 129, 216-218.	1.3	10
498	SNP genotyping with single base extension-tag microarrays. International Congress Series, 2004, 1261, 331-333.	0.2	10
499	A collaborative study of the EDNAP group regarding Y-chromosome binary polymorphism analysis. Forensic Science International, 2005, 153, 103-108.	1.3	10
500	A SNP multiplex for the simultaneous prediction of biogeographic ancestry and pigmentation type. Forensic Science International: Genetics Supplement Series, 2011, 3, e500-e501.	0.1	10
501	Genetic analysis of the SNPforID 34-plex ancestry informative SNP panel in Tunisian and Libyan populations. Forensic Science International: Genetics, 2011, 5, e45-e47.	1.6	10
502	Publications and letters related to the forensic genetic analysis of low amounts of DNA. Forensic Science International: Genetics, 2011, 5, 1-2.	1.6	10
503	Electrochemical DNA base pairs quantification and endonuclease cleavage detection. Biosensors and Bioelectronics, 2011, 27, 40-45.	5.3	10
504	SNP variation with latitude: Analysis of the SNPforID 52-plex markers in north, mid-region and south Chilean populations. Forensic Science International: Genetics, 2014, 10, 12-16.	1.6	10

#	Article	IF	Citations
505	Epidemiological Trends of Histopathologically WHO Classified CNS Tumors in Developing Countries: Systematic Review. Asian Pacific Journal of Cancer Prevention, 2015, 16, 205-216.	0.5	10
506	Altered functional connectivity of the default mode network in Williams syndrome: a multimodal approach. Developmental Science, 2016, 19, 686-695.	1.3	10
507	Human genetics: international projects and personalized medicine. Drug Metabolism and Personalized Therapy, 2016, 31, 3-8.	0.3	10
508	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
509	A replication study of JTC bias, genetic liability for psychosis and delusional ideation. Psychological Medicine, 2022, 52, 1777-1783.	2.7	10
510	Genomeâ€wide association study of stage III/IV grade C periodontitis (former aggressive periodontitis) in a Spanish population. Journal of Clinical Periodontology, 2021, 48, 896-906.	2.3	10
511	Examining facial emotion recognition as an intermediate phenotype for psychosis: Findings from the EUGEI study. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2022, 113, 110440.	2.5	10
512	Characterization of Single Nucleotide Polymorphisms of Cytochrome P450 in an Australian Deceased Sample. Current Drug Metabolism, 2012, 13, 679-692.	0.7	10
513	Alterations of gray and white matter morphology in obsessive compulsive disorder. Psicothema, 2017, 29, 35-42.	0.7	10
514	Progress in methodology and standards in European molecular genetics laboratories. Clinica Chimica Acta, 1998, 278, 163-169.	0.5	9
515	New method to measure minisatellite variant repeat variation in population genetic studies. American Journal of Human Biology, 2002, 14, 421-428.	0.8	9
516	Significance of micro-geographical population structure in forensic cases: a bayesian exploration. International Journal of Legal Medicine, 2003, 117, 302-305.	1.2	9
517	GEP proficiency testing program in forensic genetics: 10 years of experience. International Congress Series, 2004, 1261, 124-126.	0.2	9
518	Y-chromosome haplotype analysis in Antioquia (Colombia). Forensic Science International, 2005, 151, 85-91.	1.3	9
519	Relative efficiency of the linkage disequilibrium mapping approach in detecting candidate genes for schizophrenia in different European populations. Genomics, 2005, 86, 280-286.	1.3	9
520	The presence of tri-allelic TPOX genotypes in Dominican Population. Forensic Science International: Genetics Supplement Series, 2009, 2, 371-372.	0.1	9
521	Seeking genetic susceptibility variants for colorectal cancer: the EPICOLON consortium experience. Mutagenesis, 2012, 27, 153-159.	1.0	9
522	Allele frequencies of 20 STRs from Northwest Spain (Galicia). Forensic Science International: Genetics, 2012, 6, e149-e150.	1.6	9

#	Article	IF	Citations
523	Genetic epistasis in female suicide attempters. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2012, 38, 294-301.	2.5	9
524	Genetic variants associated with addictive behavior in Colombian addicted and non-addicted to heroin or cocaine. Colombia Medica, 2013, , 19-25.	0.7	9
525	HLA-DRB1*15:01 allele protects from asthma susceptibility. Journal of Allergy and Clinical Immunology, 2014, 134, 1201-1203.	1.5	9
526	Ancestry analysis in rural Brazilian populations of African descent. Forensic Science International: Genetics, 2018, 36, 160-166.	1.6	9
527	Assessment of genotyping tools applied in genetic susceptibility studies of periodontal disease: A systematic review. Archives of Oral Biology, 2018, 92, 38-50.	0.8	9
528	Tumor Profiling at the Service of Cancer Therapy. Frontiers in Oncology, 2020, 10, 595613.	1.3	9
529	Multiple Sporadic Colorectal Cancers Display a Unique Methylation Phenotype. PLoS ONE, 2014, 9, e91033.	1.1	9
530	Population Genetics of Nine STR Loci in Two Populations from Brazil. Journal of Forensic Sciences, 2000, 45, 432-435.	0.9	9
531	Forensic DNA analysis in Europe: current situation and standardization efforts. Forensic Science International, 1997, 86, 87-102.	1.3	8
532	Nine autosomal STRs genotype profiles in a sample from CÃ³rdoba (Argentina). Forensic Science International, 2004, 139, 81-83.	1.3	8
533	Forensic DNA-Typing Technologies: A Review. , 2005, 297, 001-012.		8
534	Microsatellite autosomal genotyping data in four indigenous populations from El Salvador. Forensic Science International, 2007, 170, 86-91.	1.3	8
535	Phylogeography of French male lineages. Forensic Science International: Genetics Supplement Series, 2009, 2, 439-441.	0.1	8
536	A novel mutation in the OFD1 (Cxorf5) gene may contribute to oral phenotype in patients with oralâ€facialâ€digital syndrome type 1. Oral Diseases, 2011, 17, 610-614.	1.5	8
537	Association between CASP8 â€“652 6N Del Polymorphism (rs3834129) and Colorectal Cancer Risk: Results from a Multi-Centric Study. PLoS ONE, 2014, 9, e85538.	1.1	8
538	Fine mapping of the myosin light chain kinase (MYLK) gene replicates the association with asthma in populations of Spanish descent. Journal of Allergy and Clinical Immunology, 2015, 136, 1116-1118.e9.	1.5	8
539	Long Survival and Severe Toxicity Under 5-Fluorouracilâ€“Based Therapy in a Patient With Colorectal Cancer Who Harbors a Germline Codon-Stop Mutation in TYMS. Mayo Clinic Proceedings, 2015, 90, 1298-1303.	1.4	8
540	Autism spectrum symptoms in Smithâ€“Magenis syndrome and Williams syndrome: comparisons and contrasts. International Journal of Developmental Disabilities, 2015, 61, 49-55.	1.3	8

#	Article	IF	Citations
541	Early Colorectal Cancers Provide New Evidence for a Lynch Syndrome-to-CMMRD Phenotypic Continuum. Cancers, 2019, 11, 1081.	1.7	8
542	Evolutionary Analyses of Entire Genomes Do Not Support the Association of mtDNA Mutations with Ras/MAPK Pathway Syndromes. PLoS ONE, 2011, 6, e18348.	1.1	8
543	Genetic Markers in Alcoholic Liver Cirrhosis. Human Heredity, 1992, 42, 235-241.	0.4	7
544	Allele distribution of three STRs in a population from Mozambique. International Journal of Legal Medicine, 1999, 112, 345-347.	1.2	7
545	Assessing microsatellite instability with semiautomated fluorescent technology: Application to the analysis of primary brain tumors. Electrophoresis, 2000, 21, 1471-1477.	1.3	7
546	Sequence variation of two hypervariable short tandem repeats at the D22S683 and D6S477 loci. International Journal of Legal Medicine, 2000, 113, 146-149.	1.2	7
547	Population data of Galicia (NW Spain) on the new Y-STRs DYS437, DYS438, DYS439, GATA A10, GATA A7.1, GATA A7.2, GATA C4 and GATA H4. Forensic Science International, 2003, 131, 220-224.	1.3	7
548	Ancestry vs physical traits: the search for ancestry informative markers (AIMs). International Journal of Legal Medicine, 2006, 120, 188-189.	1.2	7
549	Blepharophimosis?ptosis?epicanthus inversus syndrome (BPES). International Journal of Dermatology, 2007, 46, 61-63.	0.5	7
550	Evidence for classification of c.1852_1853AA>GC in MLH1 as a neutral variant for Lynch syndrome. BMC Medical Genetics, 2011, 12, 12.	2.1	7
551	Analysis of the SNPforID 52-plex markers in four Native American populations from Venezuela. Forensic Science International: Genetics, 2012, 6, e142-e145.	1.6	7
552	Pharmacogenomics of anti-platelet therapy focused on peripheral blood cells of coronary arterial disease patients. Clinica Chimica Acta, 2013, 425, 9-17.	0.5	7
553	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
554	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
555	Interaction between the functional SNP rs2070951 in NR3C2 gene and high levels of plasma corticotropin-releasing hormone associates to postpartum depression. Archives of Women's Mental Health, 2020, 23, 413-420.	1.2	7
556	Association of variants in MYH7, MYBPC3 and TNNT2 with sudden cardiac death-related risk factors in Brazilian patients with hypertrophic cardiomyopathy. Forensic Science International: Genetics, 2021, 52, 102478.	1.6	7
557	Efficacy and toxicity of adjuvant chemotherapy on colorectal cancer patients: how much influence from the genetics?. Journal of Chemotherapy, 2020, 32, 310-322.	0.7	7
558	The MLH1 c.1852_1853delinsGC (p.K618A) Variant in Colorectal Cancer: Genetic Association Study in 18,723 Individuals. PLoS ONE, 2014, 9, e95022.	1.1	7

#	Article	IF	Citations
559	Isoelectric Focusing of Human Hair Keratins: Correlation with Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) Patterns and Effect of Cosmetic Treatments. Journal of Forensic Sciences, 1992, 37, 425-431.	0.9	7
560	xDEEP-MSI: Explainable Bias-Rejecting Microsatellite Instability Deep Learning System in Colorectal Cancer. Biomolecules, 2021, 11, 1786.	1.8	7
561	Genomic Characterization of Host Factors Related to SARS-CoV-2 Infection in People with Dementia and Control Populations: The GR@ACE/DEGESCO Study. Journal of Personalized Medicine, 2021, 11, 1318.	1.1	7
562	Enzyme Polymorphisms in Galicia (NW Spain). Human Heredity, 1983, 33, 160-162.	0.4	6
563	Correlation between Native and Desialyzed Forms of Orosomucoid. Human Heredity, 1988, 38, 353-358.	0.4	6
564	Population distribution of six PCR-amplified loci in Madeira Archipelago (Portugal). Forensic Science International, 1999, 100, 93-99.	1.3	6
565	Bimodal allele frequency distribution at Y-STR loci DYS392 and DYS438: no evidence for a deviation from the stepwise mutation model. International Journal of Legal Medicine, 2003, 117, 287-290.	1.2	6
566	Results of the 2008 Colombian paternity testing quality control exercise. Forensic Science International: Genetics Supplement Series, 2009, 2, 93-94.	0.1	6
567	Toxicogenetics of lopinavir/ritonavir in HIV-infected European patients. Personalized Medicine, 2014, 11, 263-272.	0.8	6
568	Clinical characterization of a male patient with the recently described 8q21.11 microdeletion syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 1369-1373.	0.7	6
569	Female patient with autistic disorder, intellectual disability, and coâ€morbid anxiety disorder: Expanding the phenotype associated with the recurrent 3q13.2â€“q13.31 microdeletion. American Journal of Medical Genetics, Part A, 2015, 167, 3121-3129.	0.7	6
570	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
571	A forensic multiplex of nine novel pentameric-repeat STRs. Forensic Science International: Genetics, 2017, 29, 154-164.	1.6	6
572	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
573	Long runs of homozygosity are associated with Alzheimerâ€™s disease. Translational Psychiatry, 2021, 11, 142.	2.4	6
574	Genetic Susceptibility to Periodontal Disease in Down Syndrome: A Case-Control Study. International Journal of Molecular Sciences, 2021, 22, 6274.	1.8	6
575	The early-life exposome modulates the effect of polymorphic inversions on DNA methylation. Communications Biology, 2022, 5, 455.	2.0	6
576	The typing of Î±1-antitrypsin in human bloodstains by isoelectric focusing. Forensic Science International, 1982, 19, 181-184.	1.3	5

#	Article	IF	Citations
577	Karyological and allozymic study of allolobophora molleri complex and related taxa. Initial results. Soil Biology and Biochemistry, 1992, 24, 1241-1245.	4.2	5
578	Correspondence | Science & Justice - Volume 36, Issue 3. Science and Justice - Journal of the Forensic Science Society, 1996, 36, 204-206.	1.3	5
579	Typing Y-chromosome single nucleotide polymorphisms with DNA microarray technology. International Congress Series, 2003, 1239, 21-25.	0.2	5
580	Nineteen autosomal microsatellite data from Antioquia (Colombia). Forensic Science International, 2004, 143, 69-71.	1.3	5
581	Genetic analysis of autosomal and Y-specific STRs in the Karimojong population from Uganda. International Congress Series, 2006, 1288, 213-215.	0.2	5
582	Autosomal microsatellite data from Northwestern Colombia. Forensic Science International, 2006, 160, 217-220.	1.3	5
583	A simulation-based approach to evaluate population stratification in Argentina. Forensic Science International: Genetics Supplement Series, 2008, 1, 662-663.	0.1	5
584	Sequence variation at three X chromosomal short tandem repeats in Caucasian and African populations. Forensic Science International: Genetics Supplement Series, 2008, 1, 147-149.	0.1	5
585	Genetic data of 10 X-chromosomal loci in VitÃ³ria population (EspÃrito Santo State, Brazil). Forensic Science International: Genetics Supplement Series, 2009, 2, 394-395.	0.1	5
586	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.	0.3	5
587	Distribution of allele frequencies of 20 STRs loci in a population sample from Calabria, Southern Italy. Forensic Science International: Genetics, 2012, 6, e137-e138.	1.6	5
588	High incidence of large deletions in the PMS2 gene in Spanish Lynch syndrome families. Clinical Genetics, 2014, 85, 583-588.	1.0	5
589	Micro and macro geographical analysis of Y-chromosome lineages in South Iberia. Forensic Science International: Genetics, 2017, 29, e9-e15.	1.6	5
590	Candidate predisposing germline copy number variants in early onset colorectal cancer patients. Clinical and Translational Oncology, 2017, 19, 625-632.	1.2	5
591	White Noise Speech Illusions: A Trait-Dependent Risk Marker for Psychotic Disorder?. Frontiers in Psychiatry, 2019, 10, 676.	1.3	5
592	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. Scientific Reports, 2019, 9, 7825.	1.6	5
593	Predictive value of ERCC2, ABCC2 and MMP2 of response and long-term survival in locally advanced head and neck cancer patients treated with chemoradiotherapy. Cancer Chemotherapy and Pharmacology, 2021, 88, 813-823.	1.1	5
594	Liquid Biopsy Biomarkers for Immunotherapy in Non-Small Cell Lung Carcinoma: Lessons Learned and the Road Ahead. Journal of Personalized Medicine, 2021, 11, 971.	1.1	5

#	Article	IF	Citations
595	The use of scanning electron microscopy in the examination of seminal stains. Forensic Science International, 1982, 19, 185-188.	1.3	4
596	Definition of a Region of Loss of Heterozygosity at Chromosome 11q in Cervical Carcinoma. Diagnostic Molecular Pathology, 1999, 8, 92-96.	2.1	4
597	Data for nine autosomal STRs markers from Valencia (East Mediterranean coast of the Iberian) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.3	4
598	Population study of eight novel Y-chromosome STRs (DYS460, DYS461, GATA-A10, GATA-C4, GATA-H4,) Tj ETQq0 0 0 rgBT /Overlock 10 Y-chromosome haplotypes. International Journal of Legal Medicine, 2003, 117, 127-131.	1.2	4
599	Population specific single nucleotide polymorphisms. International Congress Series, 2004, 1261, 233-235.	0.2	4
600	Autosomic STR population data in two Caribbean samples from Colombia. Forensic Science International, 2005, 152, 79-81.	1.3	4
601	Complement Factor H. Ophthalmology, 2007, 114, 193.e1-193.e2.	2.5	4
602	Genetic polymorphism of 15 STR loci in central western Colombia. Forensic Science International: Genetics, 2008, 2, e7-e8.	1.6	4
603	Large scale analysis of HCM mutations in sudden cardiac death. Forensic Science International: Genetics Supplement Series, 2008, 1, 549-550.	0.1	4
604	Forensic validation of the Genplex SNP typing systemâ€"Results of an inter-laboratory study. Forensic Science International: Genetics Supplement Series, 2008, 1, 389-393.	0.1	4
605	Development and validation of a next generation STR ESS-pentaplex. Forensic Science International: Genetics Supplement Series, 2009, 2, 25-26.	0.1	4
606	Genetic patterns of 10 X chromosome short tandem repeats in an Asian population from Macau. Forensic Science International: Genetics Supplement Series, 2009, 2, 402-404.	0.1	4
607	Colombian results of the interlaboratory Quality Control Exercise 2009â€"2010. Forensic Science International: Genetics Supplement Series, 2011, 3, e57-e58.	0.1	4
608	Using STR, MiniSTR and SNP markers to solve complex cases of kinship analysis. Forensic Science International: Genetics Supplement Series, 2013, 4, e91-e92.	0.1	4
609	Population pharmacokinetic/pharmacogenetic model of lopinavir/ritonavir in HIV-infected patients. Personalized Medicine, 2014, 11, 693-704.	0.8	4
610	A 6q14.1â€q15 microdeletion in a male patient with severe autistic disorder, lack of oral language, and dysmorphic features with concomitant presence of a maternally inherited Xp22.31 copy number gain. Clinical Case Reports (discontinued), 2015, 3, 415-423.	0.2	4
611	The Road so Far in Colorectal Cancer Pharmacogenomics: Are We Closer to Individualised Treatment?. Journal of Personalized Medicine, 2020, 10, 237.	1.1	4
612	Population Study of HUMTH01, HUMVWA31/A, HUMF13A1, and HUMFES/FPS Systems in Azores. Journal of Forensic Sciences, 1999, 44, 1261-1264.	0.9	4

#	Article	IF	Citations
613	Pharmacogenetic Analysis of SNPs in Genes Involved in the Pharmacokinetics and Response to Lopinavir/Ritonavir Therapy. Current Drug Metabolism, 2013, 14, 729-737.	0.7	4
614	Overlapping variants in the blood, tissues and cell lines for patients with intracranial meningiomas are predominant in stem cell-related genes. Heliyon, 2020, 6, e05632.	1.4	4
615	Genetic variants associated with addictive behavior in Colombian addicted and non-addicted to heroin or cocaine. Colombia Medica, 2013, 44, 19-25.	0.7	4
616	Viability Study of Machine Learning-Based Prediction of COVID-19 Pandemic Impact in Obsessive-Compulsive Disorder Patients. Frontiers in Neuroinformatics, 2022, 16, 807584.	1.3	4
617	Comparison of different electrophoretic methods for digital typing of the MS32 (D1S8) locus. Electrophoresis, 1996, 17, 1294-1298.	1.3	3
618	Genetic data on three complex STRs (ACTBP2, D21S11 and HUMFIBRA/FGA) in the Galician population (NW) Tj ETQq0 0 0 rgBT /Overloc	1.2	3
619	Motherless case in paternity testing by Lee et al.. Forensic Science International, 2002, 125, 284.	1.3	3
620	Y-chromosome STRs in populations of Bantu origin from Mozambique: male contribution to the Africa genetic pool and forensic implications. International Congress Series, 2003, 1239, 419-424.	0.2	3
621	Cognitive Profile in Williams Syndrome: A Case Study. British Journal of Developmental Disabilities, 2005, 51, 143-153.	0.1	3
622	Analysis of STR loci in Cartagena, a Caribbean city of Colombia. Forensic Science International, 2006, 160, 221-223.	1.3	3
623	Three novel mutations in the CFTR gene identified in Galician patients. Journal of Cystic Fibrosis, 2008, 7, 520-522.	0.3	3
624	Genetic characterization of 52 autosomal SNPs in the Portuguese population. Forensic Science International: Genetics Supplement Series, 2008, 1, 358-360.	0.1	3
625	GEP-ISFG proficiency testing programs: 2007 update. Forensic Science International: Genetics Supplement Series, 2008, 1, 674-676.	0.1	3
626	Journal update. Forensic Science International: Genetics, 2010, 4, 143-144.	1.6	3
627	Comparison Between Universal Immunohistochemistry for Mismatch Repair Proteins Versus Revised Bethesda Guidelines in the Detection of Patients With Lynch Syndrome. Gastroenterology, 2011, 140, S-97.	0.6	3
628	Genetic variability of the SNPforID 52-plex identification SNP panel in Italian population samples. Forensic Science International: Genetics, 2012, 6, e185-e186.	1.6	3
629	Databases for neurogenetics: Introduction, overview, and challenges. Human Mutation, 2012, 33, 1311-1314.	1.1	3
630	CHEK2 c.1100delC mutation among non-BRCA1/2 Spanish hereditary breast cancer families. Clinical and Translational Oncology, 2013, 15, 164-165.	1.2	3

#	Article	IF	Citations
631	Targeted NGS meets expert clinical characterization: Efficient diagnosis of spastic paraplegia type 11. Applied & Translational Genomics, 2015, 5, 33-36.	2.1	3
632	affy2sv: an R package to pre-process Affymetrix CytoScan HD and 750K arrays for SNP, CNV, inversion and mosaicism calling. BMC Bioinformatics, 2015, 16, 167.	1.2	3
633	A new panel of SNPs to assess thyroid carcinoma risk: a pilot study in a Brazilian admixture population. BMC Medical Genetics, 2017, 18, 140.	2.1	3
634	Identification of Novel Regulators of Zalcitabine-Induced Neuropathic Pain. ACS Chemical Neuroscience, 2021, 12, 2619-2628.	1.7	3
635	Isoelectric Focusing of Pi Subtypes in Bloodstains. Journal - Forensic Science Society, 1986, 26, 425-431.	0.3	2
636	A simplified procedure for simultaneous detection of salivary proteins and its application in paternity testing. Forensic Science International, 1987, 33, 47-52.	1.3	2
637	The use of immobilized pH gradients for the detection of human polymorphisms in the forensic identification of bloodstains. Electrophoresis, 1992, 13, 239-243.	1.3	2
638	Minisatellite Variant Repeat Coding Using a Semiautomatic System. BioTechniques, 1997, 23, 44-46.	0.8	2
639	Minisatellite variant repeat (MVR) analysis of theHRAS1 minisatellite locus. Electrophoresis, 1998, 19, 3084-3089.	1.3	2
640	¹⁶⁰Thr Mutation in the Rhodopsin Gene Associated withRet initis pigmentosa. Human Heredity, 1998, 48, 237-240.	0.4	2
641	Behavior of loci D1S1656 and D12S391 in a sample from Maracaibo, Venezuela. American Journal of Human Biology, 2003, 15, 68-71.	0.8	2
642	The proficiency testing program on DNA typing of the Spanish and Portuguese working group of the International Society for Forensic Genetics. International Congress Series, 2003, 1239, 837-840.	0.2	2
643	Chapter 23 Forensic analysis. Journal of Chromatography Library, 2004, 69, 1073-1133.	0.1	2
644	29 Y-chromosome SNP analysis in European populations. International Congress Series, 2004, 1261, 73-75.	0.2	2
645	Finding genes that underlie cancer using genetic tools. Clinical and Translational Oncology, 2006, 8, 771-772.	1.2	2
646	Forensic validation and implementation of Y-chromosome SNP multiplexes. Forensic Science International: Genetics Supplement Series, 2008, 1, 181-183.	0.1	2
647	The distribution of allele frequencies of 15 STRs in Dominican population. Forensic Science International: Genetics Supplement Series, 2008, 1, 322-325.	0.1	2
648	Chapter 28 Forensic DNA typing technologies: a review. Handbook of Analytical Separations, 2008, 6, 945-957.	0.8	2

#	Article	IF	Citations
649	The â€˜Pokemonâ€™ (ZBTB7) Gene: No Evidence of Association with Sporadic Breast Cancer. Clinical Medicine Oncology, 2008, 2, CMO.S569.	0.2	2
650	Characterization of U.S. population samples using a 34plex ancestry informative SNP multiplex. Forensic Science International: Genetics Supplement Series, 2011, 3, e182-e183.	0.1	2
651	Asesoramiento genÃ©tico en NeurologÃa: un problema complejo que necesita regulaciÃ³n. NeurologÃa, 2011, 26, 129-136.	0.3	2
652	Longitudinal Assessment of Narrative Profile in a Williams Syndrome Patient. British Journal of Developmental Disabilities, 2011, 57, 91-99.	0.1	2
653	Making progress in education: The EUROFORGEN master degree pilot project in forensic genetics. Forensic Science International: Genetics, 2017, 28, e12-e13.	1.6	2
654	<scp>ABCC</scp>3 Polymorphisms and <scp>mRNA</scp> Expression Influence the Concentration of a Carboxylic Acid Metabolite in Patients on Clopidogrel and Aspirin Therapy. Basic and Clinical Pharmacology and Toxicology, 2017, 120, 466-474.	1.2	2
655	Introducing the Forensic Science International: Genetics Reviewer Hall of Fame. Forensic Science International: Genetics, 2018, 34, 277.	1.6	2
656	Congenital hyperinsulinism in two siblings with ABCC8 mutation: same genotype, different phenotypes. Archives of Endocrinology and Metabolism, 2018, 62, 560-565.	0.3	2
657	Una nueva delecciÃ³n de calsequestrina 2 que causa taquicardia ventricular polimÃ³rfica catecolaminÃ©rgica y muerte sÃºbita cardiaca. Revista Espanola De Cardiologia, 2019, 72, 681-683.	0.6	2
658	Genetic Diversity of Drug-Related Genes in Native Americans of the Brazilian Amazon. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 117-133.	0.4	2
659	LIPG endothelial lipase and breast cancer risk by subtypes. Scientific Reports, 2021, 11, 10436.	1.6	2
660	Discovery of a novel and a rare Kristen rat sarcoma viral oncogene homolog (KRAS) gene mutation in colorectal cancer patients. Bioengineered, 2021, 12, 5099-5109.	1.4	2
661	An Update of In Silico Tools for the Prediction of Pathogenesis in Missense Variants. Current Bioinformatics, 2011, 6, 185-198.	0.7	2
662	Exploring genetic variants in obsessive compulsive disorder severity: A GWAS approach. Journal of Affective Disorders, 2020, 267, 23-32.	2.0	2
663	ValoraciÃ³n de la prueba de ADN en las identificaciones a gran escala de personas desaparecidas. Revista Espanola De Medicina Legal, 2022, 48, 124-132.	0.3	2
664	Executive impairments in Obsessive Compulsive Disorder: A systematic review with emotional and non-emotional paradigms. Psicothema, 2020, 32, 24-32.	0.7	2
665	Semiparametric approach to match probability calculations using single locus probes. International Journal of Legal Medicine, 1996, 108, 306-312.	1.2	1
666	The situation of forensic DNA analysis in Spain. Forensic Science International, 1997, 88, 81-83.	1.3	1

#	Article	IF	Citations
667	Differences in Y-chromosome haplotype frequencies at the microgeographical level. International Congress Series, 2003, 1239, 409-412.	0.2	1
668	Significant differences between the Leeward and Windward groups of the Cabo Verde archipelago (West African Coast). International Congress Series, 2003, 1239, 79-80.	0.2	1
669	Microgeographic substructure of Northern Portuguese mitochondrial DNA lineages: the female perspective of this region history. International Congress Series, 2004, 1261, 386-388.	0.2	1
670	Typing mtDNA SNPs of forensic and population interest with snapshot. International Congress Series, 2004, 1261, 419-421.	0.2	1
671	Exploring mitochondrial DNA variation in the Italian Peninsula. Forensic Science International: Genetics Supplement Series, 2008, 1, 264-265.	0.1	1
672	Genetic characterization of 52 autosomal SNPs in two sub-Saharan African populations. Forensic Science International: Genetics Supplement Series, 2008, 1, 361-363.	0.1	1
673	The distribution of Y-chromosome STRs in Dominican population. Forensic Science International: Genetics Supplement Series, 2008, 1, 195-197.	0.1	1
674	Population data of 52 autosomal SNPs in Italian population. Forensic Science International: Genetics Supplement Series, 2009, 2, 351-352.	0.1	1
675	SNP typing of forensic samples with the GenPlexâ„¢ HID system: A collaborative study. Forensic Science International: Genetics Supplement Series, 2009, 2, 508-509.	0.1	1
676	Genetic variants related to nicotine dependence. Forensic Science International: Genetics Supplement Series, 2011, 3, e492-e493.	0.1	1
677	Role of Tumor Tissue Analysis in Rectal Cancer Pharmacogenetics. , 0, , .		1
678	The Complexity of Colorectal Cancer Biology â€" Putting Bricks on the Path to Personalized Medicine. , 0, , .		1
679	Delimiting Allelic Imbalance of TYMS by Allele-Specific Analysis. Medicine (United States), 2015, 94, e1091.	0.4	1
680	Use of ancestry-informative markers as a scientific tool to combat the illegal traffic in human kidneys. Forensic Science International: Genetics Supplement Series, 2015, 5, e302-e304.	0.1	1
681	A Novel Calsequestrin 2 Deletion Causing Catecholaminergic Polymorphic Ventricular Tachycardia and Sudden Cardiac Death. Revista Espanola De Cardiologia (English Ed), 2019, 72, 681-683.	0.4	1
682	Sudden infant death as the most severe phenotype caused by genetic modulation in a family with atrial fibrillation. Forensic Science International: Genetics, 2019, 43, 102159.	1.6	1
683	On the suppression of Forensic Science International: Genetics from the 2019 Journal Citations Report. Forensic Science International: Genetics, 2020, 48, 102357.	1.6	1
684	Obesity-related genetic determinants of stroke. Brain Communications, 2021, 3, fcab069.	1.5	1

#	Article	IF	Citations
685	Ancestry analysis using autosomal SNPs in northern South America, reveals interpretation differences between an AIM panel and an identification panel. Forensic Science International, 2021, 326, 110934.	1.3	1
686	Fast Isoelectric Focusing of Some Polymorphic Proteins and Enzymes in Miniaturized Gels Using an Automated System. Journal of Forensic Sciences, 1988, 33, 1379-1384.	0.9	1
687	Utility of Circulating Cell-Free DNA in Assessing Microsatellite Instability and Loss of Heterozygosity in Breast Cancer Using Human Identification Approach. Genes, 2022, 13, 590.	1.0	1
688	A Machine Learning Approach in Autism Spectrum Disorders: From Sensory Processing to Behavior Problems. Frontiers in Molecular Neuroscience, 2022, 15, .	1.4	1
689	Application of Pelletized Sodium Borohydride in the Spectrophotometric Determination of Arsenic. Journal of Analytical Toxicology, 1982, 6, 314-316.	1.7	0
690	The use of hybrid isoelectric focusing for the detection of polymorphic proteins in bloodstains. Forensic Science International, 1989, 43, 239-245.	1.3	0
691	Chapter 20A Forensic genetics: From classical serological genetic markers to DNA polymorphisms analyzed by microarray technology. Handbook of Analytical Separations, 2000, 2, 695-706.	0.8	0
692	Optimisation of Y-STR multiplexing combining established and newly described loci. International Congress Series, 2003, 1239, 415-418.	0.2	0
693	Y-chromosome short tandem repeat polymorphisms: a comparison between humans and chimpanzees. International Congress Series, 2003, 1239, 287-290.	0.2	0
694	Microgeographic patterns of highly informative Y-chromosome haplotypes (using biallelic markers) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Series, 2003, 1239, 61-66.	0.2	0
695	Mitochondrial DNA variability patterns in Southeast Africa and forensic implications. International Congress Series, 2003, 1239, 541-545.	0.2	0
696	Sequence structure of 12 novel Y chromosome microsatellites and PCR amplification strategies. International Congress Series, 2003, 1239, 425-429.	0.2	0
697	Population studies using single nucleotide polymorphismsâ€"how important is detailed sample origin information?. International Congress Series, 2004, 1261, 30-32.	0.2	0
698	GATA C4 allele 17 as a marker for sub-Saharan origin of Y-chromosome lineages. International Congress Series, 2004, 1261, 281-283.	0.2	0
699	Microgeographic substructure of NW Iberian Y chromosome STR haplotypes. International Congress Series, 2004, 1261, 296-298.	0.2	0
700	Dissection of mitochondrial haplogroup H using coding region SNPs. International Congress Series, 2006, 1288, 7-9.	0.2	0
701	FSI:Geneticsâ€"A new journal dedicated to the scientific advancement of forensic genetics. Forensic Science International: Genetics, 2007, 1, 75.	1.6	0
702	Chapter 29 Mitochondrial DNA: future challenges in forensic genetics. Handbook of Analytical Separations, 2008, 6, 959-967.	0.8	0

#	Article	IF	Citations
703	Increasing the discrimination power of the mtDNA test through the analysis of a large set of haplogroup H coding region SNPs: Forensic applications and validation. Forensic Science International: Genetics Supplement Series, 2008, 1, 301-302.	0.1	0
704	Population data of 5 next generation STRs in Southern Italy. Forensic Science International: Genetics Supplement Series, 2009, 2, 386-387.	0.1	0
705	Sequenom MassArrayâ„¢ application in the long QT syndrome mutation detection. Forensic Science International: Genetics Supplement Series, 2009, 2, 497-498.	0.1	0
706	Identification of Mirnas and Their Gene Targets Differentially Expressed in Microsatellite Stable and Unstable Colorectal Cancers Through an Integrated Analysis. Gastroenterology, 2011, 140, S-819.	0.6	0
707	Differential Features of Colorectal Cancer (CRC) in Patients With Probable Non-Sporadic Mismatch Repair Deficiency Without Germline Mutation. Gastroenterology, 2011, 140, S-190-S-191.	0.6	0
708	Pharmacogenetics Study of TMPT and ITPA Genes in Patients With Inflammatory Bowel Disease Treated With Azathioprine Detects Relation Between Itpase Deficiency and Clinical Response. Gastroenterology, 2011, 140, S-769.	0.6	0
709	Casework application of a stand-alone pentaplex assay of extended-ESS STRs. Legal Medicine, 2013, 15, 217-221.	0.6	0
710	Forensic Science Practice in Spain. , 2014, , 261-266.		0
711	Journal Update and Reviewer Acknowledgement. Forensic Science International: Genetics, 2016, 20, 149-150.	1.6	0
712	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
713	Forensic Science International: Genetics reviewer Hall of Fame 2018. Forensic Science International: Genetics, 2019, 40, 23.	1.6	0
714	Forensic science International: Genetics Reviewer Hall of Fame 2019. Forensic Science International: Genetics, 2020, 45, 102231.	1.6	0
715	Forensic Science International: Genetics Reviewer Hall of Fame 2020. Forensic Science International: Genetics, 2021, 52, 102480.	1.6	0
716	Abstract 1334: Implication of the 3â€²UTR region of TGFÎ²R1 with MSS HNPCC and sporadic colorectal cancer.. , 2013, , .		0
717	Abstract 139: Alcohol and breast cancer subtypes in a Spanish cohort.. , 2013, , .		0
718	Abstract 2781: Genetic susceptibility to breast cancer in a Spanish population. , 2015, , .		0
719	Exome-wide pharmacogenomic analysis of response to thiopurines in inflammatory bowel disease patients. Current Pharmacogenomics and Personalized Medicine, 2015, 13, 61-67.	0.2	0
720	Beyond the CSI effect: Keys for good forensic genetics communication. Metode, 2018, , .	0.0	0

#	Article	IF	Citations
721	Differential admixture in Latin American populations and its impact on the study of colorectal cancer. Genetics and Molecular Biology, 2020, 43, e20200143.	0.6	0
722	La puntuaciÃ³n de riesgo poligÃ©nico como factor clave enÂlosÂmodelos deÂprediccIÃ³n clÃnica cardiovascular. Revista Espanola De Cardiologia, 2020, 73, 608-610.	0.6	0
723	Genetic susceptibility to CRC. , 2022, , 513-518.		0
724	Meta-GWAS of amyloid burden endophenotype combining PET and CSF results.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052333.	0.4	0