Peter de Knijff

List of Publications by Year in descending order

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199 papers	18,863 citations	13087 68 h-index	13758 129 g-index
208 all docs	208 docs citations	208 times ranked	18081 citing authors

#	Article	IF	Citations
1	Large-scale migration into Britain during the Middle to Late Bronze Age. Nature, 2022, 601, 588-594.	13.7	86
2	On the Forensic Use of Y-Chromosome Polymorphisms. Genes, 2022, 13, 898.	1.0	9
3	Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. Leukemia, 2021, 35, 47-61.	3.3	47
4	Subdividing Y-chromosome haplogroup R1a1 reveals Norse Viking dispersal lineages in Britain. European Journal of Human Genetics, 2021, 29, 512-523.	1.4	9
5	Biallelic loss-of-function variants in PLD1 cause congenital right-sided cardiac valve defects and neonatal cardiomyopathy. Journal of Clinical Investigation, 2021, 131, .	3.9	16
6	Application of a probabilistic genotyping software to MPS mixture STR data is supported by similar trends in LRs compared with CE data. Forensic Science International: Genetics, 2021, 52, 102489.	1.6	3
7	Ten millennia of hepatitis B virus evolution. Science, 2021, 374, 182-188.	6.0	64
8	The Dutch Y-chromosomal landscape. European Journal of Human Genetics, 2020, 28, 287-299.	1.4	15
9	Deciduous Teeth as an Alternative DNA Source for Postmortem Genetic Testing. Circulation Genomic and Precision Medicine, 2020, 13, e002674.	1.6	1
10	DNA commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of Y-STR results in forensic analysis. Forensic Science International: Genetics, 2020, 48, 102308.	1.6	42
11	Generation and genetic repair of 2 iPSC clones from a patient bearing a heterozygous c.1120del18 mutation in the ACVRL1 gene leading to Hereditary Hemorrhagic Telangiectasia (HHT) type 2. Stem Cell Research, 2020, 46, 101786.	0.3	5
12	Taxonomic classification and abundance estimation using 16S and WGSâ€"A comparison using controlled reference samples. Forensic Science International: Genetics, 2020, 46, 102257.	1.6	31
13	Forensic Y-SNP analysis beyond SNaPshot: High-resolution Y-chromosomal haplogrouping from low quality and quantity DNA using Ion AmpliSeq and targeted massively parallel sequencing. Forensic Science International: Genetics, 2019, 41, 93-106.	1.6	42
14	Diagnostics of short tandem repeat expansion variants using massively parallel sequencing and componential tools. European Journal of Human Genetics, 2019, 27, 400-407.	1.4	12
15	From next generation sequencing to now generation sequencing in forensics. Forensic Science International: Genetics, 2019, 38, 175-180.	1.6	54
16	The Beaker phenomenon and the genomic transformation of northwest Europe. Nature, 2018, 555, 190-196.	13.7	503
17	The HIrisPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation. Forensic Science International: Genetics, 2018, 35, 123-135.	1.6	199
18	Demographic History and Genetic Adaptation in the Himalayan Region Inferred from Genome-Wide SNP Genotypes of 49 Populations. Molecular Biology and Evolution, 2018, 35, 1916-1933.	3.5	36

#	Article	IF	Citations
19	Short hypervariable microhaplotypes: A novel set of very short high discriminating power loci without stutter artefacts. Forensic Science International: Genetics, 2018, 35, 169-175.	1.6	51
20	A SNP panel for identification of DNA and RNA specimens. BMC Genomics, 2018, 19, 90.	1.2	47
21	Whole Transcriptome RNA Sequencing As a Comprehensive Diagnostic Tool for Acute Myeloid Leukemia. Blood, 2018, 132, 2762-2762.	0.6	0
22	FDSTools: A software package for analysis of massively parallel sequencing data with the ability to recognise and correct STR stutter and other PCR or sequencing noise. Forensic Science International: Genetics, 2017, 27, 27-40.	1.6	73
23	Effect of APOE Îµ4 allele on survival and fertility in an adverse environment. PLoS ONE, 2017, 12, e0179497.	1.1	51
24	Decay of sexual trait genes in an asexual parasitoid wasp. Genome Biology and Evolution, 2016, 8, evw273.	1.1	33
25	Male-specific risk of first and recurrent venous thrombosis: a phylogenetic analysis of the Y chromosome. Journal of Thrombosis and Haemostasis, 2016, 14, 1971-1977.	1.9	5
26	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	13.7	1,216
27	Massively parallel sequencing of short tandem repeatsâ€"Population data and mixture analysis results for the PowerSeqâ„¢ system. Forensic Science International: Genetics, 2016, 24, 86-96.	1.6	118
28	Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. Human Genetics, 2016, 135, 393-402.	1.8	41
29	High-quality mtDNA control region sequences from 680 individuals sampled across the Netherlands to establish a national forensic mtDNA reference database. Forensic Science International: Genetics, 2016, 21, 158-167.	1.6	20
30	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forensic Science International: Genetics, 2016, 22, 54-63.	1.6	190
31	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. Genome Research, 2016, 26, 417-426.	2.4	84
32	Genetic variants determining survival and fertility in an adverse African environment: a population-based large-scale candidate gene association study. Aging, 2016, 8, 1364-1383.	1.4	1
33	Large-scale recent expansion of European patrilineages shown by population resequencing. Nature Communications, 2015, 6, 7152.	5.8	69
34	Forensic nomenclature for short tandem repeats updated for sequencing. Forensic Science International: Genetics Supplement Series, 2015, 5, e542-e544.	0.1	6
35	Analysis of 36 Y-STR marker units including a concordance study among 2085 Dutch males. Forensic Science International: Genetics, 2015, 14, 174-181.	1.6	29
36	The Y-Chromosome Tree Bursts into Leaf: 13,000 High-Confidence SNPs Covering the Majority of Known Clades. Molecular Biology and Evolution, 2015, 32, 661-673.	3.5	137

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37	Determining the quality and complexity of next-generation sequencing data without a reference genome. Genome Biology, 2014, 15, 555.	3.8	30
38	De novo transcriptome of Ischnura elegans provides insights into sensory biology, colour and vision genes. BMC Genomics, 2014, 15, 808.	1.2	46
39	Gene Conversion Violates the Stepwise Mutation Model for Microsatellites in<scp>Y</scp>â€Chromosomal Palindromic Repeats. Human Mutation, 2014, 35, 609-617.	1.1	26
40	Variations in predicted risks in personal genome testing for common complex diseases. Genetics in Medicine, 2014, 16, 85-91.	1.1	63
41	Comparing six commercial autosomal STR kits in a large Dutch population sample. Forensic Science International: Genetics, 2014, 10, 55-63.	1.6	92
42	Recent Radiation within Yâ€chromosomal Haplogroup Râ€M269 Resulted in High Yâ€STR Haplotype Resemblance. Annals of Human Genetics, 2014, 78, 92-103.	0.3	36
43	TSSV: a tool for characterization of complex allelic variants in pure and mixed genomes. Bioinformatics, 2014, 30, 1651-1659.	1.8	39
44	Developmental validation of the HIrisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. Forensic Science International: Genetics, 2014, 9, 150-161.	1.6	164
45	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	1.6	214
46	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	1.4	246
47	Analysis of coprolites from the extinct mountain goat Myotragus balearicus. Quaternary Research, 2014, 81, 106-116.	1.0	34
48	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	9.4	641
49	Developmental validation of mitochondrial DNA genotyping assays for adept matrilineal inference of biogeographic ancestry at a continental level. Forensic Science International: Genetics, 2014, 11, 39-51.	1.6	29
50	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	1.1	151
51	How carrion and hooded crows defeat Linnaeus's curse. Science, 2014, 344, 1345-1346.	6.0	11
52	Patterns in Nuclear and Mitochondrial DNA Reveal Historical and Recent Isolation in the Black-Tailed Godwit (Limosa limosa). PLoS ONE, 2014, 9, e83949.	1.1	14
53	A Linguistically Informed Autosomal STR Survey of Human Populations Residing in the Greater Himalayan Region. PLoS ONE, 2014, 9, e91534.	1.1	16
54	The Contribution of DNA Metabarcoding to Fungal Conservation: Diversity Assessment, Habitat Partitioning and Mapping Red-Listed Fungi in Protected Coastal Salix repens Communities in the Netherlands. PLoS ONE, 2014, 9, e99852.	1.1	66

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55	Clinal distribution of human genomic diversity across the Netherlands despite archaeological evidence for genetic discontinuities in Dutch population history. Investigative Genetics, 2013, 4, 9.	3.3	18
56	Genome-wide analysis of macrosatellite repeat copy number variation in worldwide populations: evidence for differences and commonalities in size distributions and size restrictions. BMC Genomics, 2013, 14, 143.	1.2	29
57	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
58	Indian ocean crossroads: Human genetic origin and population structure in the maldives. American Journal of Physical Anthropology, 2013, 151, 58-67.	2.1	14
59	Population structure, migration, and diversifying selection in the Netherlands. European Journal of Human Genetics, 2013, 21, 1277-1285.	1.4	137
60	Improved analysis of long STR amplicons from degraded single source and mixed DNA. International Journal of Legal Medicine, 2013, 127, 741-747.	1.2	5
61	Quality Assessment of the Genetic Test for Familial Hypercholesterolemia in The Netherlands. Cholesterol, 2013, 2013, 1-8.	1.6	8
62	The influence of clan structure on the genetic variation in a single Ghanaian village. European Journal of Human Genetics, 2013, 21, 1134-1139.	1.4	16
63	Mosaic segmental uniparental isodisomy and progressive clonal selection: a common mechanism of late onset Â-thalassemia major. Haematologica, 2013, 98, 691-695.	1.7	11
64	Ancestral Stories of Ghanaian Bimoba Reflect Millennia-Old Genetic Lineages. PLoS ONE, 2013, 8, e65690.	1.1	5
65	Epigenetic regulation of the X-chromosomal macrosatellite repeat encoding for the cancer/testis gene CT47. European Journal of Human Genetics, 2012, 20, 185-191.	1.4	15
66	A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages. Forensic Science International: Genetics, 2012, 6, 208-218.	1.6	210
67	Combining results of forensic STR kits: HDplex validation including allelic association and linkage testing with NGM and Identifiler loci. International Journal of Legal Medicine, 2012, 126, 781-789.	1.2	52
68	Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM. Forensic Science International: Genetics, 2012, 6, 708-715.	1.6	41
69	Dissecting the genetic make-up of North-East Sardinia using a large set of haploid and autosomal markers. European Journal of Human Genetics, 2012, 20, 956-964.	1.4	13
70	Transposon proliferation in an asexual parasitoid. Molecular Ecology, 2012, 21, 3898-3906.	2.0	33
71	Developmental validation of the IrisPlex system: Determination of blue and brown iris colour for forensic intelligence. Forensic Science International: Genetics, 2011, 5, 464-471.	1.6	141
72	Clonal genetic variation in a Wolbachia-infected asexual wasp: horizontal transmission or historical sex?. Molecular Ecology, 2011, 20, no-no.	2.0	30

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73	Improving human forensics through advances in genetics, genomics and molecular biology. Nature Reviews Genetics, 2011, 12, 179-192.	7.7	407
74	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	6.0	675
75	A sensitive method to extract DNA from biological traces present on ammunition for the purpose of genetic profiling. International Journal of Legal Medicine, 2011, 125, 597-602.	1.2	44
76	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. Human Molecular Genetics, 2011, 20, 4748-4757.	1.4	13
77	Y-Chromosomal Variation in Sub-Saharan Africa: Insights Into the History of Niger-Congo Groups. Molecular Biology and Evolution, 2011, 28, 1255-1269.	3.5	122
78	Worldwide Population Analysis of the 4q and 10q Subtelomeres Identifies Only Four Discrete Interchromosomal Sequence Transfers in Human Evolution. American Journal of Human Genetics, 2010, 86, 364-377.	2.6	93
79	Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications. American Journal of Human Genetics, 2010, 87, 341-353.	2.6	324
80	Introgressive hybridization and the evolutionary history of the herring gull complex revealed by mitochondrial and nuclear DNA. BMC Evolutionary Biology, 2010, 10, 348.	3.2	30
81	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. Human Mutation, 2010, 31, E1875-E1893.	1.1	86
82	Inferring Continental Ancestry of Argentineans from Autosomal, Yâ€Chromosomal and Mitochondrial DNA. Annals of Human Genetics, 2010, 74, 65-76.	0.3	155
83	A Worldwide Survey of Human Male Demographic History Based on Y-SNP and Y-STR Data from the HGDP-CEPH Populations. Molecular Biology and Evolution, 2010, 27, 385-393.	3.5	101
84	SDHAF2 mutations in familial and sporadic paraganglioma and phaeochromocytoma. Lancet Oncology, The, 2010, 11, 366-372.	5.1	256
85	The Herring Gull Complex (Larus argentatus - fuscus - cachinnans) as a Model Group for Recent Holarctic Vertebrate Radiations. , 2010, , 351-371.		7
86	Population Genetics And The Migration Of Modern Humans (Homo Sapiens). , 2010, , 36-56.		1
87	Genetic heterogeneity in regional populations of Quebecâ€”Parental lineages in the Gaspe Peninsula. American Journal of Physical Anthropology, 2009, 139, 512-522.	2.1	20
88	Genomic complexity of the Y-STR DYS19: inversions, deletions and founder lineages carrying duplications. International Journal of Legal Medicine, 2009, 123, 15-23.	1.2	30
89	Developing a set of ancestry-sensitive DNA markers reflecting continental origins of humans. BMC Genetics, 2009, 10, 69.	2.7	47
90	A genome wide association analysis in the GENDER study. Netherlands Heart Journal, 2009, 17, 262-264.	0.3	11

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91	Improving global and regional resolution of male lineage differentiation by simple single-copy Y-chromosomal short tandem repeat polymorphisms. Forensic Science International: Genetics, 2009, 3, 205-213.	1.6	87
92	Tri-allelic SNP markers enable analysis of mixed and degraded DNA samples. Forensic Science International: Genetics, 2009, 3, 233-241.	1.6	71
93	Genetic and linguistic borders in the Himalayan Region. , 2009, , 181-202.		2
94	Geographical Affinities of the HapMap Samples. PLoS ONE, 2009, 4, e4684.	1.1	21
95	Dynamic nature of the proximalAZFcregion of the human Y chromosome: multiple independent deletion and duplication events revealed by microsatellite analysis. Human Mutation, 2008, 29, 1171-1180.	1.1	61
96	Evaluation of haplotype discrimination capacity of 35 Y-chromosomal short tandem repeat loci. Forensic Science International, 2008, 174, 182-188.	1.3	42
97	Analysis of forensically used autosomal short tandem repeat markers in Polish and neighboring populations. Forensic Science International: Genetics, 2008, 2, 205-211.	1.6	21
98	Allele frequency distribution of 21 forensic autosomal STRs in 7 populations from Yunnan, China. Forensic Science International: Genetics, 2008, 3, e11-e12.	1.6	9
99	â€œFalse positiveâ€•or true paternity: Investigating one or two STR mismatches by detailed SNP analyses. Forensic Science International: Genetics Supplement Series, 2008, 1, 518-519.	0.1	3
100	Phenotype Frequencies of Autosomal Minor Histocompatibility Antigens Display Significant Differences among Populations. PLoS Genetics, 2007, 3, e103.	1.5	68
101	Structural variation on the short arm of the human Y chromosome: recurrent multigene deletions encompassing Amelogenin Y. Human Molecular Genetics, 2007, 16, 307-316.	1.4	116
102	Inferring Human Population Sizes, Divergence Times and Rates of Gene Flow From Mitochondrial, X and Y Chromosome Resequencing Data. Genetics, 2007, 177, 2195-2207.	1.2	65
103	G.O.1 Specific sequence variations associated with FSHD. Neuromuscular Disorders, 2007, 17, 766.	0.3	0
104	Specific Sequence Variations within the 4q35 Region Are Associated with Facioscapulohumeral Muscular Dystrophy. American Journal of Human Genetics, 2007, 81, 884-894.	2.6	200
105	Allele frequency distribution for 21 autosomal STR loci in Bhutan. Forensic Science International, 2007, 170, 68-72.	1.3	27
106	Allele frequency distribution for 21 autosomal STR loci in Nepal. Forensic Science International, 2007, 168, 227-231.	1.3	33
107	Diversity of 26-locus Y-STR haplotypes in a Nepalese population sample: Isolation and drift in the Himalayas. Forensic Science International, 2007, 166, 176-181.	1.3	49
108	Hidden African Ancestors: Hidden secrets of your ancestors. European Journal of Human Genetics, 2007, 15, 509-510.	1.4	1

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109	Proportioning Whole-Genome Single-Nucleotideâ€“Polymorphism Diversity for the Identification of Geographic Population Structure and Genetic Ancestry. American Journal of Human Genetics, 2006, 78, 680-690.	2.6	164
110	Apoliprotein-E polymorphism and response to pravastatin in men with coronary artery disease (REGRESS). Acta Cardiologica, 2006, 61, 327-331.	0.3	28
111	Nepalese populations show no association between the distribution of malaria and protective alleles. Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research, 2006, 02, 101-106.	0.1	4
112	The longevity of Y chromosomes: The Human Y chromosome is not dead (yet). Heredity, 2006, 97, 377-378.	1.2	6
113	26-Locus Y-STR typing in a Bhutanese population sample. Forensic Science International, 2006, 161, 1-7.	1.3	34
114	Detection of three single nucleotide polymorphisms in the gene encoding mannose-binding lectin in a single pyrosequencing reaction. Journal of Immunological Methods, 2006, 309, 108-114.	0.6	26
115	The Role of Selection in the Evolution of Human Mitochondrial Genomes. Genetics, 2006, 172, 373-387.	1.2	395
116	Mannose Binding Lectin Gene Polymorphisms Confer a Major Risk for Severe Infections After Liver Transplantation. Gastroenterology, 2005, 129, 408-414.	0.6	1
117	Studying the biological and technical sources of variation in telomere length of individual chromosomes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2005, 65A, 35-39.	1.1	1
118	Signature of recent historical events in the European Y-chromosomal STR haplotype distribution. Human Genetics, 2005, 116, 279-291.	1.8	168
119	Elevated Levels of Mannose-Binding Lectin at Clinical Manifestation of Type 1 Diabetes in Juveniles. Diabetes, 2005, 54, 3002-3006.	0.3	54
120	Mannose Binding Lectin Gene Polymorphisms Confer a Major Risk for Severe Infections After Liver Transplantation. Gastroenterology, 2005, 129, 408-414.	0.6	125
121	Combined association and linkage analysis applied to theAPOE locus. Genetic Epidemiology, 2004, 26, 328-337.	0.6	12
122	STR analysis of artificially degraded DNAâ€”results of a collaborative European exercise. Forensic Science International, 2004, 139, 123-134.	1.3	71
123	The herring gull complex is not a ring species. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 893-901.	1.2	128
124	IVS10â€“6T>G, an ancient ATM germline mutation linked with breast cancer. Human Mutation, 2003, 21, 521-528.	1.1	27
125	A new phylogeny of swiftlets (Aves: Apodidae) based on cytochrome-b DNA. Molecular Phylogenetics and Evolution, 2003, 29, 86-93.	1.2	36
126	Estimation of Multilocus Haplotype Effects Using Weighted Penalised Log-Likelihood: Analysis of Five Sequence Variations at the Cholesteryl Ester Transfer Protein Gene Locus. Annals of Human Genetics, 2003, 67, 175-184.	0.3	42

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127	Evidence for a QTL on chromosome 19 influencing LDL cholesterol levels in the general population. European Journal of Human Genetics, 2003, 11, 845-850.	1.4	29
128	The Molecule Hunt.. American Journal of Human Genetics, 2003, 72, 221-222.	2.6	0
129	Two-locus Linkage Analysis Applied to Putative Quantitative Trait Loci for Lipoprotein(a) Levels. Twin Research and Human Genetics, 2003, 6, 322-324.	1.3	1
130	High resolution Y chromosome typing: 19 STRs amplified in three multiplex reactions. Forensic Science International, 2002, 125, 42-51.	1.3	93
131	Forensic value of 14 novel STRs on the human Y chromosome. Forensic Science International, 2002, 130, 97-111.	1.3	144
132	An Extensive Analysis of Y-Chromosomal Microsatellite Haplotypes in Globally Dispersed Human Populations. American Journal of Human Genetics, 2001, 68, 990-1018.	2.6	186
133	A powerful and rapid approach to human genome scanning using small quantities of genomic DNA. Genetical Research, 2001, 77, 129-134.	0.3	16
134	Genetic Affinities Within the Herring Gull Larus argentatus Assemblage Revealed by AFLP Genotyping. Journal of Molecular Evolution, 2001, 52, 85-93.	0.8	49
135	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
136	Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. Forensic Science International, 2001, 118, 106-113.	1.3	198
137	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
138	Genetic differentiation and phylogeography of gulls in the Larus cachinnans-fuscus group (Aves:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.0	81
139	Using a roster and haplotyping is useful in risk assessment for persons with intermediate and reduced penetrance alleles in Huntington disease. American Journal of Medical Genetics Part A, 2001, 105, 737-744.	2.4	17
140	Patterns of inter- and intra-group genetic diversity in the Vlax Roma as revealed by Y chromosome and mitochondrial DNA lineages. European Journal of Human Genetics, 2001, 9, 97-104.	1.4	67
141	Genetic polymorphisms of the reninâ€“angiotensin system and complications of insulinâ€dependent diabetes mellitus. Nephrology Dialysis Transplantation, 2000, 15, 1000-1007.	0.4	69
142	ApoE polymorphism accounts for only part of the genetic variation in quantitative ApoE levels. , 2000, 18, 331-340.		30
143	A new method for the evaluation of matches in non-recombining genomes: application to Y-chromosomal short tandem repeat (STR) haplotypes in European males. Forensic Science International, 2000, 114, 31-43.	1.3	119
144	A polymorphic L1 retroposon insertion in the centromere of the human Y chromosome. Human Molecular Genetics, 2000, 9, 421-430.	1.4	37

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145	Messages through Bottlenecks: On the Combined Use of Slow and Fast Evolving Polymorphic Markers on the Human Y Chromosome. American Journal of Human Genetics, 2000, 67, 1055-1061.	2.6	122
146	Characteristics and Frequency of Germline Mutations at Microsatellite Loci from the Human Y Chromosome, as Revealed by Direct Observation in Father/Son Pairs. American Journal of Human Genetics, 2000, 66, 1580-1588.	2.6	334
147	Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language. American Journal of Human Genetics, 2000, 67, 1526-1543.	2.6	519
148	Severe Hyperlipidemia in Apolipoprotein E2 Homozygotes Due to a Combined Effect of Hyperinsulinemia and anSstI Polymorphism. Arteriosclerosis, Thrombosis, and Vascular Biology, 1999, 19, 2722-2729.	1.1	31
149	Y-chromosome-specific microsatellite mutation rates re-examined using a minisatellite, MSY1. Human Molecular Genetics, 1999, 8, 2117-2120.	1.4	46
150	Reply: The Thomas Jefferson paternity case. Nature, 1999, 397, 32-32.	13.7	18
151	Y chromosomal polymorphisms reveal founding lineages in the Finns and the Saami. European Journal of Human Genetics, 1999, 7, 447-458.	1.4	48
152	Variants in the sulphonylurea receptor gene: association of the exon 16-3t variant with Type II diabetes mellitus in Dutch Caucasians. Diabetologia, 1999, 42, 617-620.	2.9	79
153	Ancestral Asian Source(s) of New World Y-Chromosome Founder Haplotypes. American Journal of Human Genetics, 1999, 64, 817-831.	2.6	271
154	Apolipoprotein E genotype does not affect the age of onset of dementia in families with defined tau mutations. Neuroscience Letters, 1999, 260, 193-195.	1.0	27
155	Jefferson fathered slave's last child. Nature, 1998, 396, 27-28.	13.7	240
156	Selective coâ€evolution of the D6STNFa microsatellite region with HLA class I and II loci. Tissue Antigens, 1998, 52, 213-219.	1.0	10
157	Polymorphism at the tetranucleotide repeat locus DYS389 in 10 populations reveals strong geographic clustering. European Journal of Human Genetics, 1998, 6, 583-588.	1.4	37
158	Serum apolipoprotein E level is not increased in Alzheimer's disease: the Rotterdam study. Neuroscience Letters, 1998, 248, 21-24.	1.0	58
159	Polymorphisms in the Coagulation Factor VII Gene and the Risk of Myocardial Infarction. New England Journal of Medicine, 1998, 338, 79-85.	13.9	288
160	Familial aggregation in frontotemporal dementia. Neurology, 1998, 50, 1541-1545.	1.5	187
161	The Role of a Common Variant of the Cholesteryl Ester Transfer Protein Gene in the Progression of Coronary Atherosclerosis. New England Journal of Medicine, 1998, 338, 86-93.	13.9	625
162	Role of APOE in Dementia:A Critical Reappraisal. Pathophysiology of Haemostasis and Thrombosis: International Journal on Haemostasis and Thrombosis Research, 1998, 28, 195-201.	0.5	11

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163	Analysis of Molecular Variance (AMOVA) of Y--Chromosome--Specific Microsatellites in Two Closely Related Human Populations. Human Molecular Genetics, 1997, 6, 828-828.	1.4	6
164	Estimating Y Chromosome Specific Microsatellite Mutation Frequencies using Deep Rooting Pedigrees. Human Molecular Genetics, 1997, 6, 799-803.	1.4	234
165	TNFa Microsatellite Polymorphism Modulates the Risk of IDDM in Caucasians With the High-Risk Genotype HLA DQA1*0501-DQB1*0201/DQA1*0301-DQB1*0302. Diabetes, 1997, 46, 1514-1515.	0.3	42
166	Apolipoprotein E gene and sporadic frontal lobe dementia. Neurology, 1997, 48, 1526-1529.	1.5	72
167	Genetics and Behavioral Medicine: Risk Factors for Cardiovascular Disease. Behavioral Medicine, 1997, 22, 141-149.	1.0	14
168	Factor VII Polymorphisms in Populations With Different Risks of Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 1997, 17, 1918-1923.	1.1	54
169	Evaluation of Y-chromosomal STRs: a multicenter study. International Journal of Legal Medicine, 1997, 110, 125-133.	1.2	648
170	Chromosome Y microsatellites: population genetic and evolutionary aspects. International Journal of Legal Medicine, 1997, 110, 134-140.	1.2	286
171	Applications of microsatellite-based Y chromosome haplotyping. Electrophoresis, 1997, 18, 1602-1607.	1.3	63
172	Heterogeneity at the CETP Gene Locus. Arteriosclerosis, Thrombosis, and Vascular Biology, 1997, 17, 560-568.	1.1	185
173	Tissue Plasminogen Activator and Risk of Myocardial Infarction. Circulation, 1997, 95, 2623-2627.	1.6	113
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