

Ronny Decorte

List of Publications by Citations

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

1,334
citations

16
h-index

36
g-index

48
ext. papers

1,580
ext. citations

3.9
avg, IF

3.97
L-index

#	Paper	IF	Citations
47	Mutability of Y-chromosomal microsatellites: rates, characteristics, molecular bases, and forensic implications. <i>American Journal of Human Genetics</i> , 2010 , 87, 341-53	11	268
46	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014 , 12, 12-23	4.3	171
45	Toward male individualization with rapidly mutating y-chromosomal short tandem repeats. <i>Human Mutation</i> , 2014 , 35, 1021-32	4.7	130
44	Improved age determination of blood and teeth samples using a selected set of DNA methylation markers. <i>Epigenetics</i> , 2015 , 10, 922-30	5.7	125
43	Seeing the wood for the trees: a minimal reference phylogeny for the human Y chromosome. <i>Human Mutation</i> , 2014 , 35, 187-91	4.7	121
42	The palaeogenetics of cat dispersal in the ancient world. <i>Nature Ecology and Evolution</i> , 2017 , 1,	12.3	71
41	Belgian population data for 15 STR loci (AmpFISTR SGM Plus and AmpFISTR profiler PCR amplification kit). <i>Forensic Science International</i> , 2004 , 139, 211-3	2.6	31
40	Micro-geographic distribution of Y-chromosomal variation in the central-western European region Brabant. <i>Forensic Science International: Genetics</i> , 2011 , 5, 95-9	4.3	30
39	Temporal differentiation across a West-European Y-chromosomal cline: genealogy as a tool in human population genetics. <i>European Journal of Human Genetics</i> , 2012 , 20, 434-40	5.3	25
38	Determining Y-STR mutation rates in deep-rooting genealogies: Identification of haplogroup differences. <i>Forensic Science International: Genetics</i> , 2018 , 34, 1-10	4.3	24
37	Identification and sequence analysis of discordant phenotypes between AmpFISTR SGM Plus and PowerPlex 16. <i>International Journal of Legal Medicine</i> , 2007 , 121, 297-301	3.1	24
36	Towards a consensus Y-chromosomal phylogeny and Y-SNP set in forensics in the next-generation sequencing era. <i>Forensic Science International: Genetics</i> , 2015 , 15, 39-42	4.3	22
35	Evaluation of three statistical prediction models for forensic age prediction based on DNA methylation. <i>Forensic Science International: Genetics</i> , 2018 , 34, 128-133	4.3	21
34	Deep into the roots of the Libyan Tuareg: a genetic survey of their paternal heritage. <i>American Journal of Physical Anthropology</i> , 2011 , 145, 118-24	2.5	21
33	Genetic-genealogy approach reveals low rate of extrapair paternity in historical Dutch populations. <i>American Journal of Human Biology</i> , 2017 , 29, e23046	2.7	21
32	Pseudoautosomal region 1 length polymorphism in the human population. <i>PLoS Genetics</i> , 2014 , 10, e1004578	19	
31	Genetic genealogy reveals true Y haplogroup of House of Bourbon contradicting recent identification of the presumed remains of two French Kings. <i>European Journal of Human Genetics</i> , 2014 , 22, 681-7	5.3	16

30	Allele frequencies for the new European Standard Set (ESS) loci and D1S1677 in the Belgian population. <i>Forensic Science International: Genetics</i> , 2012 , 6, e75-7	4.3	15
29	A substantially lower frequency of uninformative matches between 23 versus 17 Y-STR haplotypes in north Western Europe. <i>Forensic Science International: Genetics</i> , 2014 , 11, 214-9	4.3	14
28	A game of hide and seq: Identification of parallel Y-STR evolution in deep-rooting pedigrees. <i>European Journal of Human Genetics</i> , 2019 , 27, 637-646	5.3	14
27	A selective set of DNA-methylation markers for age determination of blood, teeth and buccal samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2015 , 5, e144-e145	0.5	13
26	Development and evaluation of multiplex Y-STR assays for application in molecular genealogy. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 57-59	0.5	12
25	Ysurnames? The patrilineal Y-chromosome and surname correlation for DNA kinship research. <i>Forensic Science International: Genetics</i> , 2020 , 44, 102204	4.3	12
24	Automated DNA extraction of single dog hairs without roots for mitochondrial DNA analysis. <i>Forensic Science International: Genetics</i> , 2012 , 6, 277-81	4.3	11
23	Y-chromosomal STR haplotypes in a Belgian population sample and identification of a micro-variant with a flanking site mutation at DYS19. <i>Forensic Science International</i> , 2005 , 152, 89-94	2.6	11
22	Automating a combined composite-consensus method to generate DNA profiles from low and high template mixture samples. <i>Forensic Science International: Genetics</i> , 2012 , 6, 588-93	4.3	10
21	Biohistorical materials and contemporary privacy concerns-the forensic case of King Albert I. <i>Forensic Science International: Genetics</i> , 2016 , 24, 202-210	4.3	9
20	Evaluation of methodology for the isolation and analysis of LCN-DNA before and after dactyloscopic enhancement of fingerprints. <i>International Congress Series</i> , 2006 , 1288, 583-585		9
19	Allele frequency data for 19 short tandem repeats (PowerPlex 16 and FFFI) in a Belgian population sample. <i>Journal of Forensic Sciences</i> , 2006 , 51, 436-7	1.8	9
18	A Historical-Genetic Reconstruction of Human Extra-Pair Paternity. <i>Current Biology</i> , 2019 , 29, 4102-4107	6.7	9
17	Increased sensitivity for amplified STR alleles on capillary sequencers with BigDye [®] XTerminator [®] <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 123-124	0.5	6
16	The Dutch Y-chromosomal landscape. <i>European Journal of Human Genetics</i> , 2020 , 28, 287-299	5.3	6
15	Defining Y-SNP variation among the Flemish population (Western Europe) by full genome sequencing. <i>Forensic Science International: Genetics</i> , 2017 , 31, e12-e16	4.3	5
14	The Paternal Landscape along the Bight of Benin - Testing Regional Representativeness of West-African Population Samples Using Y-Chromosomal Markers. <i>PLoS ONE</i> , 2015 , 10, e0141510	3.7	5
13	Comparing maternal genetic variation across two millennia reveals the demographic history of an ancient human population in southwest Turkey. <i>Royal Society Open Science</i> , 2016 , 3, 150250	3.3	5

12	DNA Degradation: Current Knowledge and Progress in DNA Analysis 2017 , 65-80		4
11	The black legend on the Spanish presence in the low countries: Verifying shared beliefs on genetic ancestry. <i>American Journal of Physical Anthropology</i> , 2018 , 166, 219-227	2.5	4
10	Controversial identification in a historical case is illustrative of the complexity of DNA typing in forensic research. Response to Charlier et al. <i>Forensic Science International: Genetics</i> , 2014 , 9, e18-9	4.3	3
9	Development of a novel miniSTR multiplex assay for typing degraded DNA samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 112-114	0.5	3
8	CSYseq: The first Y-chromosome sequencing tool typing a large number of Y-SNPs and Y-STRs to unravel worldwide human population genetics. <i>PLoS Genetics</i> , 2021 , 17, e1009758	6	2
7	Bight of Benin: a Maternal Perspective of Four Beninese Populations and their Genetic Implications on the American Populations of African Ancestry. <i>Annals of Human Genetics</i> , 2017 , 81, 78-90	2.2	1
6	Validation of a microchip electrophoresis system as a DNA amplification control. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 119-120	0.5	1
5	Validation of Y-ancestor time calculators for forensic familial searching. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 411-413	0.5	1
4	YMrCA: Improving Y-chromosomal ancestor time estimation for DNA kinship research. <i>Human Mutation</i> , 2021 , 42, 1307-1320	4.7	0
3	An interdisciplinary study around the reliquary of the late cardinal Jacques de Vitry. <i>PLoS ONE</i> , 2019 , 14, e0201424	3.7	
2	Optimization and validation of the SNPforID 34-SNPplex for POP7. <i>Forensic Science International: Genetics Supplement Series</i> , 2011 , 3, e43-e44	0.5	
1	Cell survival and DNA damage repair are promoted in the human blood thanatotranscriptome shortly after death. <i>Scientific Reports</i> , 2021 , 11, 16585	4.9	