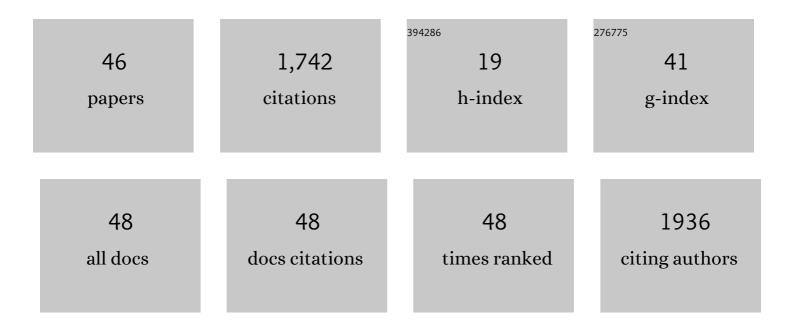
Ronny Decorte

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications. American Journal of Human Genetics, 2010, 87, 341-353.	2.6	324
2	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	1.6	214
3	Improved age determination of blood and teeth samples using a selected set of DNA methylation markers. Epigenetics, 2015, 10, 922-930.	1.3	187
4	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	1.1	151
5	Seeing the Wood for the Trees: A Minimal Reference Phylogeny for the Human Y Chromosome. Human Mutation, 2014, 35, 187-191.	1.1	141
6	The palaeogenetics of cat dispersal in the ancient world. Nature Ecology and Evolution, 2017, 1, .	3.4	113
7	Determining Y-STR mutation rates in deep-routing genealogies: Identification of haplogroup differences. Forensic Science International: Genetics, 2018, 34, 1-10.	1.6	38
8	Evaluation of three statistical prediction models for forensic age prediction based on DNA methylation. Forensic Science International: Genetics, 2018, 34, 128-133.	1.6	37
9	Micro-geographic distribution of Y-chromosomal variation in the central-western European region Brabant. Forensic Science International: Genetics, 2011, 5, 95-99.	1.6	36
10	Belgian population data for 15 STR loci (AmpFlSTR® SGM Plus and AmpFlSTR™ profiler PCR) Tj ETQq0 0 0 rgBT	/Oyerlock 1.3	10 Tf 50 38
11	Identification and sequence analysis of discordant phenotypes between AmpFISTR SGM Plusâ,,¢ and PowerPlex® 16. International Journal of Legal Medicine, 2007, 121, 297-301.	1.2	27
12	Temporal differentiation across a West-European Y-chromosomal cline: genealogy as a tool in human population genetics. European Journal of Human Genetics, 2012, 20, 434-440.	1.4	26
13	Geneticâ€genealogy approach reveals low rate of extrapair paternity in historical Dutch populations. American Journal of Human Biology, 2017, 29, e23046.	0.8	26
14	Ysurnames? The patrilineal Y-chromosome and surname correlation for DNA kinship research. Forensic Science International: Genetics, 2020, 44, 102204.	1.6	25
15	Pseudoautosomal Region 1 Length Polymorphism in the Human Population. PLoS Genetics, 2014, 10, e1004578.	1.5	24
16	Deep into the roots of the Libyan Tuareg: A genetic survey of their paternal heritage. American Journal of Physical Anthropology, 2011, 145, 118-124.	2.1	23
17	Towards a consensus Y-chromosomal phylogeny and Y-SNP set in forensics in the next-generation sequencing era. Forensic Science International: Genetics, 2015, 15, 39-42.	1.6	23
18	A Historical-Genetic Reconstruction of Human Extra-Pair Paternity. Current Biology, 2019, 29,	1.8	23

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#	Article	IF	CITATIONS
19	A selective set of DNA-methylation markers for age determination of blood, teeth and buccal samples. Forensic Science International: Genetics Supplement Series, 2015, 5, e144-e145.	0.1	22
20	A game of hide and seq: Identification of parallel Y-STR evolution in deep-rooting pedigrees. European Journal of Human Genetics, 2019, 27, 637-646.	1.4	22
21	Genetic genealogy reveals true Y haplogroup of House of Bourbon contradicting recent identification of the presumed remains of two French Kings. European Journal of Human Genetics, 2014, 22, 681-687.	1.4	18
22	CSYseq: The first Y-chromosome sequencing tool typing a large number of Y-SNPs and Y-STRs to unravel worldwide human population genetics. PLoS Genetics, 2021, 17, e1009758.	1.5	17
23	Allele frequencies for the new European Standard Set (ESS) loci and D1S1677 in the Belgian population. Forensic Science International: Genetics, 2012, 6, e75-e77.	1.6	16
24	The Dutch Y-chromosomal landscape. European Journal of Human Genetics, 2020, 28, 287-299.	1.4	15
25	Evaluation of methodology for the isolation and analysis of LCN-DNA before and after dactyloscopic enhancement of fingerprints. International Congress Series, 2006, 1288, 583-585.	0.2	14
26	A substantially lower frequency of uninformative matches between 23 versus 17 Y-STR haplotypes in north Western Europe. Forensic Science International: Genetics, 2014, 11, 214-219.	1.6	14
27	Y-chromosomal STR haplotypes in a Belgian population sample and identification of a micro-variant with a flanking site mutation at DYS19. Forensic Science International, 2005, 152, 89-94.	1.3	12
28	Development and evaluation of multiplex Y-STR assays for application in molecular genealogy. Forensic Science International: Genetics Supplement Series, 2009, 2, 57-59.	0.1	12
29	Automated DNA extraction of single dog hairs without roots for mitochondrial DNA analysis. Forensic Science International: Genetics, 2012, 6, 277-281.	1.6	12
30	Comparing maternal genetic variation across two millennia reveals the demographic history of an ancient human population in southwest Turkey. Royal Society Open Science, 2016, 3, 150250.	1.1	11
31	Biohistorical materials and contemporary privacy concerns-the forensic case of King Albert I. Forensic Science International: Genetics, 2016, 24, 202-210.	1.6	11
32	Automating a combined composite–consensus method to generate DNA profiles from low and high template mixture samples. Forensic Science International: Genetics, 2012, 6, 588-593.	1.6	10
33	Allele Frequency Data for 19 Short Tandem Repeats (PowerPlexR 16 and FFFl) in a Belgian Population Sample. Journal of Forensic Sciences, 2006, 51, 436-437.	0.9	9
34	The Paternal Landscape along the Bight of Benin – Testing Regional Representativeness of West-African Population Samples Using Y-Chromosomal Markers. PLoS ONE, 2015, 10, e0141510.	1.1	8
35	Increased sensitivity for amplified STR alleles on capillary sequencers with BigDye® XTerminator™. Forensic Science International: Genetics Supplement Series, 2009, 2, 123-124.	0.1	6
36	Defining Y-SNP variation among the Flemish population (Western Europe) by full genome sequencing. Forensic Science International: Genetics, 2017, 31, e12-e16.	1.6	6

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#	Article	IF	CITATIONS
37	Development of a novel miniSTR multiplex assay for typing degraded DNA samples. Forensic Science International: Genetics Supplement Series, 2008, 1, 112-114.	0.1	5
38	The black legend on the Spanish presence in the low countries: Verifying shared beliefs on genetic ancestry. American Journal of Physical Anthropology, 2018, 166, 219-227.	2.1	5
39	YMrCA: Improving Y hromosomal ancestor time estimation for DNA kinship research. Human Mutation, 2021, 42, 1307-1320.	1.1	5
40	Validation of a microchip electrophoresis system as a DNA amplification control. Forensic Science International: Genetics Supplement Series, 2009, 2, 119-120.	0.1	3
41	Controversial identification in a historical case is illustrative of the complexity of DNA typing in forensic research. Response to Charlier et al Forensic Science International: Genetics, 2014, 9, e18-e19.	1.6	3
42	Bight of Benin: a Maternal Perspective of Four Beninese Populations and their Genetic Implications on the American Populations of African Ancestry. Annals of Human Genetics, 2017, 81, 78-90.	0.3	3
43	Validation of Y-ancestor time calculators for forensic familial searching. Forensic Science International: Genetics Supplement Series, 2019, 7, 411-413.	0.1	3
44	Cell survival and DNA damage repair are promoted in the human blood thanatotranscriptome shortly after death. Scientific Reports, 2021, 11, 16585.	1.6	2
45	An interdisciplinary study around the reliquary of the late cardinal Jacques de Vitry. PLoS ONE, 2019, 14, e0201424.	1.1	1
46	Optimization and validation of the SNPforID 34-SNPplex for POP7â,,¢. Forensic Science International: Genetics Supplement Series, 2011, 3, e43-e44.	0.1	0