

# Kristiaan J Van Der Gaag

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1425671/publications.pdf>

Version: 2024-02-01

32  
papers

1,677  
citations

393982

19  
h-index

433756

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

2054  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of the VISAGE basic tool for appearance and ancestry inference using ForenSeq <sup>®</sup> chemistry on the MiSeq FGx <sup>®</sup> system. <i>Forensic Science International: Genetics</i> , 2022, 58, 102675.	1.6	10
2	The Dutch Y-chromosomal landscape. <i>European Journal of Human Genetics</i> , 2020, 28, 287-299.	1.4	15
3	Reducing the Number of Mismatches between Hairs and Buccal References When Analysing mtDNA Heteroplasmic Variation by Massively Parallel Sequencing. <i>Genes</i> , 2020, 11, 1355.	1.0	13
4	HlrPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms. <i>Forensic Science International: Genetics</i> , 2019, 43, 102152.	1.6	45
5	STRNaming: Standardised STR sequence allele naming to simplify MPS data analysis and interpretation. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 436-437.	0.1	0
6	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , 2018, 37, 241-251.	1.6	38
7	Short hypervariable microhaplotypes: A novel set of very short high discriminating power loci without stutter artefacts. <i>Forensic Science International: Genetics</i> , 2018, 35, 169-175.	1.6	51
8	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. <i>Forensic Science International: Genetics</i> , 2017, 27, 27-40.	1.6	73
9	Length and repeat-sequence variation in 58 STRs and 94 SNPs in two Spanish populations. <i>Forensic Science International: Genetics</i> , 2017, 30, 66-70.	1.6	28
10	Massively parallel sequencing of short tandem repeats—Population data and mixture analysis results for the PowerSeq <sup>®</sup> system. <i>Forensic Science International: Genetics</i> , 2016, 24, 86-96.	1.6	118
11	Forensic nomenclature for short tandem repeats updated for sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e542-e544.	0.1	6
12	Analysis of 36 Y-STR marker units including a concordance study among 2085 Dutch males. <i>Forensic Science International: Genetics</i> , 2015, 14, 174-181.	1.6	29
13	Comparing six commercial autosomal STR kits in a large Dutch population sample. <i>Forensic Science International: Genetics</i> , 2014, 10, 55-63.	1.6	92
14	TSSV: a tool for characterization of complex allelic variants in pure and mixed genomes. <i>Bioinformatics</i> , 2014, 30, 1651-1659.	1.8	39
15	Analysis of coprolites from the extinct mountain goat <i>Myotragus balearicus</i> . <i>Quaternary Research</i> , 2014, 81, 106-116.	1.0	34
16	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	1.1	151
17	A Linguistically Informed Autosomal STR Survey of Human Populations Residing in the Greater Himalayan Region. <i>PLoS ONE</i> , 2014, 9, e91534.	1.1	16
18	The Contribution of DNA Metabarcoding to Fungal Conservation: Diversity Assessment, Habitat Partitioning and Mapping Red-Listed Fungi in Protected Coastal <i>Salix repens</i> Communities in the Netherlands. <i>PLoS ONE</i> , 2014, 9, e99852.	1.1	66

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19	Data Concatenation, Bayesian Concordance and Coalescent-Based Analyses of the Species Tree for the Rapid Radiation of Triturus Newts. PLoS ONE, 2014, 9, e111011.	1.1	18
20	Indian ocean crossroads: Human genetic origin and population structure in the maldives. American Journal of Physical Anthropology, 2013, 151, 58-67.	2.1	14
21	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
22	Quality Assessment of the Genetic Test for Familial Hypercholesterolemia in The Netherlands. Cholesterol, 2013, 2013, 1-8.	1.6	8
23	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
24	Ancestral Stories of Ghanaian Bimoba Reflect Millennia-Old Genetic Lineages. PLoS ONE, 2013, 8, e65690.	1.1	5
25	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
26	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
27	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
28	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. Human Mutation, 2010, 31, E1875-E1893.	1.1	86
29	Inferring Continental Ancestry of Argentineans from Autosomal, Y-Chromosomal and Mitochondrial DNA. Annals of Human Genetics, 2010, 74, 65-76.	0.3	155
30	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
31	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
32	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