

# Titia Sijen

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

7,358  
citations

116194

36  
h-index

81351

76  
g-index

80  
all docs

80  
docs citations

80  
times ranked

6818  
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. Forensic Science International: Genetics, 2022, 58, 102675.	1.6	10
2	Technical note: Performing LR calculations when loci are missing between reference and trace DNA profiles. Forensic Science International: Reports, 2022, 5, 100268.	0.4	0
3	mRNA profiling of mock casework samples: Results of a FoRNAP collaborative exercise. Forensic Science International: Genetics, 2021, 50, 102409.	1.6	24
4	STRNaming: Generating simple, informative names for sequenced STR alleles in a standardised and automated manner. Forensic Science International: Genetics, 2021, 52, 102473.	1.6	10
5	Application of a probabilistic genotyping software to MPS mixture STR data is supported by similar trends in LR compared with CE data. Forensic Science International: Genetics, 2021, 52, 102489.	1.6	3
6	RMplex: An efficient method for analyzing 30 Y-STRs with high mutation rates. Forensic Science International: Genetics, 2021, 55, 102595.	1.6	12
7	On the Identification of Body Fluids and Tissues: A Crucial Link in the Investigation and Solution of Crime. Genes, 2021, 12, 1728.	1.0	34
8	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Part II: Evaluation of biological traces considering activity level propositions. Forensic Science International: Genetics, 2020, 44, 102186.	1.6	59
9	Multi-laboratory validation of DNAs including the statistical library DNASTatistX. Forensic Science International: Genetics, 2020, 49, 102390.	1.6	7
10	Reducing the Number of Mismatches between Hairs and Buccal References When Analysing mtDNA Heteroplasmic Variation by Massively Parallel Sequencing. Genes, 2020, 11, 1355.	1.0	13
11	A rapid and efficient method for DNA extraction from bone powder. Forensic Science International: Reports, 2020, 2, 100099.	0.4	8
12	An assessment of the performance of the probabilistic genotyping software EuroForMix: Trends in likelihood ratios and analysis of Type I & II errors. Forensic Science International: Genetics, 2019, 42, 31-38.	1.6	34
13	HirisPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms. Forensic Science International: Genetics, 2019, 43, 102152.	1.6	45
14	DNAs/DNASTatistX: Development and validation of a software suite for the data management and probabilistic interpretation of DNA profiles. Forensic Science International: Genetics, 2019, 42, 81-89.	1.6	37
15	Performance of EuroForMix deconvolution on PowerPlex <sup>®</sup> Fusion 6C profiles. Forensic Science International: Genetics Supplement Series, 2019, 7, 5-6.	0.1	1
16	Automated estimation of the number of contributors in autosomal STR profiles. Forensic Science International: Genetics Supplement Series, 2019, 7, 7-8.	0.1	3
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	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

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19	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Forensic Science International: Genetics, 2018, 36, 189-202.	1.6	83
20	Low-template methods yield limited extra information for PowerPlex® Fusion 6C profiling. Legal Medicine, 2018, 33, 62-65.	0.6	4
21	Validation of SmartRank: A likelihood ratio software for searching national DNA databases with complex DNA profiles. Forensic Science International: Genetics, 2017, 29, 145-153.	1.6	26
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	DNA transfer and cell type inference to assist activity level reporting: Post-activity background samples as a control in dragging scenario. Forensic Science International: Genetics Supplement Series, 2017, 6, e591-e592.	0.1	6
24	Extended specificity studies of mRNA assays used to infer human organ tissues and body fluids. Electrophoresis, 2017, 38, 3155-3160.	1.3	21
25	Development of a control region-based mtDNA SNaPshot® selection tool, integrated into a mini amplicon sequencing method. Science and Justice - Journal of the Forensic Science Society, 2016, 56, 96-103.	1.3	7
26	Advancing forensic RNA typing: On non-target secretions, a nasal mucosa marker, a differential co-extraction protocol and the sensitivity of DNA and RNA profiling. Forensic Science International: Genetics, 2016, 20, 119-129.	1.6	68
27	Is an increased drop-in rate appropriate with enhanced DNA profiling?. Forensic Science International: Genetics Supplement Series, 2015, 5, e71-e72.	0.1	2
28	Advancing forensic RNA profiling: Preventing noise signals in RNA profiling by adding the multiplex buffer last. Forensic Science International: Genetics Supplement Series, 2015, 5, e518-e519.	0.1	0
29	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. PLoS ONE, 2015, 10, e0127852.	1.1	51
30	Split DNA over replicates or perform one amplification?. Forensic Science International: Genetics Supplement Series, 2015, 5, e532-e533.	0.1	3
31	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
32	Evaluation of samples comprising minute amounts of DNA. Science and Justice - Journal of the Forensic Science Society, 2015, 55, 316-322.	1.3	11
33	The effect of varying the number of contributors on likelihood ratios for complex DNA mixtures. Forensic Science International: Genetics, 2015, 19, 92-99.	1.6	36
34	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
35	Molecular approaches for forensic cell type identification: On mRNA, miRNA, DNA methylation and microbial markers. Forensic Science International: Genetics, 2015, 18, 21-32.	1.6	134
36	Complex DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model. Forensic Science International: Genetics, 2015, 16, 17-25.	1.6	37

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37	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
38	LoCIM-tool: An expert's assistant for inferring the major contributor's alleles in mixed consensus DNA profiles. <i>Forensic Science International: Genetics</i> , 2014, 11, 154-165.	1.6	20
39	Developmental validation of the HirisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. <i>Forensic Science International: Genetics</i> , 2014, 9, 150-161.	1.6	164
40	Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. <i>Forensic Science International: Genetics</i> , 2014, 11, 241-251.	1.6	23
41	Developmental validation of mitochondrial DNA genotyping assays for adept matrilineal inference of biogeographic ancestry at a continental level. <i>Forensic Science International: Genetics</i> , 2014, 11, 39-51.	1.6	29
42	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	1.1	151
43	Development of a mRNA profiling multiplex for the inference of organ tissues. <i>International Journal of Legal Medicine</i> , 2013, 127, 891-900.	1.2	43
44	Improving a rapid DNA profiling service regularly applied in forensic casework. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e284-e285.	0.1	1
45	RNA cell typing and DNA profiling of mixed samples: Can cell types and donors be associated?. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2013, 53, 261-269.	1.3	38
46	Implementation of RNA profiling in forensic casework. <i>Forensic Science International: Genetics</i> , 2013, 7, 159-166.	1.6	76
47	Consensus and pool profiles to assist in the analysis and interpretation of complex low template DNA mixtures. <i>International Journal of Legal Medicine</i> , 2013, 127, 11-23.	1.2	32
48	Revision of the tape used in a tape-lift protocol for DNA recovery. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e270-e271.	0.1	11
49	RapidHIT <sup>®</sup> , € 200, a promising system for rapid DNA analysis. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e254-e255.	0.1	20
50	Can mRNA markers distinguish traces generated by different types of contact?. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e3-e4.	0.1	3
51	Improved analysis of long STR amplicons from degraded single source and mixed DNA. <i>International Journal of Legal Medicine</i> , 2013, 127, 741-747.	1.2	5
52	Assessment of mock cases involving complex low template DNA mixtures: A descriptive study. <i>Forensic Science International: Genetics</i> , 2012, 6, 697-707.	1.6	26
53	Combining results of forensic STR kits: HDplex validation including allelic association and linkage testing with NGM and Identifiler loci. <i>International Journal of Legal Medicine</i> , 2012, 126, 781-789.	1.2	52
54	Extended PCR conditions to reduce drop-out frequencies in low template STR typing including unequal mixtures. <i>Forensic Science International: Genetics</i> , 2012, 6, 102-107.	1.6	19

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55	Comparison of stubbing and the double swab method for collecting offender epithelial material from a victim's skin. <i>Forensic Science International: Genetics</i> , 2012, 6, 219-223.	1.6	37
56	A multiplex (m)RNA-profiling system for the forensic identification of body fluids and contact traces. <i>Forensic Science International: Genetics</i> , 2012, 6, 565-577.	1.6	185
57	Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM. <i>Forensic Science International: Genetics</i> , 2012, 6, 708-715.	1.6	41
58	A protocol for direct and rapid multiplex PCR amplification on forensically relevant samples. <i>Forensic Science International: Genetics</i> , 2012, 6, 167-175.	1.6	68
59	Vaginal microbial flora analysis by next generation sequencing and microarrays; can microbes indicate vaginal origin in a forensic context?. <i>International Journal of Legal Medicine</i> , 2012, 126, 303-310.	1.2	66
60	Revision and implementation of the SAFE kit used in the Netherlands. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e425-e426.	0.1	0
61	Implementation and first case results of a rapid DNA profiling service. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e427-e428.	0.1	7
62	Low template STR typing: Effect of replicate number and consensus method on genotyping reliability and DNA database search results. <i>Forensic Science International: Genetics</i> , 2011, 5, 316-328.	1.6	99
63	Developmental validation of the IrisPlex system: Determination of blue and brown iris colour for forensic intelligence. <i>Forensic Science International: Genetics</i> , 2011, 5, 464-471.	1.6	141
64	Post-coital vaginal sampling with nylon flocked swabs improves DNA typing. <i>Forensic Science International: Genetics</i> , 2010, 4, 115-121.	1.6	71
65	RDE-1 slicer activity is required only for passenger-strand cleavage during RNAi in <i>Caenorhabditis elegans</i> . <i>Nature Structural and Molecular Biology</i> , 2009, 16, 207-211.	3.6	68
66	Higher Capillary Electrophoresis Injection Settings as an Efficient Approach to Increase the Sensitivity of STR Typing. <i>Journal of Forensic Sciences</i> , 2009, 54, 591-598.	0.9	50
67	Tri-allelic SNP markers enable analysis of mixed and degraded DNA samples. <i>Forensic Science International: Genetics</i> , 2009, 3, 233-241.	1.6	71
68	Degraded DNA sample analysis using DNA repair enzymes, mini-STRs and (tri-allelic) SNPs. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 505-507.	0.1	11
69	Secondary siRNAs Result from Unprimed RNA Synthesis and Form a Distinct Class. <i>Science</i> , 2007, 315, 244-247.	6.0	360
70	Structural features of small RNA precursors determine Argonaute loading in <i>Caenorhabditis elegans</i> . <i>Nature Structural and Molecular Biology</i> , 2007, 14, 927-933.	3.6	80
71	Chromatin and RNAi factors protect the <i>C. elegans</i> germline against repetitive sequences. <i>Genes and Development</i> , 2005, 19, 782-787.	2.7	129
72	RDE-2 interacts with MUT-7 to mediate RNA interference in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2005, 33, 347-355.	6.5	54

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73	Transposon silencing in the <i>Caenorhabditis elegans</i> germ line by natural RNAi. <i>Nature</i> , 2003, 426, 310-314.	13.7	400
74	Negative-Strand Tospoviruses and Tenuiviruses Carry a Gene for a Suppressor of Gene Silencing at Analogous Genomic Positions. <i>Journal of Virology</i> , 2003, 77, 1329-1336.	1.5	210
75	RNA Helicase MUT-14-Dependent Gene Silencing Triggered in <i>C. elegans</i> by Short Antisense RNAs. <i>Science</i> , 2002, 295, 694-697.	6.0	141
76	On the Role of RNA Amplification in dsRNA-Triggered Gene Silencing. <i>Cell</i> , 2001, 107, 465-476.	13.5	1,172
77	Transcriptional and posttranscriptional gene silencing are mechanistically related. <i>Current Biology</i> , 2001, 11, 436-440.	1.8	263
78	Dicer functions in RNA interference and in synthesis of small RNA involved in developmental timing in <i>C. elegans</i> . <i>Genes and Development</i> , 2001, 15, 2654-2659.	2.7	1,564
79	Post-transcriptional gene-silencing: RNAs on the attack or on the defense?. <i>BioEssays</i> , 2000, 22, 520-531.	1.2	101