

Titia Sijen

List of Publications by Year in descending order

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79
papers

7,358
citations

101543

36
h-index

71685

76
g-index

80
all docs

80
docs citations

80
times ranked

6120
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	5.9	1,564
2	On the Role of RNA Amplification in dsRNA-Triggered Gene Silencing. <i>Cell</i> , 2001, 107, 465-476.	28.9	1,172
3	Transposon silencing in the <i>Caenorhabditis elegans</i> germ line by natural RNAi. <i>Nature</i> , 2003, 426, 310-314.	27.8	400
4	Secondary siRNAs Result from Unprimed RNA Synthesis and Form a Distinct Class. <i>Science</i> , 2007, 315, 244-247.	12.6	360
5	Transcriptional and posttranscriptional gene silencing are mechanistically related. <i>Current Biology</i> , 2001, 11, 436-440.	3.9	263
6	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.	3.4	210
7	The HlrPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation. <i>Forensic Science International: Genetics</i> , 2018, 35, 123-135.	3.1	199
8	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.	3.1	185
9	Developmental validation of the HlrPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. <i>Forensic Science International: Genetics</i> , 2014, 9, 150-161.	3.1	164
10	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	2.5	151
11	RNA Helicase MUT-14-Dependent Gene Silencing Triggered in <i>C. elegans</i> by Short Antisense RNAs. <i>Science</i> , 2002, 295, 694-697.	12.6	141
12	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.	3.1	141
13	Molecular approaches for forensic cell type identification: On mRNA, miRNA, DNA methylation and microbial markers. <i>Forensic Science International: Genetics</i> , 2015, 18, 21-32.	3.1	134
14	Chromatin and RNAi factors protect the <i>C. elegans</i> germline against repetitive sequences. <i>Genes and Development</i> , 2005, 19, 782-787.	5.9	129
15	Post-transcriptional gene-silencing: RNAs on the attack or on the defense?. <i>BioEssays</i> , 2000, 22, 520-531.	2.5	101
16	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.	3.1	99
17	Comparing six commercial autosomal STR kits in a large Dutch population sample. <i>Forensic Science International: Genetics</i> , 2014, 10, 55-63.	3.1	92
18	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. <i>Forensic Science International: Genetics</i> , 2018, 36, 189-202.	3.1	83

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19	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.	8.2	80
20	Implementation of RNA profiling in forensic casework. <i>Forensic Science International: Genetics</i> , 2013, 7, 159-166.	3.1	76
21	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.	3.1	73
22	Tri-allelic SNP markers enable analysis of mixed and degraded DNA samples. <i>Forensic Science International: Genetics</i> , 2009, 3, 233-241.	3.1	71
23	Post-coital vaginal sampling with nylon flocked swabs improves DNA typing. <i>Forensic Science International: Genetics</i> , 2010, 4, 115-121.	3.1	71
24	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.	8.2	68
25	A protocol for direct and rapid multiplex PCR amplification on forensically relevant samples. <i>Forensic Science International: Genetics</i> , 2012, 6, 167-175.	3.1	68
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. <i>Forensic Science International: Genetics</i> , 2016, 20, 119-129.	3.1	68
27	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.	2.2	66
28	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. <i>Forensic Science International: Genetics</i> , 2020, 44, 102186.	3.1	59
29	RDE-2 interacts with MUT-7 to mediate RNA interference in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2005, 33, 347-355.	14.5	54
30	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.	2.2	52
31	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. <i>PLoS ONE</i> , 2015, 10, e0127852.	2.5	51
32	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.	1.6	50
33	HirisPlex-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.	3.1	45
34	Development of a mRNA profiling multiplex for the inference of organ tissues. <i>International Journal of Legal Medicine</i> , 2013, 127, 891-900.	2.2	43
35	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.	3.1	41
36	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.	2.1	38

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37	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.	3.1	38
38	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.	3.1	37
39	Complex DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model. <i>Forensic Science International: Genetics</i> , 2015, 16, 17-25.	3.1	37
40	DNAXs/DNAStatistX: Development and validation of a software suite for the data management and probabilistic interpretation of DNA profiles. <i>Forensic Science International: Genetics</i> , 2019, 42, 81-89.	3.1	37
41	The effect of varying the number of contributors on likelihood ratios for complex DNA mixtures. <i>Forensic Science International: Genetics</i> , 2015, 19, 92-99.	3.1	36
42	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. <i>Forensic Science International: Genetics</i> , 2015, 19, 280-288.	3.1	36
43	An assessment of the performance of the probabilistic genotyping software EuroForMix: Trends in likelihood ratios and analysis of Type I & II errors. <i>Forensic Science International: Genetics</i> , 2019, 42, 31-38.	3.1	34
44	On the Identification of Body Fluids and Tissues: A Crucial Link in the Investigation and Solution of Crime. <i>Genes</i> , 2021, 12, 1728.	2.4	34
45	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.	2.2	32
46	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.	3.1	29
47	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.	3.1	29
48	Assessment of mock cases involving complex low template DNA mixtures: A descriptive study. <i>Forensic Science International: Genetics</i> , 2012, 6, 697-707.	3.1	26
49	Validation of SmartRank: A likelihood ratio software for searching national DNA databases with complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2017, 29, 145-153.	3.1	26
50	mRNA profiling of mock casework samples: Results of a FoRNAP collaborative exercise. <i>Forensic Science International: Genetics</i> , 2021, 50, 102409.	3.1	24
51	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.	3.1	23
52	Extended specificity studies of mRNA assays used to infer human organ tissues and body fluids. <i>Electrophoresis</i> , 2017, 38, 3155-3160.	2.4	21
53	RapidHIT [®] , € 200, a promising system for rapid DNA analysis. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e254-e255.	0.3	20
54	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.	3.1	20

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55	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.	3.1	19
56	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.	2.4	13
57	RMplex: An efficient method for analyzing 30 Y-STRs with high mutation rates. <i>Forensic Science International: Genetics</i> , 2021, 55, 102595.	3.1	12
58	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.	0.3	11
59	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.	0.3	11
60	Evaluation of samples comprising minute amounts of DNA. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2015, 55, 316-322.	2.1	11
61	STRNaming: Generating simple, informative names for sequenced STR alleles in a standardised and automated manner. <i>Forensic Science International: Genetics</i> , 2021, 52, 102473.	3.1	10
62	Evaluation of the VISAGE basic tool for appearance and ancestry inference using ForenSeq [®] chemistry on the MiSeq FGx [®] system. <i>Forensic Science International: Genetics</i> , 2022, 58, 102675.	3.1	10
63	A rapid and efficient method for DNA extraction from bone powder. <i>Forensic Science International: Reports</i> , 2020, 2, 100099.	0.8	8
64	Implementation and first case results of a rapid DNA profiling service. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e427-e428.	0.3	7
65	Development of a control region-based mtDNA SNaPshot [®] selection tool, integrated into a mini amplicon sequencing method. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2016, 56, 96-103.	2.1	7
66	Multi-laboratory validation of DNAs including the statistical library DNASTatistX. <i>Forensic Science International: Genetics</i> , 2020, 49, 102390.	3.1	7
67	DNA transfer and cell type inference to assist activity level reporting: Post-activity background samples as a control in dragging scenario. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e591-e592.	0.3	6
68	Improved analysis of long STR amplicons from degraded single source and mixed DNA. <i>International Journal of Legal Medicine</i> , 2013, 127, 741-747.	2.2	5
69	Low-template methods yield limited extra information for PowerPlex [®] Fusion 6C profiling. <i>Legal Medicine</i> , 2018, 33, 62-65.	1.3	4
70	Can mRNA markers distinguish traces generated by different types of contact?. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e3-e4.	0.3	3
71	Split DNA over replicates or perform one amplification?. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e532-e533.	0.3	3
72	Application of a probabilistic genotyping software to MPS mixture STR data is supported by similar trends in LR compared with CE data. <i>Forensic Science International: Genetics</i> , 2021, 52, 102489.	3.1	3

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73	Automated estimation of the number of contributors in autosomal STR profiles. Forensic Science International: Genetics Supplement Series, 2019, 7, 7-8.	0.3	3
74	Is an increased drop-in rate appropriate with enhanced DNA profiling?. Forensic Science International: Genetics Supplement Series, 2015, 5, e71-e72.	0.3	2
75	Improving a rapid DNA profiling service regularly applied in forensic casework. Forensic Science International: Genetics Supplement Series, 2013, 4, e284-e285.	0.3	1
76	Performance of EuroForMix deconvolution on PowerPlex ^Â Fusion 6C profiles. Forensic Science International: Genetics Supplement Series, 2019, 7, 5-6.	0.3	1
77	Revision and implementation of the SAFE kit used in the Netherlands. Forensic Science International: Genetics Supplement Series, 2011, 3, e425-e426.	0.3	0
78	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.	0.3	0
79	Technical note: Performing LR calculations when loci are missing between reference and trace DNA profiles. Forensic Science International: Reports, 2022, 5, 100268.	0.8	0