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An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA

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#	Paper	IF	Citations
485	Forensic science. 2001 , 73, 2735-43		17
484	DNA commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. <i>International Journal of Legal Medicine</i> , 2001 , 114, 305-9	3.1	104
483	DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. <i>Forensic Science International</i> , 2001 , 124, 5-10	2.6	128
482	A comparison of the characteristics of profiles produced with the AMPFISTR SGM Plus multiplex system for both standard and low copy number (LCN) STR DNA analysis. <i>Forensic Science International</i> , 2001 , 123, 215-23	2.6	157
481	DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome short tandem repeats. <i>Legal Medicine</i> , 2001 , 3, 252-257	1.9	4
480	Role of short tandem repeat DNA in forensic casework in the UK--past, present, and future perspectives. 2002 , 32, 366-8, 370, 372, passim		94
479	Molecular characterisation of the nucleic acids recovered from aged forensic samples. <i>International Journal of Legal Medicine</i> , 2002 , 116, 334-9	3.1	12
478	Archived or directly swabbed latent fingerprints as a DNA source for STR typing. <i>Forensic Science International</i> , 2002 , 127, 128-30	2.6	48
477	The propensity of individuals to deposit DNA and secondary transfer of low level DNA from individuals to inert surfaces. <i>Forensic Science International</i> , 2002 , 129, 25-34	2.6	241
476	The effectiveness of protective clothing in the reduction of potential DNA contamination of the scene of crime. <i>International Journal of Legal Medicine</i> , 2003 , 117, 170-4	3.1	37
475	STR genotyping and mtDNA sequencing of latent fingerprint on paper. <i>Forensic Science International</i> , 2003 , 137, 188-95	2.6	69
474	Use of laser microdissection greatly improves the recovery of DNA from sperm on microscope slides. <i>Forensic Science International</i> , 2003 , 137, 28-36	2.6	100
473	DNA profiling: evaluation of the evidentiary value. <i>Legal Medicine</i> , 2003 , 5 Suppl 1, S41-4	1.9	1
472	Better tools are needed for parentage and kinship studies. 2003 , 43, 979-81		22
471	Novel Y-STR typing strategies reveal the genetic profile of the semen donor in extended interval post-coital cervicovaginal samples. <i>Forensic Science International</i> , 2003 , 136, 58-72	2.6	51
470	Efficacy and limits of genotyping low copy number DNA samples by multiplex PCR of STR loci. 2003 , 1239, 795-798		18
469	Hypersensitive PCR, ancient human mtDNA, and contamination. 2003 , 75, 355-64		19

468	Efficacy and limits of genotyping low copy number (LCN) DNA samples by multiplex PCR of STR loci. 2003 , 197, 351-9		60
467	Ancient DNA analysis of the delta F508 mutation. 2003 , 75, 105-15		9
466	. 2004 ,		4
465	Ongoing controversy over Romanov remains. 2004 , 306, 407-10		7
464	Chapter 23 Forensic analysis. 2004 , 69, 1073-1133		2
463	A real-time PCR protocol to determine the number of amelogenin (X-Y) gene copies from forensic DNA samples. <i>Methods in Molecular Biology</i> , 2005 , 297, 31-44	1.4	7
462	Encoded evidence: DNA in forensic analysis. 2004 , 5, 739-51		368
461	Development of a 13-locus PCR multiplex system for paternity testing. <i>International Journal of Legal Medicine</i> , 2004 , 118, 55-61	3.1	14
460	Single sperm cell isolation by laser microdissection. <i>Forensic Science International</i> , 2004 , 146 Suppl, S151-36		46
459	Use of laser microdissection greatly improves the recovery of DNA from sperm on microscope slides. 2004 , 1261, 45-47		2
458	Attribution of DNA profiles to body fluid stains. 2004 , 1261, 53-55		6
457	Consensus profiles and databasing of casework samples amplified with 34 PCR cycles: an empirical approach. 2004 , 1261, 532-534		4
456	DNA typing from steel cable. 2004 , 1261, 473-475		3
455	Robust STR multiplexes for challenging casework samples. 2004 , 1261, 547-549		3
454	Identifying the culprit from LCN DNA obtained from saliva and sweat traces linked to two different robberies and use of a database. 2004 , 1261, 443-445		5
453	Forensic DNA-typing technologies: a review. <i>Methods in Molecular Biology</i> , 2005 , 297, 1-12	1.4	7
452	Forensic DNA Typing Protocols. 2004 ,		6
451	Forensic DNA Analysis Methods. 2005 , 45-148		

450	Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure. <i>Forensic Science International</i> , 2005 , 148, 47-53	2.6	61
449	Short tandem repeat (STR) genotyping of keratinised hair. Part 2. An optimised genomic DNA extraction procedure reveals donor dependence of STR profiles. <i>Forensic Science International</i> , 2005 , 153, 247-59	2.6	48
448	Short tandem repeat (STR) genotyping of keratinised hair. Part 1. Review of current status and knowledge gaps. <i>Forensic Science International</i> , 2005 , 153, 237-46	2.6	47
447	Whole genome amplification strategy for forensic genetic analysis using single or few cell equivalents of genomic DNA. 2005 , 346, 246-57		55
446	PENDULUM--a guideline-based approach to the interpretation of STR mixtures. <i>Forensic Science International</i> , 2005 , 148, 181-9	2.6	66
445	Validation of a 21-locus autosomal SNP multiplex for forensic identification purposes. <i>Forensic Science International</i> , 2005 , 154, 62-77	2.6	90
444	DNA as evidence--the technology of identification. 2005 , 352, 2669-71		12
443	A graphical simulation model of the entire DNA process associated with the analysis of short tandem repeat loci. 2005 , 33, 632-43		96
442	A graphical (Bayes net) molecular model of the entire DNA STR process to aid interpretation. 2006 , 1288, 468-470		1
441	Use of fluorescence in situ hybridisation and laser microdissection to isolate male non-sperm cells in cases of sexual assault. 2006 , 1288, 622-624		6
440	Low copy number: Interpretation of evidence results. 2006 , 1288, 616-618		1
439	Maximization of STR DNA typing success for touched objects. 2006 , 1288, 651-653		16
438	Introduction of the DNase in forensic analysis. 2006 , 1288, 607-609		
437	Multi-substrata analysis on Siberian mummies: A different way for validation in ancient DNA studies?. 2006 , 1288, 834-836		2
436	Early influence of the steppe tribes in the peopling of Siberia. 2006 , 78, 531-49		9
435	DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. <i>Forensic Science International</i> , 2006 , 160, 90-101	2.6	279
434	Nuclear and mitochondrial DNA quantification of various forensic materials. <i>Forensic Science International</i> , 2006 , 164, 56-64	2.6	48
433	Short amplicon STR multiplex for stain typing. <i>International Journal of Legal Medicine</i> , 2006 , 120, 160-4	3.1	31

432	Is the 2p rule always conservative?. <i>Forensic Science International</i> , 2006 , 159, 206-9	2.6	36
431	Dealing with allelic dropout when reporting the evidential value in DNA relatedness analysis. <i>Forensic Science International</i> , 2006 , 160, 134-9	2.6	10
430	Analysis of artificially degraded DNA using STRs and SNPs--results of a collaborative European (EDNAP) exercise. <i>Forensic Science International</i> , 2006 , 164, 33-44	2.6	112
429	How long does it take a static speaking individual to contaminate the immediate environment?. <i>Forensic Science, Medicine, and Pathology</i> , 2006 , 2, 157-63	1.5	27
428	Unknown biological mixtures evaluation using STR analytical quantification. 2006 , 27, 409-15		3
427	Molecular Analysis for Forensic Casework and Parentage Testing. 2006 , 495-510		
426	Biologische Spurenkunde. 2007 ,		4
425	Towards understanding the effect of uncertainty in the number of contributors to DNA stains. <i>Forensic Science International: Genetics</i> , 2007 , 1, 20-8	4.3	70
424	Identification and isolation of male cells using fluorescence in situ hybridisation and laser microdissection, for use in the investigation of sexual assault. <i>Forensic Science International: Genetics</i> , 2007 , 1, 247-52	4.3	35
423	Donor cell leukemia: a critical review. 2007 , 48, 25-38		24
422	Comparative Analysis of Luminol Formulations. <i>Journal of the Canadian Society of Forensic Science</i> , 2007 , 40, 53-63	0.5	8
421	Integrated portable polymerase chain reaction-capillary electrophoresis microsystem for rapid forensic short tandem repeat typing. 2007 , 79, 1881-9		149
420	Comparison of two whole genome amplification methods for STR genotyping of LCN and degraded DNA samples. <i>Forensic Science International</i> , 2007 , 166, 35-41	2.6	60
419	Object-oriented Bayesian networks for complex forensic DNA profiling problems. <i>Forensic Science International</i> , 2007 , 169, 195-205	2.6	57
418	LoComatioN: a software tool for the analysis of low copy number DNA profiles. <i>Forensic Science International</i> , 2007 , 166, 128-38	2.6	81
417	Investigation into the usefulness of DNA profiling of earprints. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2007 , 47, 155-9	2	6
416	The probability of achieving full allelic representation for LCN-STR profiling of haploid cells. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2007 , 47, 168-71	2	17
415	Interpreting DNA Evidence: A Review. 2007 , 71, 473-495		27

414	Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. 2007 , 16, 1099-106		3624
413	Simplified low-copy-number DNA analysis by post-PCR purification. <i>Journal of Forensic Sciences</i> , 2007 , 52, 820-9	1.8	77
412	Application of low copy number STR typing to the identification of aged, degraded skeletal remains. <i>Journal of Forensic Sciences</i> , 2007 , 52, 1322-7	1.8	28
411	Developmental validation of reduced-size STR Miniplex primer sets. <i>Journal of Forensic Sciences</i> , 2007 , 52, 1263-71	1.8	29
410	Characterization of target nuclear DNA from faeces reduces technical issues associated with the assumptions of low-quality and quantity template. 2007 , 8, 577-586		70
409	Y-STR analysis of degraded DNA using reduced-size amplicons. <i>International Journal of Legal Medicine</i> , 2007 , 121, 152-7	3.1	31
408	Increasing amplification success of forensic DNA samples using multiple displacement amplification. <i>Forensic Science, Medicine, and Pathology</i> , 2007 , 3, 182-7	1.5	5
407	STR typing of ancient DNA extracted from hair shafts of Siberian mummies. <i>Forensic Science International</i> , 2007 , 166, 218-29	2.6	39
406	The tendency of individuals to transfer DNA to handled items. <i>Forensic Science International</i> , 2007 , 168, 162-8	2.6	155
405	Sicherung und Auswertung von latenten DNA-Spuren im Bereich der Eigentumskriminalität. 2008 , 18, 251-256		2
404	DNA reviews: low level DNA profiling. <i>Forensic Science, Medicine, and Pathology</i> , 2008 , 4, 129-31	1.5	9
403	Fluorescence energy transfer-labeled primers for high-performance forensic DNA profiling. 2008 , 29, 2251-9		20
402	The next generation of DNA profiling--STR typing by multiplexed PCR--ion-pair RP LC-ESI time-of-flight MS. 2008 , 29, 4739-50		20
401	Experimental studies on identification of the driver based on STR analysis. <i>Legal Medicine</i> , 2008 , 10, 115-89		5
400	Characterization of human DNA in environmental samples. <i>Forensic Science International</i> , 2008 , 178, 7-15.6		25
399	Recovery and STR amplification of DNA from RFLP membranes. <i>Journal of Forensic Sciences</i> , 2008 , 53, 349-58	1.8	4
398	Development and validation of the AmpFISTR MiniFiler PCR Amplification Kit: a MiniSTR multiplex for the analysis of degraded and/or PCR inhibited DNA. <i>Journal of Forensic Sciences</i> , 2008 , 53, 838-52	1.8	116
397	Developmental validation of a Cannabis sativa STR multiplex system for forensic analysis. <i>Journal of Forensic Sciences</i> , 2008 , 53, 1061-7	1.8	34

396	LCN DNA: proof beyond reasonable doubt? - a response. 2008 , 9, 726; author reply 726		6
395	Direct comparison of post-28-cycle PCR purification and modified capillary electrophoresis methods with the 34-cycle "low copy number" (LCN) method for analysis of trace forensic DNA samples. <i>Forensic Science International: Genetics</i> , 2008 , 2, 318-28	4-3	64
394	Interpretation of complex DNA profiles using empirical models and a method to measure their robustness. <i>Forensic Science International: Genetics</i> , 2008 , 2, 91-103	4-3	63
393	Real-time forensic DNA analysis at a crime scene using a portable microchip analyzer. <i>Forensic Science International: Genetics</i> , 2008 , 2, 301-9	4-3	69
392	A discussion of the merits of random man not excluded and likelihood ratios. <i>Forensic Science International: Genetics</i> , 2008 , 2, 343-8	4-3	50
391	A novel fluorescence-based method in forensic science for the detection of blood in situ. <i>Forensic Science International: Genetics</i> , 2008 , 2, 363-71	4-3	20
390	Analysis of LCN DNA from synthetic ropes: A practical approach used in real homicide investigation. 2008 , 1, 446-447		3
389	Old cadaver identification from severely spoiled bones: Analytical approach to degraded DNA. 2008 , 1, 444-445		2
388	Interpretation of complex DNA profiles using Tippett plots. 2008 , 1, 646-648		13
387	Chapter 28 Forensic DNA typing technologies: a review. 2008 , 6, 945-957		
386	DNA: an Overview. 2009 ,		
385	Mixture Interpretation: DNA. 2009 ,		
384	Interpretation: Low Template DNA. 2009 ,		
383	Extracting evidence from forensic DNA analyses: future molecular biology directions. 2009 , 46, 339-40, 342-50		58
382	Mystery solved: the identification of the two missing Romanov children using DNA analysis. 2009 , 4, e4838		106
381	An information gap in DNA evidence interpretation. 2009 , 4, e8327		51
380	Evaluation of modified Yfiler amplification strategy for compromised samples. 2009 , 50, 228-38		15
379	Validity of low copy number typing and applications to forensic science. 2009 , 50, 207-17		144

378	Validation of testing and interpretation protocols for low template DNA samples using AmpFISTR Identifiler. 2009 , 50, 250-67		93
377	Impact of allelic dropout on evidential value of forensic DNA profiles using RMNE. 2009 , 25, 225-9		16
376	Integrated microfluidic systems for high-performance genetic analysis. 2009 , 27, 572-81		115
375	Scaling of nucleic acid assays on microelectrophoresis array devices: high-dynamic range multi-gene readout from less than ten transcripts. 2009 , 30, 2090-9		
374	Subtyping of Y-chromosomal haplogroup E-M78 (E1b1b1a) by SNP assay and its forensic application. <i>International Journal of Legal Medicine</i> , 2009 , 123, 357-60	3.1	15
373	Higher capillary electrophoresis injection settings as an efficient approach to increase the sensitivity of STR typing. <i>Journal of Forensic Sciences</i> , 2009 , 54, 591-8	1.8	43
372	Single nucleotide polymorphism genotyping by mini-primer allele-specific amplification with universal reporter primers for identification of degraded DNA. 2009 , 386, 85-90		20
371	An integrated microdevice for high-performance short tandem repeat genotyping. 2009 , 4, 1530-41		12
370	Aspartic acid racemization variability in ancient human remains: implications in the prediction of ancient DNA recovery. 2009 , 36, 965-972		21
369	Biology, Conservation and Sustainable Development of Sturgeons. 2009 ,		11
368	Maximizing DNA profiling success from sub-optimal quantities of DNA: a staged approach. <i>Forensic Science International: Genetics</i> , 2009 , 3, 128-37	4.3	22
367	Estimating the probability of allelic drop-out of STR alleles in forensic genetics. <i>Forensic Science International: Genetics</i> , 2009 , 3, 222-6	4.3	91
366	Interpreting low template DNA profiles. <i>Forensic Science International: Genetics</i> , 2009 , 4, 1-10	4.3	139
365	Validation issues around DNA typing of low level DNA. <i>Forensic Science International: Genetics</i> , 2009 , 3, 255-60	4.3	29
364	Genetic typing of dogstraces in biological samples. 2009 , 2, 283-285		2
363	The combination of single cell micromanipulation with LV-PCR system and its application in forensic science. 2009 , 2, 516-517		7
362	Interpretation of low-copy-number DNA profile after post-PCR purification. 2009 , 2, 542-543		4
361	Integration of the AmpFISTR Identifiler PCR Amplification Kit with SRY-specific primers for gender identification. 2009 , 2, 36-37		1

360	Low copy number typing Where next?. 2009 , 2, 553-555		4
359	Genomic identification in the historical case of the Nicholas II royal family. 2009 , 106, 5258-63		37
358	Mini-STRs. 2009 ,		
357	Whole Genome Amplification. 2009 ,		
356	Use of Knowledge-Based Systems in Forensic Science. 2009 ,		
355	Laser capture microdissection in forensic research: a review. <i>International Journal of Legal Medicine</i> , 2010 , 124, 513-21	3.1	57
354	Microchip electrophoresis of Alu elements for gender determination and inference of human ethnic origin. 2010 , 31, 981-90		9
353	Forensic trace DNA: a review. 2010 , 1, 14		186
352	A new approach to the investigation of sexual offenses-cytoskeleton analysis reveals the origin of cells found on forensic swabs. <i>Journal of Forensic Sciences</i> , 2010 , 55, 492-8	1.8	18
351	Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL. Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. <i>J Forensic Sci</i> 2009;54(4):810-21. <i>Journal of Forensic Sciences</i> , 2010 , 55, 265-8; author reply 269-72	1.8	9
350	Authors Response. <i>Journal of Forensic Sciences</i> , 2010 , 55, 269-272	1.8	7
349	Integrated DNA and fingerprint analyses in the identification of 60-year-old mummified human remains discovered in an Alaskan glacier. <i>Journal of Forensic Sciences</i> , 2010 , 55, 813-8	1.8	35
348	DNA typing for the identification of old skeletal remains from Korean War victims. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1422-9	1.8	20
347	Inclusion probabilities and dropout. <i>Journal of Forensic Sciences</i> , 2010 , 55, 1171-3	1.8	25
346	Science in court: DNA's identity crisis. 2010 , 464, 347-8		19
345	Forensic Challenges. 2010 , 315-339		4
344	Introduzione alla genetica forense. 2010 ,		1
343	Modification of a commercially available kit for the improvement of PCR efficiency. 2010 , 82, 343-51		

342	DNA Amplification (The Polymerase Chain Reaction). 2010 , 125-146		
341	Secondary DNA transfer of biological substances under varying test conditions. <i>Forensic Science International: Genetics</i> , 2010 , 4, 62-7	4-3	113
340	A universal strategy to interpret DNA profiles that does not require a definition of low-copy-number. <i>Forensic Science International: Genetics</i> , 2010 , 4, 221-7	4-3	59
339	Validation of a dual cycle ethylene oxide treatment technique to remove DNA from consumables used in forensic laboratories. <i>Forensic Science International: Genetics</i> , 2010 , 4, 239-43	4-3	18
338	Simple and highly effective DNA extraction methods from old skeletal remains using silica columns. <i>Forensic Science International: Genetics</i> , 2010 , 4, 275-80	4-3	63
337	Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFISTR SGM Plus multiplex. <i>Forensic Science International: Genetics</i> , 2010 , 4, 305-10	4-3	47
336	Tooth portion profile in criminology. 2011 , 3, e433-e434		
335	An automated approach for generating consensus profiles from low template STR typing results. 2011 , 3, e435-e436		2
334	Tackling poaching: Recovery of human DNA profiles from deer remains. 2011 , 3, e265-e266		
333	A comparison of AmpFISTR Identifiler Kit versus AmpFISTR Identifiler Plus Kit in challenging bone samples by using normal and increased PCR cycle number. 2011 , 3, e514-e515		2
332	Low Template DNA Analysis and Interpretation. 2011 ,		
331	Integrated DNA purification, PCR, sample cleanup, and capillary electrophoresis microchip for forensic human identification. 2011 , 11, 1041-8		141
330	Probabilistic expert systems for handling artifacts in complex DNA mixtures. <i>Forensic Science International: Genetics</i> , 2011 , 5, 202-9	4-3	39
329	Estimating drop-out probabilities in forensic DNA samples: a simulation approach to evaluate different models. <i>Forensic Science International: Genetics</i> , 2011 , 5, 525-31	4-3	29
328	Generating STR profile from "Touch DNA". 2011 , 18, 295-8		22
327	Powerplex ES versus Powerplex S5--casework testing of the new screening kit. <i>Forensic Science International: Genetics</i> , 2011 , 5, 57-63	4-3	11
326	A comparison of mini-STRs versus standard STRs--results of a collaborative European (EDNAP) exercise. <i>Forensic Science International: Genetics</i> , 2011 , 5, 257-8	4-3	11
325	Further Comment on "Low copy number typing has yet to achieve general acceptance" by Budowle, B., et al, 2009. <i>Forensic Sci. Int. Genetics: Supplement Series 2</i> , 551-552. <i>Forensic Science International: Genetics</i> , 2011 , 5, 7-11	4-3	7

324	Comment on "A universal strategy to interpret DNA profiles that does not require a definition of low copy number" by Peter Gill and John Buckleton, 2010, <i>Forensic Sci. Int. Genetics</i> 4, 221-227. <i>Forensic Science International: Genetics</i> , 2011 , 5, 15	4-3	4
323	Increased amplification success from forensic samples with locked nucleic acids. <i>Forensic Science International: Genetics</i> , 2011 , 5, 276-80	4-3	5
322	The use of fluorescence in situ hybridisation and laser microdissection to identify and isolate male cells in an azoospermic sexual assault case. <i>Forensic Science International: Genetics</i> , 2011 , 5, 69-73	4-3	12
321	Evaluation of nucleosome forming potentials (NFPs) of forensically important STRs. <i>Forensic Science International: Genetics</i> , 2011 , 5, 285-90	4-3	6
320	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, 316-28	4-3	84
319	Analysis and interpretation of mixed profiles generated by 34 cycle SGM Plus(®) amplification. <i>Forensic Science International: Genetics</i> , 2011 , 5, 376-80	4-3	4
318	Determination of the variables affecting mixed MiniFiler® DNA profiles. <i>Forensic Science International: Genetics</i> , 2011 , 5, 381-5	4-3	27
317	An investigation of the robustness of the consensus method of interpreting low-template DNA profiles. <i>Forensic Science International: Genetics</i> , 2011 , 5, 400-6	4-3	31
316	Reply to Comments by Buckleton and Gill on "Low copy number typing has yet to achieve general acceptance" by Budowle, B., et al., 2009. <i>Forensic Sci. Int.: Genet. Suppl. Series 2</i> , 551-52. <i>Forensic Science International: Genetics</i> , 2011 , 5, 12-14	4-3	5
315	Practical determination of the low template DNA threshold. <i>Forensic Science International: Genetics</i> , 2011 , 5, 422-7	4-3	14
314	Developmental validation of the PowerPlex(®) ESI 16 and PowerPlex(®) ESI 17 Systems: STR multiplexes for the new European standard. <i>Forensic Science International: Genetics</i> , 2011 , 5, 436-48	4-3	44
313	Selection of highly specific and sensitive mRNA biomarkers for the identification of blood. <i>Forensic Science International: Genetics</i> , 2011 , 5, 449-58	4-3	66
312	Integrated sample cleanup and capillary array electrophoresis microchip for forensic short tandem repeat analysis. <i>Forensic Science International: Genetics</i> , 2011 , 5, 484-92	4-3	22
311	Publications and letters related to the forensic genetic analysis of low amounts of DNA. <i>Forensic Science International: Genetics</i> , 2011 , 5, 1-2	4-3	6
310	Should efforts to minimise DNA contamination of forensic swabs be standardised across Australia?. 2011 , 195, 416-9		2
309	Avoiding Errors and Pitfalls in Evidence Sampling for Forensic Genetics. 2011 ,		
308	DNA profiling of spermatozoa by laser capture microdissection and low volume-PCR. 2011 , 6, e22316		18
307	An STR melt curve genotyping assay for forensic analysis employing an intercalating dye probe FRET. <i>Journal of Forensic Sciences</i> , 2011 , 56, 36-45	1.8	4

306	New optimized DNA extraction protocol for fingerprints deposited on a special self-adhesive security seal and other latent samples used for human identification. <i>Journal of Forensic Sciences</i> , 2011 , 56, 1235-40	1.8	10
305	Improving human forensics through advances in genetics, genomics and molecular biology. 2011 , 12, 179-92		305
304	Recovery of human DNA profiles from poached deer remains: a feasibility study. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2011 , 51, 190-5	2	7
303	A genetic investigation of Korean mummies from the Joseon Dynasty. 2011 , 38, 115-21		8
302	Magnitude-dependent variation in peak height balance at heterozygous STR loci. <i>International Journal of Legal Medicine</i> , 2011 , 125, 87-94	3.1	19
301	Hot flakes in cold cases. <i>International Journal of Legal Medicine</i> , 2011 , 125, 543-8	3.1	19
300	The evidentiary values of "cold hits" in a DNA database search on two-person mixture. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2011 , 51, 10-5	2	6
299	STRs, mini STRs and SNPs--a comparative study for typing degraded DNA. <i>Legal Medicine</i> , 2011 , 13, 68-74.9		30
298	LCN DNA Analysis and Opinion on Transfer: R v Reed and Reed. 2011 , 15, 161-169		7
297	New cell separation technique for the isolation and analysis of cells from biological mixtures in forensic caseworks. 2011 , 52, 293-8		11
296	Estimating the number of contributors to two-, three-, and four-person mixtures containing DNA in high template and low template amounts. 2011 , 52, 314-26		35
295	Nuclear DNA typing from ancient teeth. 2012 , 33, 211-4		15
294	Laser microdissection methodology in forensic casework. <i>Australian Journal of Forensic Sciences</i> , 2012 , 44, 135-144	1.1	5
293	Evaluating the performance of whole genome amplification for use in low template DNA typing. 2012 , 52, 223-8		6
292	Misleading DNA Evidence: Reasons for Miscarriages of Justice. 2012 , 10,		4
291	A stochastic model of the processes in PCR based amplification of STR DNA in forensic applications. <i>Forensic Science International: Genetics</i> , 2012 , 6, 17-25	4.3	34
290	PCR Amplification: Capabilities and Cautions. 2012 , 69-97		8
289	Typing short amplicon binary polymorphisms: supplementary SNP and Indel genetic information in the analysis of highly degraded skeletal remains. <i>Forensic Science International: Genetics</i> , 2012 , 6, 469-76 ^{4.3}		52

288	DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods. <i>Forensic Science International: Genetics</i> , 2012 , 6, 679-88	4-3	139
287	Assessment of mock cases involving complex low template DNA mixtures: A descriptive study. <i>Forensic Science International: Genetics</i> , 2012 , 6, 697-707	4-3	23
286	Comparison of different interpretation strategies for low template DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 716-22	4-3	25
285	Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in. <i>Forensic Science International: Genetics</i> , 2012 , 6, 749-61	4-3	44
284	Extended PCR conditions to reduce drop-out frequencies in low template STR typing including unequal mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 102-7	4-3	18
283	Developmental validation of the PowerPlex [®] ESX 16 and PowerPlex [®] ESX 17 Systems. <i>Forensic Science International: Genetics</i> , 2012 , 6, 124-31	4-3	47
282	The interpretation of low level DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 191-7	4-3	22
281	Evaluation of three DNA extraction protocols for forensic STR typing after laser capture microdissection. <i>Forensic Science International: Genetics</i> , 2012 , 6, 258-62	4-3	22
280	Composite profiles in DNA analysis. <i>Forensic Science International: Genetics</i> , 2012 , 6, 317-21	4-3	24
279	Pentaplex typing of new European Standard Set (ESS) STR loci in Indian population. <i>Forensic Science International: Genetics</i> , 2012 , 6, e86-9	4-3	2
278	Automatable full demineralization DNA extraction procedure from degraded skeletal remains. <i>Forensic Science International: Genetics</i> , 2012 , 6, 398-406	4-3	79
277	An optimized protocol for forensic application of the PreCR [®] Repair Mix to multiplex STR amplification of UV-damaged DNA. <i>Forensic Science International: Genetics</i> , 2012 , 6, 498-503	4-3	34
276	Characterization of a modified amplification approach for improved STR recovery from severely degraded skeletal elements. <i>Forensic Science International: Genetics</i> , 2012 , 6, 578-87	4-3	16
275	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
274	Modelling heterozygote balance in forensic DNA profiles. <i>Forensic Science International: Genetics</i> , 2012 , 6, 729-34	4-3	30
273	Exploratory data analysis for the interpretation of low template DNA mixtures. <i>Forensic Science International: Genetics</i> , 2012 , 6, 762-74	4-3	80
272	Comparison of STR profiling from low template DNA extracts with and without the consensus profiling method. 2012 , 3, 14		16
271	An overview of DNA typing methods for human identification: past, present, and future. <i>Methods in Molecular Biology</i> , 2012 , 830, 3-16	1.4	27

270	Interpretation guidelines for multilocus STR forensic profiles from low template DNA samples. <i>Methods in Molecular Biology</i> , 2012 , 830, 199-211	1.4	3
269	Low-Level DNA Testing: Issues, Concerns, and Solutions. 2012 , 311-346		3
268	Exploring the feasibility of bioaerosol analysis as a novel fingerprinting technique. 2012 , 403, 15-26		22
267	Forensic validation of the PowerPlex [®] ESI 16 STR Multiplex and comparison of performance with AmpFISTR [®] SGM Plus [®] . <i>International Journal of Legal Medicine</i> , 2012 , 126, 345-56	3.1	10
266	A validation study of the Qiagen Investigator DIPplex [®] kit; an INDEL-based assay for human identification. <i>International Journal of Legal Medicine</i> , 2012 , 126, 533-40	3.1	74
265	Low-Template DNA Testing. 2013 , 252-256		
264	Low Copy Number Stochastic Results. 2013 , 159-167		
263	Reliable support: Measuring calibration of likelihood ratios. <i>Forensic Science International</i> , 2013 , 230, 156-69	2.6	68
262	Evaluating DNA profiles using peak heights, allowing for dropin, dropout and stutters. 2013 , 4, e380-e381		1
261	Application of direct PCR in forensic casework. 2013 , 4, e47-e48		24
260	Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. <i>Forensic Science International: Genetics</i> , 2013 , 7, 555-63	4.3	63
259	Forensic genetic SNP typing of low-template DNA and highly degraded DNA from crime case samples. <i>Forensic Science International: Genetics</i> , 2013 , 7, 345-52	4.3	41
258	Mass spectrometry-based proteomics as a tool to identify biological matrices in forensic science. <i>International Journal of Legal Medicine</i> , 2013 , 127, 287-98	3.1	70
257	Y-SNP miniplexes for East Asian Y-chromosomal haplogroup determination in degraded DNA. <i>Forensic Science International: Genetics</i> , 2013 , 7, 75-81	4.3	8
256	High-throughput analysis using AmpFISTR [®] Identifiler [®] with the Applied Biosystems 3500xl Genetic Analyser. <i>Forensic Science International: Genetics</i> , 2013 , 7, 92-7	4.3	22
255	Developmental validation of Mini-DogFiler for degraded canine DNA. <i>Forensic Science International: Genetics</i> , 2013 , 7, 151-8	4.3	19
254	Whole genome amplification of degraded and nondegraded DNA for forensic purposes. <i>International Journal of Legal Medicine</i> , 2013 , 127, 309-19	3.1	29
253	A quantitative assessment of a reliable screening technique for the STR analysis of telogen hair roots. <i>Forensic Science International: Genetics</i> , 2013 , 7, 180-8	4.3	23

252	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	3.1	29
251	Bitemarks in foodstuffs –An approach for genetic identification of the bitter. 2013 , 4, e340-e341		3
250	Comparative study on the effects of reduced PCR reaction volumes and increased cycle number, on the sensitivity and the stochastic threshold of the AmpFLSTR Identifier® Plus kit. 2013 , 4, e306-e307		9
249	Mixture interpretation: Experimental and simulated reevaluation of qualitative analysis. <i>Legal Medicine</i> , 2013 , 15, 66-71	1.9	8
248	DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2013 , 53, 103-14	2	28
247	The forensic aspects of sexual violence. 2013 , 27, 77-90		19
246	The interpretation of single source and mixed DNA profiles. <i>Forensic Science International: Genetics</i> , 2013 , 7, 516-28	4.3	187
245	Calculating the weight of evidence in low-template forensic DNA casework. <i>Journal of Forensic Sciences</i> , 2013 , 58 Suppl 1, S243-9	1.8	26
244	Response to Grisedale and Van Daal: comparison of STR profiling from low template DNA extracts with and without the consensus profiling method. 2013 , 4, 1		22
243	Comment on Kokshoorn, B, and Blankers, BJ 'Response to Grisedale, KS and van Daal, A: comparison of STR profiling from low template DNA extracts with and without the consensus profiling method'. 2013 , 4, 2		2
242	Bona fide colour: DNA prediction of human eye and hair colour from ancient and contemporary skeletal remains. 2013 , 4, 3		46
241	A 21 marker insertion deletion polymorphism panel to study biogeographic ancestry. <i>Forensic Science International: Genetics</i> , 2013 , 7, 305-12	4.3	39
240	Automated extraction of DNA from biological stains on fabric from crime cases. A comparison of a manual and three automated methods. <i>Forensic Science International: Genetics</i> , 2013 , 7, 384-8	4.3	7
239	An improved qPCR protocol for rapid detection and quantification of <i>Clostridium difficile</i> in cattle feces. 2013 , 341, 115-21		12
238	A new methodological framework to interpret complex DNA profiles using likelihood ratios. <i>Forensic Science International: Genetics</i> , 2013 , 7, 251-63	4.3	98
237	Modified Practical Approach in Repeated DNA Studies of Biological Evidence of Sexual Assault. 2013 , 27, 4115-4122		1
236	Integrated microfluidic systems for genetic analysis. 2013 , 465-494e		0
235	Development of a multiplex system to assess DNA persistence in taphonomic studies. 2013 , 34, 3352-60		5

234	Identification of Organic Traces in Pre-Trial and Judicial Investigations, using DNA Fragment Analysis. 2013 , 27, 3821-3824		1
233	Evaluation of mixed-source, low-template DNA profiles in forensic science. 2013 , 110, 12241-6		66
232	Taphonomic Bone Staining and Color Changes in Forensic Contexts. 2013 , 330-355		7
231	Optimizing Storage and Handling of DNA Extracts. 2013 , 19-38		0
230	The National DNA Data Bank of Canada: a Quebecer perspective. 2013 , 4, 249		11
229	Preamplification procedure for the analysis of ancient DNA samples. 2013 , 2013, 734676		8
228	DNA: An Overview. 2014 , 1-19		
227	Diverse and widespread contamination evident in the unmapped depths of high throughput sequencing data. 2014 , 9, e110808		124
226	National DNA Databases, Strength of Evidence and Error Rates. 2014 , 81-129		1
225	Linear amplification of target prior to PCR for improved low template DNA results. 2014 , 56, 145-7		7
224	DNA profiles from fingerprints. 2014 , 57, 259-66		45
223	A new strategy for sperm isolation and STR typing from multi-donor sperm mixtures. <i>Forensic Science International: Genetics</i> , 2014 , 13, 239-46	4-3	10
222	Differentiation of mixed biological traces in sexual assaults using DNA fragment analysis. 2014 , 28, 301-305		1
221	A Y-short tandem repeat specific DNA enhancement strategy to aid the analysis of late reported (□ 6 days) sexual assault cases. 2014 , 54, 209-18		8
220	Statistical Evaluation of Forensic DNA Profile Evidence. 2014 , 1, 361-384		42
219	Y-chromosomal haplotyping of single sperm cells isolated from semen mixtures - a successful identification of three perpetrators in a multi-suspect sexual assault case. 2014 , 55, 537-41		6
218	Definitions. 2014 , 1-20		2
217	Current developments in forensic interpretation of mixed DNA samples (Review). 2014 , 2, 309-316		18

216	Interpreting forensic DNA profiling evidence without specifying the number of contributors. <i>Forensic Science International: Genetics</i> , 2014 , 13, 269-80	4-3	27
215	The molecular characterization of a depurinated trial DNA sample can be a model to understand the reliability of the results in forensic genetics. 2014 , 35, 3134-44		10
214	DNA analysis of fingernail clippings: an unusual case report. 2014 , 35, 96-9		2
213	Effect of dactyloscopic powders on DNA profiling from enhanced fingerprints: results from an experimental study. 2014 , 35, 68-72		14
212	Decision analysis for the genotype designation in low-template-DNA profiles. <i>Forensic Science International: Genetics</i> , 2014 , 9, 118-33	4-3	14
211	Analysis of allelic drop-out using the Identifiler(®) and PowerPlex(®) 16 forensic STR typing systems. <i>Forensic Science International: Genetics</i> , 2014 , 12, 1-11	4-3	17
210	Defining background DNA levels found on the skin of children aged 0-5 years. <i>International Journal of Legal Medicine</i> , 2014 , 128, 251-8	3-1	7
209	Forensic DNA Analysis. 2014 , 1141-1183		2
208	The successful recovery of low copy number and degraded DNA from bones exposed to seawater suitable for generating a DNA STR profile. <i>Journal of Forensic Sciences</i> , 2014 , 59, 470-3	1-8	14
207	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, 154-65	4-3	16
206	Population genetics of insertion-deletion polymorphisms in South Koreans using Investigator DIPplex kit. <i>Forensic Science International: Genetics</i> , 2014 , 8, 80-3	4-3	37
205	Qualitative and quantitative assessment of single fingerprints in forensic DNA analysis. 2014 , 35, 3165-72		8
204	STR-validator: an open source platform for validation and process control. <i>Forensic Science International: Genetics</i> , 2014 , 13, 154-66	4-3	13
203	Establishment of an ISO 17025:2005 accredited forensic genetics laboratory in Italy. 2014 , 19, 289-299		4
202	Modeling one complete versus triplicate analyses in low template DNA typing. <i>International Journal of Legal Medicine</i> , 2014 , 128, 259-67	3-1	3
201	A dropin peak height model. <i>Forensic Science International: Genetics</i> , 2014 , 11, 80-4	4-3	16
200	EuroforGen-NoE collaborative exercise on LRmix to demonstrate standardization of the interpretation of complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2014 , 9, 47-54	4-3	43
199	Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. <i>Forensic Science International: Genetics</i> , 2014 , 11, 144-53	4-3	46

198	A comparison of statistical models for the analysis of complex forensic DNA profiles. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 66-70	2	44
197	'Stochastic' effects at balanced mixtures: a calibration study. <i>Forensic Science International: Genetics</i> , 2014 , 8, 113-25	4.3	4
196	Stochastic sampling effects in STR typing: Implications for analysis and interpretation. <i>Forensic Science International: Genetics</i> , 2014 , 11, 195-204	4.3	21
195	Development of two highly sensitive forensic sex determination assays based on human DYZ1 and Alu repetitive DNA elements. 2014 , 35, 3028-35		9
194	Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles. 2015 , 16, 298		28
193	Mucosal cell isolation and analysis from cellular mixtures of three contributors. <i>Journal of Forensic Sciences</i> , 2015 , 60, 783-6	1.8	0
192	References. 2015 , 196-209		
191	Comparative study of STR loci for typing old skeletal remains with modified protocols of AmpFISTR Identifiler and AmpFISTR MiniFiler STR Kits. <i>Australian Journal of Forensic Sciences</i> , 2015 , 47, 200-223	1.1	4
190	Reduced reaction volumes and increased Taq DNA polymerase concentration improve STR profiling outcomes from a real-world low template DNA source: telogen hairs. <i>Forensic Science, Medicine, and Pathology</i> , 2015 , 11, 326-38	1.5	15
189	Analysis of forensic DNA mixtures with artefacts. 2015 , 64, 1-48		67
188	STR profiling of epithelial cells identified by X/Y-FISH labelling and laser microdissection using standard and elevated PCR conditions. <i>Forensic Science International: Genetics</i> , 2015 , 16, 1-7	4.3	9
187	Isolating cells from female/male blood mixtures using fluorescence in situ hybridization combined with low volume PCR and its application in forensic science. <i>International Journal of Legal Medicine</i> , 2015 , 129, 1211-5	3.1	4
186	Comparing different post-mortem human samples as DNA sources for downstream genotyping and identification. <i>Forensic Science International: Genetics</i> , 2015 , 19, 212-220	4.3	23
185	Evaluation of samples comprising minute amounts of DNA. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2015 , 55, 316-22	2	9
184	The future of forensic DNA analysis. 2015 , 370,		98
183	Molecular sex identification of juvenile skeletal remains from an Irish medieval population using ancient DNA analysis. 2015 , 62, 27-38		10
182	Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches-Twenty years of research and development. <i>Forensic Science International: Genetics</i> , 2015 , 18, 100-17	4.3	90
181	Restored teeth can be used as samples for genotyping?. 2015 , 5, e293-e294		

180	A novel set of DIP-STR markers for improved analysis of challenging DNA mixtures. <i>Forensic Science International: Genetics</i> , 2015 , 19, 156-164	4-3	31
179	Bone DNA typing using a new miniYSTR multiplex. 2015 , 5, e172-e174		1
178	Do low template DNA profiles have useful quantitative data?. <i>Forensic Science International: Genetics</i> , 2015 , 16, 13-16	4-3	20
177	Enhanced low-template DNA analysis conditions and investigation of allele dropout patterns. <i>Forensic Science International: Genetics</i> , 2015 , 14, 61-75	4-3	15
176	Low-Level DNA and Complex Mixtures. 2015 , 159-182		2
175	Coping with Potential Missing Alleles. 2015 , 333-348		
174	. 2016 ,		7
173	Low Template DNA Analysis and Interpretation. 2016 , 1-12		
172	Interpretation of Mixtures; Graphical. 2016 , 1-13		
171	Developmental validation of the Yfiler(®) Plus PCR Amplification Kit: An enhanced Y-STR multiplex for casework and database applications. <i>Forensic Science International: Genetics</i> , 2016 , 24, 164-175	4-3	77
170	Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. 2016 , 17, 125		44
169	Analyse von Hautkontaktspuren in der forensischen Genetik unter besonderer Berücksichtigung von Kontamination und Transferszenarien. 2016 , 26, 537-552		1
168	Low Template DNA. 2016 , 151-168		
167	DNA Analysis and Document Examination: The Impact of Each Technique on Respective Analyses. <i>Journal of Forensic Sciences</i> , 2016 , 61, 26-34	1.8	4
166	GHEP-ISFG collaborative simulated exercise for DVI/MPI: Lessons learned about large-scale profile database comparisons. <i>Forensic Science International: Genetics</i> , 2016 , 21, 45-53	4-3	13
165	Analysis and implications of the miscarriages of justice of Amanda Knox and Raffaele Sollecito. <i>Forensic Science International: Genetics</i> , 2016 , 23, 9-18	4-3	33
164	Assessing the Risk of Secondary Transfer Via Fingerprint Brush Contamination Using Enhanced Sensitivity DNA Analysis Methods. <i>Journal of Forensic Sciences</i> , 2016 , 61, 204-11	1.8	6
163	References. 2016 , 447-486		

162	Advances in DNA typing in the agro-food supply chain. 2016 , 52, 80-89		16
161	Shedding light on the relative DNA contribution of two persons handling the same object. <i>Forensic Science International: Genetics</i> , 2016 , 24, 148-157	4.3	33
160	Expected net gain data of low-template DNA analyses. 2016 , 8, 375-86		4
159	Encoding of low-quality DNA profiles as genotype probability matrices for improved profile comparisons, relatedness evaluation and database searches. <i>Forensic Science International: Genetics</i> , 2016 , 25, 227-239	4.3	4
158	A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles. <i>Forensic Science International: Genetics</i> , 2016 , 25, 85-96	4.3	54
157	Analysis of uni and bi-parental markers in mixture samples: Lessons from the 22nd GHEP-ISFG Intercomparison Exercise. <i>Forensic Science International: Genetics</i> , 2016 , 25, 63-72	4.3	6
156	Evaluation of low-template DNA profiles using peak heights. 2016 , 15, 431-445		21
155	Estimation and Preparation of the Hypervariable Regions I/II Templates for Mitochondrial DNA Typing From Human Bones and Teeth Remains Using Singleplex Quantitative Polymerase Chain Reaction. 2016 , 37, 158-64		
154	Purification of PCR Products to Improve STR Profiles. <i>Methods in Molecular Biology</i> , 2016 , 1420, 131-4	1.4	
153	The effect of mark enhancement techniques on the subsequent detection of saliva. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2016 , 56, 305-320	2	5
152	Low-template DNA: A single DNA analysis or two replicates?. <i>Forensic Science International</i> , 2016 , 264, 139-45	2.6	13
151	Forensic DNA Typing Protocols. <i>Methods in Molecular Biology</i> , 2016 ,	1.4	3
150	Rapid DNA analysis for automated processing and interpretation of low DNA content samples. 2016 , 7, 2		26
149	Could Secondary DNA Transfer Falsely Place Someone at the Scene of a Crime?. <i>Journal of Forensic Sciences</i> , 2016 , 61, 196-203	1.8	40
148	Modified DOP-PCR for improved STR typing of degraded DNA from human skeletal remains and bloodstains. <i>Legal Medicine</i> , 2016 , 18, 7-12	1.9	16
147	Revealing the challenges of low template DNA analysis with the prototype Ion AmpliSeq Identity panel v2.3 on the PGM Sequencer. <i>Forensic Science International: Genetics</i> , 2016 , 22, 25-36	4.3	31
146	Expansion of Microbial Forensics. 2016 , 54, 1964-74		49
145	Stabbing simulations and DNA transfer. <i>Forensic Science International: Genetics</i> , 2016 , 22, 73-80	4.3	32

144	Validating multiplexes for use in conjunction with modern interpretation strategies. <i>Forensic Science International: Genetics</i> , 2016 , 20, 6-19	4-3	39
143	Estimating allele dropout probabilities by logistic regression: Assessments using Applied Biosystems 3500xL and 3130xl Genetic Analyzers with various commercially available human identification kits. <i>Legal Medicine</i> , 2016 , 19, 77-82	1-9	2
142	Developmental validation and evaluation of a miniSTR pentaplex in forensic genetics. <i>Forensic Science International: Genetics</i> , 2016 , 20, e4-e9	4-3	1
141	Improving reliability in environmental DNA detection surveys through enhanced quality control. 2017 , 68, 388		25
140	DNA profiling: A metrological and signal processing perspective. 2017 , 20, 4-7		2
139	ADN, une perpétuelle avancée. 2017 , 2017, 67-76		1
138	Sensitive DIP-STR markers for the analysis of unbalanced mixtures from "touch" DNA samples. <i>Forensic Science International: Genetics</i> , 2017 , 28, 111-117	4-3	23
137	Characterisation of artefacts and drop-in events using STR-validator and single-cell analysis. <i>Forensic Science International: Genetics</i> , 2017 , 30, 57-65	4-3	11
136	An evaluation of the International Society for Animal Genetics recommended parentage and identification panel for the domestic pigeon (<i>Columba livia domestica</i>). 2017 , 48, 431-435		2
135	A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis. <i>Forensic Science International: Genetics</i> , 2017 , 31, 149-154	4-3	9
134	A preliminary evaluation study of new generation multiplex STR kits comprising of the CODIS core loci and the European Standard Set loci. 2017 , 52, 16-23		8
133	Genetic Fingerprinting Using Microsatellite Markers in a Multiplex PCR Reaction: A Compilation of Methodological Approaches from Primer Design to Detection Systems. <i>Methods in Molecular Biology</i> , 2017 , 1492, 1-15	1-4	2
132	- History of forensic DNA profiling in criminal investigations. 2017 , 20-31		
131	- Strengths and limitations of DNA profiling evidence. 2017 , 32-51		
130	Prediction of autosomal STR typing success in ancient and Second World War bone samples. <i>Forensic Science International: Genetics</i> , 2017 , 27, 17-26	4-3	19
129	<i>Staphylococcus aureus</i> Sequences from Osteomyelitic Specimens of a Pathological Bone Collection from Pre-Antibiotic Times. 2017 , 9, 43		3
128	Duplex Alu Screening for Degraded DNA of Skeletal Human Remains. 2017 , 9, 48		
127	Modified allele-specific PCR improves HER2 Ile655Val detection by reducing genotyping errors. 2017 , 37,		1

126	Likelihood ratio development for mixed Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018 , 35, 82-96	4.3	13
125	Male DNA under female fingernails after scratching: transfer and persistence evaluation by RT-PCR analysis and Y-STR typing. <i>International Journal of Legal Medicine</i> , 2018 , 132, 1603-1609	3.1	5
124	Forensic SNP Genotyping with SNaPshot: Development of a Novel In-house SBE Multiplex SNP Assay. <i>Journal of Forensic Sciences</i> , 2018 , 63, 1824-1829	1.8	5
123	Evaluation Of A Powder-Free DNA Extraction Method For Skeletal Remains. <i>Journal of Forensic Sciences</i> , 2018 , 63, 1819-1823	1.8	7
122	Forensic genetic analysis of bone remain samples. <i>Forensic Science International</i> , 2018 , 284, 167-175	2.6	15
121	A preliminary assessment of the effect of PreCRIDNA repair treatment on mixture ratios in two person mixtures. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2018 , 58, 308-314	2	1
120	Enhanced DNA mixture deconvolution of sexual offense samples using the DEPArray system. <i>Forensic Science International: Genetics</i> , 2018 , 34, 265-276	4.3	21
119	Rapidly mutating Y-STR analyses of compromised forensic samples. <i>International Journal of Legal Medicine</i> , 2018 , 132, 397-403	3.1	8
118	Determining the optimal forensic DNA analysis procedure following investigation of sample quality. <i>International Journal of Legal Medicine</i> , 2018 , 132, 955-966	3.1	3
117	Efficient construction of match strength distributions for uncertain multi-locus genotypes. 2018 , 4, e00824		2
116	NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis. <i>Forensic Science International: Genetics</i> , 2018 , 37, 172-179	4.3	27
115	Modelling allelic drop-outs in STR sequencing data generated by MPS. <i>Forensic Science International: Genetics</i> , 2018 , 37, 6-12	4.3	3
114	Evaluation of the Microhaplotypes panel for DNA mixture analyses. <i>Forensic Science International: Genetics</i> , 2018 , 35, 149-155	4.3	37
113	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions: Part I: evaluation of DNA profiling comparisons given (sub-) source propositions. <i>Forensic Science International: Genetics</i> , 2018 , 36, 189-202	4.3	56
112	Evaluation of the performance of Illumina's ForenSeq system on serially degraded samples. 2018 , 39, 2674-2684		11
111	From unknown to known: Identification of the remains at the mausoleum of fosse Ardeatine. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2018 , 58, 469-478	2	8
110	Evaluation of forensic genetics findings given activity level propositions: A review. <i>Forensic Science International: Genetics</i> , 2018 , 36, 34-49	4.3	55
109	Low-template methods yield limited extra information for PowerPlex Fusion 6C profiling. <i>Legal Medicine</i> , 2018 , 33, 62-65	1.9	3

108	The effects of extra PCR cycles when amplifying skeletal samples with the GlobalFiler PCR Amplification Kit. <i>International Journal of Legal Medicine</i> , 2019 , 133, 745-750	3.1	2
107	The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. <i>Journal of Forensic Sciences</i> , 2019 , 64, 393-405	1.8	23
106	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	4.3	18
105	Forensic molecular biomarkers for mixture analysis. <i>Forensic Science International: Genetics</i> , 2019 , 41, 107-119	4.3	32
104	CaseSolver: An investigative open source expert system based on EuroForMix. <i>Forensic Science International: Genetics</i> , 2019 , 41, 83-92	4.3	11
103	A cold case turns hot after 30 years. <i>Australian Journal of Forensic Sciences</i> , 2019 , 51, S60-S67	1.1	1
102	STRmix put to the test: 300 000 non-contributor profiles compared to four-contributor DNA mixtures and the impact of replicates. <i>Forensic Science International: Genetics</i> , 2019 , 41, 24-31	4.3	11
101	A review of direct polymerase chain reaction of DNA and RNA for forensic purposes. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2019 , e1335	2.6	6
100	Optimization of the collection and analysis of touch DNA traces. 2019 , 7, 98-99		6
99	Evaluating the amplification efficiency of the MALBAC [®] single-cell DNA Kit for trace DNA. 2019 , 7, 351-352		1
98	Efficiency of Casework Direct Kit for extraction of touch DNA samples obtained from cars steering wheels. 2019 , 7, 16-18		0
97	Forensic Spermatozoa Detection. 2019 , 40, 304-311		6
96	Successful analysis of a 100 years old semen stain generating a complete DNA STR profile. 2019 , 61, 78-81		3
95	Probabilistic genotyping software: An overview. <i>Forensic Science International: Genetics</i> , 2019 , 38, 219-224	4.3	70
94	DNA recovery and analysis from skeletal material in modern forensic contexts. <i>Forensic Sciences Research</i> , 2019 , 4, 51-59	3.6	45
93	The evolution of the field of legal medicine: A holistic investigation of global outputs with bibliometric analysis. 2020 , 69, 101885		16
92	Identifying victims of the largest Second World War family massacre in Slovenia. <i>Forensic Science International</i> , 2020 , 306, 110056	2.6	12
91	An examination of aspects of the probabilistic genotyping tool: Forensic Statistical Tool. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2020 , 2,	2.6	

90	Human Leukocyte Antigen alleles as an aid to STR in complex forensic DNA samples. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2020 , 60, 1-8	2	2
89	DNA Mixtures in Forensic Investigations: The Statistical State of the Art. 2020 , 7, 111-142		4
88	Next generation sequencing of STR artifacts produced from historical bone samples. <i>Forensic Science International: Genetics</i> , 2020 , 49, 102397	4.3	0
87	Validation. 2020 , 277-308		1
86	Effectiveness of whole genome amplification prior to short tandem repeat analysis for degraded DNA. <i>Forensic Science International: Genetics</i> , 2020 , 49, 102373	4.3	2
85	Identification of burglars using foil impressing based on tool marks and DNA evidence. <i>Forensic Science International</i> , 2020 , 316, 110524	2.6	1
84	Analysis of Low Copy Number DNA and Degraded DNA. 2020 , 1-20		
83	Allele drop-out and the stochastic threshold. 2020 , 89-110		
82	Low-template DNA. 2020 , 111-128		
81	Empirical characterization of DNA profiles. 2020 , 55-88		1
80	A Forensic Genomics Approach for the Identification of Sister Marija Crucifiksa Kozulić. <i>Genes</i> , 2020 , 11,	4.2	1
79	Generating DNA profile from low copy number DNA: Strategies and associated risks. <i>Acta Scientiarum - Biological Sciences</i> , 2020 , 42, e52239	0.3	
78	A comprehensive study of allele drop-in over an extended period of time. <i>Forensic Science International: Genetics</i> , 2020 , 48, 102332	4.3	0
77	Development of a massively parallel, genotyping-by-sequencing assay in American badger (<i>Taxidea taxus</i>) highlights the need for careful validation when working with low template DNA. <i>Conservation Genetics Resources</i> , 2020 , 12, 601-610	0.8	3
76	Direct PCR: A review of use and limitations. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2020 , 60, 303-310	2	5
75	Recovery of single source DNA profiles from mixtures by direct single cell subsampling and simplified micromanipulation. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2021 , 61, 13-25 ²		4
74	Exploring new short tandem repeat markers for DNA mixture deconvolution. <i>Wiley Interdisciplinary Reviews Forensic Science</i> , 2021 , 3,	2.6	1
73	A novel approach for visualization and localization of small amounts of DNA on swabs to improve DNA collection and recovery process. <i>Analyst, The</i> , 2021 , 146, 1198-1206	5	2

72	Integrated microfluidic systems for genetic analysis. 2021 , 511-549		0
71	Usefulness of Quantitative PCR in Forensic Genetics. 2021 , 1-26		
70	Challenges in the DNA Analysis of Compromised Samples. 2021 , 1-20		
69	Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation. <i>Australian Journal of Forensic Sciences</i> , 1-12	1.1	
68	DMSO Improves the Ski-Slope Effect in Direct PCR. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 1943	2.6	1
67	Revisiting single cell analysis in forensic science. <i>Scientific Reports</i> , 2021 , 11, 7054	4.9	2
66	Efficacy of reduced-size short tandem repeat PCR analysis for degraded DNA samples. <i>Genes and Genomics</i> , 2021 , 43, 749-758	2.1	
65	Novel extraction chemistry and alternative amplification strategies for use with rootless hair shafts. <i>Journal of Forensic Sciences</i> , 2021 , 66, 1929-1936	1.8	2
64	An inter-laboratory study of DNA-based identity, parentage and species testing in animal forensic genetics. <i>Forensic Sciences Research</i> , 1-14	3.6	0
63	Evaluation of the AGCU Expressmarker 30 Kit composed of 31 loci for forensic application. <i>Forensic Science International</i> , 2021 , 324, 110849	2.6	1
62	Can a reference 'match' an evidence profile if these have no loci in common?. <i>Forensic Science International: Genetics</i> , 2021 , 53, 102520	4.3	0
61	Evaluating the effects of whole genome amplification strategies for amplifying trace DNA using capillary electrophoresis and massive parallel sequencing. <i>Forensic Science International: Genetics</i> , 2022 , 56, 102599	4.3	0
60	A Review of Probabilistic Genotyping Systems: , and. <i>Genes</i> , 2021 , 12,	4.2	4
59	References. 2021 , 177-185		
58	Encyclopedia of Biometrics. 2009 , 573-579		2
57	Forensic Strategies Used for DNA Extraction of Ancient and Degraded Museum Sturgeon Specimens. 2009 , 85-96		1
56	Capillary electrophoresis of miniSTR markers to genotype highly degraded DNA samples. <i>Methods in Molecular Biology</i> , 2012 , 830, 31-42	1.4	4
55	Skeletal Remains Presumed Submerged in Water for Three Years Identified Using PCR-STR Analysis. <i>Journal of Forensic Sciences</i> , 2002 , 47, 15490J	1.8	20

54	Reduced Volume PCR Amplification Reactions Using the AmpFISTR® Profiler Plus Kit. <i>Journal of Forensic Sciences</i> , 2002 , 47, 15554J	1.8	38
53	Fingerprints as Evidence for a Genetic Profile: Morphological Study on Fingerprints and Analysis of Exogenous and Individual Factors Affecting DNA Typing. <i>Journal of Forensic Sciences</i> , 2003 , 48, 2002260	1.8	79
52	Infanticide in brown bear: a case-study in the Italian Alps [Genetic identification of perpetrator and implications in small populations. <i>Nature Conservation</i> , 25, 55-75		30
51	Evaluation of 17 microsatellite markers for parentage testing and individual identification of domestic yak (<i></i>). <i>PeerJ</i> , 2018 , 6, e5946	3.1	6
50	A mixed DNA profile controversy revisited. <i>Journal of Forensic Sciences</i> , 2021 ,	1.8	1
49	A proof-of-principle study on implementing polymerase chain displacement reaction (PCDR) to improve forensic low-template DNA analysis. <i>Forensic Science International: Genetics</i> , 2022 , 56, 102609	4.3	1
48	Development and validation of Kongoh ver. 3.0.1: Open-source software for DNA mixture interpretation in the GlobalFiler system based on a quantitative continuous model. <i>Legal Medicine</i> , 2021 , 54, 101972	1.9	0
47	Source Level Attribution: DNA Profiling from the ABACard® HemaTrace® Kit. <i>Forensic Sciences</i> , 2021 , 1, 116-129		1
46	DNA profiling of single sperm cells after whole genome amplification. <i>Forensic Science International: Reports</i> , 2021 , 4, 100240	1.9	0
45	References. 2004 ,		
44	An Information Gap in DNA Evidence Interpretation. <i>SSRN Electronic Journal</i> ,		1
43	Forensic Medicine. 2010 , 425-434		
42	Analisi dei risultati. 2010 , 97-118		
41	Biological Evidence and Forensic DNA Profiling. 2010 , 591-672		
40	Research on the detection of LCN DNA from traces on firearms. <i>Analytical Science and Technology</i> , 2011 , 24, 51-59		
39	Encyclopedia of Criminology and Criminal Justice. 2014 , 1114-1128		1
38	Bibliography. 2014 , 167-171		
37	DNA Methods to Identify Missing Persons. 2016 , 337-352		

36	Pengaruh Lama Paparan Pengikat Cincin Elastomer Ortodonti Terhadap Kualitas DNA. <i>Jurnal Biosains Pascasarjana</i> , 2017 , 19, 1	0.2	
35	Utilizing Short Tandem Repeats (STRs) as a Resolving Matrix in Parental Dispute DNA Analysis. <i>American Journal of Molecular Biology</i> , 2018 , 08, 156-165	0.2	
34	Formal description of the probabilistic models. 2020 , 459-476		
33	The Effectiveness of Mini Primer STR CODIS in DNA Degradation as the Effect of High-Temperature Exposure. <i>Analytical Cellular Pathology</i> , 2020 , 2020, 2417693	3-4	
32	Bibliography. 2020 , 477-495		
31	Usefulness of Mini-STRs in Analyzing Degraded DNA Samples and Their Forensic Relevance. 2020 , 205-222		
30	Casework direct kit as an alternative extraction method to enhance touch DNA samples analysis. <i>Forensic Science International: Genetics</i> , 2020 , 47, 102307	4-3	3
29	Forensic applications of micropalaeontology. 245-260		
28	DNA-Analysen in der forensischen Fallarbeit. 2007 , 279-323		1
27	The tooth for molecular analysis and identification : a forensic approach. <i>Journal of Forensic Odonto-Stomatology</i> , 2012 , 30, 22-8	0.4	3
26	Establishing an integrated pipeline for automatic and efficient detection of trace DNA encountered in forensic applications.. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2022 , 62, 50-59	2	
25	Secondary DNA transfer on denim using a human blood analogue.		
24	Analysis of Low Copy Number DNA and Degraded DNA. 2021 , 351-370		
23	Forensic DNA: From New Approaches for the Bio-stain Identification to the Evaluation of the Genetics Evidence in Courtroom. 2021 , 1-33		
22	Short tandem repeat (STR) instability in the oral mucosa of patients submitted to fixed orthodontic therapy: a limitation of STR profile quality for human identification.. <i>Forensic Science, Medicine, and Pathology</i> , 2022 , 18, 57	1.5	0
21	Total allele count distribution (TAC curves) improves number of contributor estimation for complex DNA mixtures. <i>Journal of the Canadian Society of Forensic Science</i> , 1-15	0.5	0
20	GITAD 2020: quality assurance test through 20 years of experience.. <i>International Journal of Legal Medicine</i> , 2022 , 136, 659	3.1	
19	Assessment of Multiple Annealing and Looping-Based Amplification Cycle-Based Whole-Genome Amplification for Short Tandem Repeat Genotyping of Low Copy Number-DNA.. <i>Genetic Testing and Molecular Biomarkers</i> , 2022 ,	1.6	0

18	Usefulness of Quantitative PCR in Forensic Genetics. 2022 , 773-797	
17	Forensic DNA: From New Approaches for the Bio-stain Identification to the Evaluation of the Genetics Evidence in Courtroom. 2022 , 85-117	
16	Challenges in the DNA Analysis of Compromised Samples. 2022 , 1067-1086	
15	How Long Does It Take a Static Speaking Individual to Contaminate the Immediate Environment?. <i>Forensic Science, Medicine, and Pathology</i> , 2006 , 2, 157-164	1.5
14	A new implementation of a semi-continuous method for DNA mixture interpretation. <i>Forensic Science International: Reports</i> , 2022 , 6, 100281	1.9
13	The number of alleles in DNA mixtures with related contributors. <i>Forensic Science International: Genetics</i> , 2022 , 102748	4.3
12	Investigation of Linear Amplification Using Abasic Site-Containing Primers Coupled to Routine STR Typing for LT-DNA Analysis. 2022 , 13, 1386	
11	Internal Validation of MaSTR-Probabilistic Genotyping Software for the Interpretation of 25 Person Mixed DNA Profiles. 2022 , 13, 1429	○
10	Forensic DNA Profiling. 2022 , 151-202	○
9	Characterizing the amplification of STR markers in multiplex polymerase chain displacement reaction using massively parallel sequencing. 2023 , 62, 102802	○
8	Mixture Interpretation (Interpretation of Mixed DNA Profiles With STRs). 2023 , 602-612	○
7	Using unique molecular identifiers to improve allele calling in low-template mixtures. 2023 , 63, 102807	○
6	Prevalence, Antimicrobial Resistance and Toxin-Encoding Genes of <i>Clostridioides difficile</i> from Environmental Sources Contaminated by Feces. 2023 , 12, 162	○
5	Autosomal short tandem repeat (STR) profiling of human skeletal remains. 2023 , 167-197	○
4	Challenges in forensic genetic investigations of decomposed or skeletonized human remains: Environmental exposure, DNA degradation, inhibitors, and low copy number (LCN). 2023 , 15-36	○
3	Skeletal microstructure, bone diagenesis, optimal sample selection, and pre-processing preparation techniques for DNA testing. 2023 , 81-117	○
2	Identification and characterization of novel DIP-STRs from whole-genome sequencing data. 2023 , 64, 102849	○
1	Characterizing the Amplification of STR Markers in Multiplex Polymerase Chain Displacement Reaction Using Massively Parallel Sequencing.	○

