Informative Textbooks on Forensic DNA (16)

The following informative textbooks are listed by publication date in ascending order with the most recent ones listed last.This list is not comprehensive (e.g., earlier editions of some of these textbooks not included).

1. National Research Council (1996) *The Evaluation of Forensic DNA Evidence*. National Academy Press:Washington, D.C.

2. Evett, I.W. and Weir, B.S. (1998) *Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists.* SinauerAssociates: Sunderland MA.

3. Inman, K. and Rudin, N. (2001) *Principles and Practice of Criminalistics: The Profession of Forensic Science*. CRCPress: Boca Raton.

4. Fung, W.K. and Hu, Y.-Q. (2008) *Statistical DNA Forensics: Theory, Methods and Computation*. Wiley:Chichester, UK.

5. Butler, J.M. (2010) *Fundamentals of Forensic DNA Typing*. Elsevier Academic Press: San Diego.

6. Goodwin, W., Linacre, A., Hadi, S. (2011) *An Introduction to Forensic Genetics Second Edition*. Wiley: Chichester,UK.

7. Butler, J.M. (2012) *Advanced Topics in Forensic DNA Typing: Methodology*. Elsevier Academic Press: San Diego.

8. Gill, P. (2014) *Misleading DNA Evidence: Reasons for Miscarriages of Justice*. Elsevier Academic Press: SanDiego.

9. Butler, J.M. (2015) *Advanced Topics in Forensic DNA Typing: Interpretation*. Elsevier Academic Press: San Diego.

10. Balding, D. J. and Steele, C. D. (2015). *Weight-of-evidence for Forensic DNA Profiles Second Edition*. Wiley:Chichester, UK.

11. Buckleton, J.S., Bright, J.-A., Taylor, D. (Editors) (2016) *Forensic DNA Evidence Interpretation Second Edition.*CRC Press: Boca Raton.

12. Robertson, B., Vignaux, G.A., Berger, C.E.H. (2016) *Interpreting Evidence: Evaluating Forensic Science in theCourtroom Second Edition*. Wiley: Chichester, UK.

13. Jamieson, A. and Bader, S. (Editors) (2016) *A Guide to Forensic DNA Profiling*. Wiley: Chichester, UK.

14. Amorim, A. and Budowle, B. (Editors) (2017) *Handbook of Forensic Genetics: Biodiversity and Heredity in Civiland Criminal Investigation*. World Scientific Publishing: London.

15. Bright, J.-A. and Coble, M. (2020) *Forensic DNA Profiling: A Practical Guide to Assigning Likelihood Ratios*. CRCPress: Boca Raton.

16. Gill, P., Bleka, Ø., Hansson, O., Benschop, C., Haned, H. (2020) *Forensic Practitioner's Guide to the Interpretationof Complex DNA Profiles*. Elsevier Academic Press: San Diego.

Informative Forensic DNA Reviews and Research Studies (434)

Below 26 categories are defined covering topics of interest in forensic DNA analysis and interpretation (listed arbitrarily from A to Z). Neither the categories nor this reference list are intended to be exhaustive. Suggestions for additional, appropriate references and categories are welcome. A #1 article (in bold font) was subjectively selected in each category andthen followed by reference citations defined by date in ascending order with the most recent publications at the end of each category. This letter and number system (e.g., A1, B3, F7) provides a simple method to locate specific articles and enables opportunities for expansion as the literature grows. Although some articles could logically appear under multiple categories,no duplicate listings were used. Recommended references from the SWGDAM 2020 Training Guidelines have been included as well.

A. Plain Language Guides to Forensic DNA Analysis

1. Sense about Science (2017) *Making Sense of Forensic Genetics*. A 40-page plain language guide available at https://senseaboutscience.org/activities/making-sense-of-forensic-genetics/.

2. The Royal Society (2017) *Forensic DNA Analysis: A Primer for Courts*. A 60-page plain language guide availableat https://royalsociety.org/-/media/about-us/programmes/science-and-law/royal-society-forensic-dna-analysis- primer-for-courts.pdf.

3. Press, R. (2019) *DNA Mixtures: A Forensic Science Explainer*. Available at https://www.nist.gov/featured-stories/dna-mixtures-forensic-science-explainer. (see also *Forensic Science Review* 31: 87-91 available at http://forensicsciencereview.com/Abstract/31(2)-(R&C)%20Full%20text.pdf)

B. Serology and Body Fluid Identification

1. Gaensslen, R.E. (1983) *Sourcebook in Forensic Serology, Immunology, and Biochemistry*. U.S. Department ofJustice, National Institute of Justice: Washington, D.C.

2. Schweers BA, Old J, Boonlayangoor PW, Reich KA. (2008) Developmental validation of a novel lateral flow striptest for rapid identification of human blood (Rapid Stain Identification--Blood). *Forensic Science International: Genetics* 2(3): 243-247.

3. Desroches, A.N., Buckle, J.L., Fourney, R.M. (2009) Forensic biology evidence screening: past and present. *Canadian Society of Forensic Science Journal* 42(2): 101-120.

4. Old, J.B., Schweers, B.A., Boonlayangoor, P.W., Reich, K.A. (2009) Developmental validation of RSID-saliva: alateral flow immunochromatographic strip test for the forensic detection of saliva. *Journal of Forensic Sciences* 54(4): 866-873.

5. Harteveld, J., Lindenbergh, A. and Sijen, T. (2013) RNA cell typing and DNA profiling of mixed samples: can celltypes and donors be associated? *Science & Justice* 53: 261-269.

6. Cotton, R.W. and Fisher, M.B. (2015) Review: Properties of sperm and seminal fluid, informed by research onreproduction and contraception. *Forensic Science International: Genetics* 18: 66-77.

7. Harbison, S. and Fleming, R.I. (2016) Forensic body fluid identification: state of the art. *Research and Reports inForensic Medical Science* 6: 11-23.

8. Vidaki, A., Giangasparo, F., Syndercombe Court, D. (2016) Discovery of potential DNA methylation markers forforensic tissue identification using bisulphite pyrosequencing. *Electrophoresis* 37(21): 2767-2779.

9. Silva, D.S.B.S., Antunes, J., Balamurugan, K., Duncan, G., Alho, C.S., McCord, B. (2016) Developmental validation studies of epigenetic DNA methylation markers for the detection of blood, semen and saliva samples.*Forensic Science International: Genetics* 23: 55-63.

10. Legg, K.M. and Danielson, P.B. (2017) State of the Art in Forensic Serology. In Liz Fergus (Ed.), "Sexual Assault Victimization Across the Life Span Second Edition Volume 1: Investigation, Diagnosis, and the MultidisciplinaryTeam". (vol. 1, pp. 462). STM Learning Inc.

11. Wornes, D.J., Speers, S.J., Murakami, J.A. (2018) The evaluation and validation of Phadebas® paper as apresumptive screening tool for saliva on forensic exhibits. *Forensic Science International* 288: 81-88.

12. Dørum, G., Ingold, S., Hanson, E., Ballantyne, J., Snipen, L., Haas, C. (2018) Predicting the origin of stains fromnext generation sequencing mRNA data. *Forensic Science International: Genetics* 34: 37-48.

13. Ingold, S., Dørum, G., Hanson, E., Berti, A., Branicki, W., Brito, P., Elsmore, P., Gettings, K.B., Giangasparo, F.,Gross, T.E., Hansen, S., Hanssen, E.N., Kampmann, M.L., Kayser, M., Laurent, F.X., Morling, N., Mosquera- Miguel, A., Parson, W., Phillips, C., Porto, M.J., Pośpiech, E., Roeder, A.D., Schneider, P.M., Schulze, J.K., Steffen, C.R., Syndercombe-Court, D., Trautmann, M., van den Berge, M., van der Gaag, K.J., Vannier, J., Verdoliva, V., Vidaki, A., Xavier, C., Ballantyne, J., Haas, C. (2018) Body fluid identification using a targeted mRNA massively parallel sequencing approach - results of a EUROFORGEN/EDNAP collaborative exercise. *Forensic Science International: Genetics* 34: 105-115.

14. Albani, P.P. and Fleming, R. (2019) Developmental validation of an enhanced mRNA-based multiplex system forbody fluid and cell type identification. *Science & Justice* 59(3): 217-227.

15. Kulstein, G., Pably, P., Fürst, A., Wiegand, P., Hadrys, T. (2019) "The acid test"-validation of the ParaDNA® BodyFluid ID Test for routine forensic casework. *International Journal of Legal Medicine* 133(3): 751-757.

16. Foley, M.M., Brown, C.O., Westring, C.G., Danielson, P.B., McKiernan, H.E. (2020) Effects of organic acids and common household products on the occurrence of false positive test results using immunochromatographic assays.*Forensic Science International* 308:1-6.

17. Ingold, S., Dørum, G., Hanson, E., Ballard, D., Berti, A., Gettings, K.B., Giangasparo, F., Kampmann, M.L., Laurent, F.X., Morling, N., Parson, W., Steffen, C.R., Ulus, A., van den Berge, M., van der Gaag, K.J., Verdoliva,V., Xavier, C., Ballantyne, J., Haas, C. (2020) Body fluid identification and assignment to donors using a targetedmRNA massively parallel sequencing approach - results of a second EUROFORGEN/EDNAP collaborative exercise. *Forensic Science International: Genetics* 45: 102208.

C. Collection and Storage of Biological Material

1. Mapes, A.A., Kloosterman, A.D., van Marion, V., de Poot, C.J. (2016) Knowledge on DNA success rates to optimize the DNA analysis process: from crime scene to laboratory. *Journal of Forensic Sciences* 61(4): 1055-1061.

2. Bär, W., Kratzer, A., Mächler, M., Schmid, W. (1988) Postmortem stability of DNA. *Forensic Science International* 39(1): 59-70.

3. Sweet, D., Lorente, M., Lorente, J.A., Valenzuela, A., Villanueva, E. (1997) An improved method to recover salivafrom human skin: the double swab technique. *Journal of Forensic Sciences* 42(2): 320-322.

4. Lee, H.C. and Ladd, C. (2001) Preservation and collection of biological evidence. *Croatian Medical Journal* 42(3):225-228.

5. Kline, M.C., Duewer, D.L., Redman, J.W., Butler, J.M., Boyer, D.A. (2002) Polymerase chain reaction amplification of DNA from aged blood stains: quantitative evaluation of the "suitability for purpose" of four filterpapers as archival media. *Analytical Chemistry* 74(8): 1863-1869.

6. Bond, J.W. and Hammond, C. (2008) The value of DNA material recovered from crime scenes. *Journal of ForensicSciences* 53(4): 797-801.

7. Virkler, K. and Lednev, I.K. (2009) Analysis of body fluids for forensic purposes: from laboratory testing to non-destructive rapid confirmatory identification at a crime scene. *Forensic Science International* 188: 1-17.

8. Vandewoestyne, M. and Deforce, D. (2010) Laser capture microdissection in forensic research: a review. *International Journal of Legal Medicine* 124(6): 513-521.

9. van Oorschot, R.A.H. (2012) Assessing DNA profiling success rates: need for more and better collection of relevantdata. *Forensic Science Policy and Management* 3: 37-41.

10. Goray, M., van Oorschot, R.A., Mitchell, J.R. (2012) DNA transfer within forensic exhibit packaging: potential forDNA loss and relocation. *Forensic Science International: Genetics* 6(2): 158-166.

11. Allen-Hall, A. and McNevin, D. (2013) Non-cryogenic forensic tissue preservation in the field: a review. *AustralianJournal of Forensic Sciences* 45(4): 450-460.

12. Higgins, D. and Austin, J.J. (2013) Teeth as a source of DNA for forensic identification of human remains: Areview. *Science & Justice* 53(4): 433-441.

13. Verdon, T.J., Mitchell, R.J. and van Oorschot, R.A. (2014) Swabs as DNA collection devices for sampling differentbiological materials from different substrates. *Journal of Forensic Sciences* 59(4): 1080-1089.

14. Verdon, T.J., Mitchell, R.J. and van Oorschot, R.A. (2014) Evaluation of tapelifting as a collection method for touchDNA. *Forensic Science International: Genetics* 8(1): 179-186.

15. Verdon, T.J., Mitchell, R.J., van Oorschot, R.A. (2015) Preliminary investigation of differential tapelifting forsampling forensically relevant layered deposits. *Legal Medicine* 17(6): 553-559.

16. Baechler, S. (2016) Study of criteria influencing the success rate of DNA swabs in operational conditions: A contribution to an evidence-based approach to crime scene investigation and triage. *Forensic Science International:Genetics* 20: 130-139.

17. Pickrahn, I., Kreindl, G., Müller, E., Dunkelmann, B., Zahrer, W., Cemper-Kiesslich, J., Neuhuber, F. (2017)Contamination incidents in the pre-analytical phase of forensic DNA analysis in Austria—

Statistics of 17 years. *Forensic Science International: Genetics* 31: 12-18.

18. Sujatha, G., Muruganandhan, J., Priya, V.V., Srinivasan, M.R. (2019) Determination of reliability and practicality ofsaliva as a genetic source in forensic investigation by analyzing DNA yield and success rates: A systematic
review. *Journal of Oral and Maxillofacial Surgery, Medicine, and Pathology* 31(3): 218-227.

19. Prasad, E., Hitchcock, C., Raymond, J., Cole, A., Barash, M., Gunn, P., McNevin, D., van Oorschot, R.A.(2020) DNA recovery from unfired and fired cartridge cases: A comparison of swabbing, tape lifting, vacuum filtration, anddirect PCR. *Forensic Science International* 317: 110507.

D. DNA Extraction/Purification, Differential Extraction

1. Gill, P., Jeffreys, A.J., Werrett, D.J. (1985) Forensic application of DNA 'fingerprints'. *Nature* 318: 577-579.

2. Walsh, P.S., Metzger, D.A., Higuchi, R. (1991) Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 10(4): 506-513.

3. Comey, C.T., Koons, B.W., Presley, K.W., Smerick, J.B., Sobieralski, C.A., Stanley, D.M., Baechtel, F.S. (1994)DNA extraction strategies for amplified fragment length polymorphism analysis. *Journal of Forensic Sciences* 39(5): 1254-1269.

4. Rådström, P., Knutsson, R., Wolffs, P., Lövenklev, M., Löfström, C. (2004). Pre-PCR processing: Strategies togenerate PCR-compatible samples. *Molecular Biotechnology* 26(2): 133-146.

5. Nagy, M., Otremba, P., Krüger, C., Bergner-Greiner, S., Anders, P., Henske, B., Prinz, M., Roewer, L. (2005) Optimization and validation of a fully automated silica-coated magnetic beads purification technology in forensics.*Forensic Science International* 152(1): 13-22.

6. Anslinger, K., Bayer, B., Rolf, B., Keil, W., Eisenmenger, W. (2005) Application of the BioRobot EZ1 in a forensiclaboratory. *Legal Medicine* 7(3): 164-168.

7. Montpetit, S.A., Fitch, I.T., O'Donnell, P.T. (2005) A simple automated instrument for DNA extraction in forensiccasework. *Journal of Forensic Sciences* 50(3): 1-9.

8. Castella, V., Dimo-Simonin, N., Brandt-Casadevall, C., Mangin, P. (2006) Forensic evaluation of theQIAshredder/QIAamp DNA extraction procedure. *Forensic Science International* 156(1): 70-73.

9. Loreille, O.M., Diegoli, T.M., Irwin, J.A., Coble, M.D., Parsons, T.J. (2007) High efficiency DNA extraction frombone by total demineralization. *Forensic Science International: Genetics* 1(2): 191-195.

10. Brevnov, M.G., Pawar, H.S., Mundt, J., Calandro, L.M., Furtado, M.R., Shewale, J.G. (2009) Developmental validation of the PrepFiler Forensic DNA Extraction Kit for extraction of genomic DNA from biological samples.*Journal of Forensic Sciences* 54(3): 599-607.

11. Stray, J.E., Liu, J.Y., Brevnov, M.G., Shewale, J.G. (2010) Extraction of DNA from forensic biological samples forgenotyping. *Forensic Science Review* 22(2): 159-175.

12. Stray, J.E. and Shewale, J.G. (2010) Extraction of DNA from human remains. *Forensic Science Review* 22(2): 177-
185.

13. Frégeau, C.J., Lett, C.M., Fourney, R.M. (2010) Validation of a DNA IQ™-based extraction method for TECAN robotic liquid handling workstations for processing casework. *Forensic Science International: Genetics* 4(5): 292-304.

14. Lee, S.B., Shewale, J.G. (2017). DNA Extraction Methods in Forensic Analysis. In "Encyclopedia of AnalyticalChemistry" pp 1–18. John Wiley & Sons, Ltd.

E. DNA Quantitation, Degraded DNA

1. Lee, S.B., McCord, B., Buel, E. (2014) Advances in forensic DNA quantification: a review. *Electrophoresis* 35: 3044-3052.

2. Lindahl, T. (1993) Instability and decay of the primary structure of DNA. *Nature* 362: 709-715.

3. Butler, J.M., Shen, Y., McCord, B.R. (2003) The development of reduced size STR amplicons as tools for analysisof degraded DNA. *Journal of Forensic Sciences* 48(5) 1054-1064.

4. Green, R.L., Roinestad, I.C., Boland, C., Hennessy, L.K. (2005) Developmental validation of the Quantifiler real- time PCR kits for the quantification of human nuclear DNA samples. *Journal of Forensic Sciences* 50(4): 809-825.

5. Westring, C.G., Kristinsson, R., Gilbert, D.M., Danielson, P.B. (2007) Validation of reduced-scale reactions for theQuantifiler (TM) human DNA kit. *Journal of Forensic Sciences* 52(5): 1035-1043.

6. Barbisin, M., Fang, R., O'Shea, C.E., Calandro, L.M., Furtado, M.R., Shewale, J.G. (2009) Developmental validation of the Quantifiler Duo DNA Quantification kit for simultaneous quantification of total human and humanmale DNA and detection of PCR inhibitors in biological samples. *Journal of Forensic Sciences* 54(2): 305-319.

7. Alaeddini, R., Walsh, S.J., Abbas, A. (2010) Forensic implications of genetic analyses from degraded DNA--areview. *Forensic Science International: Genetics* 4(3):148-157.

8. Grgicak, C.M., Urban, Z.M., Cotton, R.W. (2010) Investigation of reproducibility and error associated with qPCRmethods using Quantifiler® Duo DNA quantification kit. *Journal of Forensic Sciences* 55(5):1331-1339.

9. Vieira-Silva, C., Afonso-Costa, H., Ribeiro, T., Porto, M.J., Dias, M., Amorim, A. (2015) Quantifiler® Trio DNA validation and usefulness in casework samples. *Forensic Science International: Genetics Supplement Series* 5: e246-e247.

10. Holt, A., Wootton, S.C., Mulero, J.J., Brzoska, P.M., Langit, E., Green, R.L. (2016) Developmental validation of the Quantifiler(®) HP and Trio Kits for human DNA quantification in forensic samples. *Forensic Science International:Genetics* 21: 145-157.

F. PCR Amplification, Inhibition, and Artifacts

1. Walsh, P.S., Erlich, H.A. and Higuchi, R. (1992) Preferential PCR amplification of alleles: mechanisms and solutions. *PCR Methods & Applications* 1(4): 241-250.

2. Saiki, R.K., Gelfand, D.H., Stoffel, S., Scharf, S.J., Higuchi, R., Horn, G.T., Mullis, K.B., Erlich, H.A. (1988) Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. *Science* 239: 487-491.

3. Clark, J.M. (1988). Novel non-templated nucleotide addition reactions catalyzed by procaryotic and eucaryotic DNApolymerases. *Nucleic Acids Research* 16(20): 9677-9686.

4. Bloch, W. (1991) A biochemical perspective of the polymerase chain reaction. *Biochemistry* 30: 2735-2747.

5. Reynolds, R., Sensabaugh, G., Blake, E. (1991) Analysis of genetic markers in forensic DNA samples using thepolymerase chain reaction. *Analytical Chemistry* 63(1): 2-15.

6. Walsh, P.S., Fildes, N.J., Reynolds, R. (1996) Sequence analysis and characterization of stutter products at thetetranucleotide repeat locus vWA. *Nucleic Acids Research* 24(14): 2807-2812.

7. Leclair, B., Sgueglia, J.B., Wojtowicz, P.C., Juston, A.C., Frégeau, C.J,, Fourney, R.M. (2003) STR DNA typing:increased sensitivity and efficient sample consumption using reduced PCR reaction volumes. *Journal of ForensicSciences* 48(5): 1001-1013.

8. Alaeddini, R. (2012) Forensic implications of PCR inhibition—A review. *Forensic Science International: Genetics*
6(3): 297-305.

9. Kumar, P., Gupta, R., Singh, R., Jasuja, O.P. (2015) Effects of latent fingerprint development reagents onsubsequent forensic DNA typing: a review. *Journal of Forensic and Legal Medicine* 32:64-69.

10. Cavanaugh, S.E. and Bathrick, A.S. (2018) Direct PCR amplification of forensic touch and other challenging DNAsamples: A review. *Forensic Science International: Genetics* 32: 40-49.

G. Capillary Electrophoresis Separation and Detection

1. Butler, J.M., Buel, E., Crivellente, F., McCord, B.R. (2004) Forensic DNA typing by capillary electrophoresis using the ABI Prism 310 and 3100 Genetic Analyzers for STR analysis. *Electrophoresis* 25: 1397-1412.

2. Guttman, A. and Cooke, N. (1991) Effect of temperature on the separation of DNA restriction fragments in capillarygel electrophoresis. *Journal of Chromatography* 559: 285-294.

3. Issaq, H.J., Chan, K.C., Muschik, G.M. (1997) The effect of column length, applied voltage, gel type, and concentration on the capillary electrophoresis separation of DNA fragments and polymerase chain reaction products.*Electrophoresis* 18(7): 1153-1158.

4. Lazaruk, K., Walsh, P.S., Oaks, F., Gilbert, D., Rosenblum, B.B., Menchen, S., Scheibler, D., Wenz, H.M., Holt, C.,Wallin, J. (1998) Genotyping of forensic short tandem repeat (STR) systems based on sizing precision in a capillaryelectrophoresis instrument. *Electrophoresis* 19(1): 86-93.

5. Mansfield, E.S., Robertson, J.M., Vainer, M., Isenberg, A.R., Frazier, R.R., Ferguson, K., Chow, S., Harris, D.W.,Barker, D.L., Gill, P.D., Budowle, B., McCord, B.R. (1998) Analysis of multiplexed short tandem repeat (STR) systems using capillary array electrophoresis. *Electrophoresis* 19(1): 101-107.

6. Heller, C. (2001) Principles of DNA separation with capillary electrophoresis. *Electrophoresis* 22(4): 629-643.

7. Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Smerick, J.B. and Budowle, B. (2001)

Validation ofshort tandem repeats (STRs) for forensic usage: performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. *Journal of Forensic Sciences* 46(3): 647-660.

8. Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Brown, A.L. and Budowle, B. (2001) Validation ofSTR typing by capillary electrophoresis. *Journal of Forensic Sciences* 46(3): 661-676.

9. Sgueglia, J.B., Geiger, S., Davis, J. (2003) Precision studies using the ABI Prism 3100 Genetic Analyzer forforensic DNA analysis. *Analytical and Bioanalytical Chemistry* 376(8): 1247-1254.

10. Gilder, J.R., Doom, T.E., Inman, K. and Krane, D.E. (2007) Run-specific limits of detection and quantitation forSTR-based DNA testing. *Journal of Forensic Sciences* 52(1): 97-101.

11. Rakay, C.A., Bregu, J. and Grgicak, C.M. (2012) Maximizing allele detection: Effects of analytical threshold andDNA levels on rates of allele and locus drop-out. *Forensic Science International: Genetics* 6(6): 723-728.

12. Adelman, J.D., Zhao, A., Eberst, D.S. and Marciano, M.A. (2019) Automated detection and removal of capillaryelectrophoresis artifacts due to spectral overlap. *Electrophoresis* 40(14): 1753-1761.

H. Assessing Sample Suitability and Complexity, Low-Template DNA

1. Gill, P., Whitaker, J., Flaxman, C., Brown, N., Buckleton, J. (2000) An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. *Forensic Science International* 112(1):17-40.

2. Taberlet, P., Griffin, S., Goossens, B., Questiau, S., Manceau, V., Escaravage, N., Waits, L.P. Bouvet, J. (1996) Reliable genotyping of samples with very low DNA quantities using PCR. *Nucleic Acids Research* 24(16): 3189-3194.

3. Findlay, I., Taylor, A., Quirke, P., Frazier, R., Urquhart, A. (1997) DNA fingerprinting from single cells. *Nature* 389: 555-556.

4. Gill, P. (2001) Application of low copy number DNA profiling. *Croatian Medical Journal* 42(3): 229-232.

5. Graham, Eleanor A. M. (2008) DNA reviews: low level DNA profiling. *Forensic Science Medicine and Pathology*.
4(2): 129-131.

6. Balding, D.J. and Buckleton, J. (2009) Interpreting low template DNA profiles. *Forensic Science International:Genetics* 4(1): 1-10.

7. Butler, J.M. and Hill, C.R. (2010) Scientific issues with analysis of low amounts of DNA. *Profiles in DNA (Promega)*, 13(1). Available at https://www.promega.com/resources/profiles-in-dna/2010/scientific-issues-with-analysis-of-low-amounts-of-dna/.

8. Benschop, C.C., van der Beek, C.P., Meiland, H.C., van Gorp, A.G., Westen, A.A. and Sijen, T. (2011) Low template STR typing: effect of replicate number and consensus method on genotyping reliability and DNA databasesearch results. *Forensic Science International: Genetics* 5(4): 316-328.

I. Estimating the Number of Contributors

1. Buckleton, J.S., Curran, J.M. and Gill, P. (2007) Towards understanding the effect of uncertainty in the number of contributors to DNA stains. *Forensic Science International: Genetics* 1(1): 20-28.

2. Egeland, T., Dalen, I. and Mostad, P.F. (2003) Estimating the number of contributors to a DNA profile. *International Journal of Legal Medicine* 117(5): 271-275.

3. Coble, M.D., Bright, J.A., Buckleton, J.S. and Curran, J.M. (2015) Uncertainty in the number of contributors in theproposed new CODIS set. *Forensic Science International: Genetics* 19: 207-211.

4. Swaminathan, H., Grgicak, C.M., Medard, M. and Lun, D.S. (2015) NOCIt: a computational method to infer the number of contributors to DNA samples analyzed by STR genotyping. *Forensic Science International: Genetics* 16:172-180.

5. Alfonse, L.E., Tejada, G., Swaminathan, H., Lun, D.S. and Grgicak, C.M. (2017) Inferring the number ofcontributors to complex DNA mixtures using three methods: exploring the limits of low-template DNA interpretation. *Journal of Forensic Sciences* 62(2): 308-316.

6. Marciano, M.A. and Adelman, J.D. (2017) PACE: Probabilistic Assessment for Contributor Estimation- A machine learning-based assessment of the number of contributors in DNA mixtures. *Forensic Science International: Genetics*27: 82-91.

7. Norsworthy, S., Lun, D.S., Grgicak, C.M. (2018) Determining the number of contributors to DNA mixtures in thelow-template regime: Exploring the impacts of sampling and detection effects. *Legal Medicine* 32: 1-8.

8. Dembinski, G.M., Sobieralski, C., Picard C.J. (2018) Estimation of the number of contributors of theoretical mixtureprofiles based on allele counting: Does increasing the number of loci increase success rate of estimates? *Forensic Science International: Genetics* 33: 24-32.

9. Young, B.A., Gettings, K.B., McCord, B., Vallone, P.M. (2019) Estimating number of contributors in massivelyparallel sequencing data of STR loci. *Forensic Science International: Genetics* 38: 15-22.

10. Marciano, M.A. and Adelman, J.D. (2019) Developmental validation of PACE™: Automated artifact identification and contributor estimation for use with GlobalFiler™ and PowerPlex® Fusion 6C generated data. *Forensic ScienceInternational: Genetics* 43: 102140.

11. Evett, I.W. and Pope, S. (2014) Is it to the advantage of a defendant to infer a greater number of contributors to aquestioned sample than is necessary to explain the observed DNA profile? *Science & Justice* 54(5): 373-374.

12. Benschop, C.C., Haned, H., Jeurissen, L., Gill, P.D. and Sijen, T. (2015) The effect of varying the number of contributors on likelihood ratios for complex DNA mixtures. *Forensic Science International: Genetics* 19: 92-99.

J. Data Interpretation, Mixture Deconvolution, Interlaboratory Studies

1. Gill, P., Sparkes, R. and Kimpton, C. (1997) Development of guidelines to designate alleles using an STR multiplex system. *Forensic Science International* 89(3): 185-197.

2. Gill, P., Sparkes, R., Pinchin, R., Clayton, T., Whitaker, J., Buckleton, J. (1998) Interpreting simple STR mixturesusing allele peak areas. *Forensic Science International* 91(1): 41-53.

3. Clayton, T.M., Whitaker, J.P., Sparkes, R. and Gill, P. (1998) Analysis and interpretation of mixed forensic stainsusing DNA STR profiling. *Forensic Science International* 91(1): 55-70.

4. Crouse, C.A., Rogers, S., Amiott, E., Gibson, S., Masibay, A. (1999) Analysis and interpretation of short tandem repeat microvariants and three-banded allele patterns using multiple allele detection systems. *Journal of ForensicSciences* 44(1): 87-94. Erratum in: J Forensic Sci 1999 May;44(3):667.

5. Duewer, D.L., Kline, M.C., Redman, J.W., Newall, P.J. and Reeder, D.J. (2001) NIST Mixed Stain Studies #1 and #2: interlaboratory comparison of DNA quantification practice and short tandem repeat multiplex performance withmultiple-source samples. *Journal of Forensic Sciences* 46: 1199-1210.

6. Duewer, D.L., Kline, M.C., Redman, J.W. and Butler, J.M. (2004) NIST Mixed Stain Study #3: signal intensitybalance in commercial short tandem repeat multiplexes. *Analytical Chemistry* 76: 6928-6934.

7. Prieto, L., Haned, H., Mosquera, A., Crespillo, M., Aleman, M., Aler, M., Alvarez, F., Baeza-Richer, C., Dominguez, A., Doutremepuich, C., Farfán, M.J., Fenger-Grøn, M., García-Ganivet, J.M., González-Moya, E., Hombreiro, L., Lareu, M.V., Martínez-Jarreta, B., Merigioli, S., Milans Del Bosch, P., Morling, N., Muñoz-Nieto,M., Ortega-González, E., Pedrosa, S., Pérez, R., Solís, C., Yurrebaso, I. and Gill, P. (2014) Euroforgen-NoE collaborative exercise on LRmix to demonstrate standardization of the interpretation of complex DNA profiles. *Forensic Science International: Genetics* 9: 47-54.

8. Benschop, C.C., Connolly, E., Ansell, R. and Kokshoorn, B. (2017) Results of an inter and intra laboratory exerciseon the assessment of complex autosomal DNA profiles. *Science & Justice* 57(1): 21-27.

9. Butler, J.M., Kline, M.C. and Coble, M.D. (2018) NIST interlaboratory studies involving DNA mixtures (MIX05and MIX13): variation observed and lessons learned. *Forensic Science International: Genetics* 37: 81-94.

10. Lynch, P.C. and Cotton, R.W. (2018) Determination of the possible number of genotypes which can contribute to DNA mixtures: non-computer assisted deconvolution should not be attempted for greater than two person mixtures.*Forensic Science International: Genetics* 37: 235-240.

11. Tao, R., Wang, S., Zhang, J., Zhang, J., Yang, Z., Sheng, X., Hou, Y., Zhang, S., Li, C. (2018) Separation/extraction, detection, and interpretation of DNA mixtures in forensic science (review). *InternationalJournal of Legal Medicine* 132(5): 1247-1261.

12. Sanz-Piña, E., Santurtún, A., Zarrabeitia, M.T. (2019) Forensic implications of the presence of chimerism afterhematopoietic stem cell transplantation. *Forensic Science International* 302: 109862.

K. Interpretation: Binary Approaches (CPI, RMP, LR)

1. Gill, P., Brenner, C.H., Buckleton, J.S., Carracedo, A., Krawczak, M., Mayr, W.R., Morling, N., Prinz, M., Schneider, P.M. and Weir, B.S. (2006) DNA Commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Science International* 160: 90-101.

2. Schneider, P.M., Gill, P., Carracedo, A. (2006) Editorial on the recommendations of the DNA commission of theISFG on the interpretation of mixtures. *Forensic Science International* 160: 89.

3. Buckleton, J. and Triggs, C. (2006) Is the 2p rule always conservative? *Forensic Science International* 159: 206-209.

4. Morling, N., Bastisch, I., Gill, P. and Schneider, P.M. (2007) Interpretation of DNA mixtures--European consensuson principles. *Forensic Science International: Genetics* 1: 291-292.

5. Buckleton, J. and Curran, J. (2008) A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Science International: Genetics* 2(4): 343-348.

6. Schneider, P.M., Fimmers, R., Keil, W., Molsberger, G., Patzelt, D., Pflug, W., Rothämel, T., Schmitter, H., Schneider, H. and Brinkmann, B. (2009) The German Stain Commission: recommendations for the interpretation ofmixed stains. *International Journal of Legal Medicine* 123(1): 1-5. [Originally published in German in *Rechtsmedizin* (2006) 16: 401-404].

7. Budowle, B., Onorato, A.J., Callaghan, T.F., Della, M.A., Gross, A.M., Guerrieri, R.A., Luttman, J.C., McClure, D.L. (2009) Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNAprofiles in forensic casework. *Journal of Forensic Sciences* 54(4): 810-821.

8. Bieber, F.R., Buckleton, J.S., Budowle, B., Butler, J.M., Coble, M.D. (2016) Evaluation of forensic DNA mixtureevidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. *BMC Genetics* 17(1):125.

9. Marsden, C.D., Rudin, N., Inman, K., Lohmueller, K.E. (2016) An assessment of the information content oflikelihood ratios derived from complex mixtures. *Forensic Science International: Genetics* 22: 64-72.

L. Interpretation: Probabilistic Genotyping Software (Discrete, Continuous)

1. Coble, M.D. and Bright, J.-A. (2019) Probabilistic genotyping software: An overview. *Forensic Science International: Genetics* 38: 219-224.

2. Evett, I.W. (1983) What is the Probability that This Blood Came from That Person? A Meaningful Question? *Journal of the Forensic Science Society (Science & Justice)* 23:35-39.

3. Gill, P., Kirkham, A., Curran, J. (2007) LoComatioN: A software tool for the analysis of low copy number DNAprofiles, *Forensic Science International.* 166:128-138.

4. Cowell, R.G. (2009) Validation of an STR peak area model. *Forensic Science International: Genetics* 3(3): 193-199.

5. Perlin, M.W. and Sinelnikov, A. (2009) An information gap in DNA evidence interpretation. *PLoS ONE* 4(12):e8327.

6. Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N. (2010) Evaluating the weight of evidence by usingquantitative short tandem repeat data in DNA mixtures. *Applied Statistics* 59(5): 855-874.

7. Perlin, M.W., Legler, M.M., Spencer, C.E., Smith, J.L., Allan, W.P., Belrose, J.L., Duceman, B.W. (2011)Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences* 56(6): 1430-1447.

8. Cowell, R.G., Lauritzen, S.L., Mortera, J. (2011) Probabilistic expert systems for handling artifacts in complexDNA mixtures. *Forensic Science International: Genetics* 5(3): 202-209.

9. Brookes, C., Bright, J.-A., Harbison, S., Buckleton, J. (2012) Characterizing stutter in forensic STR multiplexes. *Forensic Science International: Genetics* 6(1): 58-63.

10. Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N. (2012) Statistical model for degraded DNA samplesand adjusted probabilities for allelic drop-out. *Forensic Science International: Genetics* 6: 97-101.

11. Kelly, H., Bright, J.-A., Curran, J.M., Buckleton, J. (2012) Modelling heterozygote balance in forensic DNAprofiles, *Forensic Science International: Genetics* 6: 729-734.

12. Gill, P., Gusmao, L., Haned, H., Mayr, W.R., Morling, N., Parson, W., Prieto, L., Prinz, M., Schneider, H.,Schneider, P.M., Weir, B.S. (2012) 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. *Forensic Science International: Genetics* 6(6): 679-688.

13. Bright, J.-A., Curran, J.M., Buckleton, J.S. (2013). Investigation into the performance of different models forpredicting stutter. *Forensic Science International: Genetics* 7(4), 422–427.

14. Taylor, D., Bright, J.-A., Buckleton, J. (2013) The interpretation of single source and mixed DNA profiles, *ForensicScience International: Genetics* 7:516-528.

15. Gill, P. and Haned, H. (2013) A new methodological framework to interpret complex DNA profiles using likelihoodratios. *Forensic Science International: Genetics* 7(2): 251-263.

16. Puch-Solis, R., Rodgers, L., Mazumder, A., Pope, S., Evett, I., Curran, J., Balding, D. (2013) Evaluating forensicDNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. *Forensic Science International: Genetics* 7(5): 555-563.

17. Ramos, D. and Gonzalez-Rodriguez, J. (2013) Reliable support: measuring calibration of likelihood ratios. *ForensicScience International* 230: 156-169.

18. Taylor, D., Bright, J.-A., Buckleton, J. (2014) The 'factor of two' issue in mixed {DNA} profiles, *Journal ofTheoretical Biology* 363:300-306.

19. Taylor, D., Bright, J.-A., Buckleton, J. (2014) Interpreting forensic DNA profiling evidence without specifying thenumber of contributors, *Forensic Science International: Genetics* 13:269-280.

20. Taylor, D., Bright, J.-A., Buckleton, J. (2014) Considering relatives when assessing the evidential strength of mixedDNA profiles, *Forensic Science International: Genetics* 13:259-263.

21. Bright, J.-A., Taylor, D., Curran, J.M., Buckleton, J. (2014) Searching mixed DNA profiles directly against profiledatabases, *Forensic Science International: Genetics* 9:102-110.

22. Bille, T.W., Weitz, S.M., Coble, M.D., Buckleton, J., Bright, J.-A. (2014) Comparison of the performance ofdifferent models for the interpretation of low level mixed DNA profiles, *Electrophoresis* 35: 3125-3133.

23. Kelly, H., Bright, J.A., Buckleton, J.S., Curran, J.M. (2014) A comparison of statistical models for the analysis ofcomplex forensic DNA profiles. *Science & Justice* 54(1): 66-70.

24. Steele, C.D., Greenhalgh, M., Balding, D.J. (2014) Verifying likelihoods for low template DNA profiles usingmultiple replicates. *Forensic Science International: Genetics* 13: 82-89.

25. Steele, C.D. and Balding, D.J. (2014) Statistical evaluation of forensic DNA profile evidence. *Annual Review ofStatistics and its Application* 1: 361-384.

26. Bright, J.-A., Evett, I.W., Taylor, D., Curran, J.M., Buckleton, J. (2015) A series of recommended tests when validating probabilistic DNA profile interpretation software, *Forensic Science International: Genetics* 14:125-131.

27. Gill, P., Haned, H., Bleka, O., Hansson, O., Dorum, G. and Egeland, T. (2015) Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches-Twenty years of research and development. *ForensicScience International: Genetics* 18: 100-117.

28. Perlin, M.W., Hornyak, J.M., Sugimoto, G., Miller, K.W. (2015) TrueAllele® genotype identification on DNAmixtures containing up to five unknown contributors. *Journal of Forensic Sciences* 60(4): 857-868.

29. Greenspoon, S.A., Schiermeier- Wood, L., Jenkins, B.C. (2015) Establishing the limits of TrueAllele® Casework:A validation study. *Journal of Forensic Sciences* 60(5): 1263-1276.

30. Bleka, Ø., Benschop, C.C., Storvik, G. and Gill, P. (2016) A comparative study of qualitative and quantitativemodels used to interpret complex STR DNA profiles. *Forensic Science International: Genetics* 25: 85-96.

31. Steele, C.D., Greenhalgh, M. and Balding, D.J. (2016) Evaluation of low-template DNA profiles using peak heights.
Stat. Appl. Genet. Mol. Biol. 15(5): 431-445.

32. Haned, H., Gill, P., Lohmueller, K., Inman, K., Rudin, N. (2016) Validation of probabilistic genotyping software foruse in forensic DNA casework: Definitions and illustrations. *Science & Justice* 56(2): 104-108.

33. Moretti, T.R., Just, R.S., Kehl, S.C., Willis, L.E., Buckleton, J.S., Bright, J.A., Taylor, D.A. and Onorato, A.J. (2017) Internal validation of STRmix for the interpretation of single source and mixed DNA profiles. *ForensicScience International: Genetics* 29: 126-144.

34. Bright, J.A., Taylor, D., Gittelson, S., Buckleton, J. (2017) The paradigm shift in DNA profile interpretation. *Forensic Science International: Genetics* 31: e24-e32.

35. Meuwly, D., Ramos, D., Haraksim, R. (2017) A guideline for the validation of likelihood ratio methods used forforensic evidence evaluation. *Forensic Science International* 276: 142-153.

36. Bright, J.A., Richards, R., Kruijver, M., Kelly, H., McGovern, C., Magee, A., McWhorter, A., Ciecko, A., Peck, B., Baumgartner, C., Buettner, C., McWilliams, S., McKenna, C., Gallacher, C., Mallinder, B., Wright, D., Johnson, D.,Catella, D., Lien, E., O'Connor, C., Duncan, G., Bundy, J., Echard, J., Lowe, J., Stewart, J., Corrado, K., Gentile, S.,Kaplan, M., Hassler, M., McDonald, N., Hulme, P., Oefelein, R.H., Montpetit, S., Strong, M., Noel, S., Malsom, S.,Myers, S., Welti, S., Moretti, T., McMahon, T., Grill, T., Kalafut, T., Greer-Ritzheimer, M.M., Beamer, V., Taylor, D.A., Buckleton, J.S. (2018) Internal validation of STRmix™– a multi laboratory response to PCAST. *Forensic Science International: Genetics* 34: 11-24.

37. Slooten, K. (2018) The information gain from peak height data in DNA mixtures. *Forensic Science International:Genetics* 36: 119-123.

38. Swaminathan, H., Qureshi, M.O., Grgicak, C.M., Duffy, K. and Lun, D.S. (2018) Four model variants within a continuous forensic DNA mixture interpretation framework: effects on evidential inference and reporting. *PLoSONE* 13(11): e0207599.

39. Benschop, C.C.G., Nijveld, A., Duijs, F.E. and Sijen, T. (2019) 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* 42: 31-38.

40. Bright, J.A., Cheng, K., Kerr, Z., McGovern, C., Kelly, H., Moretti, T.R., Smith, M.A., Bieber, F.R., Budowle, B., Coble, M.D., Alghafri, R., Allen, P.S., Barber, A., Beamer, V., Buettner, C., Russell, M., Gehrig, C., Hicks, T., Charak, J., Cheong-Wing, K., Ciecko, A., Davis, C.T., Donley, M., Pedersen, N., Gartside, B., Granger, D., Greer-Ritzheimer, M., Reisinger, E., Kennedy, J., Grammer, E., Kaplan, M., Hansen, D., Larsen, H.J., Laureano, A., Li, C., Lien, E., Lindberg, E., Kelly, C., Mallinder, B., Malsom, S., Yacovone-Margetts, A., McWhorter, A., Prajapati,S.M., Powell, T., Shutler, G., Stevenson, K., Stonehouse, A.R., Smith, L., Murakami, J., Halsing, E., Wright, D., Clark, L., Taylor, D.A., Buckleton. J. (2019) STRmix™ collaborative exercise on DNA mixture interpretation. *Forensic Science International: Genetics* 40:1-8.

41. You, Y. and Balding, D. (2019) A comparison of software for the evaluation of complex DNA profiles. *ForensicScience International: Genetics* 40: 114-119.

M. Report Writing and Technical Review

1. Association of Forensic Science Providers (2009) Standards for the formulation of evaluative forensic science expert opinion. *Science & Justice* 49: 161-164.

2. Cook, R., Evett, I.W., Jackson, G., Jones, P.J. and Lambert, J.A. (1998) A model for case assessment andinterpretation. *Science & Justice* 38(3): 151-156.

3. Cook, R., Evett, I.W., Jackson, G., Jones, P.J. and Lambert, J.A. (1998) A hierarchy of propositions: deciding whichlevel to address in casework. *Science & Justice* 38(4): 231-239.

4. Evett, I.W., Jackson, G., Lambert, J.A. (2000) More on the hierarchy of propositions: exploring the distinctionbetween explanations and propositions. *Science & Justice* 40(1): 3-10.

5. Evett, I.W., Jackson, G., Lambert, J.A., McCrossan, S. (2000) The impact of the principles of evidenceinterpretation on the structure and content of statements. *Science & Justice* 40(4): 233-239.

6. Doak, S. and Assimakopoulos, D. (2007) How do forensic scientists learn to become competent in caseworkreporting in practice: A theoretical and empirical approach. *Forensic Science International* 167: 201-206.

7. Ballantyne, K.N., Edmond, G. and Found, B. (2017) Peer review in forensic science. *Forensic Science International*
277: 66-76.

8. Barrio, P.A., Crespillo, M., Luque, J.A., Aler, M., Baeza-Richer, C., Baldassarri, L., Carnevali, E., Coufalova, P.,Flores, I., García, O. and García, M.A. (2018) GHEP-ISFG collaborative exercise on mixture profiles (GHEP- MIX06). Reporting conclusions: results and evaluation. *Forensic Science International: Genetics* 35: 156-163.

N. Court Testimony, Communication of Results, Juror Comprehension Studies

1. Eldridge, H. (2019) Juror comprehension of forensic expert testimony: a literature review and gap analysis. *Forensic Science International: Synergy* 1: 24-34.

2. Thompson, W.C. and Schumann, E.L. (1987) Interpretation of statistical evidence in criminal trials: the prosecutor'sfallacy and the defense attorney's fallacy. *Law and Human Behavior* 11(3): 167-187.

3. Evett, I.W. (1995) Avoiding the transposed conditional. *Science & Justice* 35(2): 127-131.

4. Evett, I.W., Gill, P.D., Jackson, G., Whitaker, J. and Champod, C. (2002) Interpreting small quantities of DNA: thehierarchy of propositions and the use of Bayesian networks. *Journal of Forensic Sciences* 47(3): 520-530.

5. Walsh, SJ (2005) Legal perceptions of forensic DNA profiling - Part I: A review of the legal literature. *ForensicScience International.* 155(1): 51-60.

6. Jackson, G., Jones, S., Booth, G., Champod, C., Evett, I.W. (2006) The nature of forensic science opinion--a possible framework to guide thinking and practice in investigations and in court proceedings. *Science & Justice*46(1): 33-44.

7. Gill, P., Brown, R.M., Fairley, M., Lee, L., Smyth, M., Simpson, N., Irwin, B., Dunlop, J., Greenhalgh, M., Way, K., Westacott, E.J., Ferguson, S.J., Ford, L.V., Clayton, T. and Guiness, J. (2008) National recommendations of theTechnical UK DNA working group on mixture interpretation for the NDNAD and for court going purposes. *Forensic Science International: Genetics* 2(1): 76-82.

8. Smith, L.L., Bull, R. and Holliday, R. (2011) Understanding juror perceptions of forensic evidence: investigating theimpact of case context on perceptions of forensic evidence strength. *Journal of Forensic Sciences* 56(2): 409-414.

9. Coyle, Heather Miller (2012) The importance of scientific evaluation of biological evidence - Data from eight yearsof case review. *Science & Justice.* 52(4): 268-270.

10. de Keijser, J. and Elffers, H. (2012) Understanding of forensic expert reports by judges, defense lawyers andforensic professionals. *Psychology, Crime & Law* 18(2): 191-207.

11. Howes, L.M., Kirkbride, K.P., Kelty, S.F., Julian, R., Kemp, N. (2013) Forensic scientists' conclusions: howreadable are they for non-scientist report-users? *Forensic Science International* 231: 102-112.

12. Taroni, F., Biedermann, A., Vuille, J., and Morling, N. (2013). Whose DNA is this? How relevant a question? (anote for forensic scientists). *Forensic Science International: Genetics* 7: 467-470.

13. Howes, L.M. (2015) The communication of forensic science in the criminal justice system: A review of theory andproposed directions for research. *Science & Justice* 55(2): 145-154.

14. Marquis, R., Biedermann, A., Cadola, L., Champod, C., Gueissaz, L., Massonnet, G., Mazzella, W.D., Taroni, F.,Hicks, T. (2016) Discussion on how to implement a verbal scale in a forensic laboratory: Benefits, pitfalls and suggestions to avoid misunderstandings. *Science & Justice* 56(5): 364-370.

15. de Keijser, J.W., Malsch, M., Luining, E.T., Weulen Kranenbarg, M. and Lenssen, D.J.H.M. (2016) Differentialreporting of mixed DNA profiles and its impact on jurists' evaluation of evidence. An international analysis. *Forensic Science International: Genetics* 23: 71-82.

16. Evett, I., Pope, S. and Puch-Solis, R. (2016) Providing scientific guidance on DNA to the judiciary. *Science &Justice* 56(4): 278-281.

17. Gittelson, S., Kalafut, T., Myers, S., Taylor, D., Hicks, T., Taroni, F., Evett, I.W., Bright, J.A. and Buckleton, J.(2016) A practical guide for the formulation of propositions in the Bayesian approach to DNA evidence interpretation in an adversarial environment. *Journal of Forensic Sciences* 61(1): 186-195.

18. Gill, P., Hicks, T., Butler, J.M., Connolly, E., Gusmão, L., Kokshoorn, B., Morling, N., van Oorschot, R.A.H., Parson, W., Prinz, M., Schneider, P.M., Sijen, T. and Taylor, D. (2018) DNA Commission of the International Society for Forensic Genetics: Assessing the value of forensic biological evidence – guidelines highlighting theimportance of propositions. Part I: Evaluations of DNA profiling comparisons given (sub-) source propositions.*Forensic Science International: Genetics* 36: 189-202.

19. Machado, H. and Silva, S. (2019) What influences public views on forensic DNA testing in the criminal field? Ascoping review of qualitative evidence. *Human Genomics* 13:23.

20. Gill, P. (2019) Interpretation continues to be the main weakness in criminal justice systems: developing roles of theexpert witness and court. *WIREs Forensic Sci.* 1:e1321. Available at https://doi.org/10.1002/wfs2.1321.

21. Gill, P. (2019) DNA evidence and miscarriages of justice. *Forensic Science International* 294: e1-e3.

O. Autosomal STR Markers and Kits

1. Butler, J.M. (2006) Genetics and genomics of core STR loci used in human identity testing. *Journal of Forensic Sciences* 51(2): 253-265.

2. Edwards, A., Civitello, A., Hammond, H.A., Caskey, C.T. (1991) DNA typing and genetic mapping with trimericand tetrameric tandem repeats. *American Journal of Human Genetics* 49(4): 746-756.

3. Frégeau, C.J. and Fourney, R.M. (1993) DNA typing with fluorescently tagged short tandem repeats: a sensitive andaccurate approach to human identification. *BioTechniques* 15(1): 100-119.

4. Hammond, H.A., Jin, L., Zhong, Y., Caskey, C.T., Chakraborty, R. (1994) Evaluation of 13 short tandem repeat locifor use in personal identification applications. *American Journal of Human Genetics* 55(1): 175-189.

5. Wallin, J.M., Buoncristiani, M.R., Lazaruk, K.D., Fildes, N., Holt, C.L., Walsh, P.S. (1998) TWGDAM validation of the AmpFISTR™ Blue PCR amplification kit for forensic casework analysis. *Journal of Forensic Sciences* 43(4):854-870.

6. Gill, P., Sparkes, R., Fereday, L., Werrett, D.J. (2000) Report of the European Network of Forensic ScienceInstitutes (ENSFI): formulation and testing of principles to evaluate STR multiplexes. *Forensic*

Science International 108(1): 1-29.

7. Cotton, E.A., Allsop, R.F., Guest, J.L., Frazier, R.R.E., Koumi, P., Callow, I.P., Seager, A. Sparkes, R.L. (2000)Validation of the AMPFlSTR® SGM Plus™ system for use in forensic casework. *Forensic Science International* 112: 151-161.

8. Ruitberg, C.M., Reeder, D.J., Butler, J.M. (2001) STRBase: a short tandem repeat DNA database for the humanidentity testing community. *Nucleic Acids Research* 29: 320-322.

9. Frank, W.E., Llewellyn, B.E., Fish, P.A., Riech, A.K., Marcacci, T.L., Gandor, D.W., Parker, D., Carter, R.R., Thibault, S.M. (2001) Validation of the AmpFlSTR Profiler Plus PCR amplification kit for use in forensic casework.*Journal of Forensic Sciences* 46(3): 642-646.

10. LaFountain, M.J., Schwartz, M.B., Svete, P.A., Walkinshaw, M.A., Buel, E. (2001) TWGDAM validation of the AmpFlSTR Profiler Plus and AmpFlSTR COfiler STR multiplex systems using capillary electrophoresis. Journal ofForensic Sciences 46(5): 1191-1198.

11. Krenke, B.E., Tereba, A., Anderson, S.J., Buel, E., Culhane, S., Finis, C.J., Tomsey, C.S., Zachetti, J.M., Masibay, A., Rabbach, D.R., Amiott, E.A. (2002) Validation of a 16-locus fluorescent multiplex system. *Journal of ForensicSciences* 47(4): 773-785.

12. Collins, P.J., Hennessy, L.K., Leibelt, C.S., Roby, R.K., Reeder, D.J., Foxall, P.A. (2004) Developmental validationof a single-tube amplification of the 13 CODIS STR loci, D2S1338, D19S433, and amelogenin: the AmpFlSTR Identifiler PCR Amplification Kit. *Journal of Forensic Sciences* 49(6): 1265-1277.

13. Gill, P., Fereday, L., Morling, N., Schneider, P.M. (2006) The evolution of DNA databases—recommendations fornew European STR loci. *Forensic Science International* 156: 242-244.

14. Mulero, J.J., Chang, C.W., Lagace, R.E., Wang, D.Y., Bas, J.L., McMahon, T.P., Hennessy, L.K. (2008). Development and validation of the AmpFℓSTR® MiniFiler™ PCR Amplification Kit: a miniSTR multiplex for theanalysis of degraded and/or PCR inhibited DNA. *Journal of Forensic Sciences* 53(4): 838-852.

15. Luce, C., Montpetit, S., Gangitano, D., O'Donnell, P. (2009) Validation of the AMPFlSTR MiniFiler PCRamplification kit for use in forensic casework*. *Journal of Forensic Sciences* 54(5): 1046-1054.

16. Wang, D.Y., Chang, C.W., Lagacé, R.E., Calandro, L.M., Hennessy, L.K. (2012) Developmental validation of the AmpFℓSTR® Identifiler® Plus PCR Amplification Kit: an established multiplex assay with improved performance.*Journal of Forensic Sciences* 57(2): 453-465.

17. Butler, J.M. and Hill, C.R. (2012) Biology and genetics of new autosomal STR loci useful for forensic DNAanalysis. *Forensic Science Review* 24(1): 15-26.

18. Green, R.L., Lagacé, R.E., Oldroyd, N.J., Hennessy, L.K., Mulero, J.J. (2013) Developmental validation of theAmpFℓSTR® NGM SElect™ PCR Amplification Kit: A next-generation STR multiplex with the SE33
locus. *Forensic Science International: Genetics* 7(1): 41-51.

19. Hares, D.R. (2015) Selection and implementation of expanded CODIS core loci in the United States. *ForensicScience International: Genetics* 17: 33-34.

20. Gettings, K.B., Aponte, R.A., Vallone, P.M., Butler, J.M. (2015) STR allele sequence variation: current knowledgeand future issues. *Forensic Science International: Genetics* 18: 118-130.

21. Ensenberger, M.G., Lenz, K.A., Matthies, L.K., Hadinoto, G.M., Schienman, J.E., Przech, A.J., Morganti, M.W., Renstrom, D.T., Baker, V.M., Gawrys, K.M., Hoogendoorn, M., Steffen, C.R., Martín, P., Alonso, A., Olson, H.R.,Sprecher, C.J., Storts, D.R. (2016) Developmental validation of the PowerPlex(®) Fusion 6C System. *Forensic Science International: Genetics* 21: 134-144.

22. Kraemer, M., Prochnow, A., Bussmann, M., Scherer, M., Peist, R., Steffen, C. (2017) Developmental validation ofQIAGEN Investigator® 24plex QS Kit and Investigator® 24plex GO! Kit: Two 6-dye multiplex assays for the extended CODIS core loci. *Forensic Science International: Genetics* 29: 9-20.

23. Gettings, K.B., Borsuk, L.A., Ballard, D., Bodner, M., Budowle, B., Devesse, L., King, J., Parson, W., Phillips, C., Vallone, P.M. (2017) STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci.*Forensic Science International: Genetics* 31: 111-117.

24. Ludeman, M.J., Zhong, C., Mulero, J.J., Lagacé, R.E., Hennessy, L.K., Short, M.L., Wang, D.Y. (2018) Developmental validation of GlobalFiler™ PCR amplification kit: a 6-dye multiplex assay designed for amplification of casework samples. *International Journal of Legal Medicine* 132(6): 1555-1573.

25. Gettings, K.B., Borsuk, L.A., Steffen, C.R., Kiesler, K.M., Vallone, P.M. (2018) Sequence-based U.S. populationdata for 27 autosomal STR loci. *Forensic Science International: Genetics* 37: 106-115.

26. Novroski, N.M.M., Woerner, A.E., Budowle, B. (2018) Potential highly polymorphic short tandem repeat markers for enhanced forensic identity testing. *Forensic Science International: Genetics* 37:162-171.

27. Novroski, N.M.M., Wendt, F.R., Woerner, A.E., Bus, M.M., Coble, M., Budowle, B. (2019) Expanding beyond thecurrent core STR loci: An exploration of 73 STR markers with increased diversity for enhanced DNA mixture deconvolution. *Forensic Science International: Genetics* 38: 121-129.

P. Mitochondrial DNA Testing

1. Parson, W., Gusmão, L., Hares, D.R., Irwin, J.A., Mayr, W.R., Morling, N., Pokorak, E., Prinz, M., Salas, A., Schneider, P.M., Parsons, T.J. (2014) DNA Commission of the International Society for Forensic Genetics: **revised and extended guidelines for mitochondrial DNA typing. *Forensic Science International: Genetics* 13:134-142.**

2. Wilson, M.R., DiZinno, J.A., Polanskey, D., Replogle, J., Budowle, B. (1995) Validation of mitochondrial DNAsequencing for forensic casework analysis. *International Journal of Legal Medicine* 108(2): 68-74.

3. Budowle, B., Allard, M.W., Wilson, M.R., Chakraborty, R. (2003) Forensics and mitochondrial DNA: Applications,debates, and foundations. *Annual Review of Genomics and Human Genetics* 4: 119-141.

4. Melton, T. (2004) Mitochondrial DNA heteroplasmy. *Forensic Science Review* 16: 2-19.

5. Danielson, P.B., Sun, H.-Y., Melton, T., Kristinsson, R. (2007) Resolving mtDNA mixtures by denaturing high-performance liquid chromatography and linkage phase determination. *Forensic Science International: Genetics*1(2): 148-153.

6. van der Gaag, K.J., Hoogenboom, J., Sijen, T. (2017) Validation and implementation of MPS mtDNA control regionanalysis for forensic casework: Determination of C-stretch lengths by the FDSTools noise correction

feature. *Forensic Science International: Genetics Supplement Series*. 6: e558-eE559.

7. Peck, M.A., Sturk-Andreaggi, K., Thomas, J.T., Oliver, R.S., Barritt-Ross, S., Marshall, C. (2018) Developmentalvalidation of a Nextera XT mitogenome Illumina MiSeq sequencing method for high-quality samples. *Forensic Science International: Genetics* 34: 25-36.

8. Holland, M.M., Makova, K.D., McElhoe, J.A. (2018) Deep-coverage MPS analysis of heteroplasmic variants withinthe mtGenome allows for frequent differentiation of maternal relatives. *Genes (Basel)* 9(3): 124.

9. Huber, N., Parson, W., Dur, A. (2018) Next generation database search algorithm for forensic mitogenome analyses.
Forensic Science International: Genetics 37: 204-214.

10. Pereira, V., Longobardi, A., Borsting, C. (2018) Sequencing of mitochondrial genomes using the Precision IDmtDNA Whole Genome Panel. *Electrophoresis* 39(21): 2766-2775.

11. Amorim, A., Fernandes, T., Taveira, N. (2019) Mitochondrial DNA in human identification: a review. *PeerJ* 7:e7314.

Q. Y-Chromosome and X-Chromosome Testing

1. Roewer, L., Andersen, M.M., Ballantyne, J., Butler, J.M., Caliebe, A., Corach, D., D'Amato, M.E., Gusmão, L., Hou, Y., de Knijff, P., Parson, W., Prinz, M., Schneider, P.M., Taylor, D., Vennemann, M., Willuweit, S. (2020) DNA commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of Y-STR results in forensic analysis. *Forensic Science International: Genetics* 48: 102308.

2. Gill, P., Brenner, C., Brinkmann, B., Budowle, B., Carracedo, A., Jobling, M.A., de Knijff, P., Kayser, M., Krawczak, M., Mayr, W.R., Morling, N., Olaisen, B., Pascali, V., Prinz, M., Roewer, L., Schneider, P.M., Sajantila,A., Tyler-Smith, C. (2001) DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. *Forensic Science International* 124(1): 5-10.

3. Butler, J.M. (2003) Recent developments in Y-short tandem repeat and Y-single nucleotide polymorphismanalysis. *Forensic Science Review* 15: 91-111.

4. Gusmão, L., Butler, J.M., Carracedo, A., Gill, P., Kayser, M., Mayr, W.R., Morling, N., Prinz, M., Roewer, L.,Tyler-Smith, C., Schneider, P.M. (2006) DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis. *Forensic Science International* 157(2-3): 187-197.

5. Diegoli, T.M. (2015) Forensic typing of short tandem repeat markers on the X and Y chromosomes. *ForensicScience International: Genetics* 18: 140-151.

6. Caliebe, A. and Krawczak, M. (2018) Match probabilities for Y-chromosomal profiles: a paradigm shift. *ForensicScience International: Genetics* 37: 200-203.

7. Tillmar, A.O., Kling, D., Butler, J.M., Parson, W., Prinz, M., Schneider, P.M., Egeland, T., Gusmão, L. (2017) DNACommission of the International Society for Forensic Genetics (ISFG): Guidelines on the use of X-STRs in kinship analysis. *Forensic Science International: Genetics* 29: 269-275.

8. Mulero, J.J., Chang, C.W., Calandro, L.M., Green, R.L., Li, Y., Johnson, C.L., Hennessy, L.K. (2006)

Developmentand validation of the AmpFlSTR Yfiler PCR amplification kit: a male specific, single amplification 17 Y-STR multiplex system. *Journal of Forensic Sciences* 51(1): 64-75.

9. Gopinath, S., Zhong, C., Nguyen, V., Ge, J., Lagacé, R.E., Short, M.L., Mulero, J.J. (2016) Developmental validation of the Yfiler(®) Plus PCR Amplification Kit: An enhanced Y-STR multiplex for casework and databaseapplications. *Forensic Science International: Genetics* 24: 164-175.

10. Thompson, J.M., Ewing, M.M., Frank, W.E., Pogemiller, J.J., Nolde, C.A., Koehler, D.J., Shaffer, A.M., Rabbach, D.R., Fulmer, P.M., Sprecher, C.J., Storts, D.R. (2013) Developmental validation of the PowerPlex® Y23 System: asingle multiplex Y-STR analysis system for casework and database samples. *Forensic Science International: Genetics* 7(2): 240-50.

11. Barbaro, A. and Cormaci, P. (2015) Validation of PowerPlex® Y23 System (Promega) using reduced reactionvolume. *Forensic Science International: Genetics Supplement Series* 5: e373-e374.

R. DNA Databases and Investigative Genetic Genealogy

1. Struyf, P., De Moor, S., Vandeviver, C., Renard, B., van der Beken, T. (2019) The effectiveness of DNA databases in relation to their purpose and content: A systematic review. *Forensic Science International* 301:371-381.

2. Werrett, D.J. (1997) The national DNA database. *Forensic Science International* 88: 33-42.

3. Bieber, F.R., Brenner, C.H., Lazer, D. (2006) Finding criminals through DNA of their relatives. *Science* 312: 1315-1316.

4. Curran, J.M. and Buckleton, J.S. (2008) Effectiveness of familial searches. *Science & Justice* 48(4): 164-167.

5. Guerrini, C.J., Robinson, J.O., Petersen, D., McGuire, A.L. (2018) Should police have access to genetic genealogy databases? Capturing the Golden State Killer and other criminals using a controversial new forensic technique. *PLoSBiology* 16(10): e2006906.

6. Murphy, E. (2018) Law and policy oversight of familial searches in recreational genealogy databases. *ForensicScience International* 292: e5-e9.

7. Phillips, C. (2018) The Golden State Killer investigation and the nascent field of forensic genealogy. *ForensicScience International: Genetics* 36: 186-188.

8. Ram, N., Guerrini, C.J., McGuire, A.L. (2018) Genealogy databases and the future of criminal investigation. *Science*
360: 1078-1079.

9. Greytak, E.M., Kaye, D.H., Budowle, B., Moore, C., Armentrout, S.L. (2018) Privacy and genetic genealogy data.
Science 361:857.

10. Samuel, G., Howard, H.C., Cornel, M., van El, C., Hall, A., Forzano, F., Prainsack, B. (2018) A response to theforensic genetics policy initiative's report "Establishing Best Practice for Forensic DNA Databases." *Forensic Science International: Genetics* 36: e19-e21.

11. Syndercombe Court, D. (2018) Forensic genealogy: Some serious concerns. *Forensic Science International:Genetics* 36: 203-204.

12. Greytak, E.M., Moore, C., Armentrout, S.L. (2019) Genetic genealogy for cold case and active investigations. *Forensic Science International* 299: 103-113.

13. Kennett, D. (2019) Using genetic genealogy databases in missing persons cases and to develop suspect leads inviolent crimes. *Forensic Science International* 301: 107-117.

14. Thomson, J., Clayton, T., Cleary, J., Gleeson, M., Kennett, D., Leonard, M., Rutherford, D. (2020) An empiricalinvestigation into the effectiveness of genetic genealogy to identify individuals in the UK. *Forensic Science International: Genetics* 46: 102263.

S. Statistical Analysis

1. Curran, J.M. (2013) Is forensic science the last bastion of resistance against statistics? *Science & Justice* 53: 251-252.

2. DNA Advisory Board (2000) Statistical and population genetics issues affecting the evaluation of the frequency ofoccurrence of DNA profiles calculated from pertinent population database (s). *Forensic Science Communications*, *2*(3), 1-8. Available at https://archives.fbi.gov/archives/about-us/lab/forensic-science-communications/fsc/july2000/dnastat.htm.

3. Foreman, L.A. and Evett, I.W. (2001). Statistical analyses to support forensic interpretation for a new ten-locus STRprofiling system. *International Journal of Legal Medicine* 114(3): 147-155.

4. Foreman, LA; Champod, C; Evett, IW; et al. (2003) Interpreting DNA evidence: A review. *International StatisticalReview.* 71(3): 473-495.

5. Aitken, C., Roberts, P. and Jackson, G. (2010) Practitioner Guide No. 1. *Fundamentals of Probability and StatisticalEvidence in Criminal Proceedings: Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses*. Royal Statistical Society's Working Group on Statistics and the Law. Available at https://www.maths.ed.ac.uk/~cgga/Guide-1-WEB.pdf.

6. Biedermann, A.; Taroni, F. (2012) Bayesian networks for evaluating forensic DNA profiling evidence: A review andguide to literature. *Forensic Science International-Genetics.* 6(2): 147-157.

7. Puch-Solis, R., Roberts, P., Pope, S. and Aitken, C. (2012) Practitioner Guide No. 2. *Assessing the Probative Valueof DNA Evidence: Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses*. Royal Statistical
Society's Working Group on Statistics and the Law. Available at
https://www.maths.ed.ac.uk/~cgga/Guide-2-WEB.pdf.

8. Roberts, P. and Aiken, C. (2014) Practitioner Guide No. 3. *The Logic of Forensic Proof: Inferential Reasoning in Criminal Evidence and Forensic Science: Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses*. Royal Statistical Society's Working Group on Statistics and the Law. Available at https://rss.org.uk/RSS/media/File-library/Publications/rss-inferential-reasoning-criminal-evidence-forensic-science.pdf.

9. Jackson, G., Aitken, C., Roberts, P. (2014) Practitioner Guide No. 4. *Case Assessment and Interpretation of ExpertEvidence: Guidance for Judges, Lawyers, Forensic Scientists and Expert Witnesses*. Royal Statistical Society's Working Group on Statistics and the Law. Available at https://rss.org.uk/RSS/media/File-library/Publications/rss- case-assessment-interpretation-expert-evidence.pdf.

T. Population Genetics

1. Balding, D.J. and Nichols, R.A. (1994) DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. *Forensic Science International* 64:125-140.

2. Hardy, G.H. (1908) Mendelian proportions in a mixed population. *Science* 28: 49-50.

3. Stern, C. (1943) The Hardy-Weinberg law. *Science* 97: 137-138.

4. Weir, B.S. and Cockerham, C.C. (1984) Estimating F-statistics for the analysis of population structure. *Evolution* 38(6): 1358-1370.

5. Guo, S.W. and Thompson, E.A. (1992) Performing the exact test of Hardy-Weinberg proportion for multiplealleles. *Biometrics* 48(2): 361-372.

6. Weir, B.S. (1994) The effects of inbreeding on forensic calculations. *Annual Review of Genetics* 28: 597-621.

7. Buckleton, J.S., Curran, J.M., Walsh, S.J. (2006) How reliable is the sub-population model in DNA testimony? *Forensic Science International* 157(2-3): 144-148.

8. Curran, J.M., Walsh, S.J., Buckleton, J. (2007) Empirical testing of estimated DNA frequencies. *Forensic ScienceInternational: Genetics* 1: 267-272.

9. Steele, C.D., Syndercombe-Court, D., Balding, D.J. (2014) Worldwide F(ST) estimates relative to five continental-scale populations. *Annals of Human Genetics* 78(6): 468-477.

10. Buckleton, J., Curran, J., Goudet, J., Taylor, D., Thiery, A., Weir, B.S. (2016) Population-specific FST values forforensic STR markers: A worldwide survey. *Forensic Science International: Genetics* 23: 91-100.

U. DNA Phenotyping (Ancestry, Appearance, Age)

1. Kayser, M. and Schneider, P.M. (2009) DNA-based prediction of human externally visible characteristics in forensics: motivations, scientific challenges, and ethical considerations. *Forensic Science International: Genetics* 3(3): 154-161.

2. Graham, Eleanor A. M. (2008) DNA reviews: predicting phenotype. *Forensic Science Medicine and Pathology*. 4(3): 196-199.

3. Walsh, S., Liu, F., Wollstein, A., Kovatsi, L., Ralf, A., Kosiniak-Kamysz, A., Branicki, W., Kayser, M. (2013) TheHIrisPlex system for simultaneous prediction of hair and eye colour from DNA. *Forensic Science International: Genetics* 7(1): 98-115.

4. Chaitanya, L., Breslin, K., Zuñiga, S., Wirken, L., Pośpiech, E., Kukla-Bartoszek, M., Sijen, T., Knijff, P., Liu, F.,Branicki, W., Kayser, M., Walsh, S. (2018) The HIrisPlex-S system for eye, hair and skin colour

prediction from DNA: Introduction and forensic developmental validation. *Forensic Science International: Genetics* 35: 123-135.

5. Vidaki, A. and Kayser, M. (2017) From forensic epigenetics to forensic epigenomics: broadening DNA investigativeintelligence. *Genome Biology* 18(1): 238.

6. Vidaki, A. and Kayser, M. (2018) Recent progress, methods and perspectives in forensic epigenetics. *ForensicScience International: Genetics* 37: 180-195.

7. Parson, W. (2018) Age estimation with DNA: from forensic DNA fingerprinting to forensic (epi)genomics: a mini-review. Gerontology 64(4): 326-332.

8. Naue, J., Hoefsloot, H.C.J., Kloosterman, A.D., Verschure, P.J. (2018) Forensic DNA methylation profiling fromminimal traces: How low can we go? *Forensic Science International: Genetics* 33: 17-23.

9. Scudder, N., McNevin, D., Kelty, S.F., Walsh, S.J., Robertson, J. (2018) Forensic DNA phenotyping: Developing amodel privacy impact assessment. *Forensic Science International: Genetics* 34: 222-230.

10. Pośpiech, E., Chen, Y., Kukla-Bartoszek, M., Breslin, K., Aliferi, A., Andersen, J.D., Ballard, D., Chaitanya, L., Freire-Aradas, A., van der Gaag, K.J., Girón-Santamaría, L., Gross, T.E., Gysi, M., Huber, G., Mosquera-Miguel, A., Muralidharan, C., Skowron, M., Carracedo, Á., Haas, C., Morling, N., Parson, W., Phillips, C., Schneider, P.M.,Sijen, T., Syndercombe-Court, D., Vennemann, M., Wu, S., Xu, S., Jin, L., Wang, S., Zhu, G., Martin, N.G., Medland, S.E., Branicki, W., Walsh, S., Liu, F., Kayser, M. (EUROFORGEN-NoE Consortium) (2018) Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. *Forensic Science International: Genetics* 37: 241-251.

11. Wienroth, M. (2018) Governing anticipatory technology practices: forensic DNA phenotyping and the forensicgenetics community in Europe. *New Genetics and Society* 37(2): 137-152.

12. Samuel, G. and Prainsack, B. (2019) Forensic DNA phenotyping in Europe: views "on the ground" from those whohave a professional stake in the technology. *New Genetics and Society* 38(2): 119-141.

13. Katsara, M.-A, and Nothnagel, M. (2019) True colors: A literature review on spatial distribution of eye and hairpigmentation. *Forensic Science International: Genetics* 39: 109-118.

14. Xiong, Z., Dankova, G., Howe, L.J., Lee, M.K., Hysi, P.G., de Jong, M.A., Zhu, G., Adhikari, K., Li, D., Li, Y., Pan, B., Feingold, E., Marazita, M.L., Shaffer, J.R., McAloney, K., Xu, S.H., Jin, L., Wang, S., de Vrij, F.M., Lendemeijer, B., Richmond, S., Zhurov, A., Lewis, S., Sharp, G.C., Paternoster, L., Thompson, H., Gonzalez-Jose, R., Bortolini, M.C., Canizales-Quinteros, S., Gallo, C., Poletti, G., Bedoya, G., Rothhammer, F., Uitterlinden, A.G., Ikram, M.A., Wolvius, E., Kushner, S.A., Nijsten, T.E., Palstra, R.T., Boehringer, S., Medland, S.E., Tang, K., Ruiz-Linares, A., Martin, N.G., Spector, T.D., Stergiakouli, E., Weinberg, S.M., Liu, F., Kayser, M. (2019) Novel genetic loci affecting facial shape variation in humans. *eLIFE* 8: e49898.

15. Peng, F., Zhu, G., Hysi, P.G., Eller, R.J., Chen, Y., Li, Y., Hamer, M.A., Zeng, C., Hopkins, R.L., Jacobus, C.L., Wallace, P.L., Uitterlinden, A.G., Ikram, M.A., Nijsten, T., Duffy, D.L., Medland, S.E., Spector, T.D., Walsh, S., Martin, N.G., Liu, F., Kayser, M. (2019) Genome-wide association studies identify multiple genetic loci influencingeyebrow color variation in Europeans. *Journal of Investigative Dermatology* 139(7): 1601-1605.

16. Liu, F., Zhong, K., Jing, X., Uitterlinden, A.G., Hendriks, A.E.J., Drop, S.L.S., Kayser, M. (2019) Update on thepredictability of tall stature from DNA markers in Europeans. *Forensic Science International:*

Genetics 42: 8-13.

17. Kukla-Bartoszeka, M., Pośpiech, E., Woźniak, A., Boroń, M., Karłowska-Pik, J., Teisseyre, P., Zubańska, M., Bronikowska, A., Grzybowski, T., Płoski, R., Spólnicka, M., Branicki, W. (2019) DNA-based predictive models forthe presence of freckles. *Forensic Science International: Genetics* 42: 252-259.

18. Heidegger, A., Xavier, C., Niederstätter, H., de la Puente, M., Pośpiech, E., Pisarek, A., Kayser, M., Branicki, W., Parson, W. (VISAGE Consortium) (2020) Development and optimization of the VISAGE basic prototype tool forforensic age estimation. *Forensic Science International: Genetics* 48: 102322.

19. Palencia-Madrid, L., Xavier, C., de la Puente, M., Hohoff, C., Phillips, C., Kayser, M., Parson, W. (2020) Evaluation of the VISAGE basic tool for appearance and ancestry prediction using PowerSeq chemistry on theMiSeq FGx System. *Genes (Basel)* 11(6): 708.

20. Xavier, C., de la Puente, M., Mosquera-Miguel, A., Freire-Aradas, A., Kalamara, V., Vidaki, A., Gross, T.E., Revoir, A., Pośpiech, E., Kartasińska, E., Spólnicka, M., Branicki, W., Ames, C.E., Schneider, P.M., Hohoff, C.,Kayser, M., Phillips, C., Parson, W. (VISAGE Consortium) (2020) Development and validation of the VISAGE
AmpliSeq basic tool to predict appearance and ancestry from DNA. *Forensic Science International: Genetics* 48:102336.

V. New Technologies (Rapid DNA, Massively Parallel Sequencing)

1. Butler, J.M. (2015) The future of forensic DNA analysis. *Philosophical Transactions of the Royal Society of London Series B, Biological Sciences* 370: 20140252.

2. Gill, P. (2001) An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensicpurposes. *International Journal of Legal Medicine* 114: 204-210.

3. Gill, P., Werrett, D.J., Budowle, B., Guerrieri, R. (2004) An assessment of whether SNPs will replace STRs in national DNA databases--joint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). *Science &Justice* 44(1): 51-53.

4. Butler, J.M., Coble, M.D., Vallone, P.M. (2007) STRs vs SNPs: thoughts on the future of forensic DNAtesting. *Forensic Science Medicine and Pathology* 3: 200-205.

5. Blackman, S., Dawnay, N., Ball, G., Stafford-Allen, B., Tribble, N., Rendell, P., Neary, K., Hanson, E.K., Ballantyne, J., Kallifatidis, B., Mendel, J., Mills, D.K., Wells, S. (2015) Developmental validation of the ParaDNA(®) Intelligence System-A novel approach to DNA profiling. *Forensic Science International: Genetics* 17:137-148.

6. Date-Chong, M., Hudlow, W.R., Buoncristiani, M.R. (2016) Evaluation of the RapidHIT 200 and RapidHIT GlobalFiler® Express kit for fully automated STR genotyping. *Forensic Science International: Genetics* 23: 1-8.

7. Parson, W., Ballard, D., Budowle, B., Butler, J.M., Gettings, K.B., Gill, P., Gusmão, L., Hares, D.R., Irwin, J.A.,King, J.L., Knijff, P., Morling, N., Prinz, M., Schneider, P.M., Neste, C.V., Willuweit, S., Phillips, C. (2016) Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the

International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. *Forensic Science International: Genetics* 22: 54-63.

8. van der Gaag, K.J., de Leeuw, R.H., Hoogenboom, J., Patel, J., Storts, D.R., Laros, J.F.J., de Knijff, P. (2016)Massively parallel sequencing of short tandem repeats-Population data and mixture analysis results for the PowerSeq™ system. *Forensic Science International: Genetics* 24: 86-96.

9. Bruijns, B., van Asten, A., Tiggelaar, R., Gardeniers, H. (2016) Microfluidic devices for forensic DNA analysis: areview. *Biosensors (Basel)* 6(3): 41.

10. Della Manna, A., Nye, J.V., Carney, C., Hammons, J.S., Mann, M., Al Shamali, F., Vallone, P.M., Romsos, E.L., Marne, B.A., Tan, E., Turingan, R.S., Hogan, C., Selden, R.F., French, J.L. (2016) Developmental validation of theDNAscan™ Rapid DNA Analysis™ instrument and expert system for reference sample processing. *Forensic Science International: Genetics* 25: 145-156.

11. Mapes, A.A., Kloosterman, A.D., de Poot, C.J., van Marion, V. (2016) Objective data on DNA success rates can aidthe selection process of crime samples for analysis by rapid mobile DNA technologies. *Forensic Science International* 264: 28-33.

12. Moreno, L.I., Brown, A.L., Callaghan, T.F. (2017) Internal validation of the DNAscan/ANDE Rapid DNA Analysisplatform and its associated PowerPlex® 16 high content DNA biochip cassette for use as an expert system with reference buccal swabs. *Forensic Science International: Genetics* 29: 100-108.

13. Wiley, R., Sage, K., LaRue, B., Budowle, B. (2017) Internal validation of the RapidHIT® ID system. *ForensicScience International: Genetics* 31: 180-188.

14. Mehta, B., Daniel, R., Phillips, C., McNevin, D. (2017) Forensically relevant SNaPshot® assays for human DNASNP analysis: a review. *International Journal of Legal Medicine* 131(1): 21-37.

15. Jäger, A.C., Alvarez, M.L., Davis, C.P., Guzmán, E., Han, Y., Way, L., Walichiewicz, P., Silva, D., Pham, N., Caves, G., Bruand, J., Schlesinger, F., Pond, S.J.K., Varlaro, J., Stephens, K.M., Holt, C.L. (2017) Developmentalvalidation of the MiSeq FGx Forensic Genomics System for targeted next generation sequencing in forensic DNAcasework and database laboratories. *Forensic Science International: Genetics* 28: 52-70.

16. Phillips, C., Gettings, K.B., King, J.L., Ballard, D., Bodner, M., Borsuk, L., Parson, W. (2018) "The devil's in the detail": Release of an expanded, enhanced and dynamically revised forensic STR sequence guide. *Forensic ScienceInternational: Genetics* 34: 162-169.

17. Alonso, A., Barrio, P.A., Müller, P., Köcher, S., Berger, B., Martin, P., Bodner, M., Willuweit, S., Parson, W.,Roewer, L., Budowle, B. (2018) Current state-of-art of STR sequencing in forensic genetics. *Electrophoresis* 39(21): 2655-2668.

18. Bruijns, B., Tiggelaar, R., Gardeniers, H. (2018) Massively parallel sequencing techniques for forensics: a review.
Electrophoresis 39(21): 2642-2654.

19. Morrison, J., Watts, G., Hobbs, G., Dawnay, N. (2018) Field-based detection of biological samples for forensic analysis: Established techniques, novel tools, and future innovations. *Forensic Science International* 285: 147-160.

20. Liu, Y.-Y. and Harbison, S. (2018) A review of bioinformatic methods for forensic DNA analyses. *Forensic ScienceInternational: Genetics* 33: 117-128.

21. Buscaino, J., Barican, A., Farrales, L., Goldman, B., Klevenberg, J., Kuhn, M., Lin, F., Nguyen, P., Salceda, S., Schueren, R., Smith, C., Troup, C., Tsou, D., Vangbo, M., King, D. (2018) Evaluation of a rapid DNA process withthe RapidHIT® ID system using a specialized cartridge for extracted and quantified human DNA. *Forensic Science International: Genetics* 34: 116-127.

22. Shackleton, D., Pagram, J., Ives, L., Vanhinsbergh, D. (2018) Development and validation of the RapidHIT™ 200utilising NGMSElect™ Express for the processing of buccal swabs. *Forensic Science International* 289: 244-252.

23. Shackleton, D., Gray, N., Ives, L., Malsom, S., Vanhinsbergh, D. (2019) Development of RapidHIT® ID using NGM SElect™ Express chemistry for the processing of reference samples within the UK criminal justice system.*Forensic Science International* 295: 179-188.

24. Shackleton, D., Pagram, J., Andrews, N., Malsom, S., Ives, L., Vanhinsbergh, D. (2019) Development of enhancedsensitivity protocols on the RapidHIT™ 200 with a view to processing casework material. *Science & Justice* 59: 411-417.

25. Sharma, V., Chow, H.Y., Siegel, D., Wurmbach, E. (2017) Qualitative and quantitative assessment of Illumina'sforensic STR and SNP kits on MiSeq FGx. *PLoS ONE* 12(11): e0187932.

26. Wu, J., Li, J.L., Wang, M.L., Li, J.P., Zhao, Z.C., Wang, Q., Yang, S.D., Xiong, X., Yang, J.L., Deng, Y.J. (2019) Evaluation of the MiSeq FGx system for use in forensic casework. *International Journal of Legal Medicine* 133(3):689-697.

27. de Knijff, P. (2019) From next generation sequencing to now generation sequencing in forensics. *Forensic ScienceInternational: Genetics* 38: 175-180.

28. Morgan, R., Illidge, S., Wilson-Wilde, L. (2019) Assessment of the potential investigative value of a decentralizedrapid DNA workflow for reference DNA samples. *Forensic Science International* 294: 140-149.

29. Mapes, A.A., Stoel, R.D., de Poot, C.J., Vergeer, P., Huyck, M. (2019) Decision support for using mobile RapidDNA analysis at the crime scene. *Science & Justice* 59: 29-45.

30. Carney, C., Whitney, S., Vaidyanathan, J., Persick, R., Noel, F., Vallone, P.M., Romsos, E.L., Tan, E., Grover, R., Turingan, R.S., French, J.L., Selden, R.F. (2019) Developmental validation of the ANDE™ rapid DNA system withFlexPlex™ assay for arrestee and reference buccal swab processing and database searching. *Forensic Science International: Genetics* 40: 120-130.

31. Romsos, E.L., French, J.L., Smith, M., Figarelli, V., Harran, F., Vandegrift, G., Moreno, L.I., Callaghan, T.F., Brocato, J., Vaidyanathan, J., Pedroso, J.C., Amy, A., Stoiloff, S., Morillo, V.H., Czetyrko, K., Johnson, E.D., deTagyos, J., Murray, A., Vallone, P.M. (2020) Results of the 2018 Rapid DNA Maturity Assessment. *Journal of Forensic Sciences* 65(3): 953-959.

W. DNA Transfer and Activity Level Reporting

1. van Oorschot, R.A.H., Szkuta, B., Meakin, G.E., Kookshoorn, B., Goray, M. (2019) DNA transfer in forensic science: a review. *Forensic Science International: Genetics* 38: 140-166.

2. van Oorschot, R.A. and Jones, M.K. (1997) DNA fingerprints from fingerprints. *Nature* 387: 767.

3. Lowe, A., Murray, C., Whitaker, J., Tully, G. and Gill, P. (2002) The propensity of individuals to deposit DNA andsecondary transfer of low level DNA from individuals to inert surfaces. *Forensic Science International* 129: 25-34.

4. Wickenheiser, R.A. (2002) Trace DNA: a review, discussion of theory, and application of the transfer of tracequantities of DNA through skin contact. *Journal of Forensic Sciences* 47(3): 442-450.

5. Port, N.J., Bowyer, V.L., Graham, E.A.M., Batuwangala, M.S. and Rutty, G.N. (2006) How Long Does It Take a Static Speaking Individual to Contaminate the Immediate Environment? *Forensic Science, Medicine, and Pathology*2(3):157-163.

6. Phipps, M., and Petricevic, S. (2007) The tendency of individuals to transfer DNA to handled items. *ForensicScience International* 168(2-3):162–168.

7. Malsom, S., Flanagan, N., McAlister, C., and Dixon, L. (2009) The prevalence of mixed DNA profiles in fingernailsamples taken from couples who co-habit using autosomal and Y-STRs. *Forensic Science International: Genetics* 3(2):57-62.

8. Goray, M., Mitchell, R.J., and van Oorschot, R.A.H. (2010) Investigation of secondary DNA transfer of skin cellsunder controlled test conditions. *Legal Medicine* 12(3): 117–120.

9. Goray, M., Eken, E., Mitchell, R. J., and van Oorschot, R.A.H. (2010) Secondary DNA transfer of biologicalsubstances under varying test conditions. *Forensic Science International: Genetics* 4(2):62-67.

10. Daly, D.J., Murphy, C., and McDermott, S.D. (2012) The transfer of touch DNA from hands to glass, fabric andwood. *Forensic Science International: Genetics* 6(1):41-46.

11. Meakin, G. and Jamieson, A. (2013) DNA transfer: review and implications for casework. *Forensic ScienceInternational: Genetics* 7: 434-443.

12. Ballantyne, K.N., Poy, A.L. and van Oorschot, R.A.H. (2013) Environmental DNA monitoring: beware of thetransition to more sensitive typing methodologies. *Australian Journal of Forensic Sciences* 45(3): 323-340.

13. Verdon, T.J., Mitchell, R.J. and van Oorschot, R.A. (2013) The influence of substrate on DNA transfer andextraction efficiency. *Forensic Science International: Genetics* 7(1): 167-175.

14. van Oorschot, R.A.H., Glavich, G., and Mitchell, R.J. (2014) Persistence of DNA deposited by the original user onobjects after subsequent use by a second person. *Forensic Science International: Genetics* 8(1): 219–225.

15. Cale, C.M., Earll, M.E., Latham, K.E., and Bush, G.L. (2015) Could Secondary DNA Transfer Falsely

PlaceSomeone at the Scene of a Crime? *Journal of Forensic Sciences* 61(1):196-203.

16. Lehmann, V.J.., Mitchell, R.J., Ballantyne, K.N., and van Oorschot, R.A.H. (2015) Following the transfer of DNA:How does the presence of background DNA affect the transfer and detection of a target source of DNA? *Forensic Science International: Genetics.* 19:68-75.

17. Fonneløp, A.E., Egeland, T., and Gill, P. (2015) Secondary and subsequent DNA transfer during criminalinvestigation. *Forensic Science International: Genetics* 17:155-162.

18. Kamphausen, T., Fandel, S.B., Gutmann, J.S., Bajanowski, T., and Poetsch, M. (2015) Everything clean? Transferof DNA traces between textiles in the washtub. *International Journal of Legal Medicine* 129(4):709-714.

19. ENFSI (2015) ENFSI Guideline for Evaluative Reporting in Forensic Science; available at http://enfsi.eu/wp-content/uploads/2016/09/m1_guideline.pdf.

20. Goray, M. and van Oorschot, RA. (2015) The complexities of DNA transfer during a social setting. *Legal Medicine* 17(2): 82-91.

21. Lapointe, M., Rogic, A., Bourgoin, S., Jolicoeur, C. and Séguin, D. (2015) Leading-edge forensic DNA analyses andthe necessity of including crime scene investigators, police officers and technicians in a DNA elimination database. *Forensic Science International: Genetics* 19: 50-55.

22. Taylor, D., Abarno, D., Rowe, E., Rask-Nielsen, L. (2016) Observations of DNA transfer within an operationalForensic Biology Laboratory. *Forensic Science International: Genetics* 23: 33-49.

23. Jones, S., Scott, K., Lewis, J., Davidson, G., Allard, J. E., Lowrie, C., McBride, B.M., McKenna, L., Teppett, G.,Rogers, C., Clayson, N. and Baird, A. (2016) DNA transfer through nonintimate social contact. *Science & Justice*56(2), 90-95.

24. Noël, S., Lagacé, K., Rogic, A., Granger, D., Bourgoin, S., Jolicoeur, C., and Séguin, D. (2016) DNA transferduring laundering may yield complete genetic profiles. *Forensic Science International: Genetics* 23:240-247.

25. Breathnach, M., Williams, L., McKenna, L. and Moore, E. (2016) Probability of detection of DNA deposited by habitual wearer and/or the second individual who touched the garment. *Forensic Science International: Genetics* 20:53-60.

26. Helmus, J., Bajanowski, T., Poetsch, M. (2016) DNA transfer-a never ending story: a study on scenarios involving asecond person as carrier. *International Journal of Legal Medicine* 130(1): 121-125.

27. Oldoni, F., Castella, V., Hall, D. (2016) Shedding light on the relative DNA contribution of two persons handlingthe same object. *Forensic Science International: Genetics* 24: 148-157.

28. Goray, M., Fowler, S., Szkuta, B., van Oorschot, R.A.H. (2016) Shedder status – an analysis of self and non-self DNA in multiple handprints deposited by the same individuals over time. *Forensic Science International: Genetics*23: 190-196.

29. Biedermann, A. and Hicks, T. (2016) The importance of critically examining the level of propositions whenevaluating forensic DNA results. *Frontiers in Genetics* 7: 8.

30. Biedermann, A., Champod, C., Jackson, G., Gill, P., Taylor, D., Butler, J., Morling, N., Hicks, T., Vuille, J., Taroni,
F. (2016) Evaluation of forensic DNA traces when propositions of interest relate to activities: analysis and discussion of recurrent concerns. *Frontiers in Genetics* 7: 215.

31. Taylor, D., Biedermann, A., Samie, L., Pun, K.M., Hicks, T. and Champod, C. (2017) Helping to distinguish primary from secondary transfer events for trace DNA. *Forensic Science International: Genetics* 28: 155-177.

32. Steensma, K., Ansell, R., Clarisse, L., Connolly, E., Kloosterman, A.D., McKenna, L.G., van Oorschot, R.A.H., Szkuta, B. and Kokshoorn, B. (2017) An inter-laboratory comparison study on transfer, persistence and recoveryof DNA from cable ties. *Forensic Science International: Genetics* 31: 95-104.

33. Meakin, G.E., Butcher, E.V., van Oorschot, R.A.H., Morgan, R.M. (2017) Trace DNA evidence dynamics: Aninvestigation into the deposition and persistence of directly- and indirectly-transferred DNA on regularly-usedknives. *Forensic Science International: Genetics* 29: 38-47.

34. Pfeifer, C.M. and Wiegand, P. (2017) Persistence of touch DNA on burglary-related tools. *International Journal ofLegal Medicine* 131(4): 941-953.

35. Kokshoorn, B., Blankers, B. J., de Zoete, J., & Berger, C. E. H. (2017) Activity level DNA evidence evaluation: Onpropositions addressing the actor or the activity. *Forensic Science International* 278: 115–124.

36. Stella, C.J., Mitchell, R.J., & van Oorschot, R. A. H. (2017) Hand activities during robberies—Relevance to consideration of DNA transfer and detection. *Forensic Science International: Genetics Supplement Series* 6: e3-e5.

37. Szkuta, B., Ballantyne, K.N., and van Oorschot, R.A.H. (2017) Transfer and persistence of DNA on the hands andthe influence of activities performed. *Forensic Science International: Genetics* 28:10-20.

38. Kanokwongnuwut, P., Martin, B., Kirkbride, K.P., and Linacre, A. (2018) Shedding light on shedders. *ForensicScience International: Genetics* 36:20-25.

39. Szkuta, B., Ballantyne, K.N., Kokshoorn, B., and van Oorschot, R.A.H. (2018) Transfer and persistence of non-selfDNA on hands over time: Using empirical data to evaluate DNA evidence given activity level propositions. *Forensic Science International: Genetics* 33:84-97.

40. Taylor, D., Kokshoorn, B. and Biedermann, A. (2018) Evaluation of forensic genetics findings given activity levelpropositions: A review. *Forensic Science International: Genetics* 36: 34-49.

41. Taylor, D., Biedermann, A., Hicks, T. and Champod, C. (2018) A template for constructing Bayesian networks in forensic biology cases when considering activity level propositions. *Forensic Science International: Genetics* 33:136-146.

42. Kokshoorn, B., Aarts, L.H.J., Ansell, R., Connolly, E., Drotz, W., Kloosterman, A.D., McKenna, L.G., Szkuta, B.,van Oorschot, R.A.H. (2018) Sharing data on DNA transfer, persistence, prevalence and recovery: Arguments for harmonization and standardization. *Forensic Science International: Genetics* 37: 260-269.

43. Voskoboinik, L., Amiel, M., Reshef, A., Gafny, R., Barash, M. (2018) Laundry in a washing machine as a

mediatorof secondary and tertiary DNA transfer. *International Journal of Legal Medicine* 132(2): 373-378.

44. Burrill, J., Daniel, B., Frascione, N. (2019) A review of trace "touch DNA" deposits: Variability factors and anexploration of cellular composition. *Forensic Science International: Genetics* 39:8–18.

45. Gosch, A. and Courts, C. (2019) On DNA transfer: the lack and difficulty of systematic research and how to do itbetter. *Forensic Science International: Genetics* 40: 24-36.

46. Rolo, M., Sampaio, L., Balsa, F., Bento, A.M., Gouveia, N., Serra, A., Brito, P., Lopes, V., Sao-Bento, M., Bogas, V., Cunha, P., Porto, M. J., Carneiro de Sousa, M.J. (2019) Assessment of individual shedder status and backgroundDNA on objects: Direct or indirect transfer? *Forensic Science International Genetics Supplement Series* 7(1): 622- 623.

47. Romero-García, C., Rosell-Herrera, R., Revilla, C.J., Baeza-Richer, C., Gomes, C., Palomo-Díez, S., Arroyo-Pardo,E., López-Parra, A.M. (2019) Effect of the activity in secondary transfer of DNA profiles. *Forensic Science International: Genetics Supplement Series* 7(1): 578–579.

48. Szkuta, B., Ansell, R., Boiso, L., Connolly, E., Kloosterman, A.D., Kokshoorn, B., McKenna, L.G., Steensma, K. and van Oorschot, R.A.H. (2019) Assessment of the transfer, persistence, prevalence and recovery of DNA traces from clothing: An inter-laboratory study on worn upper garments. *Forensic Science International: Genetics* 42: 56-68.

49. Taylor, D., Samie, L., Champod, C. (2019) Using Bayesian networks to track DNA movement through complextransfer scenarios. *Forensic Science International: Genetics* 42: 69-80.

50. Burrill, J., Daniel, B. & Frascione, N. (2020) Illuminating touch deposits through cellular characterization of handrinses and body fluids with nucleic acid fluorescence. *Forensic Science International: Genetics* 46:102269.

51. Gosch, A., Euteneuer, J., Preuss-Wossner, J., Courts, C. (2020) DNA transfer to firearms in alternative realistichandling scenarios. *Forensic Science International: Genetics* 48: 102355.

52. Gill, P., Hicks, T., Butler, J.M., Connolly, E., Gusmão, L., Kokshoorn, B., Morling, N., van Oorschot, R.A.H., Parson, W., Prinz, M., Schneider, P.M., Sijen, T. and Taylor, D. (2020) 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. *ForensicScience International: Genetics* 44: 102186.

53. Samie, L., Taroni, F., Champod, C. (2020) Estimating the quantity of transferred DNA in primary and secondarytransfers. *Science & Justice* 60(2): 128-135.

54. Samie, L., Champod, C., Taylor, D., Taroni, F. (2020) The use of Bayesian Networks and simulation methods to identify the variables impacting the value of evidence assessed under activity level propositions in stabbing cases.*Forensic Science International: Genetics* 48: 102334.

X. Non-Human DNA Testing

1. Linacre, A., Gusmão, L., Hecht, W., Hellmann, A.P., Mayr, W.R., Parson, W., Prinz, M., Schneider, P.M., Morling, N. (2011) ISFG: recommendations regarding the use of non-human (animal) DNA in forensic genetic investigations. *Forensic Science International: Genetics* 5(5): 501-505.

2. Budowle, B., Schutzer, S.E., Einseln, A., Kelley, L.C., Walsh, A.C., Smith, J.A., Marrone, B.L., Robertson, J.,Campos, J. (2003) Building microbial forensics as a response to bioterrorism. *Science* 301: 1852-1853.

3. Budowle, B., Garofano, P., Hellman, A., Ketchum, M., Kanthaswamy, S., Parson, W., van Haeringen, W., Fain, S.,Broad, T. (2005) Recommendations for animal DNA forensic and identity testing. *International Journal of Legal Medicine* 119(5): 295-302.

4. Budowle, B., Murch, R., Chakraborty, R. (2005) Microbial forensics: the next forensic challenge. *InternationalJournal of Legal Medicine* 119(6): 317-330.

5. Menotti-Raymond, M.A., David, V.A., Wachter, L.A., Butler, J.M., O'Brien, S.J. (2005) An STR forensic typingsystem for genetic individualization of domestic cat (*Felis catus*) samples. *Journal of Forensic Sciences* 50(5): 1061-1070.

6. Ogden, R. (2010) Forensic science, genetics and wildlife biology: getting the right mix for a wildlife DNA forensicslab. *Forensic Science Medicine and Pathology* 6(3): 172-179.

7. Alacs, E.A., Georges, A., FitzSimmons, N.N., Robertson, J. (2010) DNA detective: a review of molecularapproaches to wildlife forensics. *Forensic Science Medicine and Pathology* 6(3): 180-194.

8. Linacre, A. and Tobe, S.S. (2011) An overview to the investigative approach to species testing in wildlife forensicscience. *Investigative Genetics* 2(1): 2. doi: 10.1186/2041-2223-2-2.

9. Iyengar, A. (2014) Forensic DNA analysis for animal protection and biodiversity conservation: A review. *Journalfor Nature Conservation.* 22(3): 195-205.

10. Iyengar, A. and Hadi, S. (2014) Use of non-human DNA analysis in forensic science: a mini review. *Medicine,Science, and the Law* 54(1): 41-50.

11. Ogden, R. and Linacre, A. (2015) Wildlife forensic science: A review of genetic geographic origin assignment. *Forensic Science International: Genetics* 18: 152-159.

12. Arenas, M., Pereira, F., Oliveira, M., Pinto, N., Lopes, A.M., Gomes, V., Carracedo, A., Amorim, A. (2017)Forensic genetics and genomics: Much more than just a human affair. *PLoS Genetics* 13(9): e1006960.

13. Oliveira, M. and Amorim, A. (2018) Microbial forensics: new breakthroughs and future prospects. *AppliedMicrobiology and Biotechnology* 102(24): 10377-10391.

14. Metcalf, J.L. (2019) Estimating the postmortem interval using microbes: Knowledge gaps and a path to technologyadoption. *Forensic Science International: Genetics* 38: 211-218.

15. Berger, B., Heinrich, J., Niederstätter, H., Hecht, W., Morf, N., Hellmann, A., Rohleder, U., Schleenbecker, U., Berger, C., Parson, W (The CaDNAP Group) (2019) Forensic characterization and statistical considerations of theCaDNAP 13-STR panel in 1,184 domestic dogs from Germany, Austria, and Switzerland. *Forensic Science International: Genetics* 42: 90-98.

Y. Method Validation, Quality Control, and Human Factors

1. Kloosterman, A., Sjerps, M., & Quak, A. (2014) Error rates in forensic DNA analysis: Definition, numbers, impact and communication. *Forensic Science International: Genetics* 12: 77-85.

2. Wallin, J.M., Buoncristiani, M.R., Lazaruk, K.D., Fildes, N., Holt, C.L. and Walsh, P.S. (1998) TWGDAM validation of the AmpFlSTR Blue PCR amplification kit for forensic casework analysis. *Journal of ForensicSciences* 43(4): 854-870.

3. Budowle, B., Bottrell, M.C., Bunch, S.G., Fram, R., Harrison, D., Meagher, S., Oien, C.T., Peterson, P.E., Seiger, D.P., Smith, M.B., Smrz, M.A., Soltis, G.L., Stacey, R.B. (2009) A perspective on errors, bias, and interpretation inthe forensic sciences and direction for continuing advancement. *Journal of Forensic Sciences* 54(4): 798-809.

4. Buckleton, J. (2009) Validation issues around DNA typing of low level DNA. *Forensic Science International:Genetics* 3(4): 255-260.

5. Thompson, W.C. (2009) Painting the target around the matching profile: the Texas sharpshooter fallacy in forensicDNA interpretation. *Law, Probability and Risk* 8(3): 257-276.

6. Dror, I.E and Hampikian G. (2011) Subjectivity and bias in forensic DNA mixture interpretation. *Science andJustice* 51: 204-208.

7. Thompson, W.C. (2011) What role should investigative facts play in the evaluation of scientific evidence? *Australian Journal of Forensic Sciences* 43(2-3): 123-134.

8. Dror, I. E. (2012). Cognitive forensics and experimental research about bias in forensic casework. *Science &Justice* 52(2): 128-130.

9. Kassin, S.M., Dror, I.E., Kukucka, J. (2013) The forensic confirmation bias: Problems, perspectives, and proposedsolutions. *Journal of Applied Research in Memory and Cognition* 2(1): 42-52.

10. ENFSI (2014) Guidelines for the single laboratory validation of instrumental and human based methods in forensicscience. Available at http://enfsi.eu/wp-content/uploads/2017/06/Guidance-QCC-VAL-002.pdf.

11. Hansson, O., Gill, P., Egeland, T. (2014) STR-validator: an open source platform for validation and process control. *Forensic Science International: Genetics* 13: 154-166.

12. Dror, I.E. (2015) Cognitive neuroscience in forensic science: understanding and utilizing the human element. *Philosophical Transactions of the Royal Society of London Series B, Biological Sciences* 370: 20140255.

13. Bodner, M., Bastisch, I., Butler, J.M., Fimmers, R., Gill, P., Gusmão, L., Morling, N., Phillips, C., Prinz, M., Schneider, P.M., Parson, W. (2016) Recommendations of the DNA Commission of the International Society forForensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER). *Forensic Science International: Genetics* 24:97-102.

14. Peters, K.C., Swaminathan, H., Sheehan, J., Duffy, K.R., Lun, D.S., Grgicak, C.M. (2017) Production of high-fidelity electropherograms results in improved and consistent DNA interpretation: Standardizing the forensic validation process. Forensic Sci Int Genet. 31: 160-170.

15. Jeanguenat, A.M., Budowle, B., Dror, I.E. (2017) Strengthening forensic DNA decision making through a betterunderstanding of the influence of cognitive bias. *Science & Justice* 57(6): 415-420.

16. Alfonse, L.E., Garrett, A.D., Lun, D.S., Duffy, K.R. and Grgicak, C.M. (2018) A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt. *Forensic ScienceInternational: Genetics* 32: 62-70.

17. Jeanguenat, A.M. and Dror, I.E. (2018) Human factors effecting forensic decision making: workplace stress andwell-being. *Journal of Forensic Sciences* 63(1): 258-261.

18. Basset, P. and Castella, V. (2018) Lessons from a study of DNA contaminations from police services and forensiclaboratories in Switzerland. *Forensic Science International: Genetics* 33: 147-154.

19. Basset, P. and Castella, V. (2019) Positive impact of DNA contamination minimization procedures taken within thelaboratory. *Forensic Science International: Genetics* 38: 232-235.

20. Wickenheiser, R. and Farrell, L. (2020) Collaborative versus traditional method validation approach: Discussion andbusiness case. *Forensic Science International: Synergy* 2: 230-237.

21. Bodner, M. and Parson, W. (2020) The STRidER report on two years of quality control of autosomal STRpopulation datasets. *Genes (Basel)* 11(8): 901.

22. Dror, I.E. (2020) Cognitive and human factors in expert decision making: six fallacies and the eight sources of bias. *Analytical Chemistry* 92(12): 7998-8004.

23. Dror, I.E. (2020) The error in "error rate": why error rates are so needed, yet so elusive. *Journal of ForensicSciences* 65(4): 1034-1039.

Z. General Forensic Science Topics

1. National Academy of Sciences, Committee on the Conduct of Science (1989) On being a scientist. Proceedings of the National Academy of Sciences of the United States of America 86(23): 9053-9074.

2. National Research Council, Committee on Identifying the Needs of the Forensic Science Community (2009) *Strengthening Forensic Science in the United States: A Path Forward*. The National Academies Press: WashingtonDC.

3. Mnookin, J.L., Cole, S.A., Dror, I.E., Fisher, B.A.J., Houck, M.M., Inman, K., Kaye, D.H., Koehler, J.J., Langenburg, G., Risinger, D.M., Rudin, N., Siegel, J., Stoney, D.A. (2010). The need for a research culture in theforensic sciences. *UCLA Law Review* 58: 725-779.

4. Evett, I.W. (2015) The logical foundations of forensic science: Towards reliable knowledge. *PhilosophicalTransactions of the Royal Society of London Series B, Biological Sciences* 370: 20140263.

5. Butler, J.M. (2015) U.S. initiatives to strengthen forensic science & international standards in forensicDNA. *Forensic Science International: Genetics* 18: 4-20. [open access]

6. Edmond, G., Found, B., Martire, K., Ballantyne, K., Hamer, D., Searston, R., Thompson, M., Cunliffe, E.,

Kemp, R., San Roque, M., Tangen, J., Dioso-Villa, R., Ligertwood, A., Hibbert, D., White, D., Ribeiro, G., Porter, G., Towler, A. and Roberts, A. (2016) Model forensic science. *Australian Journal of Forensic Science* 48(5): 496-537.

7. President's Council of Advisors on Science and Technology (PCAST) (2016) Report to the President - Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods. Issued September 2016with an addendum in January 2017. Available at https://obamawhitehouse.archives.gov/sites/default/files/microsites/ostp/PCAST/pcast_forensic_science_report_final.pdf and https://obamawhitehouse.archives.gov/sites/default/files/microsites/ostp/PCAST/pcast_forensics_addendum_finalv2.pdf.

8. Butler, J.M. (2017) Recent activities in the United States involving the National Commission on Forensic Science and the Organization of Scientific Area Committees for Forensic Science. *Australian Journal of Forensic Sciences*49(5): 526-540 [open access]

9. National Commission on Forensic Science (2017) *Reflecting Back – Looking Toward the Future*. Available athttps://www.justice.gov/archives/ncfs/page/file/959356/download.

10. Evett, I.W., Berger, C.E.H., Buckleton, J.S., Champod, C., Jackson, G. (2017) Finding the way forward for forensicscience in the US-A commentary on the PCAST report. *Forensic Science International* 278: 16-23.

11. Edmond, G., Towler, A., Growns, B., Ribeiro, G., Found, B., White, D., Ballantyne, K., Searston, R.A., Thompson,M.B., Tangen, J.M., Kemp, R.I. and Martire, K. (2017) Thinking forensics: cognitive science for forensic practitioners. *Science & Justice* 57: 144-154.