Recent Advances in Forensic Biology and Forensic DNA Typing 2016-2019

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Review was written with Sheila Willis, Ph.D.
(former director of Forensic Science Ireland and a NIST guest researcher from 2017-2019)

Acknowledgments and Disclaimer

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Feedback on the written review from Tom Callaghan (FBI Laboratory) and Erica Romsos (NIST Applied Genetics Group)

Points of view are the presenter and do not necessarily represent the official position or policies of the National Institute of Standards and Technology.

Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

https://strbase.nist.gov/NISTpub.htm
Status of DNA Use in INTERPOL Member Countries Through 2016 (95 of 190 member countries responded)

- 84 countries use DNA in criminal investigations
- 69 countries possess a national DNA database

Overview of Papers Reviewed

- Number of Papers: 235
- Number of Journals: 35
- Topics Covered: 12 (see next slide)

17th INTERPOL Review on DNA (2010-2013) examined 114 articles (Jolicoeur 2013)
18th INTERPOL Review on DNA (2013-2016) examined 75 articles (Laurent & Pene 2016)
Topics Covered: Forensic Biology and DNA Typing

1. Core Loci Expansion
2. Rapid Analysis of STR Markers
3. Investigative Genetic Genealogy
4. Next-Generation Sequencing
5. DNA Mixture Interpretation and Probabilistic Genotyping Software
6. DNA Transfer and Activity Level Evaluations
7. Forensic Biology and Body Fluid Identification
8. DNA Phenotyping
9. Privacy and Ethical Issues
10. Guidance Documents (SWGDAM, OSAC, ASB, ENFSI, UK FS Regulator)
11. Contamination Avoidance and DNA Success Rates
12. Recent Special Issues and Review Articles of Note

Journals (Alphabetical Listing)

1. Analytical Chemistry
2. Applied Spectroscopy
3. BMC Bioinformatics
4. BMC Genetics
5. Current Issues in Criminal Justice
6. Developing World Bioethics
7. Electrophoresis
8. Forensic Science International
9. Forensic Science International: Genetics
10. Forensic Science International: Genetics Supplement Series
11. Forensic Science Review
12. Frontiers in Genetics
13. Genes (Basel)
14. Genetics in Medicine
15. Genome Biology
16. Gerontology
17. Human Genetics
18. Human Genomics
19. International Journal of Legal Medicine
20. Investigative Genetics
21. Journal of Clinical Microbiology
22. Journal of Forensic Sciences
23. Journal of Investigative Dermatology
24. MicroRNA
25. Molecular and Cellular Probes
26. New Genetics and Society
27. PLoS Biology
28. PLoS ONE
29. Proceedings of INTERPOL Forensic Science Managers Symposium
30. Proceedings of International Symposium on Human Identification
31. Proceedings of the National Academy of Sciences U.S.A.
32. Science
33. Science & Justice
34. Sensors (Basel)
35. Talanta

Most journals only have a single citation in this review.

Traditional forensic science journals are in bold font.

https://strbase.nist.gov/NISTpub.htm
Relevant (Physical and Virtual) Special Issues

**ELECTROPHORESIS**

- October 2016
- November 2018
- Volume 37, Issue 21
  - Special Issue: Forensic Analysis
- Volume 39, Issue 21
  - Special Issue: Novel Applications of Massively Parallel Sequencing (MPS) in Forensic Analysis
- 20 articles

- November 2017 to December 2018
- September 2018 to January 2019
- May 2019 to August 2019

- Virtual Issue on Forensic Genomics
- Virtual Issue on Trends and Perspectives in Forensic Genetics 2018
- Virtual Issue on Cold Cases
- 11 articles
- 11 articles
- 3 articles on DNA topics

Recent Books and Major Conferences on Forensic DNA (2016-2019)

- Forensic DNA Evidence Interpretation, Second Edition
  - CRC Press, 2016
- Handbook of Forensic Genetics
  - World Scientific, 2016

- International Symposium on Human Identification
  - Seoul, Korea
  - Sept 2017
  - 237 extended abstracts published

- International Society for Forensic Genetics
  - Prague, Czech Republic
  - Sept 2019
  - >350 extended abstracts published

- American Academy of Forensic Sciences
- ISFG Proceedings published in Forensic Science International: Genetics Supplement Series

https://strbase.nist.gov/NISTpub.htm
Topics Covered: Forensic Biology and DNA Typing

1. **Core Loci Expansion**
2. Rapid Analysis of STR Markers
3. Investigative Genetic Genealogy
4. Next-Generation Sequencing
5. DNA Mixture Interpretation and Probabilistic Genotyping Software
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Core Loci Expansion

- In January 2017, the FBI required expansion of the U.S. core loci from 13 short tandem repeat (STR) loci to 20 STR loci.

- Commercial kits that amplify more than 20 STR loci have now been adopted in many countries worldwide.

- These kits enable more international sharing of DNA data with increased compatibility between STR data going into national DNA databases.

(Effective January 1, 2017):

\[
\begin{align*}
\text{D1S1656} & \quad \text{D2S441} & \quad \text{D2S1338} & \quad \text{D10S1248} & \quad \text{D12S391} & \quad \text{D19S433} & \quad \text{D22S1045}
\end{align*}
\]

See [https://www.fbi.gov/services/laboratory/biometric-analysis/codis](https://www.fbi.gov/services/laboratory/biometric-analysis/codis)
Topics Covered: Forensic Biology and DNA Typing

1. Core Loci Expansion
2. **Rapid Analysis of STR Markers (Rapid DNA)**
3. Investigative Genetic Genealogy
4. Next-Generation Sequencing
5. DNA Mixture Interpretation and Probabilistic Genotyping Software
6. DNA Transfer and Activity Level Evaluations
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**Rapid DNA**

- Integrated instruments (sample-to-result) can produce reliable DNA results for single-source samples in <90 minutes
- Size-based analysis of 15 to 23 autosomal STR markers
- Success rates are typically >80%
- Reagent costs are approximately 10 times conventional testing ($\approx$300 per sample)
- Rapid DNA Act of 2017 signed into U.S. law on August 18, 2017
- 13 published evaluation or validation studies

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https://strbase.nist.gov/NISTpub.htm
## Rapid DNA Instrument Validation and Evaluation Studies (1)

<table>
<thead>
<tr>
<th>Publication</th>
<th>Instrument</th>
<th>STR Primer Set</th>
<th>Tests Performed and Success Rates Reported</th>
</tr>
</thead>
<tbody>
<tr>
<td>Turingan et al. 2016</td>
<td>DNAscan/ANDE 4C</td>
<td>PowerPlex 16</td>
<td>Evaluation of swabs from drinking containers, blood and buccal cells on FTA paper, blood and buccal cells on untreated paper, dried blood on ceramic tile, dried blood and dried semen on clothing, chewing gum, cigarette butt, cellphones, and bones to assess reproducibility, accuracy, concordance, sensitivity, precision, resolution, and peak height ratios</td>
</tr>
<tr>
<td>Della Manna et al. 2016</td>
<td>DNAscan/ANDE 4C</td>
<td>PowerPlex 16</td>
<td>SWGDAM developmental validation (across 8 laboratories, &gt;2300 swabs): species specificity, sensitivity, stability, inhibitors, reproducibility, mixtures, precision, accuracy, and concordance; success rate (1362 samples with 13 CODIS core loci) = 84% (auto) → 91% (manual)</td>
</tr>
<tr>
<td>Date-Chong et al. 2016</td>
<td>RapidHit 200</td>
<td>GlobalFiler Express</td>
<td>Evaluation of 34 known buccal samples and 23 negative controls; success rate = 50% (auto)</td>
</tr>
<tr>
<td>Moreno et al. 2017</td>
<td>DNAscan/ANDE 4C</td>
<td>PowerPlex 16</td>
<td>SWGDAM internal validation: contamination assessment, consistency and reliability, sizing precision, peak height ratio determination, noise and average peak height assessment, stutter percent calculation, sensitivity and interpretation threshold calculations, and stability studies; success rate (193 samples) = 75% (auto) for 13 CODIS core loci with no incorrect calls</td>
</tr>
<tr>
<td>Wiley et al. 2017</td>
<td>RapidHit ID</td>
<td>GlobalFiler Express</td>
<td>SWGDAM developmental validation: thermal cycling parameters, mock inhibition, species specificity, sensitivity, concordance and carryover, swab retrieval and re-extraction, repeatability and reproducibility, electrophoresis sizing accuracy, stutter calculations and precision studies</td>
</tr>
<tr>
<td>Salceda et al. 2017</td>
<td>RapidHit ID</td>
<td>GlobalFiler Express</td>
<td>SWGDAM developmental validation: thermal cycling parameters, mock inhibition, species specificity, sensitivity, concordance and carryover, swab retrieval and re-extraction, repeatability and reproducibility, electrophoresis sizing accuracy, stutter calculations and precision studies</td>
</tr>
</tbody>
</table>

## Rapid DNA Instrument Validation and Evaluation Studies (2)

<table>
<thead>
<tr>
<th>Publication</th>
<th>Instrument</th>
<th>STR Primer Set</th>
<th>Tests Performed and Success Rates Reported</th>
</tr>
</thead>
<tbody>
<tr>
<td>Boiso et al. 2017a, 2017b</td>
<td>RapidHit 200</td>
<td>NGM SE lect Express</td>
<td>28 runs performed in total (with 7 samples each); problems encountered with hardware, software, and consumables; found the system was not suitable for crime scene samples in its current design; success rate (155 samples) = 77% gave complete DNA profiles with samples involving (1, 2, or 5) μL blood spotted on swabs</td>
</tr>
<tr>
<td>Buscaino et al. 2018</td>
<td>RapidHit ID</td>
<td>GlobalFiler Express and NGM SE lect Express</td>
<td>Evaluation of thermal cycling parameters, sensitivity, carryover contamination risks, repeatability and reproducibility, mixtures, and mock crime scene samples</td>
</tr>
<tr>
<td>Amick &amp; Swiger 2019</td>
<td>RapidHit ID</td>
<td>GlobalFiler Express</td>
<td>SWGDAM internal validation: known and database-type samples, reproducibility, precision, sensitivity, stochastic effects, mixtures, contamination assessment, and concordance studies</td>
</tr>
<tr>
<td>Carney et al. 2019</td>
<td>ANDE 6C</td>
<td>FlexPlex (6-dye, 27plex STR assay)</td>
<td>SWGDAM developmental validation (across 6 labs, 2045 swabs, 13 instruments): species specificity, limit of detection, stability, inhibitors, reproducibility, reference material, mixtures, precision, concordance, signal strength, peak height ratio, stutter, non-template addition, resolution, and contamination assessment; first-pass success rate (1338 samples with 20 CODIS core loci) = 92%; successfully interpreted &gt;2000 samples with over 99.99% concordant alleles; data package led to receiving NDIS approval in June 2018</td>
</tr>
<tr>
<td>Shackleton et al. 2019</td>
<td>RapidHit 200</td>
<td>NGM SE lect Express</td>
<td>Development studies that included process optimization, sensitivity, repeatability, contamination checks, inhibition, swab age, concordance, and overall performance; success rate (124 samples) = 84.5% gave a full profile</td>
</tr>
<tr>
<td>Shackleton et al. 2019b</td>
<td>RapidHit 200</td>
<td>NGM SE lect Express</td>
<td>Protocol adjustments that extended the overall run times were made to enhance slightly sensitivity with mock crime scene samples (dilutions of blood and cell line DNA)</td>
</tr>
</tbody>
</table>

https://strbase.nist.gov/NISTpub.htm
Rapid DNA in Police Stations?

https://www.fbi.gov/services/laboratory/biometric-analysis/codis/rapid-dna

The capability exists but how much rapid DNA will be used remains to be seen...

Non-CODIS Rapid DNA Considerations and Best Practices for Law Enforcement Use


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**Investigative Genetic Genealogy**

- Arrest of the alleged Golden State Killer Joseph DeAngelo in April 2018 opened the doors to solving cold cases using genetic genealogy (non-law-enforcement) DNA databases

- Has raised genetic privacy concerns

- Subject of active discussions at recent forensic DNA and genetic genealogy conferences

**Golden State Killer Case**

- **Crimes:** 13+ murdered, 50+ raped, 120+ burgled (many linked by DNA evidence over the years)

- DNA from a **crime scene sample** (sexual assault kit) was examined with genetic genealogy DNA markers

- Data obtained was uploaded to a **genetic genealogy database** (GEDmatch) to locate potential distant relatives of the perpetrator

- **Family trees were created** from possible links and **detective work** reduced number of possible suspects

- **Confirmation DNA sample** was collected from a door handle and later a tissue in the garbage to verify that the **suspect’s DNA profile** matched the **crime scene DNA profile**

- DeAngelo (age 72) was arrested at his home outside of Sacramento, CA on April 24, 2018 and is awaiting trial

*Sources: numerous news articles and Wikipedia*
>60 Cold Cases in the United States Have Been Solved with Genetic Genealogy since April 2018


**GENEALOGY DATABASES AND THE FUTURE OF CRIMINAL INVESTIGATION**

The police can access your online family-tree research—and use it to investigate your relatives

Natalie Rame, Cheryl J. Goertzen,* Ann S. McMillin

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Of 1587 members of the general public questioned in May 2018, 91% said yes

PERSPECTIVE

Should police have access to genetic genealogy databases? Capturing the Golden State Killer and other criminals using a controversial new forensic technique

Christel J. Goertzen,* Jeff D. Robinson, Devon Peterson, Amy L. McGuire

Center for Medical Ethics and Health Policy, Baylor College of Medicine, Houston, Texas, United States of America

The Atlantic

The Messy Consequences of the Golden State Killer Case

Tools meant to reunite families are now being “used essentially to get families to put their members in jail.”

Sarah Zhang, Oct 1, 2019


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**DOJ Policy on Investigative Genetic Genealogy**

Released September 24, 2019 (goes into effect November 1, 2019)

This interim policy applies to:

1) all criminal investigations run by the Department of Justice (DOJ)
2) any criminal investigation in which DOJ provides funding
3) any criminal investigation in which DOJ employees or contractors conduct genealogical research
4) any federal agency or any unit of state, local, or tribal government that receives DOJ grant award funding

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Topics Covered: Forensic Biology and DNA Typing

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Next-Generation DNA Sequencing

- **Additional markers** can be run simultaneously (=10 times as many as current CE systems) with higher information content
  - May enable additional capabilities (e.g., phenotyping)
  - Privacy concerns with additional genomic information
- **Involves more sample preparation** steps and requires **more extensive data analysis**
  - Expensive per run although cost per marker is lower
  - STR allele nomenclature challenges to keep backwards compatibility
  - Data handling and storage issues
- Agreeing upon and implementing a standard STR allele nomenclature is critical for future progress

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DNA Mixture Interpretation

- Deciphering the various components present in a mixture and assigning an appropriate weight to the evidence can be challenging

- Improper use of DNA mixture interpretation approaches led to closure of several U.S. forensic DNA laboratories in 2015 and 2016

- The past few years have seen an increase in the use of probabilistic genotyping software (PGS) to assist DNA mixture interpretation
  - PGS systems use either (1) “*discrete*” (sometimes called “semi-continuous”) models that use the presence or absence of peaks along with probabilities of allele drop-out or drop-in or (2) “*continuous*” (sometimes called “fully-continuous”) models that take peak heights into account as well as the presence or absence of peaks along with probabilities of allele drop-out or drop-in

[https://strbase.nist.gov/NISTpub.htm](https://strbase.nist.gov/NISTpub.htm)
### Probabilistic Genotyping Software (PGS) – as of July 2019

<table>
<thead>
<tr>
<th>Program Name</th>
<th>Type (Model)</th>
<th>Creator(s)</th>
<th>Availability</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 CEESIt</td>
<td>Continuous</td>
<td>Catherine Grgicak</td>
<td>Open-source software: <a href="https://lftdi.camden.rutgers.edu/">https://lftdi.camden.rutgers.edu/</a></td>
<td>Swaminathan et al. 2016</td>
</tr>
<tr>
<td>2 DNAmixtures</td>
<td>Continuous</td>
<td>Therese Graversen</td>
<td>Open-source software: <a href="http://dnamixtures.r-forge.r-project.org/">http://dnamixtures.r-forge.r-project.org/</a></td>
<td>Cowell et al. 2015</td>
</tr>
<tr>
<td>4 eDNA</td>
<td>Discrete &amp; Continuous</td>
<td></td>
<td>Available through subscription service: Bullet (Semi-continuous; uses LRmix math) and BulletProof (Fully-continuous; uses EuroForMix math)</td>
<td></td>
</tr>
<tr>
<td>6 FST</td>
<td>Discrete</td>
<td>NYC OCME</td>
<td>Proprietary to NYC OCME Department of Forensic Biology</td>
<td>Mitchell et al. 2012</td>
</tr>
<tr>
<td>7 GenoProof Mixture 3</td>
<td>Continuous</td>
<td>Frank Götz</td>
<td>Commercial product: <a href="https://www.quality.de">https://www.quality.de</a></td>
<td>Götz et al. 2017</td>
</tr>
<tr>
<td>9 Lab Retriever</td>
<td>Discrete</td>
<td>David Balding; maintained by Norah Rudin and colleagues</td>
<td>Open-source software: <a href="https://scieg.org/lab-retriever/">https://scieg.org/lab-retriever/</a></td>
<td>Inman et al. 2015</td>
</tr>
<tr>
<td>10 likeLTD</td>
<td>Discrete &amp; Continuous</td>
<td>David Balding</td>
<td>Open-source software: <a href="https://sites.google.com/site/baldingstatisticalgenetics/software/likeltd">https://sites.google.com/site/baldingstatisticalgenetics/software/likeltd</a></td>
<td>Balding 2013</td>
</tr>
<tr>
<td>11 LiRa/ LiRa-HT</td>
<td>Discrete/ Continuous</td>
<td>Roberto Puch-Solis</td>
<td>Proprietary to LGC (now Eurofins)</td>
<td>Puch-Solis &amp; Clayton 2014</td>
</tr>
<tr>
<td>13 MaSTR</td>
<td>Continuous</td>
<td>Teresa Snyder-Leby</td>
<td>Commercial product: <a href="https://softgenetics.com/MaSTR.php">https://softgenetics.com/MaSTR.php</a></td>
<td>Adamowicz et al. 2016</td>
</tr>
<tr>
<td>14 STRmix</td>
<td>Continuous</td>
<td>Duncan Taylor, Jo-Anne Bright, John Buckleton</td>
<td>Commercial product: <a href="https://strmix.esr.or.nz/">https://strmix.esr.or.nz/</a></td>
<td>Taylor et al. 2013</td>
</tr>
</tbody>
</table>

### Topics Covered: Forensic Biology and DNA Typing

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The importance of DNA transfer and activity propositions has increased in recent years with use of highly sensitive DNA testing methods. There is a growing body of literature on this topic in the past three years due to the desire to address not only the source of the DNA but how the DNA got there. Several reviews highlight how little we know with certainty about how DNA transfers from the donor, the range of variables that affect transfer and persistence, the value of activity propositions, and a proposal for a more systematic approach to data collection.


The overall takeaway from this literature is that sub-source LR results in isolation cannot automatically be assumed to be connected with the crime.

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**Topics Covered: Forensic Biology and DNA Typing**

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J.M. Butler, Recent Advances in Forensic Biology and Forensic DNA Typing (2016-2019)

INTERPOL Forensic Science Managers Symposium
10 October 2019

Organizations Providing Guidance Documents on Forensic DNA

SWGDAM Documents

Validation Guidelines

Scientific Working Group on DNA Analysis Methods
Validation Guidelines for DNA Analysis Methods

Interpretation Guidelines

Scientific Working Group on DNA Analysis Methods
Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories

LR Verbal Equivalents

Scientific Working Group on DNA Analysis Methods
LR Verbal Equivalents

December 2016
January 2017
July 2018

https://strbase.nist.gov/NISTpub.htm

35 issued in the past three years

Sworn by

https://strbase.nist.gov/NISTpub.htm

15
UK Forensic Science Regulator

Codes of Practice and Conduct

- **Codes of Practice and Conduct**
  - For forensic science providers and practitioners in the Criminal Justice System
  - **Issue 4**
  - October 2017

PGS Software Validation

- **Guidance**
  - Software Validation for DNA Mixture Interpretation
  - **FSR-G-223**
  - **ISSUE 1**
  - September 2018

DNA Mixture Interpretation

- **Guidance**
  - DNA Mixture Interpretation
  - **ISSUE 2**
  - October 2018

Guidance Documents Related to Forensic DNA (1)

<table>
<thead>
<tr>
<th>Organization</th>
<th>Publication Date</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>SWGDAM</td>
<td>December 2016</td>
<td>Recommendations for the Efficient DNA Processing of Sexual Assault Evidence Kits <a href="https://docs.wixstatic.com/ugd/4344b0_4d4a2bb5512b4e2582895c4a133a0ed.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>December 2016</td>
<td>Validation Guidelines for DNA Analysis Methods <a href="https://docs.wixstatic.com/ugd/4344b0_813b241e8944497e99be465b1e3b67bd.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>January 2017</td>
<td>Contamination Prevention and Detection Guidelines for Forensic DNA Laboratories <a href="https://docs.wixstatic.com/ugd/4344b0_c4d4dbba841f0400a9eaa2e48f2291.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>January 2017</td>
<td>Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories <a href="https://docs.wixstatic.com/ugd/4344b0_50a2749756a042528a285a5b478f4c.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>July 2018</td>
<td>Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios <a href="https://docs.wixstatic.com/ugd/4344b0_dd5221694d1448588dc0937738c9e46.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>April 2019</td>
<td>Addendum to “SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories” to Address Next Generation Sequencing <a href="https://docs.wixstatic.com/ugd/4344b0_912b953944575a9f51867de7be85.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>April 2019</td>
<td>Interpretation Guidelines for Mitochondrial DNA Analysis by Forensic DNA Testing Laboratories <a href="https://docs.wixstatic.com/ugd/4344b0_6f1de6abf394c52b2813906f000ae98.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>January 2018</td>
<td>Quality Assurance Standards for Forensic DNA Testing Laboratories (draft) <a href="https://docs.wixstatic.com/ugd/4344b0_d4c50d6204b240d3a23e888b58591a.pdf">link</a></td>
</tr>
<tr>
<td>SWGDAM</td>
<td>February 2019</td>
<td>FBI Quality Assurance Standards Audit for DNA Databasing Laboratories (draft) <a href="https://docs.wixstatic.com/ugd/4344b0_7b037800b724a5b9a93b3b8d5934b5.pdf">link</a></td>
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[link](https://strbase.nist.gov/NISTpub.htm)
### Guidance Documents Related to Forensic DNA (2)

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Released September 24, 2019 (goes into effect November 1, 2019)

### Guidance Documents Related to Forensic DNA (3)

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### Guidance Documents Related to Forensic DNA (4)

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<tr>
<td>ISFG DNA Commission</td>
<td>January 2016</td>
<td>Massively parallel sequencing of forensic STRs: Considerations…on minimal nomenclature requirements (Parson et al. 2016)</td>
<td><a href="https://www.isfg.org/files/d5cc0599ee232596c75ad8a0b435190e7d7ba3035.parson2016_str.recommendations.pdf">https://www.isfg.org/files/d5cc0599ee232596c75ad8a0b435190e7d7ba3035.parson2016_str.recommendations.pdf</a></td>
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<tr>
<td>ISFG DNA Commission</td>
<td>June 2016</td>
<td>Recommendations…on quality control of autosomal short tandem repeat allele frequency databasing (STRidER) (Bodner et al. 2016)</td>
<td><a href="https://www.isfg.org/files/9864824b449971014a62a321f0d25e6c98.bodner2016_strider.pdf">https://www.isfg.org/files/9864824b449971014a62a321f0d25e6c98.bodner2016_strider.pdf</a></td>
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<tr>
<td>ISFG DNA Commission</td>
<td>September 2016</td>
<td>Recommendations on the validation of software programs performing biostatistical calculations for forensic genetic applications (Coble et al. 2016)</td>
<td><a href="https://www.isfg.org/files/225be64835df624d1ddac706f5a2e7354f916fbb.coble_software_validation_fsigen2016.pdf">https://www.isfg.org/files/225be64835df624d1ddac706f5a2e7354f916fbb.coble_software_validation_fsigen2016.pdf</a></td>
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<tr>
<td>ISFG DNA Commission</td>
<td>July 2018</td>
<td>Assessing the value of forensic biological evidence – guidelines highlighting the importance of propositions. Part I: evaluation of DNA profiling comparisons given (sub-) source propositions (Gill et al. 2018)</td>
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### Guidance Documents Related to Forensic DNA (5)

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**Guidance Documents Related to Forensic DNA (6)**

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**Biological Methods Subcommittee**
- 13 work products to SDO
- 14 additional documents under development

**Biological Data Interpretation and Reporting Subcommittee**
- 5 work products to SDO
- 14 additional documents under development

**Wildlife Forensics Subcommittee**
- 8 work products to SDO
- 9 additional documents under development

https://www.nist.gov/topics/organizationscientific-area-committees-forensic-science

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**Another Recent Review Article on Forensic DNA**

*Analytical Chemistry* 2019, 91, 673-688

Forensic DNA Analysis

Bruce R. McCord, Quentin Gauthier, Sohee Cho, Meghan N. Roig, Georgiana C. Gibson-Daw, Brian Young, Fabiana Taglia, Sara C. Zapico, Roberta Fogliatto Mariot, Steven B. Lee, and George Duncan

1Department of Chemistry, Florida International University, Miami, Florida 33199, United States
2Department of Forensic Medicine, Seoul National University, Seoul, 08826, South Korea
3Niche Vision, Inc., Akron, Ohio 44311, United States
4Forensic Science Program, Justice Studies Department, San Jose State University, San Jose, California 95192, United States

246 references cited (225 are from the 2016 to 2018 time frame)

**Topics covered:**
- Forensic serology
- Chemical & spectroscopic methods
- Body fluid identification via RNA typing
- Proteomic body fluid identification
- Epigenetics
- DNA extraction & sample recovery
- Genotyping methods using STRs
- Mixtures and probabilistic genotyping
- Estimating the number of contributors
- Y-STRs and X-STRs; Y-SNPs and X-SNPs
- SNPs; Insertion/Deletions; Mitochondrial DNA
- Ancient DNA, bones, and teeth
- Improving DNA extractions from teeth and bone
- Nonhuman DNA; Wildlife forensics
- Drug sourcing
- Massively parallel sequencing
- The microbiome as a source of DNA
- Postmortem interval

https://strbase.nist.gov/NISTpub.htm
Thank you for your attention!

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+1-301-975-4049

www.nist.gov/forensics

A pdf copy of this presentation is available at:
http://strbase.nist.gov/NISTpub.htm

Any questions?