PRESENTING PROBABILISTIC GENOTYPING AT TRIAL: Best practices & Avoiding error

WRITTEN MATERIALS

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CDAA Forensic DNA for Prosecutors
10:45 – Noon, March 14, 2018, Anaheim, CA
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Defense lawyers want to peek behind the curtain of probabilistic genotyping

This article was published in the December 2017 issue of the ABA Journal with the title “Code of Science: Defense lawyers want to peek behind the curtain of probabilistic genotyping.”

Defense lawyers want to peek behind the curtain of probabilistic genotyping

BY JASON TASHEA
DECEMBER 2017

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Three years ago, a man with a gun walked into a Shell gas station in Norton Shores, Michigan, and announced a robbery.

After grabbing the till, the robber escorted the clerk into the storeroom to get a carton of cigarettes. In the next few seconds, the clerk grabbed a gun and fired 10 shots as the robber ran for the door. As he fled, the robber left behind a shoe on the store’s floor.

Security footage failed to capture the robber’s face or the license plate of the getaway vehicle. After collecting non-DNA evidence from the shoe, police were led to El-Amin Muhammad, 40, a repeat offender with a violent history, and charged him with the stickup.

Prosecutors admitted at the time that their case against Muhammad was circumstantial. However, the prosecution used DNA analysis software, called probabilistic genotyping, to interpret the sweat found in the forlorn shoe. This analysis employed an algorithm to create a likelihood ratio that compares DNA samples. According to one of these tools, Muhammad was the largest and most likely contributor to the sample.

He was sentenced in 2016 to serve 25 to 38 years for armed robbery.

POSSIBLE OR PROBABLE?

With the use of DNA evidence increasing across the United States, DNA labs are using probabilistic genotyping to analyze hard-to-interpret samples. However, some scientists and lawyers worry that the privately held computer code behind these tools is limiting its reliability and hindering due process.
Traditional DNA analysis is challenged when there are multiple contributors to a sample or the quantity of DNA recovered is too small. Without a better analytical tool, these samples are often inconclusive, says Dan E. Krane, a professor of biological science at Wright State University.

Probabilistic genotyping is not a technique that defines the sample itself; rather it is an interpretive software that runs multiple scenarios—like the risk analysis tools used in finance—to examine the sample. This contrasts with traditional DNA analysis, which assesses whether a DNA type is present or absent.

Bjorn Sutherland, forensic development manager at the New Zealand-based Institute of Environmental Science and Research—the probabilistic genotyping company used in the case involving Muhammad—says that his software, STRMix, “enables users to compare the results against a person or persons of interest and calculate a statistic, or 'likelihood ratio,' of the strength of the match.”

By leveraging computer processing, probabilistic genotyping “gives us more information to work with,” says Chris Lindberg, a deputy district attorney in San Diego. Many, like Lindberg, are excited for this technology because it analyzes samples in a way that would have been too labor intensive previously. The cost of these tools varies by company and number of licenses purchased.

Last year, San Diego joined jurisdictions in Indiana, Louisiana and New York, among others, deploying this technology in its investigations. Sutherland says this technology has been around for less than 10 years, but the statistical models the tools use have been around for decades.

This science has created a cottage industry. Besides STRmix, those receiving the most attention in the U.S. are the Forensic Statistical Tool, used by the Office of the Medical Examiner in New York, and TrueAllele, created by the Pittsburgh-based company Cybergenetics.

In September 2016, a report on forensics from the Presidential Council on Science and Technology noted that “probabilistic genotyping software programs clearly represent a major improvement over purely subjective interpretation.” However, the report added, “careful scrutiny” is still needed to determine whether methods are scientifically valid and if the software correctly implements those methods. The report clarifies that analyzing the software “is particularly important because the programs employ different mathematical algorithms and can yield different results for the same mixture profile.”

**SCIENCE UNDER SCRUTINY**

Built on biology, computer science and statistics, the world of probabilistic genotyping is niche. With few people who can understand these tools, the challenge of analyzing them is compounded by the fact that companies developing these tools “black-box” the computer code. This means there is no or limited capability to review the math; therefore, it cannot be independently challenged.

Richard Torres, a staff attorney in the DNA unit of the New York Legal Aid Society in New York City, and scientists such as Krane are concerned about the lack of transparency.

“My biggest issue is with access to the source code,” Torres says. “It’s a confrontation issue,” a reference to the Sixth Amendment right to confront a witness who makes a claim against a defendant. Torres argues that an algorithm behind a genotyping tool is speech that makes a claim against a defendant—so the defense has a right to confront and question the algorithm, not just the scientist who made it.

Organizations like Cybergenetics and the Institute of Environmental Science and Research provide defense counsels access to the tool and supplemental materials such as validation studies, but the information is incomplete to protect the company’s intellectual property. Less frequently used tools,
including Lab Retriever, LRMix and LikeLTD, have their source code available for download without limitations.

Defense access to the source code has been litigated around the country with mixed results.

In California, *People v. Chubbs*, a cold murder case from the 1970s, brought this issue to light in 2012. The prosecution used evidence from TrueAllele, saying DNA found on the victim and Martell Chubbs’ sample was “1:62 quintillion times more probable than a coincidental match to an unrelated black person.” The trial court determined that Chubbs was entitled to examine the source code under protective order.

On appeal, this decision was overturned in 2015. The appeals court said that Chubbs’ stated reasons to access the source code, even under protective order, did not outweigh trade secret protections. Further, as the court writes, “access to TrueAllele’s source code is not necessary to judge the software’s reliability” because validation studies and expert testimony are sufficient to make that determination.

This view is shared by Mark Perlin, CEO of Cybergenetics, the company at issue in the Chubbs case. He thinks that full algorithmic transparency is not necessary, and that the scientific process can and should police forensic science.

The challenge here, says Erin Murphy, a law professor at New York University and author of *Inside the Cell: the Dark Side of Forensic DNA*, is that genotyping software validation studies are done almost entirely in-house by the company itself, putting their validity into question. She says that “one of the key ways to understand the strengths and weaknesses of these programs is to make them really transparent.”

Siding with Murphy, Judge Valerie Caproni of the U.S. District Court for the Southern District of New York determined in *Johnson v. U.S.* in July 2016 that the Forensic Statistical Tool’s “source code is ‘relevant [and] admissible,’ ” at least during a Daubert hearing, a pretrial hearing where the admissibility of expert testimony is challenged. Caproni provided a protective order, which she later lifted when journalists at ProPublica filed a motion arguing that there was a public interest in the code. The source code is now available online.

With this debate ongoing, requiring access to source code may be insufficient, says Nathan Adams, a systems engineer at Forensic Bioinformatics, a Fairborn, Ohio-based consultancy led by Krane.

“Even if it’s an open sourced program ... and there is interest” in doing an evaluation, there are resource and ability limitations, says Adams. “The field of forensic DNA hasn’t emphasized the skill set of software quality assurance,” he adds.

Frank Pasquale, a law professor at the University of Maryland and author of *The Black Box Society*, agrees with Adams, saying it is a “huge problem” to find experts in computer science, biology and law. “Before we mass-deploy these things, we have to make sure these experts are equally spread out,” he says.

Without any indication that the proliferation of these tools will wait for a cadre of experts to be created and deployed, courts and scientists will continue to grapple with questions using the resources they have.

Acknowledging this debate, Rhonda Roby, the supervising DNA criminalist at the Alameda County Sheriff’s Office forensic biology unit in California, strikes a balanced tone. “I think the bottom line is that it’s a critical time, right now, to closely evaluate and not dismiss the technology,” she says. “It’s that good that we need to consider it.”
POINTS AND AUTHORITIES

I.

THE STRMIX DNA RESULTS ARE NOT EVIDENCE DERIVED FROM A “NEW SCIENTIFIC TECHNIQUE,” AND THUS STRMIX DNA ANALYSIS IS NOT SUBJECT TO A KELLY HEARING PRIOR TO ITS ADMISSION

The admissibility of DNA results obtained through the use of STRmix software analysis is not subject to a separate preliminary hearing pursuant to People v. Kelly (1976) 17 Cal.3d 24 (Kelly). The use of STRmix software to analyze and interpret DNA evidence is not a “new scientific technique.” Rather, it is relatively-new computer software that uses long-established mathematical and statistical principles and the power of computers to more efficiently interpret complex DNA mixtures. Even assuming arguendo it is subject to a Kelly hearing, the principles and the statistical methods implemented by STRmix are generally accepted as reliable in the forensic scientific community, as clearly established by literature and decisions from other jurisdictions. Thus, a Kelly hearing is not required.

A. Established Scientific Procedures Are Not Subject To A Kelly Hearing

In California, when expert testimony relies on a “new scientific technique,” its admissibility is subject to a three-prong test requiring that: (1) “the technique is generally accepted as reliable in the relevant scientific community,” (2) the expert is properly qualified to testify about it, and (3) “the person performing the test in the particular case used correct scientific procedures.” (People v. Jackson (2016) 1 Cal.5th 269, 315–316, quoting People v. Bolden (2002) 29 Cal.4th 515, 544–545 [describing the test articulated in People v. Kelly, supra, 17 Cal.3d 24].) A judicial finding as to the reliability of scientifically based evidence is required because scientific evidence is viewed as imparting “some definitive truth which the expert need only accurately recognize and relay to the jury,” such that the jury can be misled

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1 In People v. Soto (1999) 21 Cal.4th 512, 515, footnote 3, the California Supreme Court explained that Frye v. United States (D.C. Cir. 1923) 293 F. 1013 has been superseded by the Federal Rules of Evidence. Therefore the foundational requirement for admission of new scientific evidence in California, formerly referred to as the Kelly/Frye test, is now referred to as the Kelly test.
by the “aura of infallibility” that may surround unproven scientific methods. (*People v. Stoll*

Notably, the *Kelly* rule applies only to “new” scientific testing procedures. As use of a
scientific practice or instrument becomes widespread, it is no longer new or novel.
Consequently, in such situations a *Kelly* hearing is unnecessary even though no appellate
opinion specifically establishes its general acceptance. (*People v. Municipal Court (Sansone)*
Cal.App.3d 239, 251-254 [scanning electron microscopes].) Thus, established scientific
procedures are not subject to a *Kelly* hearing. Statistical calculations have been established as

Similarly, a new method of doing an established scientific test generally does not
implicate the *Kelly* rule. (*People v. Cowan* (2010) 50 Cal.4th 401, 470 [ballistics testing using
elastomeric material]; *People v. Webb* (1993) 6 Cal.4th 494, 523-524 [fingerprint comparison
of laser-derived image of latent print]; *People v. Stevey* (2012) 209 Cal.App.4th 1400, 1411-
1419 [“mere tweaking of existing methodologies and calculations” of DNA analysis].)

Where, as here, the issue is the novelty of a change in the method of
analyzing DNA, courts have recognized that “[w]hat was once considered
revolutionary has now become rather mundane,” and the threshold issue is
“whether the improvement or refinement in DNA methodology qualifies as
another breakthrough innovation within the meaning of *Kelly*, or whether
the change represents a mere evolution of a generally accepted scientific
technique.” (*People v. Stevey*, *supra*, 209 Cal.App.4th at p. 1411.) As
discussed, the PCR-STR method of analyzing DNA has been found to be
generally accepted by many, many courts. [Citations.] When a new kit
utilizing the PCR-STR methodology comes onto the market, the issue is not
whether there are differences between it and prior kits, but whether it
significantly changes the methodology. [Citations.]

innovation in DNA testing]; see also *People v. Cordova* (2015) 62 Cal.4th 104, 127-128
[Identifiler is more sophisticated, but not novel, form of DNA testing].)
DNA testing results and the basic science behind it has been accepted in California courts for well over 20 years to prove identity in a criminal case. (*People v. Cordova* (2015) 62 Cal.4th 104, 128; *People v. Stevey* (2012) 209 Cal.App.4th 1400, 1411.) The California Supreme Court has noted that although DNA testing is continually being refined and improved, the scientific methodology remains fundamentally the same. (*Ibid.*) “*O*nce a new scientific technique becomes generally accepted, a *Kelly* prong-one hearing is not necessary to establish whether each specific methodology employing the technique is also generally accepted. [Citation.] Rather than quibble over the components of the process or the *interpretation of the results*, challenges are directed to the weight of the evidence to be determined by the [trier of fact] and not to its admissibility.’ [Citation.]” (*People v. Cordova*, supra, 62 Cal.4th at p. 128, italics added.)


In this instance, two DNA samples, 16-2 and 17-2, were collected to be examined; one sample was obtained from a swab of the interior of the right glove and the other sample was obtained from the swab of the interior of the left glove. Using the PCR kit “Global Filer,” a DNA profile was generated in electronic form as to each sample. These two DNA profiles were each inputted into the STRmix computer program, which in turn, interpreted the DNA profile and provided a weighted statistical conclusion when compared to petitioner versus a hypothetical unrelated random individual. The results support that petitioner is a possible minor contributor to the DNA mixture obtained from the gloves collected at the murder scene. Contrary to petitioner’s contentions, STRmix is not subject to a *Kelly* hearing.

As a preliminary matter, it is well-established that incrementally more-advanced DNA test kits, such as Global Filer, using the same PCR/STR foundation, are not new scientific techniques that trigger renewed scrutiny under *Kelly*. “Neither the use of PCR . . . nor STR technology to analyze mixed-source forensic samples is a new scientific technique. [Citation.] Nor are new kits as they come on the market.” (*People v. Stevey*, supra, 209 Cal.App.4th at p. 1411.)
More importantly, the use of STRmix software to analyze the previously-developed DNA data and provide an interpretative statistic does not trigger a Kelly hearing. As stated on the STRmix website: “Using standard and well-established statistical methods, the software analyzes a DNA profile and determine[s] which DNA genotypes best explain the data.” (How Does STRmix Work? <http://strmix.esr.cri.nz/#how> [as of June 12, 2017].) STRmix is probabilistic genotyping computer software which is used to compare a reference DNA profile to single source and mixed DNA profiles. Probabilistic genotyping software uses complex algorithms and computing power in a software package to break down DNA mixtures into the possible genotypes of the contributors. The software interprets this data and provides a statistical weighting. The statistical weight the software applies uses a likelihood ratio approach, which is a mathematical relationship between two different ways to explain the data. In other words, a likelihood ratio is a comparison of two probabilities and it states the likelihood of a particular explanation of the evidence compared with a different explanation of the evidence.

The mathematical and statistical principles, applied by the STRmix computer program to interpret the data, are well-established. These principles are simply being implemented via software, making cumbersome and time-consuming manual calculations no longer necessary. STRmix is a further refinement of well-accepted and long-established mathematical principles as applied to DNA interpretation. Thus, STRmix is not a “new scientific technique” and does not trigger a Kelly hearing.

As far as respondent is aware, no published California case has involved or addressed DNA interpretation using STRmix software. However, the out-of-state decisions and court

1411 [describing technology and citing cases]; see People v. Jones (2013) 57 Cal.4th 899, 937, fn. 13 [noting that “PCR has attained a consensus in the scientific community as a valid procedure”]; People v. Johnson (2006) 139 Cal.App.4th 1135, 1149 [“PCR and STR methods of DNA analysis have been held to be generally accepted in the relevant scientific community for some time now”]; People v. Hill (2001) 89 Cal.App.4th 48, 58 [Profiler Plus test kit based on PCR/STR technology, and not subject to new prong one Kelly assessment].)
orders that discuss STRmix software persuasively demonstrate that the use of STRmix
software, in interpreting DNA data, does not constitute a “new scientific technique.”

Decisions from other jurisdictions are highly relevant because they extensively discuss and
analyze the methods and principles behind STRmix DNA analysis, demonstrating that
STRmix is outside the purview of a Kelly hearing.

Recent cases in Michigan and New York are particularly helpful in understanding the
principles behind STRmix software. In the New York case of People v. Bullard-Daniel (N.Y.
March 10, 2016) 42 N.Y.S. 3d 714, the defendant was charged with sexual assault and
burglary. (Exh. A. 2) DNA testing was conducted on several pieces of evidence by the Erie
County Central Police Services Forensic Lab and STRmix was used to interpret the results.
(Id. at pp. 178-179.) The defense objected to the DNA report and testimony related to it,
contending they were not admissible at trial. The court conducted a Frye 3 hearing, and
ultimately concluded that STRmix was generally accepted in the relevant scientific
community. (Id. at p. 194.)

In its holding, the New York court described STRmix as a probability genotyping
software. (People v. Bullard-Daniel, supra, 42 N.Y.S. 3d at p. 181.) The court noted that
probabilistic genotypes have been recognized by the Scientific Working Group on DNA
Analysis Methods (SWGDAM) in the 2010 guideline, “Interpretation guidelines for
autosomal STR typing by forensic DNA testing laboratories,” and has also been recognized
by the American National Standards Institute (ANSI) in the 2011 article, “Data format for the
interchange of fingerprint, facial & other biometric information” as a valid approach to DNA
interpretation and reporting. (Id. at p. 180.)

2 In addition to the out-of-state decisions addressed in respondent’s briefing,
respondent has attached other relevant out-of-state court decisions to better assist this court in
its review of STRmix. (See Exhs. D-G.)

3 Under the Frye test, pursuant to Frye v. U.S., supra, 293 F. 1013, “one who seeks the
admission of evidence based upon a new scientific technique must make ‘a preliminary
showing of general acceptance of the new technique in the relevant scientific community.’
[Citations.]” (People v. Wilkinson (2004) 33 Ca.4th 821, 843.)
The court noted that computer interpretation methods utilize more of the quantitative short tandem repeat (STR) peak height data rather than thresholds, and have been used for over 20 years. Computer methods offer three advantages in the DNA interpretation process: (1) these methods eliminate time-consuming human review of cases, (2) these methods use a statistical model that can review the data more extensively than a human, and (3) a mathematically programmed computer can infer a genotype directly from the evidence data, without using suspect information, and then compute a match likelihood ratio (LR) statistic from this genotype, making the process more objective than traditional human mixture interpretation methods. (*People v. Bullard-Daniel*, supra, 42 N.Y.S. 3d at p. 180.)

Relying on the testimony of Dr. John Simich, the Director of the Erie County Police Services Forensic Lab, the court found that STRmix is generally accepted in the relevant scientific community. (*People v. Bullard-Daniel*, supra, 42 N.Y.S. 3d at p. 194.) Dr. Simich testified that various scientific organizations, including SWGDAM, have recommended the use of STRmix. (*Id.* at p. 182.) He stated that probabilistic genotyping, as used in the calculation step of DNA analysis, has been around for many years and involves a two-step process: deconvolution and statistical analysis. (*Ibid.*). Dr. Simich explained that deconvolution breaks a mixture down into the individual contributors and generates a DNA profile for each contributor. Statistical analysis determines the likelihood ratio based on a comparison to a person of interest. (*Ibid.*).

Dr. Simich explained some of the mathematical analysis methods and principles used in the deconvolution process, including the Markov Chain Monte Carlo (MCMC) model and the Metropolis-Hastings algorithm. MCMC is a standard statistical model. Dr. Simich also testified that STRmix employs Bayes’ theorem, “which is a general scientific principle of the likelihood ratio.” (*People v. Bullard-Daniel*, supra, 42 N.Y.S. 3d at p. 182.) Bayes’ theorem was discovered in the early 1700s and has been used for centuries in many scientific disciplines without controversy. (*Ibid.*).

Dr. Simich opined, based on his review of the STRmix software, that the science behind it was generally accepted within the forensic lab community. (*People v. Bullard-
Daniel, supra, 42 N.Y.S. 3d at p. 182.) Based upon his review of peer-reviewed journals, he further testified that the software was reliable. (Ibid.) The STRmix creators had created and provided to him a report of their internal validation process. Additionally, Dr. Simich’s lab had separately conducted an internal validation study of STRmix, finding that STRmix reliably deconvolutes DNA profiles and provides likelihood ratios that can be used in casework. (Id. at p. 183.) Dr. Simich also testified that STRmix is used by labs in Australia, New Zealand, and by the United States Army lab, the California Department of Justice, and the FBI. (Ibid.)

In determining that STRmix is generally accepted in the relevant scientific community, the court found Dr. Simich to be “well-qualified” to critique the software program, and specifically noted that it was “impressed by his background, education and wealth of practical expertise generally on forensic DNA and on the STRmix program specifically.” (People v. Bullard-Daniel, supra, 42 N.Y.S. 3d at pp. 187-188.) The court stated that the scientific principles underlying the STRmix program were similar, if not identical, to other programs that have been considered and almost universally accepted by New York courts. (Id. at pp. 186-187.) The court also found that the mathematical models applied by the software are non-controversial and have been widely used in fields such as weather forecasting, computational biology, linguistics, genetics, engineering, physics, aeronautics, finance, and social sciences. (Id. at p. 187.)

The case of People v. Alford (Mich. November 28, 2016, Docket No. 15-696-FC) (Alford) is also helpful in understanding STRmix. (Exh. B.) In Alford, the defendant was charged with the 2011 shooting and killing of Michael Adams. Prior to trial, the defendant filed a motion in limine to exclude expert testimony pertaining to the use of STRmix pursuant to Daubert v. Merrell Dow Pharmaceuticals, Inc. (1993) 509 U.S. 579.

4 Courts using the Daubert analysis to assess the reliability of DNA evidence employ the following factors: (1) testing, (2) peer review, (3) rate of error, and (4) general acceptance.
testimony related to the use of STRmix satisfied the reliability criteria set forth in Daubert and therefore such evidence was relevant and admissible. (Alford, supra, at p. 21.)

In making its determination, the Michigan court provided a thorough review and examination of STRmix software and its use as a tool in DNA analysis. The court found that STRmix “does not play a role in the detection of a DNA profile; rather, it simply interprets the DNA profile presented to the computer program. STRmix is undoubtedly the newest form of probabilistic genotyping software currently on the market.” (Alford, supra, at p. 11.) The court explained the principles behind STRmix:

     STRmix applies mathematical methods to the profile, which allows profile information previously wasted to be utilized; however, probabilistic genotyping as a method of evaluating and interpreting DNA is not novel science. Instead, it is a more innovative method of DNA profile interpretation that allows complex and lower-level DNA profiles to be tested using a form of mathematics that is “decades old.”

(Id. at pp. 11-12, italics added.) The court further described how probabilistic genotyping, as a statistical analysis, is used in the application of STRmix software:

     In this process, DNA profiles are applied to mathematical algorithms. The algorithms then compare different statistical models to the actual data and weigh the probability that the model matches the data. The result is a likelihood ratio, which explains the probability of the data given two competing hypotheses. The likelihood ratio is based on the frequency of the DNA type in the population. The algorithms used by STRmix are based on the Markov Chain Monte Carlo Method, which was first developed in the 1950s and is a technique widely used in weather forecasting, computational biology and linguistics, genetics, engineering, physics, aeronautics, the stock market, and social sciences.

(Id. at pp. 12-13.) In determining that the use of STRmix and the results are based on reliable principles and methods, the court noted that “at least two other court in Michigan, as well as courts in New York, Pennsylvania, Virginia and Ohio have deemed the principles and methods utilized by STRmix and other probabilistic genotyping software (such as TrueAllele, (Petric v. State (Ala. 2013) 157 So. 3d 176, 220.) The Daubert analysis has not been held to be applicable to California.
a competitor program that preceded the creation of STRmix) reliable and therefore, admissible.” (Id. at p. 13.)

The Michigan court held that “Strmix is generally accepted in the relevant scientific community.” (Alford, supra, at p. 18.) In forming that conclusion, the court noted that 12 labs currently utilized STRmix in the U.S. (at the time of the evidentiary hearing) and had developed and implemented internal validation procedures that adhered to procedures set out by SWGDAM. The court observed that SWGDAM is a group of approximately 50 scientists that represent Federal, State, and Local forensic labs in the U.S. and Canada and meet twice a year to create guidelines for various things, including probabilistic genotyping. (Ibid.)

The court relied on the testimony of Dr. Buckleton in determining that STRmix was generally accepted. The doctor testified as to the validation process, stating that he and the other developers of STRmix hand-calculated some of the tested samples, in order to verify that the output for the software was correct. (Alford, supra, at p. 18.) He also testified that the forensic science field in North America and much of Europe is moving or has already moved towards the adoption of probabilistic genotyping for the interpretation of DNA as opposed to the conventional method of DNA typing known as the Combined Probability of Inclusion (PCI). To support this assertion, Dr. Buckleton testified that approximately 52% of North American labs had purchased STRmix and had either gone live or were in the process of validation. (Ibid.)

In Florida v. Regisme (Fla. Nov. 22, 2016, Case No. 2015CF010815AMB), a Florida court declined to conduct a Daubert hearing on probabilistic genotype software, and denied the defendant’s motion to exclude DNA evidence. (Exh. C.) As a basis for its ruling, the court stated in its condensed order that DNA evidence, including statistical frequency in population, is generally admissible and is scientifically accepted as reliable. The court further noted that probabilistic genotype software has been used in over 65 cases throughout the U.S. and had been admitted in other cases in Palm Beach, Florida. (Florida v. Regisme, supra, at pp. 1-2.)

In People v. Stevey, supra, 209 Cal.App.4th 1400, the defendant made a motion to exclude DNA tests results generated using an Identifiler kit. (Id. at p. 1409.) On appeal,
Stevey argued that the trial court erred in failing to hold a *Kelly* prong one hearing on interpretation of test results generated on Identifiler. (*Ibid.*) The Court of Appeal rejected his argument, observing that Stevey “overlooks something much more basic – *Kelly* only applies to new scientific techniques. We conclude the interpretation of the test results does not constitute a new scientific technique within the meaning of *Kelly* and did not require an evidentiary hearing.” (*Id.* at pp. 1409-1410.)

The conclusions reached in the above-cited cases are proper here. Decisions from other jurisdictions amply demonstrate that STRmix software is not a new or novel *scientific technique or methodology*. Rather, it is a relatively-new software that implements a well-established type of interpretation of DNA. Although *People v. Stevey*, *supra*, 209 Cal.App 4th 1400, does not directly address STRmix, it is a California case that corroborates STRmix is not a “new scientific technique” subject to a *Kelly* hearing. *Kelly* applies to scientific methods, principles, methodologies and techniques; it does not apply to the specific devices used to implement them. (See *People v. Bury* (1996) 41 Cal.App.4th 1194; *People v. Nolan* (2002) 95 Cal.App.4th 1210.) STRmix is simply a more-precise method of DNA analysis, through the use of a software program, which is used to reliably and more-efficiently interpret complex mixed-source samples. The underlying scientific methodology is not new; *Kelly* does not apply.

**C. Even Assuming Arguendo STRmix DNA Constitutes a “New Scientific Technique,” A First-Prong Kelly Hearing Is Not Warranted**

Even assuming arguendo STRmix constitutes a “new scientific technique,” general acceptance of this alleged scientific technique has been amply demonstrated, thus the first-prong of the *Kelly* test is met and a hearing is not required.

“The *Kelly* requirement of ‘general acceptance’ of a scientific technique means proof of *scientific consensus* drawn from a typical cross-section of the relevant, qualified scientific community. [Citations.]” (*In re Jordan R.* (2012) 205 Cal.App.4th 111, 122 (*Jordan*), italics in original.) The first prong of the *Kelly* test is met if use of the technique is supported by a clear majority of the members of the relevant scientific community. (*People v. Guerra* (1984)
37 Cal.3d 385, 418.) “In determining the general acceptance issue, courts must consider the
quality, as well as the quantity, of the evidence supporting or opposing the scientific
technique. [Citations.]” (Jordan, supra, 205 Cal.App.4th at p. 122; see also People v. Venegas
(1998) 18 Cal.4th 47, 85.)

Published case precedent can eliminate the need to show general acceptance under
Kelly of a scientific technique or to qualify the expert witness to testify about its general
acceptance. Once a published appellate opinion has affirmed the admission of evidence based
upon a new scientific technique, that precedent is controlling on the first prong of the Kelly
test, unless the opponent can produce new evidence to establish a change in the attitude of the
scientific community. (People v. Cordova (2015) 62 Cal.4th 104, 127; People v. Stevey,
supra, 209 Cal.App.4th at p. 1415; People v. Kelly (1976) 17 Cal.3d 24, 32; see, e.g., People
v. Dooley (2009) 45 Cal.4th 390, 447-448 [PCR DQ-Alpha DNA analysis]; see also People v.
Cal.App.3d 1017, 1023-1024 [electrophoresis evidence].)

Another way of determining “general acceptance” under Kelly is by examining
scientific literature:

Considerations of judicial economy make it impractical to require that the
views of a cross-section of the relevant scientific community be presented
personally by each scientist testifying in open court. [Citation.]
“Accordingly, for this limited purpose scientists have long been permitted
to speak to the courts through their published writings in scholarly treatises
and journals.” [Citations.] “ ‘If a fair overview of the literature discloses
that scientists significant either in number or expertise publicly oppose [the
technique] as unreliable, the court may safely conclude there is no such
consensus at the present time.’ ” [Citations.]

(Jordan, supra, 204 Cal.App.4th at p. 123.)

Of course, an expert witness must still be qualified. And the proponent of the evidence
still must make a case-specific foundational showing that correct scientific procedures were
used. (People v. Morganti, supra, 43 Cal.App.4th at pp. 660-662.)
In addition to the above-cited decisions, literature proffered by petitioner in support of his claims for relief as well as SWGDAM guidelines support that the mathematical principles utilized by STRmix are accepted as reliable within the scientific community. One such article was published in the American Academy of Forensic Science journal and was co-authored by several forensic scientists, including Bruce Budowle, a renowned scientist within the field of forensic science as testified to by petitioner’s expert at the hearing. (Petitioner’s Exh. 18 [Budowle et al., *Mixture Interpretation: Defining the Relevant Features for Guidelines for the Assessment of Mixed DNA Profiles* (July 2009) American Academy of Forensic Sciences].) In the article, the authors discussed the importance of likelihood ratio (LR) as a statistical approach in DNA interpretation. This 2009 article stated that the probability of exclusion (PE), a separate DNA statistical method, is a “simplistic and less powerful analysis” compared to the LR approach. (*Id.* at p. 820.) The authors recommended that forensic scientists be trained to calculate both the PE and the LR statistical approaches. (*Id.* at pp. 821.) The authors found both calculation methods acceptable and endorsed applying both statistical methods when feasible. (*Ibid.*) This article supports that LR has been accepted within the forensic scientific community as a reliable statistical method to interpret the significance of DNA evidence for at least the past eight years.

In another article utilized by petitioner at the hearing, the authors addressed the LR method. In that article, the authors recommended “moves in favour of using the [LR] approaches” and noted that “laboratories have been embracing LR application.” (Petitioner’s Exh. 32 [Bieber et al., *Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion* (2016) BMC Genetics, at p. 3].)

Probabilistic genotyping was addressed in a report created by the President’s Council on Science and Technology. The report recommended that DNA analysis of complex mixtures “move rapidly” to appropriate methods utilizing probabilistic genotyping. (Petitioner’s Exh. 33 [*Report to the President, Forensic Science in Criminal Courts: Ensuring Scientific Validity*

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**RESPONDENT’S POINTS AND AUTHORITIES REGARDING THE COURT’S QUESTIONS RE STRMIX**
And finally, in June 2015 SWGDAM issued guidelines addressing probabilistic genotyping. In the guidelines, SWGDAM stated that probabilistic genotyping is particularly useful to interpret low-level DNA samples and complex mixtures. (Exh. H [SWGDAM, Guidelines for Validation of Probabilistic Genotyping Systems (June 15, 2015) at p. 2].)

Significantly, the guidelines noted that probabilistic genotyping approaches “can reduce subjectivity in the analysis of DNA typing results” and makes “use of more genotyping information.” SWGDAM also found this method “enhances the ability to distinguish true contributors and non-contributors” compared to traditional methods. (Ibid.)

The cited out-of-state decisions and literature overwhelmingly show that STRmix probabilistic genotyping software is generally accepted in the scientific community as a reliable method of DNA interpretation under the Kelly standard. STRmix has been empirically tested and found to be reliable and accurate, and the various mathematical and statistical principles utilized by STRmix have been long-accepted and endorsed by the scientific community. Furthermore, the literature and court decisions show that this computerized probabilistic approach and the use of likelihood ration principles, is a more-advanced method of interpreting DNA mixtures and is rapidly becoming the preferred method because of the advantages it offers over traditional human interpretation methods: STRmix is capable of considering significantly more data and making better use of that data than human review, and is considered a more-objective approach to DNA interpretation than traditional human methods of DNA interpretation. Accordingly, prong-one of the Kelly test has been sufficiently established and a hearing is not required. Upon a showing of the qualifications of the testifying expert and that correct scientific procedures were used in this case, evidence of the STRmix DNA results should be admitted at the evidentiary hearing.
Appellant, Kevin James Foley, appeals from the judgment of sentence entered on June 1, 2009, by the Honorable William J. Martin, President Judge of the Court of Common Pleas of Indiana County, Criminal Division. After careful review, we affirm.

In the early morning hours of April 13, 2006, Dr. John Yelenic, a dentist living alone in Blairsville, Pennsylvania, was brutally assaulted and murdered in his home. After an eight-day jury trial, Foley, a Pennsylvania State Police Trooper who was living with Dr. Yelenic’s estranged wife,\(^1\) was

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\(^1\) The Commonwealth refers to Dr. Yelenic’s wife as his “soon-to-be ex-wife.” Appellee’s Brief, at 37. However, Dr. Yelenic and his wife were married at the time of the murder, and representatives of Dr. Yelenic’s estate were unable to obtain a posthumous divorce. See Yelenic v. Clark, 922 A.2d 935, 936 (Pa. Super. 2007).
found guilty of first-degree murder and sentenced to life imprisonment. This timely appeal followed.

Appellant presents the following issues for our review:

I. WHETHER THE TRIAL COURT ERRED IN PRECLUDING THE TESTIMONY OF BETTY MORRIS AT TRIAL, WHERE THE EVIDENCE WAS RELEVANT AND ADMISSIBLE TO DEMONSTRATE THE MOTIVE OF ANOTHER PERSON TO COMMIT THE CRIME?

II. WHETHER THE TRIAL COURT ERRED IN ADMITTING THE TESTIMONY OF DR. MARK PERLIN, IN VIOLATION OF THE FRYE TEST FOR THE ADMISSIBILITY OF NOVEL SCIENTIFIC TESTIMONY?

III. WHETHER THE VERDICT WAS AGAINST THE WEIGHT OF THE EVIDENCE?

IV. WHETHER THE TRIAL COURT ABUSED ITS DISCRETION IN ADMITTING THE SHOE PRINT EVIDENCE AT TRIAL?

V. WHETHER THE TRIAL COURT ERRED IN INSTRUCTING THE JURY ON THE PERMISSIVE INFERENCE OF MALICE FROM THE USE OF A DEADLY WEAPON?

Appellant’s Brief, at 4. We proceed to the merits.

Foley’s first claim is that the trial court erred in excluding the testimony of Bette Morris. The trial court may exercise its discretion in deciding whether to admit evidence, and our review of the trial court’s evidentiary decisions is limited to determining whether the trial court abused

2 In his brief, Appellant refers to this witness variously as “Betty Morris,” “Bette Morris,” and “Bette Davis.” Appellant’s Brief, at 4, 23. This opinion will refer to her as Bette Morris, which is consistent with the notes of testimony and Appellee’s brief. See N.T., March 17, 2009, at 134, 141.
its discretion. *See Commonwealth v. Moser*, 999 A.2d 602, 605 (Pa. Super. 2010). The trial court abused its discretion only if its ruling “reflects manifest unreasonableness, or partiality, prejudice, bias, or ill-will, or such lack of support to be clearly erroneous.” *Id.*

During the criminal investigation of this case, Bette Morris said to a law enforcement officer that on two occasions she had observed Dr. Yelenic engaged in intimate acts with his next door neighbor, Melissa Uss. According to Foley’s counsel, if placed on the stand, Bette Morris would deny that she had ever made such observations, and then counsel would treat her as a hostile witness and impeach her with the statement she gave police. *See* N.T., March 17, 2009, at 135. When the Commonwealth objected that this evidence was irrelevant, Foley’s counsel explained that it was intended to show that Melissa Uss’s husband had a motive to kill Dr. Yelenic: “[A] jury could infer that somebody who was having a romantic affair with Dr. Yelenic, the husband might be inclined to do something and that is a fair inference from that.” *Id.*, at 137. However, when the trial court asked whether the defense had any evidence that Melissa Uss’s husband knew of the supposed intimate acts, defense counsel conceded that he had no such evidence. *See*
According to the defense, Bette Morris’s observations were made when Mr. Uss was in the military and not at home. See id., at 135.

The trial court excluded the testimony of Bette Morris on the grounds that it was “a mere suggestion of motive and therefore irrelevant and inadmissible.” Opinion and Order of Court, November 4, 2009, at 10. Generally, “proof of facts showing the commission of the crime by someone else is admissible.” Commonwealth v. Boyle, 368 A.2d 661, 669 (Pa. 1977). However, the Pennsylvania Supreme Court has held that facts suggesting that someone had a motive should not be considered by the jury if the person had no knowledge of the suggestive facts. See Commonwealth v. Giovanetti, 19 A.2d 119, 125 (Pa. 1941).

In Giovanetti, the murder victim had an employer-provided life insurance policy with his wife, the defendant, listed as the beneficiary. See id. The trial court refused the defendant’s request to instruct the jury that it could consider the insurance policy as evidence of her motive only if it found that she knew about the policy before the murder. See id. The Supreme Court reversed, holding that the wife’s knowledge of the policy was necessary for it to be considered as evidence of her motive to kill. See id.

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3 Although Foley called Melissa Uss as a witness, he did not ask her any questions regarding the alleged romantic relationship with Dr. Yelenic. See N.T., March 16, 2009, at 106-15. Foley did not call her husband as a witness.
The trial court’s decision to preclude the testimony of Bette Morris had a sufficient basis in the governing law and was not an abuse of discretion. Although intimate contact between the victim and Melissa Uss may suggest that her husband had a motive, “merely suggesting that someone else may have had a motive is not evidence.” Commonwealth v. Rivers, 644 A.2d 710, 715 (Pa. 1994). The trial court acted within its discretion in rejecting the testimony as irrelevant because the husband had no knowledge of the intimate contact. See Giovanetti, 19 A.2d at 125. Because there was no other evidence corroborating the suggestion that Mr. Uss was a killer motivated by jealousy, the trial court’s decision to preclude the testimony of Bette Morris was a permissible exercise of discretion.

Foley’s reliance on Commonwealth v. Ward, 605 A.2d 796 (Pa. 1992), is misguided. In that case, the defendant was a police informant who was convicted of arson. The trial court precluded evidence that the people whom he had informed against had threatened him and had committed the arson in retaliation against him. See id., at 797. In addition, the trial court precluded testimony from “an American Red Cross worker as to appellant's request for assistance following the fire, the organization's investigation, and its subsequent provision of emergency fund vouchers for clothing,” which the defendant sought to introduce in order to “undermine the Commonwealth’s evidence of motive by arguing the unlikelihood that appellant would destroy
all of his own worldly possessions merely because of a disagreement with his brother.” *Id.*

**Ward** is distinguishable from the instant case. In **Ward**, the defendant’s offer of proof indicated that the other potential perpetrators *knew* that the defendant had given information about them to the police. *See id.* Further, the precluded evidence from the Red Cross worker concerned the defendant’s own motive to commit the crime rather than someone else’s motive. Unlike the testimony at issue in the instant case, the evidence at issue in **Ward** was relevant, and its exclusion violated the defendant’s fundamental right to introduce relevant, admissible evidence. *See id.* (citing *Chambers v. Mississippi*, 410 U.S. 284 (1973)).

Foley’s next claim is that the trial court erred in admitting the DNA-related testimony of Dr. Mark Perlin. A sample containing DNA from the victim and another person was found underneath the fingernail of the victim. This mixed sample was tested in a laboratory at the FBI, and three experts – Dr. Perlin, Dr. Robin Cotton, and Jerrilyn Conway, an FBI forensic scientist – used the FBI’s data in developing their testimony. Each of the experts determined that Foley’s DNA profile was consistent with DNA found in the sample. The experts differed in their estimates of the probability that someone other than Foley would possess DNA matching the DNA found in the sample – Conway testified that the probability that another Caucasian could be the contributor was 1 in 13,000; Dr. Cotton testified that the
probability was 1 in 23 million; and Dr. Perlin testified that it was 1 in 189 billion.

As with other evidentiary decisions, the trial court may exercise its discretion in deciding whether to admit expert testimony. See Commonwealth v. Ventura, 975 A.2d 1128, 1140 (Pa. Super. 2009). The trial court’s decision will be reversed only if the appellate court finds an abuse of discretion or an error of law. See id.

Foley claims that Dr. Perlin’s testimony is inadmissible because it fails the Frye test for the admissibility of scientific evidence. See Appellant’s Brief, at 31. Pennsylvania continues to adhere to the Frye test, which provides that “novel scientific evidence is admissible if the methodology that underlies the evidence has general acceptance in the relevant scientific community.” Betz v. Pneumo Abex LLC, 998 A.2d 962, 972 (Pa. Super. 2010) (en banc) (citing Grady v. Frito-Lay, Inc., 839 A.2d 1038 (Pa. 2003)). The Frye test is a two-step process. See id. First, the party opposing the evidence must show that the scientific evidence is “novel” by demonstrating “that there is a legitimate dispute regarding the reliability of the expert’s conclusions.” Id. If the moving party has identified novel scientific evidence, then the proponent of the scientific evidence must show that “the expert’s methodology has general acceptance in the relevant community.”

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4 Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).
scientific community” despite the legitimate dispute. *Id.* (internal quotation marks omitted).

The trial court did not expressly determine whether Dr. Perlin’s testimony was “novel scientific evidence.” Opinion and Order of Court, March 3, 2009, at 2-3. Instead, the court found that Dr. Perlin’s methodology was a refined application of the “product rule,” a method for calculating probabilities that is used in forensic DNA analysis. *See id.*, at 2. The Pennsylvania Supreme Court has held that scientific evidence based on the product rule is admissible in the Commonwealth. *See Commonwealth v. Blasioli*, 713 A.2d 1117, 1118 (Pa. 1998). Because Dr. Perlin’s calculations were made using newer technology, the trial court rhetorically asked “at what point does the use of the product rule become novel science.” Opinion and Order of Court, March 3, 2009, at 2. The trial court went on to find that Dr. Perlin’s methodology was generally accepted. *See id.*, at 3, 5.

We find that Dr. Perlin’s testimony was not “novel” as that term is defined in the governing law, and thus the trial court did not abuse its discretion in admitting the testimony. The “novelty” of scientific testimony turns on whether “there is a legitimate dispute regarding the reliability of the expert’s conclusions,” which is not necessarily related to the newness of the technology used in developing the conclusions. *Betz*, 998 A.2d at 972. In *Betz*, the court noted that novelty “is not restricted to new science,” and “even ‘bedrock’ scientific principles may be subject to a Frye analysis” if
those principles become disputed. *Id.*, at 973-74. Conversely, where there is no dispute, *Frye* should be “construed narrowly so as not to impede admissibility of evidence that will aid the trier of fact in the search for truth.” *Id.*, at 972.

Here, we find no legitimate dispute regarding the reliability of Dr. Perlin’s testimony. Dr. Perlin used proprietary software called TrueAllele to interpret the data he received from the FBI. *See* N.T., March 12, 2009, at 130. Foley claims that Dr. Perlin’s testimony should have been excluded for three reasons: (1) “as of the date of the pre-trial hearing, no forensic laboratory in the United States used Perlin’s TrueAllele [sic] method in analyzing a mixed sample of DNA for forensic purposes”; (2) “the TrueAllele [sic] system had never been used in a court of law in any jurisdiction in the United States on a mixed DNA sample to give a likelihood ratio”; and (3) no outside scientist can replicate or validate Dr. Perlin’s methodology because his computer software is proprietary. Appellant’s Brief, at 35.

Foley’s first claim does not amount to a showing of “novelty” because it does not show a “legitimate dispute regarding the reliability of the expert’s conclusions.” *Betz*, 998 A.2d at 972. Regardless, Foley understates the extent of usage of Dr. Perlin’s system. As Dr. Perlin testified:

The TrueAllele technology is used by New York State for all of their data banking and bringing their casework system on board. The Allegheny County Crime Lab has been using our system as a service and recently purchased the system for looking at mixtures in complex cases and DNA evidence. The World Trade Center engaged us to reanalyze all of the data and rematch it.
using our methods from the eighteen thousand (18,000) or so victim remains and the three thousand (3000) missing people and so on and there are other groups that we work with.

N.T., Mar. 12, 2009, at 132.

In addition, the United Kingdom’s Forensic Science Service uses TrueAllele technology to analyze crime scene evidence and build the UK National DNA Database, which is the largest of its kind in the world. See Forensic Science Service Expands License for Cybergenetics Automated DNA Data Review Technology; Pioneering TrueAllele Software Helps Builds [sic] World’s Largest DNA Database, Business Wire, July 26, 2004, available at http://tinyurl.com/8yxh8hd (last visited Nov. 21, 2011); see also Opinion and Order of Court, March 3, 2009, at 5.

Foley’s second reason for excluding the testimony is not persuasive because “novelty” of a scientific methodology does not turn on its previous use in court. During cross-examination, Dr. Perlin testified that he did not know whether any users of TrueAllele had used it in a case that went to trial. See N.T., March 12, 2009, at 133-34. Even if Foley is correct that TrueAllele has never been used in court, this would not prove novelty. The Commonwealth’s “continued adherence to the Frye test is based upon its interest in having judges be guided by scientists when assessing the reliability of a scientific method, and not the other way around.” Betz, 998 A.2d at 979 (internal quotation marks omitted). If this court assessed “novelty” of scientific evidence based on its previous use in court, we would
be failing to defer to scientists in assessing the reliability of scientific methods. Rather than looking to previous uses in court, we find “novelty” only if there is a dispute among scientists. See Betz, 998 A.2d at 972.

Foley’s third reason for exclusion is misleading because scientists can validate the reliability of a computerized process even if the “source code” underlying that process is not available to the public. TrueAllele is proprietary software; it would not be possible to market TrueAllele if it were available for free. See N.T., Hearing, February 18, 2009, at 54. Nevertheless, TrueAllele has been tested and validated in peer-reviewed studies. One study used laboratory-generated DNA samples and found that quantitative analysis performed by TrueAllele was much more sensitive than qualitative analysis such as that performed by the FBI. See Perlin & Sinelnikov, An Information Gap in DNA Evidence Interpretation, 4 PLoS ONE e8327, at 10 (2009), available at http://dx.doi.org/10.1371/journal.pone.0008327. A recent paper entitled “Validating TrueAllele® DNA Mixture Interpretation” used DNA samples from actual cases and reached similar results. See Perlin et al., Validating TrueAllele® DNA Mixture Interpretation, 56 Journal of Forensic Sciences 1430 (2011). The study “validated the TrueAllele genetic calculator for DNA mixture interpretation” and found that “[w]hen a victim reference was available, the computer was four and a half orders of magnitude more
efficacious than human review.”\textsuperscript{5} \textit{Id.}, at 1444. Both of these papers were published in peer-reviewed journals; thus, their contents were reviewed by other scholars in the field.

Because Foley has failed to establish the existence of a legitimate dispute over Dr. Perlin’s methodology, he has failed to show that Dr. Perlin’s testimony constituted “novel” scientific evidence. \textit{See Betz}, 998 A.2d at 972. Therefore, we find that the trial court’s decision to admit the testimony was not an abuse of discretion. Absent a legitimate dispute, there is no reason to “impede admissibility of evidence that will aid the trier of fact in the search for truth.” \textit{Id.}

Foley’s next claim is that the trial court abused its discretion when it admitted evidence related to bloody shoeprints found at the murder scene. Foley claims that a new trial should be awarded because this evidence was irrelevant and highly prejudicial. \textit{See} Pa. R. Evid. 402, 403. As noted above, this court will find an abuse of discretion only if the trial court’s ruling “reflects manifest unreasonableness, or partiality, prejudice, bias, or ill-will, or such lack of support to be clearly erroneous.” \textit{Commonwealth v. Moser}, 999 A.2d 602, 605 (Pa. Super. 2010).

Foley claims the shoeprint evidence was irrelevant because “[t]he shoe prints found at the scene could not be authoritatively determined to be any

\textsuperscript{5} In this case, a victim reference was available because the evidence was taken from the victim’s fingernail. \textit{See} N.T., March 12, 2009, at 89.
particular brand, style, or size of shoe.” Appellant’s Brief, at 61. At trial, the Commonwealth introduced expert testimony from an FBI forensic examiner that the shoeprints at the crime scene apparently were left by an Asics brand running shoe with the model name “Gel Creed” or “Gel Creed Plus.” N.T., March 13, 2009, at 45. The FBI forensic examiner noted that he could not state his opinion with one hundred percent certainty because the FBI database does not contain reference information for every shoe manufactured in the world. *See id.*, at 47

The Commonwealth also introduced testimony from Terry Schalow, a product manager for Asics America Corporation. He testified that the shoeprint was left by an Asics Gel Creed, Gel Creed Plus, or a knockoff of this type of shoe. *See id.*, at 18-19. The size was between ten and twelve and a half. *See id.*, at 18. Only about 25,000 Gel Creed shoes were sold in the United States. *See id.*, at 20. Importantly, Foley ordered a size ten Gel Creed from Asics in August 2003. *See id.*, at 25, 27.

Contrary to Foley’s position, the uncertainty in this testimony goes to its weight rather than its admissibility. Foley emphasizes that neither expert could state with absolute certainty that the shoeprints were left by size 10 shoes manufactured by Asics and purchased by Foley. However, to be relevant and admissible, “evidence need not be conclusive.” *Commonwealth v. Crews*, 640 A.2d 395, 402 (Pa. 1994). Evidence is relevant if it logically tends to establish a material fact in the case or tends
to support a reasonable inference regarding a material fact. See id. Here, the shoeprint evidence supported a reasonable inference that Foley was at the scene of the crime. This relevant, though inconclusive, evidence was admissible, and “its weight and persuasiveness were properly matters for the jury to determine.” Id., at 403.

Foley’s charge that the shoeprint evidence was “highly prejudicial” is also not persuasive. See Appellant’s Brief, at 64. The Pennsylvania Rules of Evidence provide that “[a]lthough relevant, evidence may be excluded if its probative value is outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by considerations of undue delay, waste of time, or needless presentation of cumulative evidence.” Pa. R. Evid. 403 (emphasis added). Evidence is not unfairly prejudicial simply because it is harmful to the defendant’s case. See Commonwealth v. Page, 965 A.2d 1212, 1220 (Pa. Super. 2009). Rather, exclusion of evidence on this ground “is limited to evidence so prejudicial that it would inflame the jury to make a decision based upon something other than the legal propositions relevant to the case.” Id. While the shoeprint evidence tended to support an inference that Foley committed the crime, there is no reason to believe that it improperly inflamed the jury. Thus, the trial court did not abuse its discretion by admitting the shoeprint evidence.

Next, we turn to Foley’s claim that the jury’s verdict was against the weight of the evidence. Foley preserved this claim for appellate review by
raising it with the trial judge in a post-sentence motion. See Pa. R. Crim. P. 607; see also Opinion and Order of Court, November 4, 2009, at 1. Our standard of review is well-settled:

The finder of fact is the exclusive judge of the weight of the evidence as the fact finder is free to believe all, part, or none of the evidence presented and determines the credibility of the witnesses.

As an appellate court, we cannot substitute our judgment for that of the finder of fact. Therefore, we will reverse a jury’s verdict and grant a new trial only where the verdict is so contrary to the evidence as to shock one’s sense of justice. A verdict is said to be contrary to the evidence such that it shocks one’s sense of justice when “the figure of Justice totters on her pedestal, or when “the jury’s verdict, at the time of its rendition, causes the trial judge to lose his breath, temporarily, and causes him to almost fall from the bench, then it is truly shocking to the judicial conscience.”

Furthermore,

where the trial court has ruled on the weight claim below, an appellate court’s role is not to consider the underlying question of whether the verdict is against the weight of the evidence. Rather, appellate review is limited to whether the trial court palpably abused its discretion in ruling on the weight claim.


We find that the trial court did not abuse its discretion in finding that the verdict was not against the weight of the evidence. Over the course of the eight-day trial, copious evidence linking Foley to the crime was presented to the jury. This evidence was comprehensive and credible enough to support the verdict.
At the time of the murder, Foley was living with Dr. Yelenic’s estranged wife. Foley had expressed his hatred of Dr. Yelenic to numerous individuals – Foley had said that he wished Dr. Yelenic would die, and on one occasion Foley asked a fellow police officer to help him kill Dr. Yelenic. On three occasions, Foley attempted to have Dr. Yelenic investigated and arrested for child abuse, and Foley was frustrated by his lack of success.

Foley had an opportunity to commit the crime. At the approximate time of the murder, he was driving from a hockey game in Delmont to his home in Indiana, which took him past Blairsville, where Dr. Yelenic resided.

Foley’s DNA profile was consistent with DNA found under Dr. Yelenic’s fingernail, and the most conservative estimate of the likelihood that someone else would possess a consistent profile was one in 13,000. On the night before the murder, Foley had no abrasion on his forehead, but on the morning following the murder he had an injury on his forehead described by three eyewitnesses as “a fingernail scratch” and by others as a cut that appeared to be “fresh.”

The shoeprint evidence, discussed above, supported a reasonable inference that Foley was present at the scene. Foley said that he did not remember what happened to the size 10 pair of Gel Creed shoes he ordered in 2003.

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6 Foley does not challenge the reliability of the scientific methodology underlying this estimate.
Dr. Yelenic was slashed by a sharp instrument, and Foley was known by his colleague to be a “knife guy” who habitually flicked open and shut a knife that he carried with him. In fact, Foley once accidentally sliced open a supervisor’s pair of pants in the groin area when he was walking past him. When informed of Dr. Yelenic’s death shortly after the discovery of the murder, Foley was unemotional, expressed no curiosity about the nature or cause of death, and only asked which law enforcement agency was in charge of the investigation. After the murder, Foley stopped playing with his knife and started wearing Nike brand shoes instead of Asics.

Given this evidence, the verdict is hardly shocking to the judicial conscience. The court below acted within the bounds of its discretion as the finder of fact. Thus, we reject Foley’s claim that the verdict was against the weight of the evidence.

Finally, we turn to Foley’s argument that the trial court erred in instructing the jury on the permissive inference of malice from the use of a deadly weapon. The trial court instructed the jury that “[i]f you believe that the defendant intentionally used a deadly weapon on a vital part of John J. Yelenic’s body, you may regard that as an item of circumstantial evidence from which you may, if you choose, infer that the defendant acted with malice.” N.T., March 18, 2009, at 229.

Foley concedes that the Supreme Court of Pennsylvania has approved this charge in a homicide case. See Commonwealth v. Jones, 912 A.2d
Nevertheless, Foley argues that “this is an unconstitutional charge that deprived him of due process and should now be overruled.” Appellant’s Brief, at 65. However, this court has a “duty and obligation to follow the decisional law of [the Supreme Court of Pennsylvania].” Commonwealth v. Shaffer, 734 A.2d 840, 844 n.6 (Pa. 1999). “The primary role of the Superior Court is to apply existing law to the cases that come before us. It is not our function to attempt reversing viable Supreme Court rulings . . . .” L.B. Foster Co. v. Charles Caracciolo Steel & Metal Yard Inc., 777 A.2d 1090, 1096 (Pa. Super. 2001).

Because the challenged jury instruction has been approved by the Supreme Court, we find that the trial court accurately instructed the jury on the law of the Commonwealth. See Jones, 912 A.2d at 279-80. Accordingly, we reject Foley’s claim and affirm the judgment of sentence.

Judgment of sentence affirmed. Jurisdiction relinquished.
47 Misc. 3d 850
Supreme Court, Schenectady County, New York.

The People of the STATE of New York v.
John WAKEFIELD, Defendant.

Feb. 9, 2015.

Synopsis
Background: Defendant was charged with murder in first degree, murder in second degree, and robbery in first degree. Defendant moved to suppress scientific evidence of DNA using computerized probabilistic genotype analysis, on grounds that evidence was novel, as abandoning human review and analyzing data that fell below thresholds incorporated in standard practice by DNA laboratories.

[ Holding: ] The Supreme Court, Schenectady County, Michael V. Coccoma, J., held that in matter of first impression, DNA evidence using computerized probabilistic genotype analysis is admissible as generally accepted under Frye standard.

Motion denied.

Attorneys and Law Firms

**541 John Wakefield, pro se, and Frederick Rench and Catherine Bonventre, for defendant.

Robert M. Carney, District Attorney (Peter H. Willis of counsel), for plaintiff.

Opinion

MICHAEL V. COCCOMA, J.

*851 The Defendant John Wakefield is charged with Murder in the First Degree (PL § 125.27(1)), Murder in the Second Degree (PL § 125.25(1)(a) (vii)), Murder in the Second Degree (PL § 125.25(3)), Robbery in the First Degree (PL § 160.15(1)), and Robbery in the First Degree (PL § 160.15(3)).

The People seek to introduce at trial scientific evidence of deoxyribonucleic acid (DNA) using a probabilistic genotype analysis. The Defendant does not argue that the principles and procedures applied to the evidence in this case to derive the DNA data prior to entry into the Cybergenetics TrueAllele Casework software are novel nor does the Defendant argue that the use of statistical models and likelihood ratios in reporting the probative value of DNA evidence is novel. Instead, the Defendant asks the Court to suppress that evidence as being novel in that it abandons the human element in analysis and it analyzes data that falls below the thresholds incorporated in standard practice by DNA laboratories.

Peter H. Willis, Esq., appeared on behalf of the People; the Defendant appeared in person and by Frederick Rench, Esq. and Catherine Bonventre, Esq. A hearing was held over numerous days at which the Court had a full opportunity to consider the evidence presented in this proceeding,
including the testimony offered and the Exhibits received (see attached Table A). The Court further had the opportunity to observe the demeanor of the witnesses—Dr. Mark W. Perlin, Dr. Barry W. Duceman and Jay Caponera—and has made determinations on issues of credibility with respect to these witnesses and the weight to give to their respective testimony. The Court has also considered the arguments of counsel and the points of law referenced in their respective Memorandums.

[1] [2] [3] Since Cybergenetics TrueAllele Casework has never been accepted in a New York Court, it is by nature novel scientific evidence. To be admissible in New York Courts, it must pass the Frye test as first formulated in Frye v. United States, 293 F. 1013 (1923) and subsequently adopted by the New York Court of Appeals in People v. Middleton, 54 N.Y.2d 42, 444 N.Y.S.2d 581, 429 N.E.2d 100 (1981). That protocol requires that expert testimony be based on a scientific principle or proceeding which has been “sufficiently established to have gained general acceptance in the particular field in *852 which it belongs” (Frye, at 1014). A Frye inquiry is concerned with the basis of an expert's opinion and not whether the particular opinion is sound (Lugo v. New York City Health & Hosps. Corp., 89 A.D.3d 42, 929 N.Y.S.2d 264 [2nd Dept.2011] ). In other words, Frye is not concerned with the reliability of an expert's conclusions, but instead with whether the expert's deductions **542 are based on principles that have gained general acceptance as reliable (see Nommon v. City of New York, 32 A.D.3d 91, 819 N.Y.S.2d 705 [1st Dept.2006] ).

And in deciding the admissibility of novel scientific evidence, a court may consider “opinions, texts, laboratory standards or scholarly articles” as well as expert testimony (see People v. Wesley, 83 N.Y.2d 417, 611 N.Y.S.2d 97, 633 N.E.2d 451 [1994] ).

DNA identification is a powerful forensic tool for solving and preventing crime. Two common sources of data ambiguity in biological evidence are DNA mixtures from multiple contributors and low-template (evidence samples below the threshold) DNA. Although some American laboratories are moving to quantitative modeling of DNA mixture data, most still use Combined Probability of Inclusion (CPI) or Combined Likelihood Ratio (CLR), using the qualitative Boolean logic of all-or-none allele (the number of repeated words) events. Both approaches apply thresholds to the DNA data that cut off quantitative information. Their analysts subjectively apply these analytical or stochastic thresholds manually to data peaks to decide whether or not they believe the evidence peak represents an allele in the genetic material. But the more complex data that has mixtures or low-template DNA limits the applicability of such qualitative procedures.

Computer interpretation methods use more of the quantitative short tandem repeat (STR) peak height data rather than thresholds and have been used for over 20 years. Computers offer three principal advantages in the interpretation process: (1) productively-eliminates the often time-consuming human review of cases that
are impossible to solve, (2) information-human review typically makes simplifying assumptions that can discard considerable identification information containing DNA evidence whereas a computer can use a statistical model to fully examine the quantitative peak height data, and (3) objectivity-human mixture interpretation methods sometimes use the suspect genotype (pair of allele) to help infer or report results whereas a mathematically programmed computer can infer a genotype directly from the evidence data without using any suspect information and then afterward compute a match likelihood ratio (LR) statistic from this genotype.

*853 Probabilistic genotypes have been recognized by regulatory bodies such as the Scientific Working Group on DNA Analysis Methods (SWGDAM)\(^1\) in its 2010 “Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories” and the American National Standards Institute (ANSI) in the 2011 article “Data format for the interchange of fingerprint, facial & other biometric information” as a valid approach to DNA Interpretation and reporting. There are two probabilistic approaches:

1 A forensic DNA advisory group to the FBI director that is comprised of forensic scientists who serve as DNA technical leaders or CODIS administrators in their laboratories.

(1)semi-continuous\(^2\)—information is determined from the allele present-peak heights are not considered, and

2 e.g. LRmix, Like LTD, FST, Lab Retriever, Armed Expert, Geno Proof Mixture.

(2)fully continuous\(^3\)—incorporation of biological parameters.

3 e.g. TrueAllele Casework, STRmix, DNA–View Mixture Solution, DNA mixtures

Cybergenetics TrueAllele Casework is a fully continuous probabilistic approach that analyzes the electropherograms (EPG) (computerized DNA data that a local laboratory extracted and amplified) and considers **543 the genotypes (pair of alleles) at every locus (pair of DNA sentences) of each contributor, taking into consideration the mixture weights of the contributors, the DNA template mass, polymerase chain reaction (PCR) stutter, relative amplification, DNA degradation, and the uncertainties of all these variables. Its genetic calculator uses Markov chain Monte Carlo (MCMC)\(^4\) to give the probabilities of all the different possibilities, not just a maximum possibility, and by using Bayes theorem\(^5\), it decomposes that calculation into a prior probability and a likelihood function that compares genotypes relative to a population and computes a match LR.

This was first published in the 1950's, and according to Dr. Perlin, “he would be hard pressed to know any field where MCMC has not been used” (October 6, 2014 Transcript, p. 45).

An algebraic (p (A/B) = p(B/A) p(A)/p(B)) way to work out the likelihood of something in the face of some particular piece, or pieces, of evidence in use since 1812.

[4] The Defendant's expert, and others, question this approach. They argue that there is a lack of validation software,
it is costly and time consuming, and it uses “black box” technology. The acknowledged success of Cybergenetics TrueAllele Casework has begun to erode these barriers and there is a move in the direction of probabilistic modeling, but the use thereof *854 would still represent a minority of casework. However, the test is not whether a particular procedure is unanimously endorsed by the scientific community (Cornell v. 360 W. 51st St. Realty, LLC, 22 N.Y.3d 762, 986 N.Y.S.2d 389, 9 N.E.3d 884 [2014] ), but whether it is generally accepted as reliable (People v. Wernick, 89 N.Y.2d 111, 651 N.Y.S.2d 392, 674 N.E.2d 322 [1996] ).

PEER REVIEW
There have been numerous articles published relative to Cybergenetics TrueAllele Casework (see People's Exhibit 15) in all the leading journals of the DNA community, including the American Journal of Human Genetics, the Journal of Forensics Sciences (the Official Scientific Journal of the American Academy of Forensic Sciences), Forensic Science International: Genetics, Plos One, Genometrics, The Croatian Medical Journal, and Science and Justice. Prior to being published, each of these articles had to be reviewed by two anonymous scientists in the DNA community to ensure a quality assurance that the manuscript and scientific results are up to the standards of the level of that journal, that the results are reported properly, that the results make sense, and that the conclusions that are drawn from the data are supported by the data. In addition thereto, there have been numerous forensic collaborations (see People's Exhibit 16) with other scientists in the DNA community.

VALIDATION STUDIES
Dr. Perlin testified that Cybergenetics TrueAllele Casework's source code is a trade secret, which he will not reveal. The Defendant argues that without that code, no outside scientist can replicate or validate Dr. Perlin's methodology and, therefore, Cybergenetics TrueAllele Casework evidence should not be admissible in this case. However, scientists can, and have, validated the reliability of Cybergenetics TrueAllele Casework even though the source code underlying the process is not available to the public. Cybergenetics TrueAllele Casework has undergone 20 unpublished validating studies and 6 published validation studies (People's Exhibits 3, 4, 5, 6, 7, 27) to confirm that the laboratory is producing the same type of reliable **544 results or determining the extent of reliability for the method or technology that's already been developmentally validated. Four of these were independent validation studies-Massachusetts, Virginia, and 2 by the New York State Police as addendums to People's Exhibit 5 (People's Exhibits 30 and 31). Without exception, each of these validation studies found Cybergenetics *855 TrueAllele Casework to be sensitive (the extent to which interpretation identifies the correct person) and specific (the extent to which the interpretation does not misidentify the wrong person). And Cybergenetics TrueAllele Casework was shown to have provided objectivity, achieved greater genotype accuracy, and proved
reproducible (the extent to which the interpretation gives the same answer to the same question).

SCIENTIFIC COMMUNITY
On May 20, 2011 the New York State Commission on Forensic Science DNA Subcommittee unanimously approved Cybergenetics TrueAllele Casework for use by the New York State Police for their forensic casework. Pursuant to Executive Law § 995–b(13), this Subcommittee was comprised of a chair appointed by the chair of the Commission who then appointed six other members to the subcommittee, one of whom shall represent the discipline of molecular biology and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall represent the discipline of population genetics and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be representative of the discipline of laboratory standards and quality assurance regulation and monitoring and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be a forensic scientist and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be representative of the discipline of population genetics and be appointed upon the recommendation of the commissioner of criminal justice services and one of whom shall be representative of the discipline of forensic science and be appointed upon the recommendation of the commissioner of criminal justice services-all respected scientists who do research on different areas of DNA analysis. The subcommittee in this case consisted of Jack Ballantyne, Ph.D., Chairman, George Carmody, M.D., Eric Buell, Ph.D., Charles Hirsch, Ph.D., Mark Batzen, Ph.D., Anne Welsh, Ph.D., and Ranajit Chakraborty, Ph.D. (Defendant's expert). It was their duty to assess and evaluate all DNA methodologies proposed to be used for forensic analysis. In that regard, it reviewed and evaluated Cybergenetics TrueAllele Casework over 1 1/2 years and heard presentations by Dr. Perlin, Joe Galdi (runs the DNA laboratory in Suffolk County), J.D. Bellvose, Russ Gedick (the DNA technical lead at the *856 Albany laboratory), and Dr. Barry W. Duceman (Director of the Biological Science Section of the New York State Police Forensic Investigation Center) before recommending its use by the New York State Police.

Thereafter, on July 15, 2011 the full Commission on Forensic Science unanimously approved Cybergenetics TrueAllele Casework technology for forensic casework without any mention of the type of forensic casework and without limitation (People's Exhibit 12). This full Commission was composed of the chair of the New York State Crime Laboratory Advisory Committee, the director of a forensic laboratory located in New York State, the director of the Office of Forensic Services within the Division of Criminal Justice Services, two scientists having experience in the areas of laboratory standards or quality assurance regulation and monitoring, **545 a representative of a law enforcement agency, a representative of
prosecution services, a representative of the public criminal defense bar, a representative of the private criminal defense bar, two members-at-large, and an attorney or judge with a background in privacy issues and biomedical ethics. The committee in this case consisted of Sean M. Byrne, Esq., Chairman, Gina L. Bianchi, Esq., Kathleen Corrado, Ph.D., Joseph D’Amico, Hon. William T. Fitzpatrick, Richard W. Jenny, Ph.D., Hon. Peter J. McQuillan, Hon. James A. Murphy, III, Peter Neufeld, Esq., Marvin E. Schechter, Esq., Barry Scheck, Esq., Nirav R. Shah, M.D., M.P.H., Marina Stajic, Ph.D., and Ann Willey, J.D., Ph.D. It was their duty, inter alia, to evaluate and approve or reject any forensic methodology. In that regard, it sets minimum standards designed to increase and maintain the effectiveness, efficiency, reliability, and accuracy of forensic laboratories in accordance with the highest scientific standards practicable.

This approval by the New York State Commission on Forensic Science DNA subcommittee and the full Commission on Forensic Science clearly constitutes “general acceptance.” Nevertheless, the New York State Police still undertook three separate validation studies specifically designed around the Quality Assurance Standards of the FBI to ensure that Cybergeneics TrueAllele Casework was a reliable way to interpret mixed and single-source DNA evidence and provide its DNA laboratory with a standardized interpretation approach that thoroughly examined data, eliminated examiner bias, accurately preserved identification information, quantified match strength (whether positive and negative) and yielded reproducible *857 results prior to its use thereof. These studies proved that Cybergeneics TrueAllele Casework is reliable, and that is the standard for admissibility (see People v. Wernick, 89 N.Y.2d 111, 651 N.Y.S.2d 392, 674 N.E.2d 322 [1996]).

LEGAL ACCEPTANCE
Cybergeneics TrueAllele Casework has also been used in the World Trade Center 9/11 victim identification,6 the Allegheny County Crime Lab in Pittsburgh, the country of Oman, the United Kingdom Forensic Science Service and 23 states7 (People's Exhibit 29, page 4). In that regard, there have been admissibility hearings in Pennsylvania, Virginia, California, Ohio, and, now, New York, as well as in Northern Ireland, Australia, and England, with Cybergeneics TrueAllele Casework being admitted in all but the England case (there was no decision in that case).

6 The Office of the Chief Medical Examiner of the City of New York asked Cybergeneics TrueAllele Casework to deconvolute mixtures from victim remains from the site relative to the 2,700 missing persons.

7 Kern County, California and the State of Virginia are presently using Cybergeneics TrueAllele Casework for all forensic casework.

This case is similar to the situation the Court of Appeals was presented with, and sanctioned, in People v. Wesley, supra. At the time of the hearing in that case only three laboratories in the world were performing RLFP based DNA typing. The only articles written on the
subject were authored by scientists affiliated with those laboratories and many law enforcement entities, including the FBI, had not employed the technique. At the time that Court considered the issue the scientific community had not widely adopted the procedure, but it still found that RLFP based profiling had been accepted as reliable within the scientific community.

**546 EXPERT TESTIMONY**

While the superiority of continuous systems like Cybergenetics TrueAllele Casework has been acknowledged for over a decade, implementation has lagged (People's Exhibit No. 25). The problem, according to Dr. Perlin, is one of education, not lack of general acceptance. In that regard, Dr. Perlin has given over 50 talks, testified in numerous court proceedings (domestically and internationally), and has been the keynote speaker for the American Academy of Forensic Sciences, the International *858 Conference on Forensics Inference and Statistics, and the International Symposium on Human Identification (Promege). He has even been a lecturer for the American Bar Association at several continuing legal education programs.

The National Institute of Standards and Technology (NIST), the scientific wing of the United States Department of Commerce, whose mission is to advocate science in the United States and guide the forensic DNA community, uses Cybergenetics TrueAllele Casework to insure that its scientific reference material used in testing laboratories is what they describe it as (to assess a mixture weight and thereby determine the variability of different amplifications). This means that Cybergenetics TrueAllele Casework is used, albeit indirectly, by almost every laboratory in the United States since they all obtain control samples from NIST. Michael D. Coble and John M. Butler, both from the NIST Applied Genetics Group, gave a presentation entitled “Exploring the Capabilities of Mixture Interpretation Using True Allele Software” on September 3, 2011 at the 24th Congress of the International Society for Forensic Genetics. They concluded by summarizing their results and finding that Cybergenetics TrueAllele Casework makes better use of the data than the RMNE (random man not excluded) approach, the statistical equivalent of CPI. And this was not the only time that NIST acknowledged the effectiveness and reliability of Cybergenetics TrueAllele Casework—at the Green Mountain DNA conference on July 28–30, 2014 in Burlington, Vermont, Michael D. Coble presented the results of a study entitled “Mix 13: Overview and Lessons Learned” and reported that Cybergenetics TrueAllele Casework was the only expert system to correctly exclude the suspect in a controlled study involving 100 laboratories, it made poster presentations at conferences for the International Symposium on Human Identification and the International Society for Forensic Genetics, and it even put on a webinar two-part series pertaining to probabilistic gene typing and advocated the use of this method (October 8, 2014 Transcript, page 561).
FINDINGS

[5] The evidence shows that computerized probabilistic approaches and likelihood ratio principles used by Cybergenetics TrueAllele Casework are superior to current methods. Moreover, Cybergenetics TrueAllele Casework has been demonstrated to be one of, if not, the most advanced method of interpreting DNA profiles from mixed and low-template DNA. It has been proved to be more accurate than CPI and CLR, preserves more of the identification information, eliminates examiner bias, produces a match value which human review may not, and permits standardization of mixture reporting whereas human review approaches can lead to very different match statistics on the same DNA data.

Here, there is a plethora of evidence in favor of Cybergenetics TrueAllele Casework, and there is no significant evidence to the contrary. The Court recognizes that the lack of critical work does not guarantee the absence of controversy; however, the reality is that Cybergenetics TrueAllele Casework has been around since 1999, a time frame that would certainly allow for a thorough critical review to be put forth if it was warranted.

Based upon the evidence produced at this hearing, the Court finds:

(1) that Cybergenetics TrueAllele Casework has been empirically tested and found to be relevant, reliable, and accurate,

(2) that Cybergenetics TrueAllele Casework has been subjected to favorable peer review and extensive publication,

(3) that Cybergenetics TrueAllele Casework's average efficacy has been proved to be at least 4 ½ orders of magnitude more efficacious than human review on the same data,

(4) that Cybergenetics TrueAllele Casework has been validated and found to be reproducible,

(5) that the various scientific principles used by Cybergenetics TrueAllele Casework have been long ago accepted and endorsed by the scientific community, and

(6) that the on-going administrative investigation at the New York State Police Forensic Investigation Center has no bearing on the validation studies performed in July 2013 and/or March 2014 (see Affidavit of Timothy J. Munro, sworn to January 23, 2015).

CONCLUSION

Accordingly, the Court finds that Cybergenetics TrueAllele Casework is not novel but instead is “generally accepted” under the Frye standard. The Court therefore DENIES the Defendant's Motion to Preclude, subject to sufficient foundational showings by the People as to their experts' qualifications and adherence to accepted procedures for collection, storage,
People's Exhibits:

1. Curriculum Vitae—Dr. Mark W. Perlin
2. Computer Interpretation of Quantitative DNA Evidence
3. *PLOS One*—“An Information Gap in DNA Evidence Interpretation”
4. *Journal of Forensic Sciences*—“Validating TrueAllele DNA Mixture Interpretation”
5. *Journal of Forensic Sciences*—“New York State TrueAllele Casework Validation Study”
7. *Journal of Forensic Sciences*—“TrueAllele Genotype Identification on DNA Mixtures Containing Up to Five Unknown Contributors”
8. Virginia TrueAllele Validation Study: Casework Comparison
10. DNA Subcommittee approval letter
11. Commission on Forensic Science approval letter
12. Citation Index
13. Forensic Collaborations
14. Workshop announcement
15. 9th International Conference on Forensic Inference and Statistics Abstracts
16. Exploring the Capabilities of Mixture Interpretation Using TrueAllele Software
18. Examination of DNA Mixture Proportion Variability Using Multiple STR Typing Kits and NIST Standard Reference Material 239fc, Component D
19. Certificate of Analysis
20. Mix13: Overview and Lessons Learned
**548 Defendant's Exhibit:**

**A. Forensic Science International: Genetics**—“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”

All Citations

STATE OF MICHIGAN

IN THE 14TH CIRCUIT COURT FOR THE COUNTY OF MUSKEGON

THE PEOPLE OF THE
STATE OF MICHIGAN,

vs.

ELAMIN MUHAMMAD,

Defendant.

HON. WILLIAM C. MARIETTI
Case No. 14-65263-FC

ROBERT E. HEDGES (P36846)
Prosecuting Attorney

SCOTT E. PEDERSON (P33518)
Attorney for Defendant

OPINION

The primary issue in this case involves statistical implications of DNA analysis conducted on a shoe recovered from an armed robbery crime scene. The Defendant does not object to the analysis' results but contends that the statistical evaluation attached to it is unreliable and inadmissible.

While the analysis of a piece of evidence for the presence of DNA may be subject to MRE 702's rigorous screening process as a prerequisite to admission, statistical evaluation of the analysis's results is a matter of evidentiary weight, not admissibility. People v Chandler, 211 Mich App 604; 536 NW2d 799 (1995). For this reason alone, the court will admit the statistical evidence evaluating the results of the analysis for the jury to accord whatever weight it deserves.

Notwithstanding this ruling, the Court also considers the admissibility of the statistical evidence. The technique employed in this case is probabilistic genotyping.
Probabilistic genotyping is the foundation for a software program known as STRmix. The program generates a match probability from the results of a DNA analysis. In this case, STRmix analyzed the results of a two-donor DNA sample harvested from the recovered shoe.

Defendant contends that STRmix is a novel theory that ignores generally accepted thresholds for DNA analysis and it lacks proper validation. Specifically, he provided testimony from an expert DNA analyst who criticized the validation process because it relies on "mock" samples produced in laboratory conditions that cannot replicate the degradation of field samples.

Admissibility of science or mathematics-based testimony in the form of expert opinions must comply with the requirements of MRE 702. As the staff comments to this rule note, it is an implementation of the requirements of Daubert v Merrill Dow, 509 US 579; 113 S Ct 2786; 125 L Ed 2d 469 (1993). The primary goal is to admit expert opinion that is based on reliable data and principles. Of course, the evidence must also be relevant. Michigan courts long ago settled that matter; DNA analysis is relevant only if it is accompanied by an evaluation or interpretation. People v Coy, 258 Mich App 1; 669 NW2d 831 (2003). Thus, the probability assessment opinion generated by STRMix is relevant. The question remains as to whether, under the Daubert standards, STRMix is reliable.

Several factors require consideration when answering that inquiry. The Court finds that the STRMix program received adequate validity testing. STRMix's co-developer, Dr. Buckleton, a recognized expert in the field of DNA analysis and statistical

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1 The parties agreed with the court's view that the controlling principles for admissibility set forth in Daubert, supra, have supplanted the requirements of People v Davis, 343 Mich 348; 72 NW2d 269 (1955).
interpretation thereof, testified that these validation tests comported with FBI Quality Assurance Standards by a properly accredited laboratory. Exhibit 1, appendix 3. Additionally, the Erie County Forensic Laboratory, the San Diego Forensic Laboratory, the United States Army, and the Federal Bureau of Investigation all conducted independent validation studies.

Defendant’s witness, Dr. Reich, also an acknowledged expert in Dr. Buckleton’s field, testified that the validation tests upon which STRmix relies are unreliable because they rely upon mock samples simulated in a laboratory that cannot replicate the degradation found in field samples.

On redirect, Dr. Buckleton testified that mock samples mimic those found in the field. In that regard, Dr. Simich, the director of the Erie County New York Forensic Laboratory testified that he conducted validation studies in compliance with guidelines that were promulgated by the Scientific Working Group on DNA Analysis Methods (SWGDAM). That organization is a body of 50 scientists representing Federal, State and Local forensic DNA laboratories in the United States and Canada. Exhibits 7, 13 and 14.

Dr. Buckleton testified that the validation studies have been published for peer review and he is unaware of any submitted critiques. Moreover, Dr. Simich presented his test results to the DNA subcommittee of the New York State Commission on Forensic Science. The subcommittee reviewed the submission and recommended approval for STRmix’s use. Exhibit 15. The full body of the NYSCFS considered and later approved STRmix for use. Exhibit 16. The validation studies conducted by Buckleton and Simich contained both mock samples and field samples from adjudicated
cases. Other than a few samples involving extremely low levels of DNA, the hundreds of tests conducted did not detect any errors.\(^2\)

Following the NYSCFS approval, at least two cases in New York utilized opinions based on STRmix evaluations. The U.S. Army used the STRmix program for evidence submitted in court-martials following validation testing by laboratories that adhered to the SWGDAM standards. Exhibit 21. Many of these validation tests were published for peer review. The only evidence submitted of any criticism of the validation testing’s methodology came from Dr. Reich. He acknowledged that the only other critic he was aware of was a scientist employed in his laboratory who had been involved in the development of a software program similar to STRmix known as True Allele.\(^3\)

According to Dr. Reich, there are approximately 400 laboratories in this country. Two critics do not seemingly comprise a widespread challenge. To the contrary, there is general acceptance of STRmix among very significant figures in the field of DNA analysis. It is also clear that STRmix validity testing comported with recognized standards in this discipline and was subjected to peer review publications along with the program’s algorithm. Exhibit 1.

Another factor ripe for consideration is whether mathematical experts outside litigation rely upon the concepts forming the STRmix program. The concept that STRmix relies upon is probabilistic genotyping and the mathematical principle supporting probabilistic genotyping is Monte Carlo Markov Chain (MCMC). This

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\(^2\) Subsequent to the hearing in this matter, Dr. Buckleton provided information that miscoding in a prior version of STRmix resulted in miscalculation of likelihood ratios in 60 cases involving three or more person mixtures. The code was replaced in January 2015 and the instant case is a two-person mixture.

\(^3\) Dr. Buckleton testified that True Allele is based upon the same principles as STRmix and he wasn’t aware of any significant differences in the two programs. Of interest, then, is the fact that True Allele results have been admitted into evidence in courts in Pennsylvania, Virginia, New York and Ohio. Exhibits 2, 3, 4, 5 and 6.
technique is widely used in weather forecasting, computational biology and linguistics, genetics, engineering, physics, aeronautics, the stock market, and social sciences. Exhibit 1.

In conclusion, this Court finds: 1. Multiple entities have extensively tested STRmix for validity, 2. The testing process adhered to generally accepted standards, 3. Experts in the field analyzed STRmix through peer review publication, 4. Of the hundreds of tests done, the only errors discovered involved extremely low levels of DNA but no specific error rate has been developed, 5. The concept of probabilistic genotyping is accepted in the community of DNA analysts and is in the process of achieving preferred status over conventional approaches like CPI (Exhibit 21), 6. The MCMC principles underlying probabilistic genotyping and the STRmix program are relied upon by experts in many fields outside the context of litigation, and 7. Courts in New York have admitted STRmix results, and courts in Pennsylvania, Virginia, New York and Ohio have admitted results from a program based upon similar principles. STRmix meets the reliability criteria for admission under MCR 702.


Hon. William C. Marietti
STATE OF MICHIGAN

IN THE 14TH CIRCUIT COURT
FOR THE COUNTY OF MUSKEGON

* * *

PEOPLE OF THE
STATE OF MICHIGAN,

    Plaintiff           File #14-65263-FC

v

ELAMIN MUHAMMAD,

    Defendant.

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DAUBERT HEARING

BEFORE THE HONORABLE WILLIAM C. MARIETTI

Muskegon, Michigan, December 3, 2015

APPEARANCES:

For the People:          ROBERT HEDGES

For the Defendant:       PETERSON

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People versus Muhammad, 15-65263. This is the time scheduled for the Court to conduct a hearing regarding the proposed statistical analysis of the results of some DNA testing that was done and the - it’s my understanding you have an expert witness you wish to have testify at this proceeding. And it’s also my understanding the defense has an expert witness that the delay here is we’ve been trying to get a telephone or skype or polycam arrangement and we’re back to the good old telephone as I understand it. And I’ve indicated that the expert that the defendant has is certainly welcome to listen to the testimony here via the telephone and apparently he’s going to be calling at some point in the course of this testimony and we’ll just put him on the speakerphone at that point so he can hear.

You can call your witness Mr. Hedges. Go ahead.

MR. HEDGES: Thank you your honor. I think the agreement is that Dr. Buckleton, who is our witness, will be allowed to listen to the testimony.

THE COURT: Oh yeah. I want everybody to listen to everybody’s testimony so that they can comment.

Absolutely.

MR. HEDGES: And then I am anticipating that
we will have a third witness after the defense witness testifies. He will be testifying by telephone as well from New York.

THE COURT: All right.

MR. HEDGES: The People call Dr. John Buckleton.

THE CLERK: Would you raise your right hand. Do you swear that the testimony you are about to give will be the truth, the whole truth and nothing but the truth, so help you God?

DR. BUFFLETON: I do.

THE CLERK: Please have a seat and state your name for the record.

THE WITNESS: My name is John Buckleton.

JOHN BUCKLETON, called as a witness at 9:29:17; testified as follows:

DIRECT EXAMINATION

BY MR. HEDGES:

Q Good morning Dr. Buckleton.

A Yes, good morning.

Q Dr. Buckleton, I want to begin with a brief description of your qualifications. I presented to the Court last night and to defense counsel this morning a series of exhibits and Exhibit Number 1 is a combination of both your report in this case and it includes your curriculum vitae.
MR. HEDGES: Yes.

And also the validation work you did on this STR Mix analysis, is that correct?

A Yes.

MR. HEDGES: So with that I will move for admission of Exhibit 1 and then I will go more quickly through Dr. Buckleton’s qualifications.

MR.: Your honor, I have no objection to this expert’s qualifications as a DNA expert. The only objection that we have is that his software program, which is called STR Mix, is not reliable. So to move it along I’ll qualify to his expertise.

THE COURT: OK. He’s got a CD; you’ve got that as an exhibit, Exhibit 1, right?

MR.: Yes.

THE COURT: So let’s not spend a lot of time on that.

(Ppl. Exhibit 1 admitted at 9:30:35)

MR. HEDGES: So with the Exhibit admitted I would then skip over Dr. Buckleton’s qualifications.

THE COURT: You say he’s qualified to testify as an expert in the area of DNA analysis and statistical evaluation?

MR. PETERSON: Absolutely.

THE COURT: OK. Go ahead.
**BY MR. HEDGES:**

**Q** Dr. Buckleton can you tell us, give us a basic overview of what probabilistic genotyping is?

**A** In DNA analysis sometimes an alleleal amplified form will peak and that is called dropout and the modern method to deal with dropout is called probabilistic genotyping. And there are a number of softwares now available to implement probabilistic genotyping. And the essence of such methods is that they assign a probability to the event of dropout.

**Q** So how does probabilistic genotyping differ from the calculation methods or probability methods that are presently used in DNA results?

**A** The most prevalent method used in the United States is CPI or Cumulative Probability Inclusion and that requires that any locus that could have dropout be disregarded or in DNA parlance, treated as inconclusive. In weak profiles this causes a loss of all the information content of the profile. Probabilistic genotyping methods can recover that information content and make an expression of the weight of evidence for those profiles.

**Q** And how does it - how does probabilistic approaches DNA interpretation account for those alleles in the dropout or drop in situation?

**A** Sure. There are - there are a number of implementations that go from relatively simplistic to quite sophisticated
and they date back to 1999 and a piece of work I did with Peter Gill and Jonathan Wittaker and that is the progenitor of probabilistic genotyping methods. In the simplest manifestation they simply attribute a probability of dropout. So if you consider a single peak, for instance allele A, it could have come from a donor who is an AA homozygote and hasn’t exhibited dropout or a donor who is an A anything else heterozygote and the term used in some places for anything else is Q. So an AQ heterozygote where the Q allele has dropped out. By assigning probabilities to this we don’t have to go yes or no. We get the ability to utilize the evidence by assigning a probability to the different events.

And then once the probability to the different events are assigned how does the probabilistic genotyping approach work? I understand it’s a computer algorithm. They’re all computer algorithms. You can only apply probabilistic genotyping if it’s by hand to a single-source sample. You couldn’t possibly do a real mixture except with software, so they’re all implemented by softwares. And if you’ll allow me to pass to the one I’m actually speaking to here, STR Mix, it creates these probabilities using modern mathematical methods and models representing the behavior of peak heights in PCR reactions.
Q: And what kind of scientific foundation is used in the computerized approach to evaluating the evidence?

A: So if I split the construction of the software into having two fundamental principles, the mathematical principles and the molecular biology principles, the mathematical principles are standard mathematical principles and they date back to the early 1900s. And they're called (indistinguishable) and they're a dominant method now in mathematical procedures treating these types of problems. If we come to the molecular biology these are based on empirical studies of the variability of peak and stutter heights in different multiplexes and at different template levels and they're published in peer-reviewed articles. They're published in peer-reviewed articles and then that — those are then incorporated into the formula or the algorithm that's used in this case in the algorithm for STR Mix?

A: Yes.

Q: And then the — tell us about what the computer — you explained a little bit about MC or Markov chain Monte Carlo. Is that an accepted procedure scientifically in the world of science?

A: Absolutely. It's quite dominant in certain fields, in physics and engineering and in (indistinguishable) genetic reconstruction and in some things that you might think are...
a little more unusual like weather forecasting and stock market production and code cracking is actually part of the method that was used to break, for instance, the enigma code in the Second World War. You may have seen the film with Alan Turing and breaking the enigma code. So that was a mark of chain.

Q So there’s nothing controversial about the mathematical approaches or the statistical approaches of the MCMC?

A No, the mathematics are thoroughly established and well before my career in science.

Q You’ve looked at bibliographies of MCMC to see how dominant it is in-

A I think I’ve put the numbers in one of the reports that you’ve got in front of you. I looked up on SCOPUS, which is a scientific (indistinguishable) search engine. And I think I searched for MCMC and I think it got about 22,000 scientific documents referencing that.

Q So MCMC itself is a well-respected scientific approach.

A Yes.

Q And so the - so what STR Mix has done is coupled the statistical approach using MCMC and applied that to what has already existed in the application of statistics to DNA results.

A Yes. So we’ve been aware that if you amplified the same sample again you wouldn’t get exactly the same peak
heights. Peak heights vary if you repeated the analysis. And this peak height variability is the essential element we need to model. With historically used peak height variability all the way back to 1995, manually so with using rules and assessing and (indistinguishable) it’s called a peak height ratio and if two peaks differed by that they could not have come from a heterozygote. So the concept of utilizing peak heights has a deep pitted (indistinguishable). In particular, to implement the Markov chain we need to understand the variability of peak heights and it’s empirical models for that that have been incorporated into STR Mix.

Q Now the - you are one of the creators of the STR Mix product of probabilistic genotyping?

A Yes.

Q And who are the other creators of that?

A Duncan Tyler from forensic science, South Australia and Adelaide, Australia and Joe Bright from my organization which is the New Zealand Government Forensic Service in New Zealand.

Q Are you an employee of, it’s called ERZ for short?

A ESR. Yes I am an employee of ESR.

Q You receive a salary for that?

A I am a civil servant and receive a salary.

Q When a product-
MR. : I’m sorry to interrupt but apparently my expert is on the line. Can we just make sure he can hear from this point what’s going on?

THE CLERK: Can you hear all right what’s going on Mr. Reich?

MR. REICH: Yes I can. I have to have my microphone off so the noises in the lab don’t affect you. Can you hear me?

THE CLERK: Yes.

MR. REICH: No problem.

MR. PETERSON: Thank you your honor.

BY MR. HEDGES:

Q So I think we left off you receive a salary from ESR. And do you profit personally from when STR Mix is purchased?

A I do not get any direct or indirect benefit from a sale of STR Mix. I don’t even get my (indistinguishable)

Q STR Mix itself, are there two divisions or two types of probabilistic genotyping?

A Yes.

Q And those are continuous and semi-continuous?

A Semi-continuous and continuous.

Q What’s the difference of the two and which type is STR Mix?

A STR Mix is continuous and the difference is whether you treat peak heights as a continuous variable or not. So
the semi-continuous ones were the first created and they
are in reasonably extensive use across Europe and they
simply have a probability of dropout. The continuous ones
have moved further forward and utilize peak heights
directly.

Q And what are some of the examples of the semi-continuous
probabilistic genotype products that are in use?
A The Hallmark one is LR Mix which is a EURO4GEN which is
the European Union For Gene Project product and it’s
freeware and it’s utilized across much of Europe.

Q Is Lab Retriever.
A Lab Retriever is a product, freeware again, available in
America and has been used I believe in at least one case
in the United States which is some particular state versus
Mitchell in a published paper.

Q And what are some of the other continuous types of
probabilistic genotyping?
A So there are a number of these available now, but the two
in use in America are TrueAllele which has been in use
since about ‘08 and STR Mix. There are some other ones
that I’m not aware of ever having been used in casework.

Q I want to discuss somewhat in detail the approach that you
have taken to validate the performance of STR Mix. And I
think if we’re going to follow along I think in Exhibit 1
we had the third attachment or Appendix 3 to that, which
begins on Page 21 of 38 of Exhibit 1, that’s Appendix 3, The Summary of Developmental Validation Experiments for STR Mix Expert Software for Interpretation for Interpretation of Forensic DNA.

First of all, can you give us a summary of the validation work that was done on STR Mix, and then we’ll go into the various categories of validation.

A Sure.

THE WITNESS: Sir, in New Zealand I have to ask for permission to look at my notes. I actually don’t quite know the rule here but am I allowed to look at my notes?

A

THE COURT: It’s up to you guys. If you’ve got a problem with it let me know; if not he can do anything he wants. No problem Mr. Peterson?

MR. PETERSON: No.

THE COURT: OK, go ahead.

THE WITNESS: OK, so we’ve done a number of tests on STR Mix. I’m guessing you don’t want me to actually read the executive summary since you both have it before you, but we’ve done such things as repeat the calculations by hand for 500 steps of the Markov chain and there are certain circumstances where you can know the answer and so we’ve checked to get that answer for those.
Then one of the most extensive types of testing we’ve done now is called True Donor and False Donor tests. So we make up mixtures where we know the answer and we run it and check that we do get that answer. And then we make up thousands of false donors by simulation on a computer and run it for those and again check that we get a proper exclusion for those. We’ve also tested STR Mix against other softwares and against human interpretation.

Q What other softwares have you tested STR Mix against?

A So we’ve tested STR Mix against LR Mix, Lab Retriever and TrueAllele.

Q And are the results that you get, they’re probably not perfectly consistent but are they relatively consistent?

A In nearly all cases you get the same type of answer. So for instance if it’s an exclusion you also get an exclusion. In very rare instances we get a different answer from TrueAllele and in the particular test I’m referring to that’s one where we had the known ground truth or known inputs and I was able to check that in fact our answer was correct and the TrueAllele answer incorrect.

Q But you indicated that’s very rare.

A Yeah, that was in fewer than one percent of the trials and nearly always because of an artifact in the PCR.

Q I think you’ve mentioned repeat calculations and
comparisons to ground truth. What other testing have you done?

A So that’s – I think that’s probably pretty much it. Is there something on the list I’ve missed?

Q No. Has STR Mix gone through various validation studies at places where it’s been implemented?

A Oh yeah, very much so. It’s been validated. Broadly speaking there are two types of validation: Developmental validation, which is what I do and lab-based validation which is what a lab does when it’s going to switch on. That’s happened in all the labs that are implementing and there are four labs in the United States now that are switched on and have gone through that.

Q What are the labs that are switched on or that are actually approved to use STR Mix now?

A US Army Criminal Investigation Laboratory were the first and then Erie County in New York State the second, San Diego Police Department the third and the FBI switched on on the first of December of this year.

Q So is the FBI done with its validation work or is that still in process?

A No, they’ve completed the validation and started casework. I was intimately involved in the internal validations for Erie and the FBI so I’m familiar with those internal validations.
Q All right. And are there other users of STR Mix that are presently in the validation process?
A If we’re speaking to the United States, the answer is yes. Every state and territory in Australia has been in use with STR Mix for a number of years now except Tasmania and Australian Capital Territories. So those labs have also done their internal evaluations.
Q And what about the State of Michigan? Does STR Mix have anything – is STR Mix doing anything in regard to the Michigan State Police Crime Lab system?
A Michigan State Police have purchased STR Mix and undergone training and are in the implementation phase.
Q And did you conduct that training?
A Yes I did, with others.
Q That was earlier this year in Lansing?
A That was in May this year.
Q What kind of peer review has been conducted regarding the validation work for STR Mix? There’s a fire truck passing so maybe we should wait a moment before you answer.
A Booth published all the mathematical and foundations for STR Mix as well as a number of specialist trials and certain specialist applications and the like produced a list fee. In addition we also placed STR Mix with a number of third party users with the opposite of a non-disclosure agreement. So the opposite of a non-disclosure
agreement is they were entitled to say anything they wanted without reference to us. And at least two of those, two other organizations have completed a by-hand analysis of STR Mix output. That’s California Department of Justice and United States Army Criminal Investigation Laboratory.

Q Has STR Mix - have there been test results of STR Mix published in peer-reviewed scientific literature?

A Yes.

Q To what extent?

A I think I’ve given you a list, about 16 or 18.

Q And those are included in that appendix? That was the list that you gave me.

A I think that was the list that I gave you more recently.

Q That was 16 - you gave me a list of 16 peer-reviewed articles that did not involve your or somebody from STR.

A That 16 to which you’re referring, are on the general subject of probabilistic genotyping. They’re not all on STR Mix. In fact I think very few of them are. Most of them are STR Mix are by myself and my co-developers.

Q But the articles that are published are in peer-review publications.

A Yes.

Q And subject to review by the readers of those.

A So there’s two possible stages of review. Every article
you put up for publication goes out to two reviewers who
give comments and may, for instance deem the paper
unpublishable. Once it’s published anyone is permitted to
write a letter to the editor criticizing the work in some
way so those are the two levels of peer review that occur.

Q Is probabilistic genotyping being taught at scientific
seminars throughout the United States and throughout the
world over the last few or even several years?

A It’s probably been taught across the United States and
Europe very extensively in the last two or three years,
but in Europe definitely back to about ‘06 it was being
taught.

Q And in some of those presentations is, in particular does
it address the STR Mix product?

A Yes.

Q Do those include presentations by the National Institute
for Standards Technology or what’s referred to as NIST?

A Yes.

Q And also ISFG?

A So ISFG is the International Society for Forensic
Geneticists and doesn’t actually publish work. It’s not a
– it’s not an organization in the sense of NIST. They do
have a DNA commission on this and the DNA Commission has
published on it in 2012 and 2006 and recommended the
probabilistic genotyping methods and NIST has definitely
given many presentations on the subject.

Q Are you familiar with an organization that goes by the initials SWGDAM or sometimes referred to as SWIGDAM?

A Yes.

Q What is SWIGDAM?

A SWGDAM is an FBI-sponsored organization. The initials stand for Scientific Working Group DNA Analysis Methods and it is a policy-making group of about 50 scientists sourced predominantly from within the United States but with invited international attendees.

Q Do you know whether SWGDAM has published any guidelines for the validation of probabilistic genotyping?

A Yes, they published them this year.

Q In our packet that I provided to defense counsel and to the Court that’s been marked as Exhibit 7, let me show it to you Doctor, is this the publication dated June 15, 2015?

A Yes.

THE COURT: I noted in reviewing that exhibit it said that these guidelines are not to be applied retroactively. That was highlighted in there. Why is that significant?

BY MR. HEDGES:

Q Can you answer that question as to why that’s significant?

A I think there is a general concern among SWGDAM that
anything they publish now causes a mess of back litigation situations and in fact there is such a situation happening in Texas at the moment. It’s been pointed out to me by my legal commentators that whatever SWGDAM says or does doesn’t actually change the law of any state of this nation and back litigation can happen whether SWGDAM desires it or not.

Q Well even prior to the adoption of the guidelines in June of this year this Exhibit 7, there’s been previous SWGDAM publications regarding probabilistic genotyping software?

A So in 2010 SWGDAM published guidelines that mentioned probabilistic genotyping. Also SWGDAM put out for comment the guidelines so we were aware of the draft guidelines much earlier and validations for STR Mix have complied with the draft and that for a number of months now.

Q You’re saying the validation studies that were done of STR Mix complied with the guidelines set forth in Exhibit 7?

A Yes.

THE COURT: You were aware of them on a proposed basis before they actually became.

THE WITNESS: Yes, they came for public comment.

THE COURT: OK.

BY MR. HEDGES:

Q There’s been a criticism leveled that the validation
process for STR Mix does not adequately address real world situations. Do you understand my question?

A Yes.

Q How do you respond to that Dr. Buckleton?

A The nature of that criticism is that many of our validations are done on mock samples, so samples where we’ve taken DNA from donors and mixed them and created mixtures where we know the answer and then run the software on it. The advantage of this is that we know the answer and in casework you never actually know the answer. The disadvantage relates to the question of whether that does truly mimic real life. There are a couple of possible bits of information I could put before you.

First of all, we actually do quite a lot of what’s called insult to the samples. So the samples are for instance degraded or inhibited artificially and they probably overly mimic casework. We actually go to an extreme of insult beyond what normal casework would represent. But in addition some studies have been done and published that show that mock samples from pristine DNA are actually a really good surrogate for casework, not a bad one at all.

Q There’s been a criticism made that probabilistic genotyping is not accepted in the general scientific community. Do you agree with that statement?
I saw that statement and it’s very hard to see what the factual basis for that could be. There are a very large number of publications now and they’re all pro probabilistic genotyping. I cannot think of a single publication that’s negative and I did a small survey for you on my scientific search engine and they’re all pro or irrelevant. I cannot find a single negative comment.

Q I thought you said there was one that actually did have a negative comment on it.

A There was one in a previous search I did that had a comment that suggested that - I can’t quite remember the multi-person mixtures, was some difficulties. It was a Japanese publication. Interestingly, they are now embracing probabilistic genotyping, that same group of researchers. So for instance they invited my co-developer Duncan Tyler to go across and speak with them.

Q So the literature is running, from your analysis of the literature, strongly in favor of acceptance?

A I would say in the last two years 100 percent in acceptance, in favor of implementation of it as an answer to deficiencies in previous methods.

Q Now I want to ask some questions specifically about Erie County, New York. You were involved in the validation work for the implementation of STR Mix in Erie County, New York?
Q: Do you know who you worked with at Erie County?
A: Don Simich.

Q: Dr. Simich is the director of the crime lab there?
A: He’s the - I don’t know if he’s the director. He’s the technical lead for the DNA group. I believe he has a director above him.

Q: And you worked with Dr. Simich in the validation work?
A: Yes.

Q: And that covered several months of work in New York?
A: Many months. We were sent back by the New York committee to do further validations. We’ve done very extensive work.

Q: And as a result of the work you did, was it presented to the - in New York they have a commission on scientific evidence?
A: Yes. They have a forensic science commission and that has a DNA subcommittee and we had to present to the DNA subcommittee.

Q: And the DNA subcommittee do you know, is that made up of scientists or people beyond scientists?
A: All scientists. Well the commission, the DNA subcommittee is all scientists. The commission itself is a mix of scientists and lawyers.

Q: So the subcommittee that is made up of scientists, do you
know how they voted?
A They gave a binding recommendation to accept it.
THE COURT: To Accept STR Mix?
THE WITNESS: Yes.

BY MR. HEDGES:
Q To accept and implement STR Mix for casework?
A Yes, yes.
Q Do you know if that was unanimous?
A No, but you might.
Q Well we’ll ask Dr. Simich, he knows. The - and I think some of the documents that we’ve attached in our package indicate that.
A So that was presented to the DNA subcommittee in New York.
A Yes.
THE COURT: You presented the validation studies from Erie County?
MR. HEDGES: From Erie County, yes your honor. Thank you.

BY MR. HEDGES:
Q And so now STR Mix has gone active in casework in Erie County.
A Yes.
Q And you’ve indicated that it’s now gone active with the FBI.
D

A Yes.

Q And the other, the last question I think that I want to cover with you, the work that was done, the actual DNA testing or the traditional workup was done by a company called - do you recall?

A Oh, in this case?

Q Yes.

A Mitotyping.

Q All right. So they did the traditional DNA workup?

A Yes.

Q And then you used the data that they provided.

A Yes.

Q Now is Mitotyping Technologies, have they gone through any validation process for STR Mix such as you’re doing presently with the Michigan State Police or what you did with Erie County, New York or with the FBI?

THE COURT: Well I didn’t think that was at issue here.

MR. HEDGES: I don’t think it’s at issue here.

THE COURT: Well I’ve got enough on my plate. I don’t want to get into that.

MR. HEDGES: All right, thank you. I have no further questions.

THE COURT: Mr. Peterson, go ahead.
CROSS-EXAMINATION

BY MR. PETERSON:

Q  Is it Dr. Buckleton?
A  Yes sir.

Q  So you came all the way here from New Zealand?
A  I live in Maryland now.

Q  Maryland?
A  Maryland. I have a (indistinguishable)

Q  I did quite a bit of reading about your, ESR is the company you work for?
A  Yes.

Q  Do you still work for them?
A  Yes.

Q  That’s basically a governmental agency in New Zealand, is that as I understand it?
A  Yes.

Q  So they have an office now in Maryland?
A  Not really sir, it’s just me. I’ve come here because of the interest in this situation in the United States.

Q  OK, and when did you come here?
A  This is my second time living in the United States. And this time I came here in October, 2014.

Q  OK. And it’s true that your software, it’s called STR Mix TM, right?
A  Yes.
Q That is a software program.
A Yes.
Q It’s not a laboratory analysis. You don’t run a laboratory like Mitotyping did, correct?
A No.
Q You take your results, you stick it in your computer program and you come out with a different probability than they did, correct?
A Yes. I’ve no knowledge of their probability but yes it would.
Q All right. You didn’t read their report?
A No.
Q And you didn’t read the report from the Michigan State Laboratory?
A No.
Q All right. You didn’t take their results, did you, the Michigan State Laboratory and put it into your STR Mix program?
A No.
Q Do you know what the source of the DNA is here on this shoe?
A I’ve been told.
Q OK, you don’t know for yourself, by your own analysis?
A Well I’ve been told it comes from the toe of a shoe but I have never seen the shoe.
Q You don’t know if it’s blood, saliva?
A No.
Q All right. Does it make a difference in your program whether it’s blood, saliva-
A No.
Q —or some other source for the DNA?
A No.
Q All right. What was the other software program that was coming to the United States, Allolee you said?
A TrueAllele.
Q TrueAllele.
A And it’s not coming, it predates us.
THE COURT: TrueAllele is already being used according to several of these cases that I’ve read.
THE WITNESS: Yes.

BY MR. PETERSON:
Q Yes, I just want to make sure I heard it right because I understand—
A I think it’s one word and it’s TrueAllele—
Q Yes.
A —and you could hit it on the net by typing in the word Cybergenetics and TrueAllele and it predates us, so—
Q Yeah, it predates you and was that another organization out of New Zealand or Australia?
A Cybergenetics is based in Pittsburgh, Pennsylvania.
Q All right. And in your - your software was commercially available in the United States in February of 2014?
A That sounds about right sir, yeah.
Q And do you know if the FBI is using it for preparation for use in federal courts?
A They’re using it in all their casework as of the first of December so that would be federal and state courts. They take some from state laboratories.
Q Do you know as you sit here today whether the FBI, through any United States Attorney has presented it as evidence in any court in the United States?
A I wouldn’t have thought so. They only went live on the first so I doubt that they’d even have a report written yet.
Q All right. And you said the Army has purchased the software, correct?
A The Army is the longest term US-based user. They’ve been live for over a year.
Q I take it the Army is using it because of these complex mixtures or low degraded samples of DNA and your program seems to be magical. It seems to tell people - tell the Army who the dead body is, correct?
A It’s actually, very regrettably, largely sex assault cases in the Army they’re using it for. And it’s useful for good template as well as more complex situations. You can
use it for the whole range. Its advantage comes in the
more complex ones.

Q Well that’s what this whole probabilistic genotyping is
about, where other laboratories it’s too complex or too
degraded or below the threshold, your software comes in
and says well we can fix that.

A Yes.

Q Correct?

A Yes.

Q You would have to admit it’s controversial.

A No, no, I cannot think of a single criticism to be honest.

Q Well you’re making probability determinations on DNA
that’s below the threshold. Do you know what I mean by
that?

A You must mean the stochastic threshold?

Q Yes.

A So yes.

Q OK, isn’t that controversial?

A No. I cannot name a single scientific paper that is
critical of the use of probabilistic genotyping. In fact
that’s the exact situation it was designed for.

Q You would agree with me that you cannot manually
replicate. If you manually replicate the sample you could
have different results. In other words, you could have a
false positive.
Can you have another go at that question sir?

THE COURT: I don’t understand the question either.

MR. PETERSON: All right, that’s fair enough.

BY MR. PETERSON:

Q Has there been any expert, expert criticism that the danger of false positive is great by the use of your software?

A No.

Q In your validations studies, your own that you’ve mentioned, did you discover false positives?

A We’ve done some massive tests of false donors, hundreds of millions and the - we get occasionally a weak indication of inclusion so weak ratio at exactly the error rate expected from genetic principles. So they’re not false positives by the software; they’re false positives because we’ve, by doing so many, replicated someone who is genetically similar to the true donor.

Q OK.

A If you give us a genotype that’s the same as a true donor we will include them. That’s the nature of DNA. It’s just that similar genotypes are quite rare.

Q I want to talk about the State of Michigan for a second. You said the State of Michigan Laboratory-
THE COURT: OK, wait a minute. I want to get some clarification to the answer to that question. So have you had false positives or not?

BY MR. PETERSON:

Q I think you’re saying no you didn’t have any except when you intentionally did it, correct? That’s what you’re saying?

A The software has never made a false positive. If we create a genotype that should be included, it is. I think the nearest answer is no sir.

Q OK.

THE COURT: OK. So the error rate is what?

THE WITNESS: We’ve never detected a false positive or false negative that was created by the software.

THE COURT: OK.

THE WITNESS: There are some that are inherent to the sample. The DNA sample can provoke a false negative.

THE COURT: So you’re telling me that you have a zero error rate?

THE WITNESS: Zero would be a big call sir. We’ve just never found one.

THE COURT: OK. All right. So as of today you have zero error rate.
THE WITNESS: Yes sir. But to claim perfection is a big claim.

BY MR. PETERSON:

Q Let’s talk about the State of Michigan. You said the State of Michigan Lab that does DNA testing for the State of Michigan purchased your software?

A Yes.

Q And when did they do that?

A I don’t know, but the training was run in May of this year. I have nothing to do with the commercial side of this at all.

Q OK.

A I attended the training and that’s the only first-hand knowledge I have.

Q Where did you attend the training at?

A Lansing, Michigan.

Q How many - I take it you train people to run your software.

A Yes, to run the software and to understand the scientific principles behind the software.

Q Is there anybody qualified, as you sit here now today, qualified to run your software in the State of Michigan based on your training?

A Once they complete their internal validations yes, they all can do it.
Q All right. When will that be?
A I’m sorry sir. You have to ask them. I just don’t know that.
Q You don’t know if they’re ready now.
A They’re not ready now. I know that.
Q Do you know if anybody in the laboratory at the State of Michigan is preparing results based on your software for use in courts?
A I believe they’re doing studies now.
Q Just studies at this point?
A Correlation and implementation studies.
Q And who’s doing those studies?
A The Michigan State Police.
Q Who’s in charge of that study?
A Jeffrey Nye.
Q Jeffrey Nye, N Y E?
A N Y E.
Q OK, is he an expert in your software?
A He’s been trained and he seems a very intelligent man and he’s finished the training.
Q How long was the training?
A Four days.
Q And that’s in Lansing?
A Yes.
Q And that’s where you sit with him and go through your
software program?

A Myself and two others did training to him and a group of colleagues from Michigan State Police.

Q Now we’ve gone over, Bob has given me results from the State of New York. In New York some of the courts have admitted your STR Mix. And one in Pennsylvania, correct?

A Not that I’m aware of in Pennsylvania, no.

MR. HEDGES: Those court cases are with a different product, the TrueAllele product.

MR. PETERSON: All right, that’s what I wanted to get at.

THE COURT: They deal with that TrueAllele.

BY MR. PETERSON:

Q Yours is not – I just want to be clear with the Court and my client sitting here, yours is different from the TrueAllele?

A We don’t know how different it is; it’s actually got a lot of similarities.

Q Well have you ever run their program?

A I can’t run STR Mix. I’ve never run either of them. They – we’ve run trials. Other people have run them back to back against each other.

Q OK. Are these key code specific? In other words, you can’t run – I can’t sit here and run your program if I’m a DNA expert unless I have the key codes, isn’t that
correct?

A What’s a key code?

Q Well, I have to rely on my expert here. Something about a code that you need to run the software.

A If I gave you my laptop you could run it right now if you chose to.

Q OK. All right. So as we sit here now you’re - your software program has not been admitted by any court in the United States?

A I don’t know that. It’s been admitted at Court Marshall and this is my first Frye or Daubert associated with STR Mix. The US Army has testified multiple times in Court Marshall which I understand are not courts. I have never testified on STR Mix, but it’s highly likely that Erie County might have. But I can’t say.

Q You can’t say.

A I have no first-hand knowledge of that.

Q This is your first Daubert hearing in the United States on this particular?

A On STR Mix. I did two in 1995 in South Carolina I think.

Q Were they admitted?

A On a different subject.

Q A different subject, what do you mean?

THE COURT: It wasn’t STR Mix.

THE WITNESS: It wasn’t STR Mix at all.
BY MR. PETERSON:

Q Oh, OK, not STR Mix.

A This is my first STR Mix Daubert or Frye ever.

Q That’s remarkable. Do you know what I mean by stutter peaks?

A Yes.

Q What are they?

A Stutter peaks are a byproduct of the PCR reaction where the PCR reaction miscopies either one repeat shorter, most often, or one repeat longer.

Q OK, that is a problem with your software, wouldn’t you agree?

A No, that’s one of the strengths of the software is the way it manages stutter peaks.

Q How about, you know what artifact peaks are?

A Yes.

Q What are those?

A They’re - it’s a generic term for peaks that aren’t allelic. It includes stutter and other peaks such as pull-up and spikes.

Q OK. Is that a problem with your software?

A No. Again that’s one of the strengths of the software.

Q Now, Mitotyping determined there were two contributors to the DNA.

THE COURT: One was the stutter peaks and
then what was other reference you made?

MR. PETERSON: Artefact. It’s A R T E F A C T.

THE WITNESS: In the United States it’s actually A R T I F A C T.

MR. PETERSON: OK.

THE WITNESS: That’s a British-US change.

MR. PETERSON: Guess that’s what I’m using here.

BY MR. PETERSON:

Q Now the Mitotyping said that there were two contributors. Do you assume there were two contributors for your software?

A Yes.

Q The State of Michigan lab found four contributors. Isn’t that a problem with your software?

A That’s in different samples as I understand it. And that wouldn’t be a problem with the software.

Q Why wouldn’t it be a problem because isn’t determining the contributors a major problem with your software?

A You have to determine the number of contributors. That’s an input so that wouldn’t be a problem with the software. That would be a problem with an input.

Q All right. So you inputted two contributors—

A Yes.
Q -in this case?
A Yes. The profile can be explained by two contributors. There’s no evidence of more than two in this profile.
Q You’re not aware then of the State of Michigan Laboratory result?
A Yes, I’ve been told about it second-hand or third-hand even.
Q As I read it there were four contributors in the State of Michigan lab result. Maybe a different area of the shoe, but-
A That’s how I understand it.
Q He didn’t run a test on the four contributors then.
A I haven’t seen those profiles, no. Happy to do so sir if you wish.

THE COURT: I am quite confused about this. Are you saying there were two different samples and you - your results relate to the sample that had two contributors and the State Police results relate to a sample that had four contributors?

THE WITNESS: That’s how I understand it sir.

THE COURT: OK, so you looked at one sample, the State Police looked at a different sample?

THE WITNESS: Yes.

THE COURT: Oh, OK now I understand.
MR. PETERSON: That’s correct your honor.

BY MR. PETERSON:

Q And just to be clear you’ve run no – you didn’t run your software on the State of Michigan result?

A No.

Q You wouldn’t know until you tried. You wouldn’t know if you’d get the same probability or not.

A I can give you an educated prediction.

Q All right, go ahead.

A The four-person mixtures are a lot harder than two so I’d almost certainly get a lower loci ratio.

Q OK. You said you don’t profit from this, that all the profit goes to ESR?

A No. Well first of all I don’t profit from it. And no, the profit gets split in a number of ways to our co-developers and our American agents.

Q OK, and you’re a co-developer, correct?

A Oh, sorry to our co-developer organization. I do not obtain financial or any other benefit from STR Mix.

Q You just get a paycheck from your company and that’s all you get?

A I get a paycheck essentially from the New Zealand government and that’s what I get and that’s what I’ll get next year as well.

Q All right. So whether you sell 100 of these software...
programs or one doesn’t make any difference in terms of how much money you make.

A That’s correct sir, yeah.

Q And you’re pushing the software because you think it works.

A Pushing is a big word sir. I enjoy training with intelligent young people and there are many of those in the United States and a real need. I’ve got to say there’s a disincentive to the success of the software. I’m just exhausted running around the States and Texas and places doing this job. So, I actually would like to go home.

Q We all want to go home.

THE COURT: Me too.

THE WITNESS: I obtain no material benefit. I certainly obtain an intellectual benefit.

BY MR. PETERSON:

Q OK. You didn’t actually write the software. I take it you’re not a computer guy.

A No sir.

Q You’re just a DNA forensic expert.

A My math is reasonably strong.

Q Well OK, you have to have math skills. I understand that. You didn’t write the software.

A No, I probably wrote many of the algorithms and the
software was largely written by my collaborator Dr. Duncan Tyler.

Q And he’s one of the co-developers. And what company actually developed-

THE COURT: Wait a minute here. But you developed a lot of the algorithms-

THE WITNESS: Yes sir.

THE COURT: -that were then put in code for the software.

THE WITNESS: Yes sir.

MR. PETERSON: Thank you your honor.

BY MR. PETERSON:

Q What was the development company if it wasn’t ESR?

A It’s not a company. It’s the Government Laboratory for South Australia in Australia and its laboratory is in Adelaide, Australia. So he’s a civil servant as well.

Q OK.

MR. PETERSON: I have no further questions.

MR. HEDGES: I have no further questions.

THE COURT: OK, thank you Doctor. You may stand down.

(Witness excused at 10:24:32)

MR. HEDGES: Your honor, I intend to call Dr. Simich later, but I think the agreement we worked out is that the defense is-
THE COURT: Is he on the phone now?
MR. PETERSON: Yes.
THE COURT: What is this gentleman’s name?
MR. PETERSON: Dr. Karl Reich, R E I C H.
THE COURT: R E I C H?
MR. PETERSON: Yes.
THE COURT: As in the third? OK. You want to place Dr. Reich under oath?

THE CLERK: OK Dr. Reich, please raise your right hand.

DR. REICH: Yes.

THE CLERK: Do you swear that the testimony you are about to give will be the truth, the whole truth and nothing but the truth, so help you God?

DR. REICH: I do.

THE CLERK: Please state your name for the record.

THE WITNESS: My last name is Reich. That’s R E I C H. First name Karl, K A R L. Middle initial A. And just for the record it’s been many years since I’ve heard that joke being the third but that’ll work for me.

THE COURT: Well that tells you how old I am.

MR. PETERSON: Your honor, I do have proposed Exhibits A and B. One is a report generated by
Dr. Reich regarding the STR Mix software and also his curriculum vitae.

MR. HEDGES: I have no objection.

THE COURT: OK, Exhibits A and B will be received.

(Dfd. Exhibits A and B admitted at 12:26:12)

K A R L A. R E I C H, called as a witness at 10:26:15; testified as follows:

DIRECT EXAMINATION

BY MR. PETERSON:

Q State your name for the record again.

A My last name is R E I C H. First name K A R L. Middle initial A.

Q And what is your - what do you do for a living?

A I am the Chief Science Officer of Independent Forensics which is an independent forensic laboratory in Lombard, Illinois.

Q And is this your laboratory?

A I don’t own the laboratory but I am the managing partner and I am responsible for the science that leaves all this facility.

Q I’ve just given the Court Defendant’s Exhibit A, your curriculum vitae which you gave to me last week. Is that up to date?

A I believe so.
Q  And it explains all your writings, all your articles, where you’ve been admitted as an expert?
A  It should be relatively complete. It should list the places I have worked for the last oh I don’t know, 30 years is my guess. It lists my education, lists the papers that I have published and the various scientific fields I have worked in. There is a list, probably not 100 percent complete, of the abstracts we have submitted in forensics. There’s a list, probably mostly complete, of the workshops we have performed for meetings and law enforcement. There is a short, I think it’s accurate, list of the states where I have been qualified as a witness in courts. It’s a pretty standard resume for a scientist.
Q  OK, and your expertise is DNA analysis and laboratory testing, is that correct?
A  That’s correct. So our laboratory is a fully accredited forensic DNA laboratory that performs biology so that’s generally, sometimes that’s called serology. It’s the identification of one of four forensic bodily fluids and/or sperm and epithelial cells as well as performing forensic DNA identity both for family studies and for law enforcement.
Q  OK. And we’ve been talking about - you’ve been listening to the testimony of Dr. Buckleton this morning?
A  I have.
Q: All right. Are you familiar with the type of probabilistic genotyping he’s talking about?
A: Yes I am. It’s a, I won’t call it a hot topic but it’s certainly a topic of huge interest in this field.
Q: Are you familiar with his software program STR Mix?
A: I am familiar with it. I have not run the software myself. I have not seen the source code of course but I am familiar with how it has to operate in terms of being able to make a prediction from raw data files.
Q: OK. And you have received Dr. Buckleton’s report prior to your testimony here today, correct?
A: Yes I have.

MR. PETERSON: I’d like to offer Dr. Reich as an expert in this area of DNA analysis.
MR. HEDGES: DNA analysis I don’t have any objection. If we’re crossing the line into probabilistic genotyping I may have an objection.

THE COURT: Go ahead and cross-examine him on that if you want to voir dire.

MR. HEDGES: I just wait to the cross-examination stage.

THE COURT: Well then do you have any objection to him being-

MR. HEDGES: I don’t have any objection to him being looked at as an expert.
BY MR. PETERSON:

Q State to the Court Dr. Reich what your position is on STR Mix.

A My position on STR Mix is that it is a experimental approach to try and determine one of the most controversial topics in forensic DNA at the moment which is the unraveling or the deconvolution of mixtures and that it is not, in my opinion, clear how that problem deconvoluting mixtures can best be done. There are certainly examples where mixtures are not controversial and where in general analysts and forensic laboratories would agree on what the conclusions are.

Interestingly, there have been a number of surveys done to try to determine how forensic labs in the United States process and analyze mixtures. Some of those surveys have been done by the Army and some of those surveys have been done by NIST, the National Institute of Standards and Technology which is one of the research laboratories in this field. There is absolutely no generally held method. There is absolutely no consensus as to how mixtures are being interpreted or even how they should be interpreted. This has been a surprise I think to the individuals who started these surveys but that’s what’s been published and discussed.
The probabilistic approach to deconvoluting mixtures has certainly received a lot of, I won’t say publicity but a lot of scrutiny and interest because mixture interpretation is a problem in this field. My objections, or my concerns probably more precisely, about using this approach do not come from the underlying concept of using probability to make future predictions. Our work in paternity is based on probability and there are many examples in manufacturing and in other fields where probabilistic predictions are used all the time successfully.

My concerns relate to what our view is of a weakness in the basic molecular biology that has to be the foundation for all of the probabilistic approaches. And that is that the generation of the tester sets of the laboratory results that are used to rate the internal tables of these kinds of software. And I tried to make those concerns clear in the report I was asked to write.

Q All right. We’re all here Dr. Reich trying to follow what you’re saying. You’re saying that it’s not a reliable test, is that what you’re saying?

A I want to be precise, so the probabilistic interpretation method is not itself a test. It’s a re-analysis of the results that were obtained by a forensic laboratory. That’s part one.
D

Two, I don’t think that the
close conclusions that the software provides are necessarily
have been shown to be completely accurate for all of the
conditions that are needed in order to make the claims
that the software developers have.

Q What are those conditions? Can you explain?
A I’m sorry, could you repeat that?
Q What are those conditions that you’re talking about, meet
all those conditions?
A The – it was alluded to slightly earlier that the tester
sets, the laboratory produced mixtures that are used by
the software developers to develop their tables are based
on perfect samples. There’s no choice. You make them in
the lab and they are perfect. It was alluded to slightly
earlier that there is a way of trying to damage those
samples. That unfortunately is not accurate. There is no
molecular biological method to make a damaged sample in a
way that a forensic sample is damaged because we have no
idea of how a forensic sample has been damaged, its extent
of inhibition or how uncertain that amplification is. We
don’t know how it was made in the field so we cannot
reproduce that in the laboratory and there is no method to
in fact degrade DNA and make it look like a forensic
sample that is damaged. That is simply not true.
So those underlying tests which the
lab builds so the software can learn, and I apologize for trying to simplify what is a more complicated and sophisticated approach, that fundamentally cannot be reproduced in a laboratory. Forensic samples are degraded. They are inhibited. Active labs, ours, Michigan, Erie, they all see samples which are labeled either as degraded or inhibited. This is a fact of life for those of us who use real samples.

That changes how the kits operate. It changes the results that are seen on the electropherogram. I do not believe, I know TrueAllele does not model that at all. I do not know this particular software well enough to say that it doesn’t, but I know that those tester sets do not model that real world experience. They cannot. And that will change what the software has learned. And that is a weakness in the probabilistic approach.

Q Well you heard the Doctor say that he has zero percent false positive. Did you hear that?

A I did. So he and I both know that there is no human test without error and he was careful to know up to now he’s not aware of any. We both know that any human endeavor, any human test, has error. There are no exceptions to that fact.

The field of - This field of forensics is not a medical field; it is not part of health care. I
used to work for Abbott Laboratories as listed on my CV. And in that field the FDA demands an error rate for all diagnostic tests. You cannot submit a diagnostic test to the FDA without providing them with an error rate. Forensics does not have an error rate. Forensics does not have an error rate. They are not asked for it. The field doesn’t discuss it, makes no effort to determine it. It wouldn’t be an easy thing to determine but it is possible. So there is an error rate. There has to be and there will be. We don’t know what it is for the software or for the general testing that is done by all forensic labs, ours included. We know there are errors.

Interestingly, one possible confusion was discussed by Dr. Buckleton, in that if he tests his software with similar genotypes I don’t recall the details of whether he can confuse the software or whether the software misrecognizes a similar genotype. But that’s an interesting example not of an error necessarily, although it could be interpreted as an error, but of a possible confusion based on someone whose DNA profile is similar to the defendant but who is not known to the Court.

THE COURT: Let me just interrupt and ask a question. This is the Judge speaking Dr. Reich. Are you saying that you would have the same criticism of the TrueAllele method as you do of STR Mix with regard to the
development of these testing sets?

    THE WITNESS: Absolutely your honor. That
has been the discussion for some time.

    THE COURT: OK.

    THE WITNESS: I’m quite familiar with
TrueAllele for a variety of reasons. Again, I don’t know
the actual software code. It has not been released. But
I know how the system works in the general form and I know
how those tester sets were made for that software. The
scientist who did that work works in my laboratory and
also he had discussed how those tester systems were built.

    THE COURT: Are you aware that TrueAllele
has been accepted from an evidentiary basis in courts in
the United States? Are you aware of that?

    THE WITNESS: I am. I am very aware of that
your honor and that-

    THE COURT: OK, just a minute, just a
minute. Hold on. Just answer my question if you would
please. OK, so you’re aware of that. Did you - did you
have the opportunity to present your critique with regard
to the TrueAllele method in any of those cases that you’re
aware of?

    THE WITNESS: I was not your honor.

    THE COURT: OK, thank you. Go ahead Mr.

   Peterson.
BY MR. PETERSON:

Q We were talking about the testing and this false positive stuff and trying to reproduce - him using perfect samples. Is that one of the problems with this software is that you cannot manually reproduce the actual DNA sample? Am I stating that correctly?

A I am not sure that you might be asking two separate questions. So one-

Q Go ahead.

A One perspective on your question refers to a validation so in one type of validation, and appropriately Dr. Buckleton mentioned there are several kinds, the laboratory is supposed to show that a new method provides the same accurate and reliable results if they introduce a new approach. So for example, our laboratory uses software to calculate the random match probability or to calculate the probability of a paternity test. Every year we have to do 10 or 15 cases manually that show that the numerical value we came up with by calculating it by hand comes up with the same number as the software we use. So we have to compare that the results are the same. I don’t know if that same need would also be for the probabilistic software but I think if it did that would be hard to do.

Q Yeah, that’s what I’m getting at. There’s literature out there that says that counter-checking it manually has not
been done or has come up with different results. Is that correct?

A I am not familiar with those approaches, with that work.

Q OK. You don’t know if it’s been done or not done?

A I don’t know if it’s been done.

Q OK. You mentioned source code and I tried to get into this with Dr. Buckleton. What do we mean by source code and why is it important for the software?

A The way computer software is written is it’s written in a language so there is a series of instructions. You can think of it very broadly as writing an essay where there is, or a manual. Let’s talk about a manual for fixing something. So there’s a list of instructions that you would do: take out a screwdriver, open this screw, undo this nut, etcetera. The software is a series of instructions.

And there is at least one lawsuit that I’m aware of in New York to force TrueAllele to divulge those set of instructions, the source code for what the software does to arrive at its final result. Many analysts, scientists feel that the ability to examine the instruction set, the source code, is important in order to understand how the software truly performs its functions.

Now I don’t know with STR Mix whether that’s an issue for them. For TrueAllele the gentleman
who has put that together has fought that tooth and nail for years.

Q And the reason that’s important, let’s say I hired you as an expert and I wanted you to review the result of the STR Mix software result in this case. You can’t do it without those source codes. Is that correct?

A I could review the output of the software because that’s gonna generated report or a series of numbers, however, they have devised their output. But I would not be able to tell you whether the steps were appropriate or what assumptions had been made at each one of the individual instruction steps, that’s correct.

Q And that’s important because you tell the Court that this software uses assumptions, isn’t that correct?

A It has to. That’s its purpose. Making assumptions is not the issue. It’s what assumptions are made and how do those assumptions affect the outcome.

Q OK. And without the source code you cannot review that, is that what you’re saying?

A I am not the only one who cannot review it. Without knowing those set of instructions nobody knows except for the developer maybe how - what those assumptions are and what those assumptions mean for the end result.

Q OK. One thing I talked about was threshold levels and the fact that this probability analysis will take a degraded
sample below threshold. Can you tell the Court what is meant by that?

A I can try. Maybe a sentence on what thresholds are might be helpful for the Court. The electropherogram is a visual representation of the raw data that the machine that does the profiling generates. And the electropherogram is a complicated piece of paper. It has a lot of information and one of the pieces of information that is on that electropherogram is the strength of the signal and in analyst speak the size or the height of the peak. The more DNA in a sample, the larger the peak; the less DNA there is in a sample the smaller the peak. At some point if you don’t have enough DNA the amount of signal that is recorded by the machine becomes unreliable. It is no longer enough signal for the software or for the analyst to believe that it’s a true signal versus the noise that’s inherent in all measurements. So that minimum peak height, that minimum amount of signal is a threshold. It’s a value that the analyst sets, the laboratory sets in order to obtain what they consider reliable and accurate results.

What was alluded to earlier is that there’s more than one kind of threshold. That is accurate, but in any event for our discussion here in order to develop the tables for the probabilistic method
the software looks below what is the threshold that the analyst him or herself would use. That threshold which was the staple in the forensic laboratory and still is for many years is the dividing line between what the lab will accept as reliable data and below which the lab will not measure or take as reliable.

So in order to use the probabilistic model they have to go below that threshold that the lab is used to using for their hand analysis. Whether that’s controversial or not is a different issue. And Dr. Buckleton of course said that that’s what would have to be done and he is correct. That raises, I don’t say hackles, it raises some form of uncertainty in what might be happening below that threshold.

Q So is that why you want to see - what do you say to this Court as to the reliability of this testing?

A I think the reliability of this testing is still under - undergoing discussion. There are a couple of ways of expressing that. There are about 400 forensic laboratories in the US. There’s only a tiny handful of labs like ours which are commercial labs. The vast majority, 395 of them or something, are state and governmental labs. For a technique to be generally accepted you would expect that 201 labs or so would have to use this method. That is certainly not the case and...
there are certainly not 201 laboratories that would
consider this fully ready for everyday use.

Q Of the 395 labs do you know of any, any that’s government
labs that are currently using STR Mix?

A I believe there was a list already spoken to by Dr.
Buckleton about which labs are beginning to implement it
and which labs have begun to validate it. I knew of some
of those. He of course has the more complete list; he
would know. But that is far from generally accepted.

Q In other words you’re saying the 395 just taking the
number of 201, if 201 were using it you would consider
that generally accepted?

A I think an argument could be made in courts that that
would be generally accepted. I would like to point out
that numbers do not always determine scientific
reliability. There were thousands of hair analyses
performed by the FBI. That method is complete junk and
has been repudiated publically with the revision of
hundreds of cases. The same can be said for ballistic
lead analysis, also a method used by the FBI for years,
fully repudiated as scientific fantasy. So just because
there are labs that use it, even a majority of
laboratories, is not necessarily a indicator of accurate
science or longevity in this analysis field.

MR. PETERSON: I have nothing further.
CROSS-EXAMINATION

BY MR. HEDGES:

Q Good morning Dr. Reich. My name is Robert Hedges. I am the prosecutor on the case and I’ll be asking you questions on cross-examination.

A Nice to meet you.

Q Nice to meet you sir. This is your first time testifying in a Michigan court, is that correct?

A I believe so.

Q Have you ever testified on the issue of probabilistic genotyping before?

A This is the first time.

Q Have you done any consulting work as an expert on the issue of probabilistic genotyping? It sounds like maybe you’ve done some work on the TrueAllele product.

A Yes I have, so there’s — I don’t know the status but I know there were challenges in New York and in Maryland and I have done consulting work for attorneys in those states and the topic of probabilistic interpretation, specifically TrueAllele was one of those topics.

Q This is your first case looking at STR Mix, is that right?

A I’ve known about it because the method has been published and the analysis method is known in the field. I go to many of the meetings and it’s discussed there.

Q Have you published any peer-reviewed work on probabilistic
genotyping?
A I have not. I have had no opportunity to do so.
Q Have you published any papers in a non peer-reviewed publication-
A No.
Q -on probabilistic genotyping?
A No.
Q Have you presented as a speaker at any scientific seminars, and what I’m trying to exclude, you also present at seminars for attorneys and we applaud you for that.
A I do.
Q But eliminating those seminars, have you presented as a speaker at any scientific seminars on the topic of probabilistic genotyping?
A I have not. I would not be asked to do that. I’m not one of the developers. I would just be someone who is examining what the results might be. That’s not a topic for a scientific meeting.
Q Have you presented as a speaker at scientific seminars, again not seminars to lawyers, on other DNA issues?
A Absolutely.
Q Are there any authorities in the field that you can point to on the subject of probabilistic genotyping that contend that this is not reliable science?
A I don’t think anybody knows whether it’s reliable science.
THE COURT: Just a minute, just a minute, that wasn’t his question.

THE WITNESS: Excuse me your honor. Could you repeat it for me?

BY MR. HEDGES:

Q Yes. Can you point us to someone that you consider to be an authority on probabilistic genotyping that contends that it is not reliable science?

A The answer is probably yes because I am one of them and so is the scientist that I hired from TrueAllele. He did the initial lab work for that software and it’s known what the weaknesses are.

Q Who is that scientist? What’s his name?

A His name is Alexander Sinelnikov and his name is on the publications, the early publications for TrueAllele.

Q Are you familiar with Norah Rudin?

A Yes, I am familiar with the name.

Q She’s not a friend or an acquaintance of yours?

A I don’t know not even that much.

Q OK.

A I just know the name.

Q Keith Inman. Do you know Keith Inman?

A I’m sorry, could you repeat that?

Q Do you know who Keith Inman is?

A Only by name.
Q All right. Are you familiar with Norah Rudin’s product called Lab Retriever?

A I didn’t hear that last word. I apologize for the phone quality.

Q It might be just my voice. Are you familiar with Norah Rudin’s product called Lab Retriever?

A No I’m not.

Q You don’t question the scientific validity of such things as Bayes Theorem or Bayes Statistics and Probabilities do you?

A I do not. We use those, or a version of them every day.

Q You don’t question the scientific validity of Markov Chain Monte Carlo approaches or methods?

A No. That’s a method for more rapidly arriving at an end point calculation and it’s used in many forms of calculations.

Q You would agree that MCMC, it’s called MCMC for short, is that right? Markov Chain Monte Carlo is usually called MCMC? I have a few more questions.

A Sure you can use an acronym. That’ll make it easier.

Q You know that it’s used in chemistry, physics, astronomy, gaming, stock market.

A Absolutely.

Q It was used in the development of atomic weapons even?

A I don’t know all of its uses. It’s a fairly - it’s a
standard mathematical approach to try to arrive at an end point calculation rather than doing it by brute force.

Q And you would not question its scientific validity?

A Of the Markov approach, no. But it’s only a tool to arrive at one particular end point. It’s like using a wrench. A wrench is a wrench depending on what you use it on.

Q Well when we say Markov, first it was Markov then it was Monte Carlo and then the two became used in conjunction with each other, isn’t that correct?

A I don’t know the history of the method but I’m sure you’re correct.

Q Well I mean for example, would you consider yourself an expert on the Markov Chain Monte Carlo?

A Certainly not.

Q You would not consider yourself qualified to teach a class on it?

A I would not be.

Q So if I asked you questions to define the Metropolis Hastings algorithms and compare it to the Gibbs Sampler you wouldn’t be able to do that would you?

A I would not, nor do I suspect are you able to. It’s not a relevant factor for the probabilistic software we are discussing.

Q Well you understand that STR Mix uses Markov Chain Monte
Carlo?

A That’s how it has been described and that’s not an inherent weakness in the approach.

Q All right. You don’t know which approach of MCMC it uses?

A No idea. I don’t think it’s relevant to the fundamental molecular biology I was discussing earlier.

Q So the problem is not the probabilistic approach using MCMC, the problem is the inputted data, the biology, the DNA results themselves? Am I understanding you?

A Not the results themselves. It’s how you get those results and whether the results in the laboratory can mimic appropriately, reliably and accurately the variety that forensic samples produce in that same laboratory. That is the fundamental weakness of all of the probabilistic approaches. It is not the fact that it arrives at its final calculation using a mathematical tool that is well understood. It is the garbage in/garbage out problem.

Q And if I understand correctly that criticism would apply to TrueAllele too.

A It does. It’s exactly the same weakness for both of the methods. There’s no avoiding that weakness in my opinion.

Q And that would apply to many scientific disciplines where any time you test science in the lab and then the question is always how well does that replicate real life. We can
test drugs, for example, before they go on the market and we can test them for a multitude of variables but when they’re finally turned loose on the market there’s going to be variables that you just can’t test for in the controlled environment. Isn’t that true?

A That is accurate. There is also an issue of degree. You brought up the fact – the issue of pharmaceuticals and that’s an interesting one because the assumption everyone makes is that forensics uses the same kind of approaches for accuracy and reliability and adverse effects, if you will, as the pharmaceutical market. And it does not. And I wish to remind you that the number of pharmaceuticals that are released and then are pulled because the number of adverse effects were either hidden by the company or were found afterwards when it was released into the general public.

Q One of your criticisms of probabilistic genotyping is that it ignores the stochastic thresholds of the prior methods, is that correct?

A It’s not that it ignores it. It doesn’t use them in any way because it’s not relevant for how the probabilistic method has to generate its internal set of results. What I am always surprised at is that the forensic laboratories that pushed and have developed the thresholds, there was the analytical threshold that I tried to describe earlier;
there’s the stochastic threshold which you have just again mentioned. They are happy to just ignore all of those thresholds when the probabilistic version comes up. I don’t understand how they can spend years developing different thresholds, hold everyone to those thresholds and then abandon them when this approach appears.

Q Don’t be offended by the question but you’re saying you just don’t understand it?

A I don’t understand why the labs would go through that effort then turn a blind eye to the fact that the probabilistic software has to look under the thresholds which the lab itself has deemed unreliable.

Q Well you are familiar with SWGDM, the Scientific Working Group for DNA Analysis Methods?

A I know about them and I know who they are, yes.

Q And they are a respected guideline and policy-making entity?

A I don’t know if I would use the word respected but they are the entity that makes the recommendations that are eventually turned into standards against which the labs are inspected against.

Q Even those stochastic thresholds that you talked about, those pretty much came from SWGDM didn’t they?

A They did. They did not exist for approximately 10 years and then they were instituted late, that is correct.
Q OK, well I need you to clarify. I mean do you consider SWGDM authoritative or don’t you? You don’t respect them?
A You don’t have a choice. They make the decisions in the field. Do I feel that all of the decisions are based on science and logic, that’s a different question.
Q Are you familiar with the publication dated June 15, 2015 by SWGDM that’s entitled Guidelines for the Validation of Probabilistic Genotyping Systems?
A I know it exists.
Q Have you read it?
A I’m sorry, could you repeat that?
Q Have you read it?
A I have not.
Q Well as an expert criticizing the admissibility of probabilistic genotyping don’t you think you should be familiar with the SWGDM guidelines for probabilistic genotyping?
A No, not necessarily. I’m not implementing it in our laboratory.
Q But you’re testifying on it in court.
A The issues I’ve discussed have not been - are not listed in that document.
Q Well I mean if you had read the document it says, and I’ll quote a part of it: “That probabilistic genotyping does not utilize the stochastic threshold. Instead it
incorporates probabilities of alleles dropping out or in
and making use of more genotyping information by
performing statistical calculations and evaluating
potential DNA contributors. Probabilistic genotyping
enhances the ability to distinguish true contributors and
non-contributors”. So that’s what it says on Page 2 of
that document that you haven’t read yet.

A You’re describing what I just said in that it is ignoring
the threshold that the field has used for 10 years.
That’s correct.

Q Or it’s deciding that there’s a new tool that has the
power through the use of statistical approaches such as
MCMC, which you’ve also indicated you don’t really
understand well enough to teach; that it has the power of
those new tools that it doesn’t need those thresholds and
in fact can produce a better result without them.

A There is no positive indication that the results are
better. There is an indication that it provides different
or more results but there is certainly no consensus and no
generally accepted test to determine whether they are
better. That’s not the case.

Q Are you aware that STR Mix was sold to Erie County, New
York and proceeded through a validation process that took
several months and then was presented to the DNA
subcommittee of the New York Commission on Forensic
Evidence?

A Yes, I heard that discussed earlier this morning.

Q And do you realize that the DNA subcommittee is made up of a panel of all PhD experts and that they unanimously approved STR Mix for casework?

A They are allowed their opinion. I work in a laboratory that has forensic cases all day long and I am much more skeptical and much more realistic about the day-to-day uses of this software then perhaps the committee from New York State is. That would be my comment.

Q Can you point us to any publications in any peer-reviewed documents that share your opinion regarding the limitations or the unsuitability of probabilistic genotyping for courtroom use?

A No I cannot. You asked - that was asked also of Dr. Buckleton. Such a paper would be extremely difficult to publish. The scientific literature does not readily accept that kind of manuscript and the only way that that paper could be written is if the software is released and made available to a wide range of researchers to do that work. Neither of those two factors are currently available. If the software becomes more generally used you can be assured that there will then be an opportunity to provide a serious test of the method but a much more wide-ranging analyst set and then you might see those
papers. It’s too early to see them now.

Q Dr. Reich, I think that we had a little bit of telephone
trouble at the beginning and honestly since we went over
some of the things so quickly I think Dr. Buckleton
testified, but certainly it’s contained within the Exhibit
1 which is the report which I know that you have looked at
in this case. That unlike TrueAllele, in the STR Mix
product all the significant algorithms have actually been
published. Are you aware of that?

A Yes, I am aware of that. We looked - we read some of
those papers as best we are able to and the thought, which
is the intellectual nugget which is very important of
course, those have been described and I’m aware of that
fact. That is not the same as the source code or the
computer instructions that was discussed earlier, but it
is correct that there’s much more openness for STR Mix
than there is for TrueAllele and Dr. Buckleton is to be
commended for that in my opinion.

Q And I know you’re on the telephone and you weren’t in the
courtroom, but when you were talking about that I went out
to the audience area and asked Dr. Buckleton about the
code and he indicates that he would be willing to give
that to anyone who simply asks for it. You did not ask
for it in this case did you?

A Of course not. It’s a commercial piece of software that
we would normally have to purchase or rent and then we would need several hours. He mentions four days to get the laboratory up and running for it. And there certainly has not been time or resources to do that. I would be interested in being able to do that but I don’t believe that’s the subject of this hearing.

Q Are you aware that the United States Army Criminal Division has been using STR Mix and has used it in their Court Marshall litigation several times with no reported problems?

A So I’ve heard. That’s an interesting laboratory and it’s completely outside of the regular forensic world because of course it belongs to the US military. They are a well-respected facility but they are not under the same rules or guidelines or standards as let’s say the rest of us, but you get the idea.

Q All right. Prior to today were you aware that the FBI has not only purchased STR Mix but has begun using it on casework, it sounds like earlier this week?

A I knew that they had been looking at it because that was partially disclosed at an earlier forensic meeting. I was not aware until this morning of the extent of their use. I’ve already described the rather unfortunate and public history of that laboratory. We will have to wait and see whether or not this was a decision that was good or bad.
MR. HEDGES: Thank you. I have no further questions.

MR. PETERSON: Nothing further.

THE COURT: OK. Thank you Dr. Reich very much for your input.

THE WITNESS: My pleasure.

THE COURT: Do you want him to remain on the phone while we have the other witness?

MR. PETERSON: No.

THE COURT: You may be recalling Dr. Buckleton.

MR. PETERSON: I wouldn’t be able to recall Dr. Reich anyways, I don’t think.

THE COURT: Well it’s up to you. I don’t want to cut him off until you’re ready because I have some more questions for Dr. Buckleton at some point.

MR. HEDGES: Well here’s what I was going to propose. Well what I was going to propose is that we take a relatively brief break, maybe 15 minutes. I will see if I need to put Dr. Buckleton on. Well obviously I’m going to if you have some more questions for him. And then I will make contact with our expert in New York and see how quickly we can have him.

THE COURT: OK, but we’re only going to make that a five-minute break, not 15. We’re break for five
minutes. Let’s try to focus on the flashpoint here. The flashpoint seems to be insofar as Dr. Reich is concerned, is this, and I’m quoting him now, I’m not saying I’m making this finding, “this problem with the replication of the natural environment in the lab”, so let’s try to focus on that and not spend a lot of time on things that don’t seem to be at issue. OK? For example, MCMC doesn’t seem to be under fire here. OK? So I don’t think we have to spend a lot of time with that.

MR. PETERSON: I’m sorry?

THE COURT: For example, MCMC doesn’t seem to be under criticism so let’s not spend a lot of time with it. It’s interesting, but let’s focus when we bring Dr. Buckleton back where the disagreement seems to be which is in this alleged weakness in the process used apparently by TrueAllele as well as STR Mix in the replication of the natural environment. I mean, you can get into other stuff if you think it’s relevant, but that’s what I’ve gleaned from this testimony up to this point.

(Off record at 11:20:20)
DECISION & ORDER

DNA Analysis Admissibility
Ind. #: 2015-15

ORAL NICHOLAS HILLARY,
Defendant.

Mary E. Rain, District Attorney, Canton, for the People.

William Fitzpatrick, District Attorney, Syracuse, for the People.

The Legal Aid Society, New York (Jessica Goldthwaite of counsel), for the Defendant.

The Legal Aid Society, New York (Richard Torres of counsel), for the Defendant.

Dumas & Narrow, Canton (Peter Dumas of counsel), for the Defendant.


Siegel, Teitelbaum & Evans, LLP, New York (Norman Siegel of counsel), for the Defendant.

The Legal Aid Society, New York (Clinton Hughes of counsel), for the Defendant.

The Bronx Defenders, New York (Adnan Omar Sultan of counsel), for the Defendant.

CATENA, J.:

A motion was filed by defendant to preclude the prosecution from offering expert testimony as to the use of, or any results produced by, the forensic software tool STRmix alleging that the use
of this software for probabilistic genotyping is not generally accepted in the relevant scientific and legal communities as required by Frye v. United States, 293 F. 1013 (see, People v. Middleton, 54 NY2d 42 ["the test is not whether a particular procedure is unanimously indorsed by the scientific community, but whether it is generally acceptable as reliable"]). The defendant also filed a motion to preclude the use of a modified random match probability statistic ("RMP"). The defendant also challenged the admissibility of the evidence. The people filed an affirmation in opposition to the motion dated June 24, 2016, and oral argument was held on Friday July 1, 2016. By decision and order dated July 11, 2016, this court granted a limited Frye hearing on the issue of whether STRmix can "generate results accepted as reliable within the scientific community generally" on extreme mixture ratios where the DNA from the minor contributor is low template. Trial foundation for the admissibility of the evidence was made part of the hearing (People v. Wesley, 83 NY2d 417, 429). The hearing was held on Monday July 25, 2016, at the courthouse in Canton, New York. Further oral argument was held on the record on August 17, 2016.

On October 24, 2011, the Potsdam Police Department received a call from a neighbor of the victim stating that she heard moans and the word "help" coming from the victim's apartment. An officer of the Potsdam Police Department arrived at the apartment at approximately 5:16 p.m., knocked on the door, and heard what sounded like someone walking around the apartment. Shortly thereafter, the Officer entered the apartment with the landlord and found the victim unconscious in the bedroom. No one else was in the apartment and the victim was pronounced dead at 7:18 p.m. that evening. The cause of death was determined to be strangulation.

As part of the investigation, the police collected dozens of samples of DNA from multiple areas in the apartment including the body and clothing of the victim. The police also obtained a
sample of the defendant’s DNA as he had lived briefly with the victim, having an intimate relationship with the victim’s mother. Because this was a New York State Police investigation, the New York State Police crime lab processed the samples. The defendant was excluded from all samples taken at the apartment where comparisons could be made except for a DNA mixture profile from fingernail scrapings taken from the victim’s left hand. Due to insufficient genetic information, the defendant could neither be included nor excluded as a possible contributor to the mixture.

Beginning in 2013, the New York State Police crime lab contacted Cybergenetics, Inc., to run the data obtained from the fingernail scrapings through their probabilistic genotyping software program called TrueAllele. The results were inconclusive. Nonetheless, the defendant was indicted for the victim’s murder in 2014 and the New York State Police crime lab sent its data at the behest of the prosecution to the Institute of Environmental Science and Research (“ESR”) which ran it through their probabilistic genotyping software program called STRmix1. The People also requested their expert, Dr. John S. Buckleton, one of the developers of STRmix, to calculate a random match probability statistic which was presented in a report dated July 1, 2016.

Dr. Buckleton conceded at the hearing that no internal validation studies were performed by the New York State Police crime lab for the use of STRmix on casework samples developed at the

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1District Attorney Fitzpatrick first contacted Dr. Buckleton by email on November 2, 2015, stating in pertinent part “I am currently assisting a colleague in prosecuting a murder case in Saint Lawrence County . . . On 10/24/2011 a 12 year old boy [ ] was strangled to death in his apartment in Potsdam NY. No physical evidence was discovered at the scene except for [ ] fingernail scrapings . . . Those scrapings were analyzed at the New York State Police crime lab and the DNA profile generated appears to be consistent with a mixture of two individuals with the victim as the major contributor and the obligate alleles (7) being consistent with the defendant. I am hoping that you or someone you recommend might be able to provide a statistical weight to the results using a likelihood ratio or some other method. I can provide the analyst’s report and the electropherograms if you decide to take a look.”
lab. As a result Dr. Buckleton was forced to pick and choose data from different “reliable sources” and input parameters into the program in such a way that he believed the system would tolerate. The reason for this was because the New York State Police crime lab was not authorized by the New York State Commission on Forensic Science to generate data from DNA samples for STRmix.

2Dr. Buckleton testified that “[a]ll labs in the United States of America are following the SWGDAM guidelines”. The Scientific Working Group on DNA Analysis Methods (SWGDAM) provides guidelines for validation of probabilistic genotyping systems such as STRmix. As stated in the guidelines, “[v]alidation is a process by which a procedure is evaluated to determine its efficacy and reliability for forensic casework and/or database analysis.” Further, “[i]nternal validation studies is the accumulation of test data within the laboratory to demonstrate that the established parameters, software settings, formulae, algorithms and functions perform as expected . . . In particular, complex mixtures and low-level contributors should be evaluated thoroughly during internal validation, as the data from such samples generally help to define the software’s limitations, as well as sample and/or data types which may potentially not be suitable for computer analysis.”

STRmix has six laboratory specific parameters to determine prior to its use. Concerning one of these parameters called stutter ratios, Dr. Buckleton testified that he received data from the New York State Police crime lab to look at “forward stutter” which “did not serve the purpose” but nonetheless was used in the April 2016 analysis. Concerning “drop-in” rates, Dr. Buckleton stated that he inputted a zero drop-in rate as the crime lab did not “have a drop-in rate because they do not do low copy number on high sensitivity methods.” A “drop-in” rate greater than zero would have benefitted the defendant. And in his affidavit dated August 18, 2016, Dr. Buckleton further stated that he used a “drop-in rate” that was based partly on “our own experience.”

Dr. Buckleton further testified that “[b]est practice is clearly validation in the lab specifically, and that is -- the optimal way is the way we recommend. It's not available to me in this case because the New York State lab has not done the relevant validation. I have two options first with that. I have the option of doing the next best practice or not doing anything. I’ve done next best practice. I’ve done this a couple times before and I’m not pertaining it’s best practice, and I have candidly acknowledged in my statement that exact fact. What I’ve done is attempt to take data from different reliable sources that I think applies to the circumstance. I’m also aware of the forgiveness of the system for slight inaccuracies in certain of the parameters, so I have input parameters in such a way that I believe the forgiveness of the system will tolerate any inaccuracies I’ve made” (emphasis supplied).
analysis. And although ESR had performed the necessary internal validations to be accredited by the relevant agencies for the use of STRmix, those validations were specific to data generated by ESR. Here, the only data generated was from the New York State Police crime lab.

"The New York State Commission on Forensic Science (the "Commission") is the governmental body tasked with developing minimum standards and accreditation programs for all forensic laboratories in New York State. In addition, the Commission approves forensic laboratories to perform specific forensic methodologies. The Commission's objectives are to increase and maintain the effectiveness, efficiency, reliability, and accuracy of forensic laboratories, ensure that forensic analyses are performed in accordance with the highest scientific standards practicable, and set forth minimum requirements for the quality and maintenance of equipment. The DNA Subcommittee of the New York Commission on Forensic Science ("DNA Subcommittee") is the

3 The lab was authorized to generate data for TrueAllele analysis. The People stated at the August 17, 2016, oral argument that "each individual laboratory has to go through essentially an accreditation process to determine whether or not . . . they have the trained personnel and expertise to accurately employ [STRmix]". The People further discussed the Onondaga County crime lab stating "Onondaga is going through . . . their own internal validation process to make sure that their people are properly trained to use STRmix, get accurate results with blind proficiency testing and then ultimately will present their process to ASCLD/LAB . . . for the accreditation process. Then that laboratory . . . has to go through a two year accreditation process in front of the Forensic Science Commission for that discipline." It is clear that the New York State Police crime lab had not gone through the accreditation process and, thus, did not have the "trained personnel and expertise to accurately employ" STRmix. The People conceded this stating "there [were] no internal validation studies by the State Police regarding STRmix."

4 The Federal Bureau of Investigation's quality assurance standards for Forensic DNA Testing Laboratories define "Forensic DNA analysis" as "the process of identification and evaluation of biological evidence in criminal matters using DNA technologies." The quality assurance standards further define "internal validation" as "the accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory." Quality Assurance Standard 8.1.3 requires that internal validation be performed for forensic casework analysis.
body appointed by the Commission to perform accreditation of all DNA laboratories in New York. Further, the DNA Subcommittee is charged with assessing all DNA methodologies proposed to be used for forensic analysis. It has the sole authority to grant, deny, review, or modify a DNA forensic laboratory accreditation, which the DNA Subcommittee exercises by issuing a binding recommendation to the Commission. While the Commission can request that the DNA Subcommittee reconsider its findings, the DNA Subcommittee is the final decision maker regarding laboratory accreditation” (U.S. v. Morgan, 53 F.Supp.3d 732; Executive Law 995-b[1]).

The Commission requires laboratories to comply with the standards promulgated by the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (“ASCLD/LAB”) (9 NYCRR §6190.3[b]). These standards require that DNA mixture interpretation be based on validation data (id.). Here, by sending its raw data to ESR, an accredited lab for STRmix analysis, the People argue that the New York State Police crime lab could bypass Commission approval for its participation in the STRmix process inasmuch as it did not run the computer program. This minimizes the importance of raw data generation in the STRmix process and emphasizes the People’s heavy reliance on the expertise of Dr. Buckleton to account for any deficiencies in the data. Such reliance appears contrary to Commission and ASCLD/LAB requirements (see, State v.
Wakefield, 57 Misc.3d 850; see, People v. Vincent Bullard-Daniel, Co Ct. Niagara County, March 10, 2016, Murphy, J., Ind. No. 2015-88).

As stated by this court in its earlier order granting the pre-trial hearing herein, "the test pursuant to Frye v. United States (293 F 1013) poses the . . . question of whether the accepted techniques, when properly performed, generate results accepted as reliable within the scientific community generally . . . The issues of proper foundation and of the adequacy of laboratory procedures [] are not before [the Court at a Frye hearing]" (People v. Wesley, supra). To that end, this court notes that the New York State Commission on Forensic Science issued a binding recommendation for use of STRmix in the analysis of DNA profiles upon recommendation from its DNA Subcommittee (Executive Law §995-a; People v. Wakefield, supra at 856 [approval by the Commission constitutes general acceptance]). And STRmix was found by a New York State court after a Frye hearing to be generally accepted in the relevant scientific community (People v. Vincent Bullard-Daniel, supra). Based upon a review of the record, this court finds that STRmix has been developmentally validated and is generally accepted as reliable within the scientific community (id.; People v. Muhammed, 14th Cir. Ct., Muskegon Co, Dec. 15, 2015). Issues concerning the manner

7 ASCLD/LAB accreditation requirement 5.4.5.2 from ISO/IEC 17025:2005:

"Procedures for DNA profile interpretation must be based on validation data. The interpretation of a DNA profile containing a mixture of two or more individuals must be guided by a procedure that includes specific defined steps that will enable different analysts in the same laboratory to reach the same conclusion; and a competent person from outside the laboratory using the same procedure to understand how the conclusion was reached. DNA mixture interpretation procedures must be tested on mixture profiles from known contributors representing the range of mixture types (e.g., different numbers of contributors, mixture proportions, and template quantities) to which the procedure will be applied in casework. The results of this validation must be used to define the capabilities and limitations of the procedure and to verify that it produces the expected results (e.g., inclusions and exclusions)."
in which STRmix accounts for stochastic effects in its probability computations where mixture ratios are extreme and the minor contributor’s DNA is low template goes to weight (People v. Debraux, 50 Misc.3d 247; People v. Megnath, 27 Misc.3d 405).

“The issue [now] shifts to a second phase, admissibility of the specific evidence--i.e., the trial foundation--and elements such as how the sample was acquired, whether the chain of custody was preserved and how the tests were made . . . Once Frye has been satisfied, the question is ‘whether the accepted techniques were employed by the experts in this case’. The focus moves from the general reliability concerns of Frye to the specific reliability of the procedures followed to generate the evidence proffered and whether they establish a foundation for the reception of the evidence at trial. The trial court determines, as a preliminary matter of law, whether an adequate foundation for the admissibility of this particular evidence has been established” (People v. Wesley, supra at 428-429). Here, the lack of internal validation by the New York State Police crime lab, as candidly admitted by Dr. Buckleton, precludes use of the STRmix results (id.; see, State v. Wakefield, supra; see, People v. Vincent Bullard-Daniel, supra).

Concerning RMP, while this court finds that it has been generally accepted as reliable within the scientific community under certain circumstances, the results produced in this case are unreliable based upon Dr. Buckleton’s testimony that it cannot adequately account for the absence of defendant’s alleles in the composite profile. As Dr. Buckleton stated, “the exact difficulty that we’ve come upon in this case and certain circumstances that the Random Match Probability is not conservative and doesn't do a fair job for the defendant, and this is one of those circumstances. The specific diagnostic is called a -- it's called a non-major allele between the profile and the accused. And we have a number of those where the accused has an allele that is not seen in the profile and
Random Match Probability is incapable of [punishing] the statistic for non-matches . . . So, in fact, it is the exact weakness of the 2p rule that has motivated me to make a probabilistic genotyping system” (emphasis supplied). Further, the defendant’s expert, Dr. Dan E. Krane, testified that “[t]he Random Match Probability is and has been considered generally accepted in many circumstances. The particulars of the evidence sample in this case do not fit within the category of those that would cause to be generally accepted. If I can put it just a different way. I’ve testified for many years that there is no generally accepted means of attaching a reliable statistical weight to a mixed sample, such as the evidence sample in this case where drop-out may have occurred, which, again, seems very likely to have occurred with the evidence sample in this case. So, on those two counts it would be quite inappropriate to rely upon a Random Match Probability approach to generate a statistical weight.”

Given Dr. Krane’s testimony, the use of RMP in this case where the People’s own expert witness testified that it “is not conservative and doesn’t do a fair job for the defendant” must be precluded as unreliable (People v. Wesley, supra). In any event, even if this court were to agree with the prosecution that “[d]efendant’s concern with the methodology used by Dr. Buckleton in calculating the statistic goes to ‘the weight of the evidence, not its admissibility’”, to allow such evidence would be unduly prejudicial to the defendant (People v. Morris, 21 NY3d 588 [“Weighing the evidence’s probative value against its potential prejudice to the defendant is a matter of discretion for the trial court”]; People v. Caban, 14 NY3d 369 [“Evidence, though relevant, may be excluded where ‘it’s probative value is substantially outweighed by the danger that it will unfairly prejudice the other side or mislead the jury’”], quoting People v. Scarola, 71 NY2d 769, 777). In determining the motions herein, this court is reminded that “[f]orensic DNA analysis should be governed by the
highest standards of scientific rigor in analysis and interpretation” (People v. Wesley, supra) (Kaye, J., concurring). Neither the STRmix nor the RMP results may be used in this case (id.).

It is, therefore,

ORDERED that the defendant's motion to preclude the prosecution from calling an expert witness to testify on their direct case regarding any conclusion reached by the use of STRmix is granted as the prosecution cannot lay a foundation for the introduction of evidence that had not been internally validated; and it is further

ORDERED that the defendant's motion to preclude the prosecution from offering expert testimony as to any statistical results obtained by using the random match probability on the composite minor component of mixture is granted.

The above constitutes the decision and order of this Court.

Signed this 26th day of August, 2016, at Fonda, New York.

HON. FELIX J. CATENA
County Court Judge
54 Misc.3d 177
County Court, Niagara County, New York.

The PEOPLE of the State of New York, Plaintiff,
v.
Vincent BULLARD—DANIEL, Defendant.

March 10, 2016.

Synopsis

Background: Defendant, charged with predatory sexual assault and first-degree burglary, questioned admissibility of DNA evidence, and Frye hearing was held.

Ford.

[ Holding: ] The County Court, Niagara County, Matthew J. Murphy, J., held that DNA evidence was sufficiently reliable to be admissible.

Ordered accordingly.

Attorneys and Law Firms

**715 Robert A. Zucco, Esq., John P. Granchelli, Esq., Assistant District Attorneys, Appearing for the People.

Christopher A. Privateer, Esq., Assistant Public Defender, Appearing for Defendant.

Opinion

MATTHEW J. MURPHY, J.

*178 Defendant is charged with Predatory Sexual Assault (Penal Law § 130.95[1][a] ) and Burglary in the First Degree (Penal Law § 140.30[1] ). During pretrial proceedings, the Court learned that the People intended to introduce DNA evidence as part of their case in chief. Defense counsel was provided with copies of the DNA report. Following his review of the report, defense counsel raised the question of the admissibility of the report as well as testimony relating to the report and thereafter sought a Frye hearing (see Frye v. United States, 293 F. 1013 [D.C.Cir.1923] ). After consideration of written submissions, the Court concluded that it would conduct a Frye Hearing.

The specific issue here is the admissibility of the forensic DNA testing results performed on a number of items of evidence discovered at the crime scene (the victim's house) and on cuttings from a dried red-stained area of a sock found in Defendant's bedroom. DNA testing on those items was conducted by the Erie County Central Police Services Forensic Laboratory *179 ("the Lab") and the results were interpreted using a relatively new software program referred to as "STRmix." 1

According to the STRmix website (http://strmix.esr.cri.nz), "STRmix is a breakthrough for forensic analysts as it can assist investigations using DNA evidence that was previously considered too complex to interpret. The software has been developed by New Zealand Crown research institute ESR, with Forensic Science South Australia."

The parties have provided the Court with voluminous submissions in support of their respective positions. Those submissions include references to relevant cases,
articles from scientific journals, and expert affidavits. The Court recognizes that the science behind DNA analysis and statistical probabilities is complex. This Court, however, previously rendered a Decision involving the admissibility of a DNA “kit” (see People v. Borden, Decision attached to People's Memorandum of Law, dated December 23, 2015) and therefore is familiar generally with the scientific principles at issue.

Before summarizing the testimony from the Frye Hearing, the Court believes that some background discussion of DNA analysis and interpretation is necessary. Rather than attempt to reinvent the wheel, the Court has taken the liberty of quoting at length from Judge Michael Coccom's recent decision involving a similar probabilistic genotyping program:

DNA identification is a powerful forensic tool for solving and preventing crime. **716 Two common sources of data ambiguity in biological evidence are DNA mixtures from multiple contributors and low-template (evidence samples below the threshold) DNA. Although some American laboratories are moving to quantitative modeling of DNA mixture data, most still use Combined Probability of Inclusion (CPI) or Combined Likelihood Ratio (CLR), using the qualitative Boolean logic of all-or-none allele (the number of repeated words) events. Both approaches apply thresholds to the DNA data that cut off quantitative information. Their analysts subjectively apply these analytical or stochastic thresholds manually to data peaks to decide whether or not they believe the evidence peak represents an allele in the genetic material. But the more complex data that has mixtures or low-template DNA limits the applicability of such qualitative procedures.

*180 Computer interpretation methods use more of the quantitative short tandem repeat (STR) peak height data rather than thresholds and have been used for over 20 years. Computers offer three principal advantages in the interpretation process: (1) productivity—eliminates the often time-consuming human review of cases that are impossible to solve, (2) information—human review typically makes simplifying assumptions that can discard considerable identification information containing DNA evidence whereas a computer can use a statistical model to fully examine the quantitative peak height data, and (3) objectivity—human mixture interpretation methods sometimes use the suspect genotype (pair of allele) to help infer or report results whereas a mathematically programmed computer can infer a genotype from the evidence data without using any suspect information and then afterward compute a match likelihood ratio (LR) statistic from this genotype.

Probabilistic genotypes have been recognized by regulatory bodies such as the Scientific Working Group on DNA Analysis Methods (SWGDAM) in its 2010 “Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories” and the American National Standards Institute (ANSI) in the 2011
article “Data format for the interchange of fingerprint, facial & other biometric information” as a valid approach to DNA Interpretation and reporting. There are two probabilistic approaches:

(1) semi-continuous—information is determined from the allele present—peak heights are not considered, and

(2) fully continuous—incorporation of biological parameters.


Wakefield involved the issue of whether “Cybergenetics True Allele Casework,” otherwise referred to as TrueAllele, met the Frye standard. That court concluded that it did.

THE FRYE HEARING

The Frye hearing was held on January 11, 14, and 21, 2016. The People's only witness was Dr. John Simich, the Director of *181 the Lab (I–12). 3 Dr. Simich testified that he was also the “DNA technical leader” for the Lab, and taught forensic science at SUNY Buffalo at both the graduate and undergraduate levels. Dr. Simich has been conducting DNA analysis since 1993 and the Lab has always used commercial “kits.” The “kits” contain “all of the components that are required for the polymerase chain reaction [PCR] process **717 to proceed and to generate the DNA results” (I–21). The Lab has used different kits over the years (I–19). The kits are used to “generate the PCR reaction and to look at the STR [short tandem repeat] genetic markers that are provided in the kit” (I–21). According to Dr. Simich, PCR/STR testing is used in all forensic labs worldwide.

3 The Frye hearing consists of two volumes, but each hearing date is consecutively paginated. The January 11 Hearing references will be preceded by (“I”), the January 14 Hearing References by (“II”), and the January 21 Hearing references by (“III”). After the PCR/STR process is complete, an instrument called a Genetic Analyzer reads the “various amplified fragments of DNA, and then that translates it into something that a human can see which is the electropherogram” (I–24). Once the Lab generates a DNA profile from the sample, that profile is compared to an individual—victim, suspect, or elimination sample—“to determine if they are the source of that DNA” (I–27). An electropherogram is a print-out of the “graph of the various DNA types that were identified at each of the genetic markers” (I–27). Exclusion can be made by visual comparison of the electropherograms. If there is no exclusion, the Lab needs “to determine the weight of the evidence” (I–28).

The electrophoresis step produces a chart, which gives the value of the DNA marker at a certain point and the “strength” of the signal (a measure of how many of the DNA molecules were examined at a particular value) (I–32). In July 2015, the Lab began using STRmix to make this calculation. STRmix allows the Lab to report the results as a likelihood ratio. 4

4 Different computer software has been used by the Lab over the years to calculate a probability ratio,
expressed in a mathematical term, e.g., one in 500,000
individuals. In a likelihood ratio, the results are
expressed as follows: a match between the suspect and
the evidence is (x number) of times more probable
than a coincidental match.

STRmix uses “continuous probability
genotyping” software (I–34). That software
uses information that has been available for
“years” (I–34). STRmix was recommended
by different scientific organizations as “the
best way to perform reporting of the
weight of the DNA evidence” (I–34). A
“continuous” *182 software program like
STRmix, according to Dr. Simich, is “more
discriminating;” it looks at “all of the
information” (I–35).

Dr. Simich testified about various scientific
organizations that review the software
programs: SWGDAM (Scientific Working
Group for DNA Analysis Methods),
NIST (National Institute of Standards
and Technology), and ISFG (International
Society of Forensic Genetics). According
to his undisputed testimony, all three have
recommended STRmix. STRmix addresses
the problem of mixed samples, that is, DNA
with more than two contributors. STRmix
“is able to break [the DNA sample] down
into its component mixtures” (I–38).

Dr. Simich discussed the concept of
“probabilistic genotyping,” 5 as used in
the calculation step of DNA analysis, and
testified that the principle “has been around
for many years.” (I–40). He described
the two steps involved in the process:
deconvolution and statistical analysis.
Deconvolution breaks a mixture “down into
**718 the individual contributors
and generate[s] DNA profiles for each of
them” (I–41). Statistical analysis determines
“the likelihood ratio of a person of interest
[the Lab] is asked to compare to” (I–41).

5 According to the Draft Guidelines for the Validation
of Probabilistic Genotyping Systems, published by
SWGDAM and introduced into evidence as People's
Exh. 3, “A probabilistic genotyping system is
comprised of software, or software and hardware,
with analytical and statistical function that entail
complex formulae and algorithms. Particularly useful
for low-level DNA samples and complex mixtures,
probabilistic genotyping approaches can reduce
subjectivity in the analysis of DNA typing results,
as compared to historical methods of mixture
interpretation (e.g., deconvolution of the mixture into
individual components), and quantifies uncertainty in
the analysis.”

Dr. Simich was familiar with some of
the mathematical analysis methods and
principles used in the deconvolution process,
for example, the MCMC (Markov Chain
Monte Carlo) model, and the Metropolis–
Hastings algorithm. MCMC is a standard
statistical modeling process. STRmix also
employs Bayes' theorem, which is a general
scientific principle of the likelihood ratio.
Bayes' theorem was developed in the early
1700s and has been used for centuries
in various scientific disciplines without
controversy (I–45).

After reviewing the STRmix software, Dr.
Simich concluded that the science behind it
was generally accepted within the forensic
lab community. He further concluded that
the software was reliable, based upon his
review of peer-reviewed journals *183 (I–
48). The creators of STRmix provided
Dr. Simich with a report of their internal
validation process (I–50). The Lab also
conducted its own validation study of
STRmix and published a report, which
was submitted to the New York State Commission on Forensic Science DNA Subcommittee (“the DNA Subcommittee”) (I–54; see People's Exh. 2). The Lab study concluded that STRmix “does reliably deconvolute DNA profiles and provide likelihood ratios that can be used for casework” (I–55). The Lab underwent an external audit by the National Forensic Science Training Center in August 2015, after it had begun using STRmix. The Lab undergoes a regular accreditation process as well as an internal audit (I–25–26).

Dr. Simich testified that he had considered other software programs, including Forensic Statistical Tool (FST) and TrueAllele. He concluded that “STRmix is accurate and reliable and can be utilized to generate likelihood ratios for mixture deconvolutions” (I–59).

Dr. Simich testified about the approval of STRmix by the New York State Commission on Forensic Science (“the Commission”). The Commission is the “organization that actually will evaluate and grant ... New York State accreditation” (I–60). The DNA Subcommittee, made up of experts in various scientific disciplines related to DNA analysis, evaluates the DNA aspect of forensic labs in New York. Dr. Simich appeared before the Subcommittee three times and presented his validation studies; Dr. Buckleton, one of the creators of STRmix, also appeared before the Subcommittee. In May 2015, the Subcommittee voted 4–0 (with one member abstaining) on a binding recommendation to the Commission to allow the Lab to use STRmix for casework analysis (see minutes of the meeting of the DNA Subcommittee approving STRmix, People's Exh. 5; letter from the Subcommittee to the Chair of the Commission with the binding recommendation, People's Exh. 6) (I–63). The DNA Subcommittee also issued a general recommendation on the use of probabilistic genotyping software (People's Exh. 7).

Dr. Simich testified without any contradiction that STRmix is used in other labs in Australia and New Zealand, and by USACIL (United States Army lab), the California Department of Justice, and the FBI. He was aware that some labs use FST (New York City's Office of the Chief Medical Examiner, or “OCME”) or TrueAllele (Virginia, some labs in Pennsylvania). He believed that other labs in New York *184 State have purchased STRmix and will be using it soon, including the OCME, which will be replacing FST.

On cross-examination, Dr. Simich explained why he selected STRmix for the Lab over other software programs. He admitted that there were other acceptable **719 methods to perform forensic statistics (I–79) and explained the differences among the various accepted methods (I–80). He opined that, in this case, the DNA profile was “15,000 times more probable if the sample originated from [Defendant] and three unknown unrelated individuals because it's a four-person mixture rather than if it originated from four unknown unrelated individuals in the U.S. population” (I–88).
Dr. Simich was asked about the “reproducibility” of the results reached by STRmix, in the context of his testimony that every time a sample was analyzed there would be a different likelihood ratio (I–115). He testified that variations among the different results were not “statistically significant” (I–115). The People rested, relying solely on the testimony of Dr. Simich and the accompanying exhibits.

Defendant presented the testimony of Dr. Gary Skuse, who teaches biological sciences at the Rochester Institute of Technology, with a specialization in a field called bioinformatics, which involves the interaction between biology and computers (III–4). His experience with DNA forensics consists of working “with criminal defense attorneys primarily helping them understand the processes that go into using DNA in criminal cases and help them interpreting the results” (III–6–7). He testified in the Wakefield case about the “way the DNA was isolated, the way the laboratory interpreted the DNA results” (III–7). With respect to STRmix, he reviewed various articles as well as material from the company, and the protocols established by the Lab. He criticized the amount of “human intervention and human judgment” involved in setting up the software (III–9). He was “interested that a laboratory acknowledged that the software itself gives different answers every time it's run” (III–9). He discussed the notion of “objective science” and opined that STRmix was not acceptable in accordance with general scientific principles (III–10).

On cross-examination, Dr. Skuse conceded that he had no training in forensic DNA analysis and that he had never been to the Lab. He apparently has visited the Monroe County Forensic Laboratory on rare and sporadic occasions. He had never used the STRmix program (III–50).

*185 On re-direct examination, Dr. Skuse was critical of what he called “directed science,” that is, “you're doing something to achieve a result that you expect” (III–55). In his view, there was an intrinsic bias with directed science (III–56). He was also critical of the peer review process in biological publications that has evolved over the past few years (III–56–57).

Defendant rested, and the parties provided the Court with further written submissions; oral argument was held on February 25, 2016.

THE LAW

THE FRYE STANDARD

[1] [2] Frye established the general proposition that scientific expert witnesses are only permitted to give opinion evidence when their testimony is based upon scientific principle or discovery that has passed the mere experimental stage and become demonstrable scientific knowledge generally accepted as valid within the relevant scientific community. Even though the Federal system, and a number of states, have moved away from the Frye standard to one embracing a more hands-on gatekeeper function for the trial judge (see Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S.
579, 113 S.Ct. 2786, 125 L.Ed.2d 469 [1993] ), New York continues to follow the Frye approach. Initially, the proponent of the evidence provides case citations indicating that other courts have already addressed the issue and approved its admissibility. Such cases can come from any competent court and **720 jurisdiction, whether in the United States or elsewhere. The proponent will also typically reference learned scientific treatises, published papers, books or other learned writings demonstrating acceptance of the scientific principle within the applicable scientific community (see People v. Hughes, 59 N.Y.2d 523, 466 N.Y.S.2d 255, 453 N.E.2d 484 [1983] ). When there are no such published materials, or when they are sparse or conflicting, the proponent must augment his proffer by expert testimony at a pretrial Frye hearing.

[3] At such a hearing, the proponent bears the burden of proof. The standard that the proponent must meet does not seem to have been clearly delineated by New York courts. At oral argument, the People indicated they were unable to find any specific authority on this issue (Transcript of Feb. 25, 2016, at 21). The People rejected Defendant's suggestion that the appropriate standard is, “beyond a reasonable doubt,” and argued that the more appropriate standard is, “preponderance of the *186 evidence.” In Daubert, the U.S. Supreme Court stated that, like any preliminary question regarding the admissibility of evidence, the standard is “a preponderance of proof” under the Federal Rules of Evidence (Daubert, 509 U.S. at 590 n. 10, 113 S.Ct. 2786). Such a standard has been suggested in New York (see People v. Owens, 187 Misc.2d 838, 725 N.Y.S.2d 178 [Sup.Ct., Monroe Co.2001] ). To the extent that it is necessary for this Court to apply a legal standard, the “preponderance of the evidence” test seems more appropriate and it has been that standard that this Court has applied in the analysis of the issues in this hearing.

The proponent of the evidence must establish that the scientific principles and techniques he advocates, when properly performed, generate consistent results accepted generally as reliable within the relevant scientific community (see People v. Wesley, 83 N.Y.2d 417, 611 N.Y.S.2d 97, 633 N.E.2d 451 [1994] ). At such a hearing, it is not the court's duty to reach its own conclusion about the reliability of the proposed scientific procedure, but rather to determine whether most of the relevant scientific community believes the procedure or technique under consideration is reliable (see id.). As Justice Mark Dwyer reminded us: “a court assessing the admissibility of evidence under Frye is not charged with deciding the validity of novel scientific procedures. It would hardly be sensible to assign that task to the judiciary, most of which is patently unqualified to perform the task as is this court. Judges should be ‘counting scientists' votes,’ and not verifying the soundness of a scientific conclusion' ” (People v. Collins, 49 Misc.3d 595, 15 N.Y.S.3d 564 [Sup.Ct., Kings Co.2015], quoting Parker v. Mobil Oil Corp., 7 N.Y.3d 434, 446–447, 824 N.Y.S.2d 584, 857 N.E.2d 1114 [2006], quoting People v. Wesley, 83 N.Y.2d 417, 439, 611 N.Y.S.2d 97, 633 N.E.2d 451 [1994] [Kaye, C.J., concurring] ).
While the issue of the admissibility of DNA has long since been resolved, new issues have arisen regarding the interpretation of the results of DNA testing. There are numerous cases in New York regarding software programs that interpret DNA results, although none involve STRmix. Although the scientific principles underlying the STRmix program are similar to the principles if not identical to the programs that have been considered, and almost universally accepted by courts in New York, this case concerns the first judicial review, as far as this Court is aware, of STRmix in New York. For that reason, the Court decided to conduct a Frye hearing. *187 The People argue, and the Court agrees, that the only question before it is whether the scientific principles underlying the STRmix software are accepted generally in the relevant scientific community. The People contend that STRmix **721 is a form of probabilistic genotyping, which is accepted generally in the scientific community of forensic DNA analysis. There is only one reported decision involving STRmix, from Michigan, where the court applied Daubert, and upheld the admissibility of the DNA test results (People v. Muhammad [14th Cir.Ct., Muskegon Co., Dec. 15, 2015] [attached to the People's submission of Dec. 23, 2015]). This Court is aware that all of the New York decisions involving software programs similar to STRmix have found the tests results to be admissible, with one exception that this Court finds distinguishable.

Defendant's primary objection to the admissibility of the results of the DNA testing, advanced in the Memorandum of Law received on February 16, 2016, is that the relevant scientific community for purposes of deciding whether STRmix is accepted is “an insular community of professionals whose careers and livelihoods focus on the prosecution of criminal cases and upon the discovery' of inculpatory evidence.” Defendant urges this Court to “take the warnings of Frye and Leone to heart.” 6 Although the People's proof was limited to the testimony of Dr. Simich and the accompanying exhibits, the Court concludes that his testimony, in conjunction with a number of other factors, supports the admissibility of DNA testing undertaken in this case.

6 Presumably, Defendant is referring to the admonition in People v. Leone, 25 N.Y.2d 511, 518, 307 N.Y.S.2d 430, 255 N.E.2d 696 (1969) that scientific “tests” can have an undue influence on juries and therefore, courts must be “most careful in admitting into evidence the results of such tests unless their reasonable accuracy and general scientific acceptance is clearly recognized.”

First, Dr. Simich was thoroughly familiar with the application of the STRmix software. While he could not expound on the underlying mathematics, his Lab conducted validation studies (People's Exh. 2) and he reviewed numerous articles regarding the software. As noted in Muhammad, the mathematical models are themselves non-controversial and have been widely used in fields such as weather forecasting, computational biology, linguistics, genetics, engineering, physics, aeronautics, finance, and social sciences. As the director of a forensics lab, Dr. Simich is well-qualified to critique software *188 programs like
STRmix. The Court was impressed by his background, education and wealth of practical experience generally on forensic DNA and on the STRmix program specifically. At least one other court has credited Dr. Simich's work on this particular topic (People v. Muhammad, supra). Dr. Simich is, in the Court's opinion, part of the relevant scientific community for Frye purposes.

With all due respect to Dr. Skuse and not in any way to denigrate the intelligence and experience that he so obviously possesses, this Court does not believe that he can be can considered as an expert in the field of forensic DNA analysis in general or on the specific topic of the scientific acceptance of probabilistic genotyping as utilized. 7

7 Having said that, this Court is not making a finding on whether he is qualified as an expert to testify at a jury trial about questions related to DNA in general.

Although the Court would have preferred to hear from other experts in the relevant scientific community, 8 Dr. Simich's testimony cannot be considered in a vacuum. He appeared before the Commission on three occasions. He testified that, following his initial presentation of the Lab's validation studies, he performed additional experiments and reorganized data at the request of the Commission (I–62). At Dr. Simich's second appearance, the Commission required additional work, so he reorganized “all of the material and performed additional studies following the SWGDAM guidelines and then made the final presentation to the DNA Subcommittee in May of 2015” (I–62).

8 For example, in the only case of which the Court is aware that STRmix was the subject of an admissibility hearing, there was testimony from Dr. Simich and Dr. Buckleton, the New Zealand scientist who helped develop STRmix. Some of the other cases reviewed by the Court discussed the testimony of several experts, on both sides of the issue, and thus those courts had the benefit of hearing from a greater portion of the relevant scientific community.

The role of the Commission and the DNA Subcommittee in this Court's decision, while not dispositive, certainly cannot be discounted. In 1994, the Legislature created the Commission (Executive Law Art. 49–B) to “develop minimum standards and a program of accreditation for all forensic laboratories in New York state ... and approval of forensic laboratories for the performance of specific forensic methodologies” (Executive Law § 995–b[1], emphasis added). To achieve its mission, the Commission is designed to “ensure that forensic analyses, including forensic DNA testing, are performed in accordance with the *189 highest scientific standards practicable” (Executive Law § 995–b[2][b] ). Insofar as relevant here, the Commission, “[u]pon the recommendation of the DNA subcommittee ... shall designate one or more approved methodologies for the performance of forensic DNA testing” (Executive Law § 995–b[11] ). Moreover, the Commission is charged with promulgating standards “ for a determination of a match between the DNA records contained in the state DNA identification index and a DNA record of a person submitted for comparison therewith” (Executive Law § 995–b[12] ).
The record establishes that the DNA Subcommittee met on May 29, 2015, and voted unanimously (4–0, with one abstention) “to issue a binding recommendation to the [Commission] that the use of STRmix by [the Lab] be approved for forensic casework” (People's Exhs. 5 and 6). The DNA Subcommittee met again on August 14, 2015, to discuss a June presentation by Dr. Michael Coble at the National College for Forensic Science Litigation on the topic of “Software Systems for Interpreting Low Level Samples and Complex Mixtures” (People's Exh. 7). The letter sent to the Commission following that meeting is informative. It states in relevant part:

The Subcommittee indicated that the presentation addresses some of the challenges involved in handling complex mixtures and some of the advantages of using probabilistic models to aid in interpretation. Subcommittee members agreed that Dr. Coble's presentation substantiates the need to embrace new technologies, especially when challenging mixtures require additional analytical methods to assist in their interpretation. The presentation addressed the benefits of using these software tools and revealed that those laboratories not using deconvolution software tools are at a disadvantage. Members noted that interpretations without the software were “all over the road.”

In sum the Subcommittee members expressed that they are pleased that New York State labs are moving forward to validate these software systems. All Subcommittee members were resolute that the development and use of these software tools is a significant advancement and will greatly assist laboratories in the analysis, interpretation and reporting of DNA mixtures.

The Commission voted on June 19, 2015, to approve the binding recommendation of the DNA Subcommittee.

**723** *190 The Court finds it significant that the DNA Subcommittee, which consists of scientists in various disciplines, voted unanimously to approve STRmix. The DNA Subcommittee consists of scientists in the fields of molecular biology, population genetics, laboratory standards and quality assurance, and forensic science (Executive Law § 995–b[13][a] ). As noted by the court in *People v. Rodriguez* (Sup.Ct., N.Y.Co.2013), “It would be bizarre indeed for a body of such highly accomplished forensic scientists, charged by law with this solemn duty, to recommend software program for use in DNA analysis unless confident that it was firmly based upon principles and methodology accepted as reliable by colleagues in the field.”

In addition to the votes of the bodies appointed by State law to consider the use of various forensic DNA methodologies, the Court is also faced with the almost unanimous approval of the courts that have considered similar software programs. Of course, there is no reported case in New York regarding the admissibility of the STRmix software program, but the Court is persuaded by the analysis of those courts that have reviewed similar programs (see...

Only two of the New York cases are worth discussing in detail. The first is People v. Wakefield, supra, which involved TrueAllele. TrueAllele, like STRmix, involves probabilistic genotyping. The Court recognizes that STRmix and TrueAllele are not identical and in fact Defendant argues that the differences between the two are so significant that the Wakefield decision cannot be used to support a ruling in favor of STRmix. The Court also recognizes that TrueAllele is a competitor of STRmix. 9 Indeed, the Court was advised during its consideration of the scheduling of the Frye hearing that Dr. Perlin might *191 testify on behalf of Defendant. That ultimately did not happen and this Court draws no inference, either favorable or unfavorable, because of the omission.

9 In one of Defendant’s many submissions to the Court, dated November 3, 2015, there is a letter from Dr. Mark W. Perlin, the Chief Scientific and Executive Officer of TrueAllele, to Jerry D. Varnell, Contract Specialist, Procurement Section, Department of Justice, Federal Bureau of Investigation. Dr. Perlin was responding to the FBI’s decision that STRmix was the only software that satisfied its requirements for DNA interpretation technology.

In any event, the court in Wakefield discussed at length the role of the Commission and the DNA Subcommittee, both of which voted to approve TrueAllele, and concluded that “approval” by the Commission and the DNA Subcommittee “clearly constitutes ‘general acceptance’” (Wakefield, 47 Misc.3d at 856, 9 N.Y.S.3d 540). After discussing the expert testimony adduced at the Frye hearing and the legal acceptance of TrueAllele, Judge Coccoma in Wakefield concluded that “computerized probabilistic approaches and likelihood ratio principles” used by TrueAllele “are superior **724 to current methods” (id. at 858, 9 N.Y.S.3d 540). The court stated that there was a “plethora of evidence” in favor of TrueAllele and “there is no significant evidence to the contrary” (id.). The same is true here.

People v. Collins, 49 Misc.3d 595, 15 N.Y.S.3d 564 (Sup.Ct., Kings Co.2015) is the outlier among the forensic DNA software program cases in New York. Collins involved FST, used by OCME. At least two other trial courts, at the time that Collins was decided, had already ruled in favor of FST as being generally accepted in the forensic DNA community. In Collins, the People presented testimony from national experts on DNA forensics and the DNA subcommittee’s vote approving FST. In response, the defendant presented testimony from an expert referred to by the court as “the father of American DNA analysis.” The
court in *Collins* rejected the view of the other courts that had considered whether FST was generally accepted in the relevant scientific community, and minimized the weight given to the DNA Subcommittee's approval of FST. With all due deference to the *Collins* court, this Court does not believe that it is in a position to assess the reliability of STRmix; rather, its role is simply to determine whether the scientific principles behind the STRmix software are accepted generally in the relevant scientific community. That does not mean that there must be unanimity within the scientific community (see *People v. Middleton*, 54 N.Y.2d 42, 49, 444 N.Y.S.2d 581, 429 N.E.2d 100 [1981]).

Additionally, Justice Dwyer's criticism in *Collins* that validation studies are not “conclusive” because they are only *tautological* begs the question. This Court has considered People's Exhibit 2, the Lab's 41–page STRmix Implementation and Internal Validation Study–2015, and finds that it tests the program's assumptions in a variety of ways and that the program properly handles problematic issues such as stutter, drop-in and peak height parameters. Moreover, page 41 of the Study references other validation experiments and tests of the STRmix program and thus supports this Court's conclusion that it has found general acceptance within the relevant scientific community.  

The *Collins* decision was criticized in *People v. Carter*, 50 Misc.3d 1210(A), 2016 WL 239708 (Sup.Ct., Kings Co.2016), the latest case involving FST. The *Carter* court found that there was “a possible lack of objectivity guiding the testimony of several of the defense experts in *Collins*” and that the recommendation of the DNA subcommittee is entitled to greater weight than the court in *Collins* gave it.

The last submission by Defendant, received by the Court on February 16, 2016, perhaps in an attempt to lighten the tone of these otherwise dreary briefs, contains the following quotation from Ernest Rutherford: “If your experiment needs a statistician, you need a better experiment.” 

The analysis of DNA is not an experiment; the science behind it is well-established. All that STRmix, TrueAllele, FST, and others of their kind are doing is improving the ability of forensic labs to confirm or deny the identity of DNA samples, particularly when multiple sources are involved.

In the Court's research to put this quotation in its proper context, it found the quotation to be, “If your experiment needs statistics, you ought to have done a better experiment.” Without impugning the integrity and brilliance of Rutherford, a Nobel Prize winner in Chemistry (although his true field was Physics), the Court makes two points. First, Rutherford died in 1937 and it is unlikely that he could have envisioned the scope and breadth of scientific advances that have been made in the late 20th and early 21st centuries, particularly in the fields of genetics and computing. Second, Rutherford has also been widely quoted for the following: “The energy produced by the breaking down of the atom is a very poor kind of thing. Anyone who expects a source of power from the
transformation of these atoms is talking moonshine.”  
With the advent of supercomputers, the future is already a thing of the past.

*193 Dr. Skuse's chief criticism of STRmix in his testimony does not relate to probabilistic genotyping in general or even to STRmix in particular but to a line in the Lab protocol that “says that STRmix should only be run one time because-well, actually the way it says it is results tend to vary. So each time a sample is analyzed it should only be run once” (III–16). That issue is addressed by Dr. Simich in his cross-examination as follows: there is a different result “if you run the program twice with the same input ... [b]ecause the MCMC process is a random process, and it generates a random number to begin the process every time you do the analysis. So you will get a different likelihood ratio every time you ... put the same data in” (I–114–115).

In a broader and and more general sense, Dr. Skuse countered that “traditional scientists” will do an experiment three times and if the results are “close, you report them ... or you figure out what's wrong and try it again” (III–12).

The Court finds that whether the procedure is performed once as recommended, or three times (or more) as Dr. Skuse seems to suggest, it does not affect the question this Court is called upon to decide, namely, general acceptance of the probabilistic genotyping procedure within the relevant scientific community. Of course, this Court would expect that the statement referred to above would add another arrow in the quiver of defense counsel that would be used to undermine the STRmix results when the issue is presented to the trial jury, but it does not affect the issue of the general acceptance of STRmix within the relevant scientific community.

People v. Muhammad, supra is the only other reported case in the country regarding the admissibility of STRmix. There, the court concluded as a preliminary matter that “statistical evaluation of the DNA analysis's results is a matter of evidentiary weight, not admissibility.” Thus, the court's determination of admissibility falls into the category of dicta. Nonetheless, the court reached several conclusions, which are persuasive insofar as this Court is faced with identical issues. First, the Muhammad court found that STRmix “received adequate validity testing.” Indeed, Dr. Buckleton testified in Muhammad and it was anticipated, based on preliminary representations made to this Court by the People, that he would testify here. His testimony could have resolved several questions *194 raised by the cross-examination testimony of Dr. Simich and the direct testimony of Dr. Skuse. Notwithstanding Dr. Buckleton's failure to testify here, Dr. Simich's testimony was sufficient to meet the People's burden of establishing, by a preponderance of the evidence, that STRmix was generally accepted in the relevant scientific community. Significantly, Dr. Simich testified in Muhammad and that court found his testimony relevant and significant. Dr. Simich reported the results of the Commission and the DNA **726 subcommittee and the Muhammad court discussed those results in a positive light.
In conclusion, the Court would like to commend the parties for their passionate and thorough advocacy on behalf of their respect positions. Contrary to the statement in the last submission by defense counsel, received by the Court on February 16, 2016, the Court does not expect its decision to be “unassailable throughout the state for the remainder of eternity.” The Court is aware that there is a case pending in Erie County, with a Frye hearing scheduled, on this very issue. As other laboratories throughout New York and the country adopt STRmix, courts will deal with the same questions presented here. At oral argument the parties agreed that there were other programs similar to STRmix being used in labs. Dr. Simich testified that he considered several programs before settling on STRmix. This Court's decision is based on the testimony adduced at the hearing, the accompanying exhibits, and the relevant case law. It may be among the first words in New York courts on the admissibility of STRmix, but the Court certainly does not expect it to be the last.

All Citations
54 Misc.3d 177, 42 N.Y.S.3d 714, 2016 N.Y. Slip Op. 26313
IN THE COURT OF APPEAL OF THE STATE OF CALIFORNIA
SECOND APPELLATE DISTRICT
DIVISION FOUR

THE PEOPLE,

Petitioner,

v.

THE SUPERIOR COURT OF
LOS ANGELES COUNTY,

Respondent;

MARTELL CHUBBS,

Real Party in Interest.

Jackie Lacey, District Attorney, Roberta Schwartz and Matthew Brown, Deputy District Attorneys, for Petitioner.
No appearance for Respondent.
Angelyn Gates for Real Party in Interest.
Real party in interest Martell Chubbs was charged in a November 28, 2012 information with the murder of Shelley H. in 1977 (Pen. Code, § 187, subd. (a)). The charge was filed after a DNA sample from the victim was found to be a match for Chubbs. The People petition for a writ of mandate to overturn the order of the superior court compelling the disclosure of a computer source code for software, TrueAllele® Casework (TrueAllele), which was used in the DNA analysis. The People contend that the source code is a protected trade secret of the creator and owner of the software, Mark W. Perlin, and his company, Cybergenetics. We grant the petition.

FACTUAL AND PROCEDURAL BACKGROUND

Preliminary Hearing Evidence

In December 1977, Long Beach Police Department officers found the 17-year-old victim in her Long Beach apartment. She was lying on the end of the bed with her feet touching the ground and with an electrical wire tied around her neck. During an autopsy, swabs were taken from the victim’s vagina and smeared onto slides.

In June 2011, as part of a cold case investigation, Sorenson Forensics (Sorenson) conducted a DNA test on the vaginal swabs from the victim. Sorenson generated a DNA report that indicated three contributors to the DNA: a major sperm DNA profile attributable to an unidentified male, a minor sperm DNA

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1 All unspecified statutory references are to the Penal Code.

2 The People have not included the transcript of the preliminary hearing, instead relying on a declaration from the deputy district attorney who appeared at the preliminary hearing, summarizing the evidence.
Although the record before us does not include the basis for the arrest, Long Beach Police Department detectives arrested Chubbs in August 2012. Chubbs confirmed that he lived in Long Beach in the 1970s.

In September 2012, Sorenson compared the DNA profile of Chubbs, an African-American, to the major sperm DNA profile and found a match. The frequency of the profile occurrence in the general population was determined to be one in approximately 10,000 for African Americans.

At the preliminary hearing in November 2012, Chubbs was held to answer for one count of murder. The information charged Chubbs with one count of murder and alleged six prior convictions of serious felonies (§ 667, subd. (a)(1)) that also qualified as strikes under the Three Strikes law (§§ 667, subds. (b)-(i), 1170.12, subds. (a)-(d)). In January 2013, Chubbs pleaded not guilty to the murder charge.

As part of trial preparation, in September 2013, the People sent the victim’s vaginal slide to Cybergenetics’ lab in Pittsburgh, Pennsylvania for further testing. Cybergenetics prepared a supplemental report, explaining that it had used its TrueAllele software to “infer possible DNA contributor genotypes from the samples,” then compared the evidence genotypes to the reference genotypes (which included Chubbs’ and Hankins’ genotypes) to compute likelihood ratio DNA match statistics. “TrueAllele assumed that the evidence sample data . . . contained two or three contributors, and objectively inferred evidence genotypes solely from these data.” Perlin concluded in the supplemental report that the DNA

3 Hankins is sometimes referred to in the record as the victim’s boyfriend, rather than her husband.
match between the vaginal sperm sample and Chubbs is “1.62 quintillion times more probable than a coincidental match to an unrelated Black person.” Perlin also concluded that the DNA match with Hankins was “2.82 million times more probable than a coincidental match to an unrelated Black person.”

Defense Discovery Efforts

In November 2013, Chubbs made his third informal discovery request, which included the request at issue here, for Cybergenetics’ source codes for TrueAllele. In January 2014, Chubbs filed a motion to compel discovery that included the request for Cybergenetics’ source codes. Defense counsel cited statements in Cybergenetics’ supplemental report indicating that TrueAllele made assumptions and inferences in computing its DNA match statistics. According to defense counsel, the TrueAllele program was “brand new” and had not been the subject of a Kelly hearing, and without the source codes there would be no way to cross examine Perlin about the efficacy and accuracy of the program.4

The defense received several discovery items related to Cybergenetics and TrueAllele, including the following: the September 2013 supplemental report, a November 2013 case packet by Cybergenetics, published articles by Perlin.

4 The three-pronged test established in People v. Kelly (1976) 17 Cal.3d 24 “provides a framework within which courts can analyze the reliability of expert testimony based on new or novel scientific methods or techniques.” (People v. Lucas (2014) 60 Cal.4th 153, 223.) “The first prong requires proof that the technique is generally accepted as reliable in the relevant scientific community. [Citation.] The second prong requires proof that the witness testifying about the technique and its application is a properly qualified expert on the subject. [Citation.] The third prong requires proof that the person performing the test in the particular case used correct scientific procedures.”[Citation.]” (Id. at p. 223, fn. 31.) The test is also known as the Kelly/Frye test. (In re Jordan R. (2012) 205 Cal.App.4th 111, 115, fn. 3; see Frye v. U.S. (D.C. Cir. 1923) 293 F. 1013.)
regarding DNA analysis and the TrueAllele software, a data disc from Sorenson, TrueAllele manuals from March 2014, a data disc from Cybergenetics, and a PowerPoint presentation to be used by Perlin. However, the dispute here focuses on the source codes for TrueAllele, which were not produced.

On January 15, 2014, the People filed an opposition to the motion to compel discovery, arguing that the defense was not entitled to a discovery order because the People had voluntarily complied with their discovery obligations, citing section 1054.5, subdivision (a). As pertinent here, the People explained that they requested the source code from Cybergenetics, but Cybergenetics did not turn it over because it is a trade secret. The People argued that disclosure of the source code would be “financially devastating” to Cybergenetics.

The People stated in their opposition that, although Cybergenetics is unwilling to disclose its source code, it “is willing to conduct additional TrueAllele testing on a limited set of defense-provided data to further defense understanding of the system, its operation and its reliability. Cybergenetics is also willing to meet with defense experts (in person or via an Internet meeting) to show them the results in this case, and explain to them on a TrueAllele computer how the system operates, though Cybergenetics cannot provide [the] defense with a[n] executable version of the TrueAllele casework system which costs $60,000.”

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5 The statute provides: “No order requiring discovery shall be made in criminal cases except as provided in this chapter. This chapter shall be the only means by which the defendant may compel the disclosure or production of information from prosecuting attorneys, law enforcement agencies which investigated or prepared the case against the defendant, or any other persons or agencies which the prosecuting attorney or investigating agency may have employed to assist them in performing their duties.” (§ 1054.5, subd. (a).)
Chubbs then filed an application for an out-of-state subpoena duces tecum, seeking the source codes for the TrueAllele software. He argued that the source codes were essential to his defense because the DNA evidence from the vaginal slide was the only evidence against him. He pointed out the discrepancy between the random match probability calculated by Sorenson (1 in approximately 10,000) and the likelihood ratio calculated by Cybergenetics (1.62 quintillion times more probable than a coincidental match) to argue that the source codes were necessary to cross-examine Perlin about the accuracy of TrueAllele.

In a declaration submitted with the application, defense counsel stated that forensic experts and other attorneys who work with DNA evidence advised her to obtain the source codes for TrueAllele. She stated that “other experts in the field have developed a similar software program as TrueAllele for which their source codes are open for public review.” Defense counsel further stated that Allan Jamieson, an expert in DNA analysis who had experience with TrueAllele, told her that she could not properly defend against the TrueAllele results without the source codes.

Jamieson stated in his declaration that “access to this code is the only satisfactory and professionally recommended way to fully consider the validity of the TrueAllele analysis” in this case. He stated that “[o]ther analysts who have developed computer-assisted DNA comparison software . . . do not hide their source codes” and instead make them freely available, which allows others to fully review and verify the reliability of the method and results in any given case.

Motion to Quash

On May 16, 2014, the People filed a motion to quash the subpoena duces tecum. Contrary to its earlier argument in its opposition to the motion to compel
discovery, the People now argued that Cybergenetics was not a third party to the investigation but instead was an investigatory agency within the meaning of section 1054.5, subdivision (a).

The trial court denied the People’s motion to quash and issued a certificate for an out-of-state subpoena, ordering Perlin to produce the source codes. On June 16, 2014, a Pennsylvania court issued an order directing compliance with the subpoena duces tecum. The Pennsylvania court reasoned that Perlin was a material witness, and the means by which he arrived at his opinions likewise was material. The court thus ordered Perlin to appear with the source codes and stated that any issue regarding the disclosure of trade secrets should be determined by the California court.

The People moved to quash the subpoena duces tecum. The People argued that the materials are a trade secret, that Chubbs has not established the source codes are material or necessary, and that the discovery is not permitted by section 1054, subdivision (e).  

On June 24, 2014, the trial court issued and held a body attachment for Perlin based on his failure to appear pursuant to the subpoena duces tecum. The People subsequently withdrew the contention that Perlin was an expert employed by the prosecution pursuant to subdivision (a) of section 1054.5, noting that Perlin had retained private counsel regarding the trade secret privilege.

Perlin, represented by California counsel, submitted a brief in support of his assertion of the trade secret privilege. The People filed a motion to reconsider the

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6 Section 1054 states that the chapter on discovery “shall be interpreted to give effect to all of the following purposes,” including “[t]o provide that no discovery shall occur in criminal cases except as provided by this chapter, other express statutory provisions, or as mandated by the Constitution of the United States.” (§ 1054, subd. (e).)
court’s May 16 order denying the People’s motion to quash the subpoena duces tecum, and for an order granting the motion and quashing the body attachment held for Perlin.

At a July 29, 2014 hearing, the court ruled the source codes are not necessary pursuant to *Kelly/Frye*, but that Chubbs’ right to confront and cross-examine witnesses required the production of the source codes. The prosecutor again invoked the trade secret privilege on Perlin’s behalf. The court found that nondisclosure of the source codes does “work injustice” in the sense that it denies Chubbs a right to confront and cross-examine witnesses (Evid. Code, § 1060), and that a protective order can protect Perlin’s interest. The court indicated that it would follow the procedure set forth in Evidence Code sections 1061 and 1062, by issuing a protective order and, if needed, excluding the public from the proceedings. The court held the body attachment for Perlin until August 26 and ordered the prosecution to provide the source codes on that date.

On August 26, 2014, the court deemed the TrueAllele source code a trade secret for purposes of the trial. Perlin brought an encrypted form of the source code. However, before turning over the source code, the prosecution raised the issue of a protective order. The court explained that although it would grant a protective order to minimize disclosure of the source code, the source code would be revealed to a certain extent at trial. The People subsequently did not proffer a protective order, but instead refused to turn over the source code. Defense counsel requested the exclusion of the TrueAllele results at trial. The court granted the request based on Chubbs’ rights under the confrontation clause and the fact Perlin was to be a main prosecution witness against Chubb.

The People petitioned for a writ of mandate to this court. We issued an alternative writ of mandate ordering the superior court to vacate the July 29 and
August 26, 2014 orders compelling the disclosure of the computer source codes, or to show cause why a peremptory writ of mandate should not issue. The superior court did not vacate its ruling, and the matter is now before us.

**DISCUSSION**

The People contend that the trial court improperly applied the trade secret privilege and that Chubbs failed to make a prima facie showing sufficient to overcome the privilege. “The court’s ruling on a discovery motion is subject to review for abuse of discretion. [Citation.]” *(People v. Jenkins* (2000) 22 Cal.4th 900, 953.) “A trial court has abused its discretion in determining the applicability of a privilege when it utilizes the wrong legal standards to resolve the particular issue presented. [Citation.]” *(Seahaus La Jolla Owners Assn. v. Superior Court* (2014) 224 Cal.App.4th 754, 766.)

We begin by setting forth the statutes and law regarding the trade secret privilege.

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7 We further issued a temporary stay of the trial.

8 We disagree with Chubbs’ contention that the trial court’s ruling was an evidentiary ruling not subject to writ review. Although the trial court’s ultimate ruling was to exclude the TrueAllele evidence, this was based on the People’s refusal to disclose the source codes. “Extraordinary review of a discovery order will be granted when a ruling threatens immediate harm, such as loss of a privilege against disclosure, for which there is no other adequate remedy. [Citation.]” [W]here the petitioner seeks relief from a discovery order that may undermine a privilege, we review the trial court’s order by way of extraordinary writ. [Citation.]” *(Doe v. Superior Court* (2011) 194 Cal.App.4th 750, 754; see also § 1512, subd. (a) [authorizing the people to seek review of an order granting a defendant’s motion for discovery by a petition for a writ of mandate]; *People v. Superior Court (Mouchaourab)* (2000) 78 Cal.App.4th 403, 413 [“writ review is appropriate when the petitioner ‘seeks relief from a discovery order which may undermine a privilege, because appellate remedies are not adequate once the privileged information has been disclosed’”].)
I. **Trade Secret Privilege**

Evidence Code section 1060 provides: “If he or his agent or employee claims the privilege, the owner of a trade secret has a privilege to refuse to disclose the secret, and to prevent another from disclosing it, if the allowance of the privilege will not tend to conceal fraud or otherwise work injustice.” In the instant case, it is undisputed that the source codes in issue constitute a trade secret. (See Evid. Code, § 1062, subd. (a) [for purposes of Evidence Code sections 1061, 1062, and 1063, which apply to criminal cases, “[t]rade secret” is defined in Civil Code section 3426.1 or Penal Code section 499c, subdivision (a)(9)].)

In civil cases, a burden-shifting procedure is used to evaluate assertion of the trade secret privilege. Based on the language and legislative history of Evidence Code section 1060, the court in *Bridgestone/Firestone, Inc. v. Superior Court* (1992) 7 Cal.App.4th 1384 (*Bridgestone*) held that “the party claiming the [trade secret] privilege has the burden of establishing its existence. [Citations.] Thereafter, the party seeking discovery must make a prima facie, particularized showing that the information sought is relevant and necessary to the proof of, or defense against, a material element of one or more causes of action presented in the case, and that it is reasonable to conclude that the information sought is essential to a fair resolution of the lawsuit. It is then up to the holder of the privilege to demonstrate any claimed disadvantages of a protective order.” (*Id.* at p. 1393; see also *Raymond Handling Concepts Corp. v. Superior Court* (1995) 39 Cal.App.4th 584, 590-591 [relying on the procedure enunciated in *Bridgestone* and concluding that the information was discoverable and that the trial court did not abuse its discretion in entering a protective order].)
Chubbs contends that when a defendant in a criminal case seeks disclosure of an item meeting the definition of a trade secret, Evidence Code section 1060 does not permit the owner of the trade secret to refuse to disclose. Rather, according to Chubbs, Evidence Code sections 1061 and 1062 supersede section 1060, and authorize only (on a proper showing) the remedy of a protective order (§ 1062) and exclusion of the public from portions of the trial at which a trade secret might be revealed (§ 1062). Evidence Code section 1061 provides: “In addition to Section 1062, the following procedure shall apply whenever the owner of a trade secret wishes to assert his or her trade secret privilege, as provided in Section 1060, during a criminal proceeding.” (Evid. Code, § 1061, subd. (b).) The statute then sets forth a procedure under which the holder of the trade secret privilege or an authorized representative may move for a protective order (Evid. Code, § 1061, subd. (b)(1)), any party to the proceeding may oppose the motion (id., subd. (b)(2)), and the court, on a finding “that a trade secret may be disclosed . . . unless a protective order is issued and that the issuance of a protective order would not conceal a fraud or work an injustice, . . . issue[s] a protective order limiting the use and dissemination of the trade secret” (id., subd. (b)(4)).

Evidence Code section 1061 provides in relevant part: “(b) In addition to Section 1062, the following procedure shall apply whenever the owner of a trade secret wishes to assert his or her trade secret privilege, as provided in Section 1060, during a criminal proceeding:

“(1) The owner of the trade secret shall file a motion for a protective order, or the people may file the motion on the owner’s behalf and with the owner’s permission. The motion shall include an affidavit based upon personal knowledge listing the affiant’s qualifications to give an opinion concerning the trade secret at issue, identifying, without revealing, the alleged trade secret and articles which disclose the secret, and presenting evidence that the secret qualifies as a trade secret under either subdivision (d) of Section 3426.1 of the Civil Code or paragraph (9) of subdivision (a) of Section 499c of the Penal Code. The motion and affidavit shall be served on all parties in the proceeding.
“(2) Any party in the proceeding may oppose the request for the protective order by submitting affidavits based upon the affiant’s personal knowledge. The affidavits shall be filed under seal, but shall be provided to the owner of the trade secret and to all parties in the proceeding. Neither the owner of the trade secret nor any party in the proceeding may disclose the affidavit to persons other than to counsel of record without prior court approval.

“(3) The movant shall, by a preponderance of the evidence, show that the issuance of a protective order is proper. The court may rule on the request without holding an evidentiary hearing. However, in its discretion, the court may choose to hold an in camera evidentiary hearing concerning disputed articles with only the owner of the trade secret, the people’s representative, the defendant, and defendant’s counsel present. If the court holds such a hearing, the parties’ right to examine witnesses shall not be used to obtain discovery, but shall be directed solely toward the question of whether the alleged trade secret qualifies for protection.

“(4) If the court finds that a trade secret may be disclosed during any criminal proceeding unless a protective order is issued and that the issuance of a protective order would not conceal a fraud or work an injustice, the court shall issue a protective order limiting the use and dissemination of the trade secret, including, but not limited to, articles disclosing that secret. The protective order may, in the court’s discretion, include the following provisions:

“(A) That the trade secret may be disseminated only to counsel for the parties, including their associate attorneys, paralegals, and investigators, and to law enforcement officials or clerical officials.

“(B) That the defendant may view the secret only in the presence of his or her counsel, or if not in the presence of his or her counsel, at counsel’s offices.

“(C) That any party seeking to show the trade secret, or articles containing the trade secret, to any person not designated by the protective order shall first obtain court approval to do so:

“(i) The court may require that the person receiving the trade secret do so only in the presence of counsel for the party requesting approval.

“(ii) The court may require the person receiving the trade secret to sign a copy of the protective order and to agree to be bound by its terms. The order may include a
Evidence Code section 1062 similarly provides a procedure under which “the court, upon motion of the owner of a trade secret, or upon motion by the People with the consent of the owner, may exclude the public from any portion of a criminal proceeding where the proponent of closure has demonstrated a substantial probability that the trade secret would otherwise be disclosed to the public during that proceeding and a substantial probability that the disclosure would cause serious harm to the owner of the secret, and where the court finds that there is no provision recognizing the owner of the trade secret to be a third-party beneficiary of that agreement.

“(iii) The court may require a party seeking disclosure to an expert to provide that expert’s name, employment history, and any other relevant information to the court for examination. The court shall accept that information under seal, and the information shall not be disclosed by any court except upon termination of the action and upon a showing of good cause to believe the secret has been disseminated by a court-approved expert. The court shall evaluate the expert and determine whether the expert poses a discernible risk of disclosure. The court shall withhold approval if the expert’s economic interests place the expert in a competitive position with the victim, unless no other experts are available. The court may interview the expert in camera in aid of its ruling. If the court rejects the expert, it shall state its reasons for doing so on the record and a transcript of those reasons shall be prepared and sealed.

“(D) That no articles disclosing the trade secret shall be filed or otherwise made a part of the court record available to the public without approval of the court and prior notice to the owner of the secret. The owner of the secret may give either party permission to accept the notice on the owner’s behalf.

“(E) Other orders as the court deems necessary to protect the integrity of the trade secret.

“(c) A ruling granting or denying a motion for a protective order filed pursuant to subdivision (b) shall not be construed as a determination that the alleged trade secret is or is not a trade secret as defined by subdivision (d) of Section 3426.1 of the Civil Code or paragraph (9) of subdivision (a) of Section 499c of the Penal Code. Such a ruling shall not have any effect on any civil litigation.”
overriding public interest in an open proceeding. No evidence, however, shall be excluded during a criminal proceeding pursuant to this section if it would conceal a fraud, work an injustice, or deprive the People or the defendant of a fair trial.”

(Evid. Code, § 1062, subd. (a).)\textsuperscript{10}

\textsuperscript{10} Section 1062 provides in full: “(a) Notwithstanding any other provision of law, in a criminal case, the court, upon motion of the owner of a trade secret, or upon motion by the People with the consent of the owner, may exclude the public from any portion of a criminal proceeding where the proponent of closure has demonstrated a substantial probability that the trade secret would otherwise be disclosed to the public during that proceeding and a substantial probability that the disclosure would cause serious harm to the owner of the secret, and where the court finds that there is no overriding public interest in an open proceeding. No evidence, however, shall be excluded during a criminal proceeding pursuant to this section if it would conceal a fraud, work an injustice, or deprive the People or the defendant of a fair trial.

“(b) The motion made pursuant to subdivision (a) shall identify, without revealing, the trade secrets which would otherwise be disclosed to the public. A showing made pursuant to subdivision (a) shall be made during an in camera hearing with only the owner of the trade secret, the People’s representative, the defendant, and defendant’s counsel present. A court reporter shall be present during the hearing. Any transcription of the proceedings at the in camera hearing, as well as any articles presented at that hearing, shall be ordered sealed by the court and only a court may allow access to its contents upon a showing of good cause. The court, in ruling upon the motion made pursuant to subdivision (a), may consider testimony presented or affidavits filed in any proceeding held in that action.

“(c) If, after the in camera hearing described in subdivision (b), the court determines that exclusion of trade secret information from the public is appropriate, the court shall close only that portion of the criminal proceeding necessary to prevent disclosure of the trade secret. Before granting the motion, however, the court shall find and state for the record that the moving party has met its burden pursuant to subdivision (b), and that the closure of that portion of the proceeding will not deprive the People or the defendant of a fair trial.

“(d) The owner of the trade secret, the People, or the defendant may seek relief from a ruling denying or granting closure by petitioning a higher court for extraordinary relief.
Although Chubbs does not expressly acknowledge it, an implicit premise of his contention seeking disclosure of the source codes is that a criminal defendant need not make a prima facie showing of the relevance and necessity of the trade secret before disclosure occurs. Rather, upon a defense request for material that qualifies as a trade secret, the holder of the trade secret privilege cannot object on the ground that no showing of relevance and necessity has been made. To the contrary, the privilege holder’s only remedies, even for material as to which there is no relevance and necessity, are to seek a protective order limiting the terms of disclosure (but not precluding disclosure) under Evidence Code section 1061, and closing the proceedings at which the trade secret might be disclosed under Evidence Code section 1062.

We decline to read Evidence Code sections 1061 and 1062 in such a manner. In short, it makes no sense to require the holder of a trade secret privilege to submit to disclosure of the trade secret, even subject to a protective order and the closing of certain proceedings, without a showing that the trade secret is relevant and necessary to the defense. (See People v. Superior Court (Barrett) (2000) 80 Cal.App.4th 1305, 1318 [“A criminal defendant has a right to discovery by a subpoena duces tecum of third party records on a showing of good cause -- that is, specific facts justifying discovery.”].) We thus conclude that the test for trade

“(e) Whenever the court closes a portion of a criminal proceeding pursuant to this section, a transcript of that closed proceeding shall be made available to the public as soon as practicable. The court shall redact any information qualifying as a trade secret before making that transcript available.

“(f) The court, subject to Section 867 of the Penal Code, may allow witnesses who are bound by a protective order entered in the criminal proceeding protecting trade secrets, pursuant to Section 1061, to remain within the courtroom during the closed portion of the proceeding.”
secret disclosure adopted in Bridgestone -- a prima facie, particularized showing that the source code is relevant and necessary to the defense -- is required for Chubbs to require disclosure of the source codes.

The trial court here correctly began with a determination under Evidence Code section 1060 that the source code is a trade secret and then moved to the issue of a protective order pursuant to Evidence Code section 1061. However, because we find that Chubbs did not meet his prima facie burden for disclosure, we conclude that the People should not have been compelled to produce the source code, whether or not subject to a protective order.

II. Chubbs’ Evidence Regarding Necessity of Source Code

Chubbs submitted declarations from defense counsel and Jamieson to support his contention that the source code is essential to his defense. Defense counsel relied on the fact that the DNA evidence was the only evidence connecting Chubbs to the victim.

Defense counsel further declared that without the source code, “there is no way for my expert to determine what assumptions, among other things, have been made and if they are appropriate in this particular case.” In her application for the subpoena duces tecum, she declared that her DNA experts, another forensic DNA consultant (who has helped develop a program similar to TrueAllele with source codes open for public review), and unidentified attorneys “who focus on DNA

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11 Chubbs attached to his return a declaration from Dr. Travis Doom regarding the necessity of the source codes. We decline to consider the declaration because it was not submitted to the trial court. (See Pomona Valley Hospital Medical Center v. Superior Court (2013) 213 Cal.App.4th 828, 835, fn. 5 [“Writ review does not provide for consideration of evidence not before respondent court at the time of its ruling.”].)
evidence regarding TrueAllele” advised her to request the source codes and pseudo
source codes.

In Jamieson’s declaration, he claimed ten years of forensic experience, as
well as familiarity with TrueAllele’s “claimed methodology and use” and
“experience” in court with TrueAllele. He opined that “access to this code is the
only satisfactory and professionally recommended way to fully consider the
validity of the TrueAllele analysis” in this case. He claimed that others who have
developed computer-assisted DNA comparison software “do not hide their source
codes” and instead make them freely available, which allows others to fully review
and verify the reliability of the method and results in any given case.

In considering whether Chubbs has made a prima facie showing of the
necessity of the source code to his defense, we consider not only Chubbs’ evidence
but also Perlin’s declaration, which was submitted in support of the People’s
motion to quash the subpoena duces tecum. (See Bridgestone, supra, 7
Cal.App.4th at p. 1395 [“while the burden of making a prima facie showing of the
particularized need for a trade secret is on the party seeking discovery, the trial
court need not ignore evidence presented by the opposing party on the question
whether the information sought is a trade secret”].)

Perlin explained that TrueAllele is useful when uncertainty in DNA analysis
arises, such as when two or more people contribute to the evidence, and it
decreases uncertainty by comparing information to a suspect. TrueAllele is
“Cybergenetics’ computer implementation of [a] two-step DNA identification
inference approach.” This process involves, first, “objectively inferring genotypes
from evidence data, accounting for allele pair uncertainty using probability,” and
“subsequently matching genotypes, comparing evidence with a suspect relative to a
population, to express the strength of association using probability.”
Perlin declared that TrueAllele is widely accepted, having been used in approximately 200 criminal cases in courts in California, Pennsylvania, and Virginia, and it has been subjected to numerous validation studies, five of which were published in peer-reviewed scientific journals.

Perlin explained that software source code is the programming language used to write a computer program. The source code “details step-by-step human-readable instructions that describe to the computer and programmers how the program operates,” and is “translated into computer-readable ‘executable’ software.” He stated that TrueAllele has about 170,000 lines of computer source code and opined that reading through the source code would not yield meaningful information.

As to the proprietary nature of the source code, Perlin explained that others “can easily copy a computer program if they have its source code,” which “contains the software design, engineering know-how, and the algorithmic implementation of the entire computer program.” Cybergenetics has invested millions of dollars over 20 years to develop TrueAllele, which it offers to crime labs for a base license fee of $60,000.

Perlin differentiated TrueAllele from the open source DNA analysis software programs referenced in the declarations of defense counsel and Jamieson, stating that open source programs “typically are not validated prior to release, because the process of perfecting software is costly.” In addition, open source forensic programs “tend to be relatively short programs consisting of several hundreds of lines of code,” in contrast to the 170,000 lines of code in TrueAllele.

Cybergenetics accordingly has never disclosed the source code to anyone outside the company and does not distribute it to businesses or government agencies that license the software. Cybergenetics does, however, disclose
TrueAllele’s methodology and its “underlying mathematical model” to enable others to understand its genotype modeling mechanism. The company “provides opposing experts the opportunity to review the TrueAllele process, examine results, and ask questions.”

Cybergenetics keeps the source code secret because of the “highly competitive commercial environment” in which it operates. Perlin declared that Cybergenetics’ competitors are interested in replicating TrueAllele and that disclosure of the source code would enable its competitors to copy the product, causing the company irreparable harm. Perlin believed that source code is not revealed for other commercial forensic DNA software because the source code is not needed to assess the software programs’ reliability.

Jamieson’s general statement that a criminal defendant cannot “receive a diligent and fair verification of a DNA testing or analysis method” without the source codes does not address Perlin’s explanations of what the source code actually is and why it is not needed to test the methodology or reliability of TrueAllele’s analysis. Jamieson also generally states that access to the source code is the only way to consider the validity of the TrueAllele analysis in Chubbs’ case, but he does not explain how access to the source code would allow him to test the reliability of TrueAllele’s analysis. (See Bridgestone, supra, 7 Cal.App.4th at p. 1396 [“nowhere did [the real parties’ expert] describe with any precision how or why the [trade secret] formulas were a predicate to his ability to reach conclusions in the case”].)

Similarly, defense counsel generally states in her declaration that others have told her she needs to request the source codes and that there is “no way [she] can properly prepare to defend against the TrueAllele results without the source codes and pseudo source codes.” However, these general declarations do not address
why the source code is needed to review the reliability of the TrueAllele analysis, how the source code would be used to review the TrueAllele results, or what could be revealed by the source codes that would be useful to Chubbs’ defense. Indeed, her declarations regarding TrueAllele’s methodology, inferences, and reliance on the likelihood ratio rather than the random match probability illustrate her understanding of TrueAllele and thus undercut her argument that the source codes are necessary to understanding TrueAllele. This is particularly true in light of the fact that defense counsel received the patent documents regarding TrueAllele, numerous published articles regarding TrueAllele, and TrueAllele operating manuals. Further supporting the position that the source code is not necessary to an understanding of TrueAllele is Perlin’s statement in his declaration that Cybergenetics discloses to opposing experts TrueAllele’s methodology, how it applies its method to the data, and how the software works. The supplemental report prepared by Cybergenetics also explained the assumptions made by TrueAllele in its analysis. The vague statements by defense counsel and Jamieson do not describe in any way how the source code would have any bearing on the reliability of the analysis.

In his declaration, Perlin cited Commonwealth v. Foley (Pa. Super. 2012) 38 A.3d 882, in which the Superior Court of Pennsylvania held that the trial court did not abuse its discretion in admitting Perlin’s DNA-related testimony. (Id. at p. 890.) Although this out-of-state case does not carry precedential weight, we agree with its conclusion that access to TrueAllele’s source code is not necessary to judge the software’s reliability. Similar to Chubbs’ case, Perlin’s estimate of the probability of a DNA match to the defendant in Foley was much higher (1 in 189 billion) than the estimates of the other scientific experts (1 in 13,000 and 1 in 23 million). (See id. at p. 887.) As pertinent here, the Pennsylvania court rejected the
defendant’s argument that Perlin’s testimony should have been excluded, reasoning that “scientists can validate the reliability of a computerized process even if the ‘source code’ underlying that process is not available to the public. TrueAllele is proprietary software; it would not be possible to market TrueAllele if it were available for free. [Citation.]” (Id. at p. 889.) The court further reasoned that TrueAllele “has been tested and validated in peer-reviewed studies,” citing several papers that “were published in peer-reviewed journals” and thus “reviewed by other scholars in the field.” (Id. at pp. 889-890.)

“[I]t is not enough that a trade secret might be useful to real parties.” (Bridgestone, supra, 7 Cal.App.4th at p. 1395.) Instead, “the party seeking discovery must make a prima facie, particularized showing that the information sought is relevant and necessary to the proof of, or defense against, a material element of one or more causes of action presented in the case, and that it is reasonable to conclude that the information sought is essential to a fair resolution of the lawsuit.” (Id. at p. 1393.) Chubbs has received extensive information regarding TrueAllele’s methodology and underlying assumptions, but he has not demonstrated how TrueAllele’s source code is necessary to his ability to test the reliability of its results. We therefore conclude that Chubbs has not made a prima facie showing of the particularized need for TrueAllele’s source code.

III. **Right to Confront Witnesses**

The trial court relied on Chubbs’ constitutional right to confrontation to conclude that the People were required to produce the source code. However, our state supreme court has stated, “invocation of the confrontation or compulsory process clauses in a claim involving pretrial discovery ‘is on weak footing’ because it is unclear whether or to what extent those constitutional guarantees
grant pretrial discovery rights to a defendant. [Citations.]” (People v. Clark (2011) 52 Cal.4th 856, 982-983; see also People v. Hammon (1997) 15 Cal.4th 1117, 1126 [examining United States Supreme Court precedent and concluding, “it is not at all clear ‘whether or to what extent the confrontation or compulsory process clauses of the Sixth Amendment grant pretrial discovery rights to the accused’”] (Hammon).)

“In [Hammon], the Supreme Court held the trial court properly quashed a subpoena duces tecum the defendant served on psychotherapists treating the alleged victim without first conducting an in camera review of the material. ‘[R]eject[ing the] defendant’s claim that pretrial access to such information was necessary to vindicate his federal constitutional rights to confront and cross-examine the complaining witness at trial or to receive a fair trial’ [citation], Hammon held ‘the trial court was not required, at the pretrial stage of the proceedings, to review or grant discovery of privileged information in the hands of third party psychotherapy providers’ [citation].” (People v. Petronella (2013) 218 Cal.App.4th 945, 958 (Petronella).)

Hammon reasoned that United States Supreme Court precedent addressing a criminal defendant’s right under the confrontation clause to information protected by state-created evidentiary privileges applied to a defendant’s trial rights, not pretrial rights. (Hammon, supra, 15 Cal.4th at pp. 1123-1127.) The court further reasoned that, “[w]hen a defendant proposes to impeach a critical prosecution witness with questions that call for privileged information, the trial court may be called upon . . . to balance the defendant’s need for cross-examination and the state policies the privilege is intended to serve. [Citation.] Before trial, the court typically will not have sufficient information to conduct this inquiry; hence, if pretrial disclosure is permitted, a serious risk arises that privileged material will be
disclosed unnecessarily.” (Id. at p. 1127.) The court thus “decline[d] to extend the defendant’s Sixth Amendment rights of confrontation and cross-examination to authorize pretrial disclosure of privileged information.” (Id. at p. 1128.)

Similarly, *Petronella* concluded that the trial court’s pretrial ruling upholding a privilege claim against the defendant’s subpoena did not violate the defendant’s constitutional rights to confrontation and due process. (*Petronella*, supra, 218 Cal.App.4th at pp. 958-959.) Pursuant to *Hammon* and *Petronella*, we conclude that Chubbs’ right to confrontation does not apply to pretrial discovery of the source code, which is privileged information.

Chubbs relies on the concurring and dissenting opinions in *Pennsylvania v. Ritchie* (1987) 480 U.S. 39 (*Ritchie*) to argue that the confrontation clause applies to pretrial discovery. However, *Hammon* specifically addressed *Ritchie* in concluding that the Sixth Amendment right to confrontation did not confer a right to discover privileged information before trial. (*Hammon*, supra, 15 Cal.4th at pp. 1125-1127.) We therefore conclude that the trial court abused its discretion in relying on the confrontation clause to order disclosure of the TrueAllele source codes.
DISPOSITION

Let a peremptory writ of mandate issue directing respondent court to vacate its order compelling disclosure of the source code, and to issue a new order denying the motion to compel discovery.

NOT TO BE PUBLISHED IN THE OFFICIAL REPORTS

WILLHITE, J.

We concur:

EPSTEIN, P. J.

MANELLA, J.
2015 WL 5665920 (Cal.) (Appellate Brief)
Supreme Court of California.

Martell CHUBBS, Petitioner,

v.

SUPERIOR COURT OF LOS ANGELES COUNTY, Respondent,

No. S228995.
September 22, 2015.

Original Proceedings Los Angeles County Superior Court
The Honorable Richard R. Romero, Judge Presiding
2d Dist. No. B264911
LASC No. Na093179

Answer to Petition for Review

Jackie Lacey, District Attorney of Los Angeles County, Phyllis C. Asayama, Deputy District Attorney, State Bar No. 88919, Matthew Brown, Deputy District Attorney, State Bar No. 238867, Appellate Division, 320 West Temple Street, Suite 540, Los Angeles, California 90012, (213) 893-0238, (213) 217-9112 fax, for real party in interest.

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*6
Petitioner Martell Chubbs seeks the source code for TrueAllele® Casework (TrueAllele), which was a program used to analyze DNA evidence in his case. This petition is just the latest salvo in his nearly two-year obsession with obtaining the TrueAllele source code - which is a protected trade secret - even though it is not necessary to understand the DNA evidence in his case. The trial court denied his request, the Court of Appeal summarily denied his writ petition, and this Court should deny review.

First, extraordinary relief is not proper. There is no novel question of law because the Court of Appeal addressed the same issue on a prior writ petition in Chubbs's case. He did not petition for review of that decision, and there is no need for the same court to revisit it. Also, Chubbs has not provided an adequate record for review because he omitted TrueAllele materials shown to the lower court. The lower court denied his discovery request, in part, because these materials were adequate to understand how the program worked. Since he failed to provide important materials, his petition should be denied.

Second, on the merits Chubbs's claim also fails. California provides a privilege for trade secrets, and the court may only order discovery based on *necessity*, not mere relevance. Here, Chubbs already has the step-by-step methodology behind TrueAllele, the raw data in his case, and several validation studies that have been published in peer-reviewed scientific journals. On top of this, the creator of TrueAllele has offered to further explain the program to Chubbs's experts, and answer questions. The source code would not add anything that these resources do not already provide.

Third, disclosing the TrueAllele source code poses several practical problems, none of which Chubbs addresses. For example:

- How long would it take to analyze the approximately 170,000 lines of code, which were developed over two decades?

- How much would this analysis cost, since the program took millions of dollars to develop into its current form?

- Would the court pay for this (presumably) expensive and lengthy analysis?

- Would the current defense expert, Dr. Doom, conduct the analysis? If so, does Dr. Doom's interest in developing other DNA software pose a conflict of interest?

- Chubbs has proposed no procedure for analyzing the code, so would the trade secret be protected?
Are the People even required to provide the code under the criminal discovery statutes, since the code is owned by a Pennsylvania corporation that the People do not have the right to control?

Similarly, should the trade secret issue be decided in California or Pennsylvania?

Since he fails to address these practical concerns, there is no way to know if analyzing the source code could yield results in a reasonable time and at a reasonable expense when compared with Chubbs's other options.

In short, Chubbs has pursued the TrueAllele source code with a quixotic obsession, and has ignored the ample materials available to him. Since he has not demonstrated that the code is necessary to his case, nor that it could practically be analyzed, his request has properly been denied at all stages, and the Court should deny this petition for review.

*8 STATEMENT OF THE CASE AND FACTS

This is a cold case murder from 1977. The victim, Shelly H., was murdered in her own home. Vaginal swabs taken at the time were analyzed for DNA evidence in 2011 by Sorenson Forensics. Initially, the analysis indicated three profiles: a major sperm DNA profile for an unknown male, a minor sperm DNA profile, and a partial DNA profile attributable for the victim. Nolan Hankins, variously described as the victim's husband or boyfriend, was excluded as the source of the major profile.

In 2012, Sorenson Forensics matched the major profile to Chubbs, but with a low probability: the profile occurred in approximately one in every 10,000 African Americans. Chubbs was charged with murder, and held to answer based primarily on this DNA evidence.

In 2013, the People had the DNA profiles analyzed by a Pennsylvania company, Cybergenetics, using their proprietary TrueAllele software. The primary advantage of a program like TrueAllele is that it is able to more accurately infer individual genotypes from DNA mixtures than a human analyst. Here, TrueAllele was able to make a much stronger probability match to Chubbs as the major profile contributor: 1.62 quintillion times more likely than a random match to an unrelated African American person. To date, the People have provided extensive TrueAllele discovery to Chubbs: a
case packet for Chubbs's case, a PowerPoint presentation explaining the analysis, a CD containing TrueAllele's manuals and procedures, and several articles and validation studies on TrueAllele. (Exh. D, pp. 64-65.) Chubbs included none of these materials with his writ petition.

Starting in November of 2013, Chubbs began making discovery requests for the TrueAllele source code. (Exh. B, p. 6.) Source code is the human-readable instructions for a computer program, which is then compiled into computer-readable executable software. (Id. at p. 20.) In addition to requesting the code from the People, Chubbs also issued an out-of-state subpoena duces tecum for Dr. Mark Perlin, the creator of TrueAllele. (Id. at p. 8.) The trial court initially granted Chubbs's request and ordered disclosure of the source code, and then excluded the TrueAllele result from evidence when Dr. Perlin refused. (Id. at p. 10.) This order was then reversed by the Court of Appeal in case B258569 based on the trade secret privilege. (Id. at pp. 23, 25.) Chubbs did not petition for review of that decision.

In April of 2015, Chubbs made a second request for the TrueAllele source code, citing only Penal Code section 1054.1. (Exh. C, pp. 27, 42.) The motion contained a declaration from Dr. Travis Doom, a computer science professor who is also familiar with forensic DNA testing. (Id. at p. 50.) He posited that the source code was necessary to evaluate what TrueAllele did. (See ibid.) Dr. Doom's declaration did not state that he reviewed any of the TrueAllele materials previously provided to Chubbs. Chubbs's motion did not state that Dr. Perlin has refused discovery of any information related to TrueAllele's methodology.

The People filed a written motion opposing the second discovery request. (Exh. D, p. 62.) The motion listed the discovery that had already been provided regarding TrueAllele. (See id. at pp. 64-65.) The motion once again asserted that the TrueAllele source code was a protected trade secret, and that Chubbs had failed to demonstrate disclosure was necessary. (Id. at pp. 66, 67.)

The opposition included a declaration from Dr. Perlin. (Exh. D, p. 78.) He described TrueAllele as a “probabilistic genotyping computer system that interprets DNA evidence using a statistical model.” (Id. at p. 79.) Its reliability has been tested in over twenty validation studies, five of which have been published in peer-reviewed scientific journals. (Id. at p. 81.) In addition, regulators in New York and Virginia had independent scientists review the validations before approving TrueAllele for use in those states. (Ibid.) Moreover, Cybergenetics allows experts to review TrueAllele's process, examine the results, and ask questions. (Id. at p. 84.) Anybody can obtain TrueAllele validation data to assess its reliability. (Id. at p. 85.)

Dr. Perlin also explained what source code is. (See Exh. D, p. 82.) Source code is the language used to write computer programs, which is then translated into something the computer can execute. (Ibid.) TrueAllele is written in MATLAB, “a high level mathematical language for programming
and visualizing numerical algorithms.” *(Ibid.)* For example, the following lines of code program a Metropolis-Hastings statistical sampling:

\[
U = \log(\text{rand}(\text{nchain},\text{nsamples}));
\]

for \( i = 1: \text{burnin} : \text{nsamples} \)

\[y = \text{proprnd}(x0);\]

\[q1 = \log\text{proppdf}(x0,y);\]

\[q2 = \log\text{proppdf}(y,x0);\]

\[\rho = (q1??(y))-(q2??(x0));\]

\[U_i = U(:,i??);\]

\[\text{acc} = U_i <= \text{min}(\rho,0);\]

\[x0(\text{acc},:) = y(\text{acc},:);\]

\[\text{accept} = \text{accept}(\text{acc});\]

end

*(Ibid.)* TrueAllele contains around 170,000 lines of code, written over two decades by multiple programmers. *(Id. at p. 83.)* Source code is therefore technically in a form that people can understand, but only if fluent in the *MATLAB* programming language. *(Id. at p. 82.)* Dr. Perlin estimates that it could take hours to decipher a few dozen lines of MATLAB code. *(Id. at p. 83.)*

Cybergenetics protects TrueAllele as a trade secret. TrueAllele represents a technological breakthrough that has yet to be replicated in full by any other company. *(Exh. D, p. 83.)* The source code has never been disclosed to the public. *(Id. at p. 84.)* Disclosing its source code would let others copy the program more easily, and would damage Cybergenetics' business. *(Id. at p. 83.)* This is the norm for commercial software, including several programs used for forensic DNA identification. *(Id. at p. 85.)* Examples include Life Technology’s “Genemapper ID,” the FBI's “Popstats,” and Microsoft Excel. *(Ibid.)*

Although the source code is not public, the methodology behind TrueAllele is disclosed. *(Exh. D, p. 85.)* The core mathematics have been published for over 10 years. *(Ibid.)* Based on this, at leave
five other groups have developed software using TrueAllele's method. (Ibid.) The source code is therefore not necessary to understand how TrueAllele works, or to assess its reliability. (Ibid.)

In addition to the declaration from Dr. Perlin, the People's opposition attached news releases showing that Dr. Doom also had an interest in developing his own DNA software. He, along with Dan Krane and Dr. Michael Raymer, have developed Genophiler, a program that interprets the automated DNA analysis generated by crime labs. (Exh. D, p. 104.) Dr. Doom's declaration did not mention this potential conflict of interest.

The court heard arguments on April 23, 2015. (Exh. E, p. 110.) The People showed the court the raw data provided by Cybergenetics. (Id. at p. 140.) After perusing some of this material, the court remarked, “I didn't realize you had all this material. I thought all they had was that little two-page report that's really bare bones.” (Id. at p. 140:26-28.) After being shown a PowerPoint that Dr. Perlin intended to use at trial, the court again remarked:

Ms. Gates [Chubbs's attorney], I didn't realize all this was available. It sounds to me like, it's not a definitive ruling, but you don't need the source code. The data is here. Your experts can dispute whether this can be done or it is inaccurate. The Court of Appeals has imposed or set forth -- I shouldn't say imposed -- set forth a rather stringent standard here.

(Exh. E, p. 144:7-13.) Despite the impression made on the court, Chubbs did not include any of these materials with his writ petition.

The People also emphasized that Dr. Doom's declaration failed to point out any errors in TrueAllele that the code could help resolve. (Exh. E, p. 155.) Providing the source code would just lead to a fishing expedition. (Ibid.) Ultimately, the court denied the request for the source code:

I am sympathetic to the argument made by Chubbs, but I don't believe the particularized need has been shown here. It is a wish list. The request for discovery of the source [code] is denied.

(Exh. E, p. 163:17-20.)

Chubbs filed a petition for writ of mandate in the Court of Appeal on June 18, 2015, which was summarily denied on August 20. He filed this petition for review on September 1.

ARGUMENT
I PRETRIAL REVIEW IS NOT APPROPRIATE SINCE THE COURT OF APPEAL PREVIOUSLY DECIDED THE NOVEL LEGAL QUESTION, AND CHUBBS DID NOT PROVIDE AN ADEQUATE RECORD HERE

Although technically reviewable, Chubbs's writ petition does not present a novel legal issue, nor has he demonstrated irreparable harm from the denial of his motion. His writ petition was properly denied.

“Interlocutory review of a discovery order on a petition for writ of mandate is appropriate if the ruling threatens immediate harm for which there is no other adequate remedy.” ( *13 Ibarra v. Superior Court (2013) 217 Cal.App.4th 695, 700.) Pretrial writ review is also appropriate where an order undermines a privilege or presents a novel question of law. (Story v. Superior Court (2003) 109 Cal.App.4th 1007, 1013.) Discovery orders are reviewed for abuse of discretion. (People v. Superior Court (Mouchaourab) (2000) 78 Cal.App.4th 403, 413.)

Here, the issue presented is not novel as to Chubbs. The Court of Appeal previously decided the main legal issue - the application of the trade secret privilege in a criminal case - in a prior unpublished opinion in Chubbs's case. (Exh. B.) Chubbs did not seek review of that decision. This petition therefore does not present an important question of law for extraordinary review. 5

Moreover, the party petitioning for a writ of mandate has the burden of providing an adequate record showing the claimed error. (People v. Superior Court (Dorsey) (1996) 50 Cal.App.4th 1216, 1222.) Here, the main question is whether Chubbs will have a fair opportunity to assess TrueAllele's accuracy and reliability at trial. But he has conspicuously omitted any of the materials shown to the trial court, including the raw data in his case. 6 Indeed, these materials apparently persuaded the trial court that the source code was not necessary. (See Exh. E, pp. 140, 144.) This is a tacit admission that those materials would damage his claim by showing that he has adequate means of testing TrueAllele's results.

Thus, even before reaching the merits, Chubbs has not shown that he is entitled to extraordinary relief. This Court should deny review.

*14 II THE TRUEALLELE SOURCE CODE IS NOT DISCOVERABLE

A Trade Secrets May Only Be Disclosed Based Upon Necessity, Not Mere Relevance

California recognizes a trade secret privilege:

If he or his agent or employee claims the privilege, the owner of a trade secret has a privilege to refuse to disclose the secret, and to prevent another from disclosing
it, if the allowance of the privilege will not tend to conceal fraud or otherwise work injustice.

(Evid. Code, § 1060, italics added.) A trade secret is defined in Civil Code section 3426.1, subdivision (d): 8

(d) “Trade secret” means information, including a formula, pattern, compilation, program, device, method, technique, or process, that:

(1) Derives independent economic value, actual or potential, from not being generally known to the public or to other persons who can obtain economic value from its disclosure or use; and

(2) Is the subject of efforts that are reasonable under the circumstances to maintain its secrecy.

(Civ. Code, § 3426.1, subd. (d); see also Pen. Code, § 499c, subd. (a)(9).)

*15 Here, there is no dispute that the source code for TrueAllele is a trade secret. Cybergenetics maintains the secrecy of the TrueAllele source code, which benefits the business by preventing competitors from easily copying the program. (See Exh. D, p. 83.) The only question here is whether it is discoverable despite the privilege. Chubbs therefore needed to show that protecting the code would either “conceal fraud” or “work injustice” before the court could order disclosure.

Case law further clarifies that disclosure of the secret must be necessary to the case, not merely relevant or convenient. The leading case on the trade secret privilege is Bridgestone/Firestone, Inc. v. Superior Court (1992) 7 Cal.App.4th 1384 (Bridgestone). There, plaintiffs sought the rubber formulas for tires they alleged were defective, and which the defendants claimed as a trade secret. (Id. at pp. 1388-1389.) The trial court ordered disclosure with a protective order, but the Court of Appeal issued a writ of mandate vacating that order. (Id. at pp. 1389, 1397.) The court held that disclosure could not be ordered based upon mere relevance, since this would render the privilege meaningless. (Id. at p. 1390.) It is also not enough to show that the trade secret might be useful in the litigation. (Id. at p. 1396.) Instead, the party seeking discovery must demonstrate that disclosure is necessary. (Id. at p. 1393.) 9 There, the formulas could help an expert determine whether the tires were defective as the result of a manufacturing defect, rather than a design defect, and were important in determining why a tire failed. (Id. at p. 1396.) But the expert could not state exactly how the formulas (as opposed to the nonprivileged specifications) were necessary to form a conclusion in the case. (Ibid.) The formulas themselves were therefore not necessary for the plaintiffs to carry their burden of proof. (Id. at p. 1397.)
The prior writ proceeding in this case dealt with whether the trial court misapplied this trade secret privilege, and ultimately held that Chubbs failed to make the prima facie showing required by Bridgestone. *16 (Exh. B, p. 23.) There, Chubbs unsuccessfully argued that Evidence Code section 1060 is superseded by Evidence Code sections 1061 and 1062, 10 reasoning that the secret must be disclosed, but would be subject to a protective order. (Exh. B, p. 13.) The Court of Appeal rejected this interpretation. (Id. at p. 15.) Chubbs does not explain in the instant petition why this was wrong, or why the same court should reconsider this holding. He therefore needed to establish that the TrueAllele source code was necessary for his case, not merely relevant. He failed to do so.

B Source Code Is Not Necessary to Understand a Scientific Process When the Underlying Method Is Disclosed

Chubbs's entire argument is based on a fundamental error: that he only has a vague “theory” on how TrueAllele infers genotypes from DNA mixture data, but has no idea how it actually does so. (See Petition for Review, p. 30.) This is not true. The mathematics behind TrueAllele have been published for over a decade, which give Chubbs a step-by-step guide to TrueAllele’s procedures. (See Exh. D, p. 85.) Given this, and the raw data, Chubbs has full access to how TrueAllele reached the results in his case. Thus, his entire argument falls apart.

Chubbs's argument misunderstands that it is the source code that is a trade secret, not the description of the process by which TrueAllele infers individual genotypes from DNA mixtures. According to Dr. Perlin's uncontradicted declaration, Chubbs has had the specific methodology behind TrueAllele from the beginning, including its core mathematics. (Exh. D, p. 85; see also ante page 8 [linking an article describing the process].) Indeed, the method behind TrueAllele is patented 11, which *17 requires disclosure of the underlying method in detail. (See 35 U.S.C. § 112(a); Exh. D, p 83 [stating technology is patented].) Chubbs has much more than a vague theory or description of the process. Instead, he has the step-by-step procedure TrueAllele uses to infer genotypes from DNA mixtures. It is therefore not the metaphorical “black box” that Chubbs implies.

The ability to test and evaluate TrueAllele is confirmed by the validation studies. There have been over twenty studies to establish both the reliability of the underlying method and the TrueAllele software. (Exh. D, p. 81.) Five of these have been published in peer-reviewed scientific journals. (Ibid.) Peer-reviewed articles are an important means of evaluating a process in the scientific community. (See People v. Smith (2003) 107 Cal.App.4th 646, 669 [noting support of peer-reviewed literature when evaluating Profiler Plus and COFiler systems in DNA analysis]; see also Daubert v. Merrell Dow Pharms. (1993) 509 U.S. 579, 593 [113 S.Ct. 2786, 125 L.Ed.2d 469] [discussing peer review as one factor when determining the admissibility of a new scientific technique].) These studies demonstrate that other scientists are able to evaluate TrueAllele without
its source code. Moreover, from these many studies, Chubbs is able to further determine whether TrueAllele is reliable.

If Chubbs had further questions about the TrueAllele process, he could watch Dr. Perlin's several YouTube videos explaining it. The webinar series is particularly helpful. These are not the actions of a charlatan peddling a black box, but rather a scientist explaining the process to other scientists.

From this wealth of material, Chubbs's experts can understand the TrueAllele results, and challenge them on their merits, if possible. The trial court did not abuse its discretion by denying disclosure of the source code. Beyond this, Chubbs's motion is most notable for what it omits, rather than what it contains. He has ignored obvious avenues of *discovery in his zeal for the TrueAllele source code, exposing his request as merely harassment.

First, Chubbs has not provided any indication that the probabilistic genotyping model is flawed, or that the validation data raises any questions about TrueAllele's reliability. There is therefore no indication that there is a flaw in the program that access to the code will help to resolve. This is just a classic fishing expedition.

Second, there is no indication that Chubbs has had the data in his case analyzed by another lab to dispute the TrueAllele results. While Dr. Perlin states that TrueAllele itself has not been successfully replicated, at least five other groups have developed similar software. (Exh. D, p. 83.) Included with the People's opposition were six other related systems, including DNAmixtur's, STRmix, and MixSep. (Id. at p. 98.) His failure to have the evidence evaluated by his own experts is telling, since this would be the most obvious way to contest the evidence in his case, if possible.

Third, Chubbs has never demonstrated that analyzing the source code is better at exposing errors than testing the program's operation itself. Testing is the most obvious way to evaluate any machine, and one can have a detailed knowledge of how a machine works without knowing how it is actually constructed. For example, one can know exactly how a calculator works, and test its reliability, without actually examining its circuit board. Poring over the source code would not expose errors that testing could not. Without some credible showing to the contrary, the validation studies were enough to establish TrueAllele's reliability.

Finally, even though Chubbs claims ignorance of various parts of TrueAllele's processes, he has never asked Dr. Perlin to provide the information directly. Cybergenetics allows opposing experts to observe the TrueAllele process, examine the results, and ask questions. (Exh. D, p. 84.) In addition, any party can provide validation data in order to test TrueAllele's reliability (i.e., whether it gives the expected results given a known sample). (Id. at p. 85.) There is no indication
that Chubbs has done either. In short, Chubbs has focused only on the source code, to the exclusion of other means of learning about TrueAllele.

Chubbs's attached declaration from Dr. Doom does not address any of these issues. Dr. Doom does not note any dispute about TrueAllele's reliability in the scientific community, or that any of the validation data raises questions about TrueAllele's programming. (See Exh. C, pp. 50-60.) Instead, it is just a wish list describing hypothetical problems. This does not establish that the source code was necessary for Chubbs's case, even if Dr. Doom would personally like to see it. It was therefore insufficient to overcome the trade secret privilege.

Furthermore, Dr. Doom's declaration contain several non sequiturs. For example, Dr. Doom declares that “black box” testing (i.e., where the internal components are not known) cannot be performed on systems that produce likelihood ratios (like DNA match statistics) “because the correct answer cannot be known and therefore cannot be compared to the results generated by the program.” (Exh. C, pp. 51-52.) This statement does not withstand minimal scrutiny. First, DNA programs would obviously be tested with known samples, so the expected result would be known. Second, since the method is known, given the input data, one can compare the actual output data with the expected output data to test for computational errors. Third, if it were truly impossible to test a DNA program's output, then why would knowing the code make any difference? The “correct answer” is unknowable either way. Dr. Doom's statement makes no sense.

As another example, Dr. Doom states that the “hundreds of variables” incorporated by TrueAllele are not evaluated by the validation studies. (Exh. C, p. 56.) This is misleading, since even if these parts of the model are not explicitly listed in a validation study, it does not mean they *20 are secret. Again, Dr. Doom does not state he has reviewed the patent for the linear genotyping model (which discloses the mathematics behind TrueAllele), or that Chubbs has asked for any information directly. There is no indication that Dr. Perlin has refused to provide the raw data for each step of the TrueAllele analysis. Thus, this statement by Dr. Doom is pointless as well, and distracts from the main issue in the case.

In sum, since Chubbs never established a prima facie case for disclosure, the court correctly denied discovery of the TrueAllele source code. The Court of Appeal properly denied his writ petition, and this Court should deny review.

**C Analyzing the Source Code Is Impractical Compared with Other Alternatives**

Beyond the question of necessity, Chubbs has never demonstrated that examining the TrueAllele source code could be done within a reasonable time and at reasonable expense. This alone should be enough to deny his petition.
The available evidence demonstrates that examining the TrueAllele source code would be a mammoth task. Without contradiction, Dr. Perlin stated that it could take a skilled analyst several hours to analyze even a few dozen lines of MATLAB code. (Exh. D, p. 83.) TrueAllele contains about 170,000 lines of code. (Ibid.) Cybergenetics has developed TrueAllele over twenty years at a cost of millions of dollars. (Ibid.) Dr. Doom's declaration contains no estimates of time or cost for analyzing TrueAllele's code. Thus, granting this motion could potentially commit the court to a million-dollar validation study that would take several years. Given that it has already been the subject of numerous validation studies, analyzing the source code is not reasonable or practical.

Moreover, Chubbs does not explain how he would secure Cybergenetics' trade secret during this analysis. A protective order from a California court is cold comfort when a violation could only be discovered years later through expensive litigation, if at all. This is all the more troubling given Dr. Doom's undisclosed conflict of interest. As pointed out in the People's opposition, Dr. Doom, along with Dan Krane and Dr. Michael Raymer, have developed Genophiler, a program that interprets the automated DNA analysis generated by crime labs. (Exh. D, p. 104.) By failing to disclose this fact in his declaration, he destroys any claim to be a disinterested expert. This raises serious security issues, and Dr. Perlin cannot be expected to turn over the code if Chubbs takes such a cavalier attitude about its protection.

In sum, Chubbs has basically proposed his own personal validation study, presumably at court expense, without considering any of the practical limitations. This is not reasonable. His motion was properly denied.

**D Proprietary Information Is the Norm in Criminal Cases, Not the Exception**

Chubbs cites no pertinent authority for the discovery he wants. None of his cases involve source code or trade secrets. Most of the authorities the People can locate involving source code from other states deny disclosure, or generally admit evidence even when based on pro-prietary information so long as the reliability of the process can be established.

Regarding TrueAllele itself, Pennsylvania upheld its admissibility in Commonwealth v. Foley (Pa.Super.Ct. 2012) 38 A.3d 882, 889, despite the nondisclosure of the source code. Similarly, a trial court in New York has rejected the idea that the source code is necessary to understand TrueAllele or to determine its reliability. (See People v. Wakefield (N.Y.Sup.Ct.) 47 Misc.3d 850, 854-855 [9 N.Y.S.3d 540, 544]; see also People v Belle (N.Y.Sup.Ct.) 47 Misc.3d 1218(A) [involving another program, and concluding that its source code was irrelevant].)

*22 Moreover, TrueAllele is not the only DNA analysis tool that contains proprietary information. GeneScan and GenoTyper from Applied Biosystems contain proprietary information. (State v. Foreman (Conn. 2008) 954 A.2d 135, 162.) Profiler Plus and Cofiler kits manufactured
by Perkins-Elmer also contain proprietary primers that are not publicly available. (*People v. Hill* (2001) 89 Cal.App.4th 48, 56; *State v. Traylor* (Minn. 2003) 656 N.W.2d 885, 890.) There is no indication that proprietary information makes these tools unverifiable or inadmissible in criminal cases.

Outside of DNA, there has been extensive litigation in other states regarding disclosure of source codes for DUI breath-testing equipment. While there are some exceptions, the general trend is that disclosure is not necessary in order to test the machines' accuracy. Several courts have denied requests for the breath test source code simply because it was not in the state's possession. Still others have required a showing of materiality, which requires some suggestion that an error exists in the code before ordering its disclosure. This makes sense, since the only real question is reliability and accuracy, which can be tested without knowing the source code.

Two cases where the breath test source code was disclosed are distinguishable from the present situation. First, the *Underdahl* litigation in Minnesota produced two opinions from that state's supreme court: *In re Comm'r of Pub. Safety* (Minn. 2007) 735 N.W.2d 706, 712 (*Underdahl I*) and *State v. Underdahl* (Minn. 2009) 767 N.W.2d 677, 681 (*Underdahl II*). These cases are unique because, in *Underdahl I*, the court upheld a finding that the state had possession and control over the code at issue. (*Underdahl I, supra*, at pp. 712-713.) This holding was reiterated in *Underdahl* (*Underdahl supra*, at pp. 686-687.) But even given this finding, the court reversed disclosure as to one of the defendants because he made no particularized showing of relevance. (*Id. at p. 685.*) Thus, even in Minnesota, defendants may not go on fishing expeditions for errors.

The second case involving disclosure is *State v. Chun* (N.J. 2008) 943 A.2d 114, from the New Jersey Supreme Court. Their high court, in a lengthy opinion, adopted the findings of special master regarding the machine at issue. (See *id. at p. 120.*) Findings, in turn, involved the analysis of the machine's proprietary source code. (See *id. at p. 122.*) Still, its eventual disclosure in that case was complicated. First, the company apparently did not (initially) release any of its algorithms. (See *State v. Chun* (N.J. Feb. 13, 2007) 2007 N.J. LEXIS 39, *78 [findings of the special master].) This was therefore truly a "black box" situation, where no party knew how the machine reached its results. Second, the parties eventually reached an agreement to disclose the code to an independent software house. (*Id. at pp. *78 - *79.*) This was therefore not a forced disclosure, although apparently "encouraged" by the threat of an adverse inference. (*Id. at p. *11.*) There is also no discussion in the case about any trade secret privilege. *Chun* is therefore distinguishable from Chubbs's situation because Chubbs has TrueAllele's underlying methodology. He also cites no authority indicating that California and New Jersey share the same approach to scientific evidence.

Thus, although there are some exceptions, it is common for cases to proceed without the parties having access to proprietary source code. All that is required is access to the program's
methodology, and validation studies verifying its results. Consistent with these authorities, the trial court correctly denied disclosure here. This was not an abuse of discretion.

**III THE TRUEALLELE SOURCE CODE HAS NOTHING TO DO WITH THE RIGHT TO EFFECTIVE ASSISTANCE OF COUNSEL**

Chubbs asserts that disclosure is necessary so that his attorney can provide constitutionally effective assistance. (Petition for Review, p. 26.) The only cases he cites describe a general duty of counsel to investigate the case. (*Id.* at pp. 27-29.) He cites no authority indicating that the right to counsel mandates any discovery from a third party. This whole argument is superficial, and should be summarily rejected.

Incidentally, Chubbs unsuccessfully argued in the prior writ proceeding that he was entitled to the source code under the confrontation clause. (See Exh. B, p. 21.) The Court of Appeal rejected this argument. (*Id.* at p. 25.) This was consistent with this Court's decision in *People v. Hammon* (1997) 15 Cal.4th 1117, 1128, which declined to find a pretrial discovery right for privileged information. It was also correct because there is no right to “cross-examine” machine data. (*People v. Banks* (2014) 59 Cal.4th 1113, 1167-1168.) Chubbs's repackaging of these arguments here is much weaker, and should similarly fail to overcome the trade secret privilege.

**IV DISCOVERY OF THE SOURCE CODE IS NOT NECESSARY FOR A KELLY HEARING**

Although he has not yet raised this issue below, it is worth noting that the source code is not necessary to evaluate TrueAllele as a novel scientific technique, if it is indeed novel. Discovery of the source code would be far in excess of what is required to show that it is generally accepted and that that analyst followed proper scientific procedures.

In California, the admissibility of scientific evidence is based on the three-prong *Kelly* test. The proponent must show “(1) the reliability of the new technique has gained general acceptance in the relevant *scientific* community, (2) the expert testifying to that effect is qualified to give an opinion on the subject, and (3) the correct scientific procedures were used.” (*People v. Doolin* (2009) 45 Cal.4th 390, 445.) No prong requires production of computer source code.

The first prong requires “general acceptance” of reliability in the scientific community, not reliability as a matter of fact. (*People v. Soto* (1999) 21 Cal.4th 512, 519.) The reliability is therefore judged by the scientific community, not the court. Thus, defendants are not entitled to conduct their own validation studies (much less at court expense), and would not be entitled to the source code for a *Kelly* hearing.
The second prong plainly does not require the source code since it only goes to the qualifications of the operator.

Finally, this Court has explained that the third prong does not require new scientific evidence, but rather that the testifying expert be familiar with the technique at issue:

Proof of that compliance does not necessitate expert testimony anew from a member of the relevant scientific community directed at evaluating the technique's validity or acceptance in that community. It does, however, require that the testifying expert understand the technique and its underlying theory, and be thoroughly familiar with the procedures that were in fact used in the case at bar to implement the technique.

(\textit{People v. Venegas} (1998) 18 Cal.4th 47, 81.) Thus, while the third prong requires an inquiry into the actual procedures used in the case, there is no indication that it is a back door for conducting an exhaustive validation study that is not required under the first prong. The source code is therefore not required for any prong of the \textit{Kelly} test.

Chubbs is essentially trying to circumvent \textit{Kelly} by requiring the People to produce material far in excess of what is required to admit the material at trial and deem it reliable. His overbroad request should be denied.

\textbf{*26 V CHUBBS'S MOTION POSES OTHER PROCEDURAL PROBLEMS}

In his quest for the TrueAllele source code, Chubbs overlooks two crucial preliminary questions: what procedural vehicle allows this discovery, and which state's laws should govern the code's discovery? As the petitioning party, it was imperative for him to show why he was entitled to the discovery at issue. Because of this, this answer brief will not fully address each issue, but will instead show that the answers are not obvious. Chubbs's petition should be denied for his failure to explain why he was entitled to the discovery at issue.

First, the People do not need to produce the source code as part of its discovery obligation. Although Chubbs's writ petition cited \textit{Penal Code section 1054.1} \textsuperscript{18} (see Petition for Writ of Mandate, pp. 44-45), albeit without analysis, his petition for review omits any authority for the disclosure. But the People have already complied with our discovery obligation by providing Chubbs with the reports and raw data in his case. While the prosecutor has a duty to disclose information in the possession of law enforcement, it has no duty to seek out information in the possession of third parties. (\textit{In re Littlefield} (1993) 5 Cal.4th 122, 135.) Here, Cybergenetics is a
Pennsylvania corporation located in Pittsburgh, and is not part of law enforcement. (Exh. D, p. 79.) The People therefore do not have an obligation to seek out trade-secret information.

*27 Next, the information might be available to Chubbs via subpoena duces tecum. 19 (See People v. Superior Court (Barrett) (2000) 80 Cal.App.4th 1305, 1319-1320.) But this raises another question: does California law govern the disclosure, or Pennsylvania? The People have assumed for this petition that California law applies, but it is not clear that this is so. (See State v. Peters (Mont. 2011) 264 P.3d 1124, 1131 [holding that Montana would give full faith and credit to Kentucky court's ruling that a Kentucky company's code was a trade secret]; Phillips v. State (Ga.Ct.App. 2013) 751 S.E.2d 526, 530 [holding out-of-state SDT for source code was decided in the other state, not Georgia].) Chubbs never addresses the choice-of-law issue.

The People are somewhat hesitant to raise these issues since they may only result in further harassment of Dr. Perlin. Still, since Chubbs apparently wants the People to suffer a discovery sanction, it is important to point out how we have already complied with our discovery obligation, and that any sanction would be unfair. Chubbs's failure to address these issues are further reasons to deny his petition for review.

*28 CONCLUSION

The People respectfully request that this Court deny the petition for review. Chubbs did not demonstrate that he was entitled to extraordinary relief, or that it was error to deny discovery of the TrueAllele source code, which is a trade secret. The code is not necessary for Chubbs to understand the evidence in his case.

Footnotes

1 These facts are taken from the unpublished Court of Appeal opinion on the prior writ proceeding, which in turn were taken from a declaration by the prosecutor. These facts are undisputed for the purposes of this petition, and are provided only for context.

2 Exhibit designations are to those accompanying Chubbs's Petition for Writ of Mandate in the Court of Appeal. Page numbers refer to the continuous pagination in the lower corner.

3 Though not apparent from this record, Chubbs is African American.

4 This article was not directly included below, but was referred to in part of the People's opposition as part of Chubbs's discovery. (See Exh. D, p. 96.)

5 Although the question might be important in the abstract, the Court of Appeal denied the People's request for publication, and this court denied the publication request in case S224140.

6 The case packet is nearly a hundred pages. We have not included it with this answer since the question is whether review is appropriate. We would include it in any return filed in the Court of Appeal.

7 Further statutory references are to the Evidence Code unless otherwise indicated.

8 Section 1061, subd. (a)(1), references Civil Code section 3426.1 and Penal Code section 499c for the definition of “trade secret”: (a) For purposes of this section, and Sections 1062 and 1063:
(1) “Trade secret” means “trade secret,” as defined in subdivision (d) of Section 3426.1 of the Civil Code, or paragraph (9) of subdivision (a) of Section 499c of the Penal Code. Although referring to subsequent sections, logically the same definition would apply to section 1060 by implication.

Pennsylvania follows a similar standard, requiring a demonstration that “production of the trade secret is relevant and necessary, and that the necessity outweighs the harm of disclosure.” (Crum v. Bridgestone/Firestone N. Am. Tire, LLC (Pa.Super.Ct. 2006) 907 A.2d 578, 587.)

These sections, respectively, provide for a protective order in criminal cases, and for closed proceedings during testimony about the secret.


Available at <https://www.youtube.com/user/TrueAllele>.

Chubbs attached a news article reporting an alleged coding error found in another DNA analysis program, STRmix, in Australia. (Exh. C, p. 48.) Crucially, the article does not describe how the error was initially discovered. The point is not that humans can never make coding errors; it is that examining the source code itself is not an effective means of uncovering those errors. If the STRmix error was uncovered by testing, then Chubbs’s position is completely undercut. The People have not located anything explaining how the STRmix error was found.

Further information about Dr. Doom’s involvement with this company, Forensic Bioinformatics, is available at <http://www.bioinformatics.com/>.


The relevant part of that section reads: “The prosecuting attorney shall disclose to the defendant or his or her attorney all of the following materials and information, if it is in the possession of the prosecuting attorney or if the prosecuting attorney knows it to be in the possession of the investigating agencies:[¶][¶][¶] (f) Relevant written or recorded statements of witnesses or reports of the statements of witnesses whom the prosecutor intends to call at the trial, including any reports or statements of experts made in conjunction with the case, including the results of physical or mental examinations, scientific tests, experiments, or comparisons which the prosecutor intends to offer in evidence at the trial.”

In the prior writ proceeding, Chubbs did issue an out-of-state SDT for Dr. Perlin to produce the source code. (Exh. B, p. 8.) The Pennsylvania court ordered him to appear, but did not decide the issue of whether the trade secret should be disclosed. (Id. at p. 9.)
SUPERIOR COURT OF CALIFORNIA, COUNTY OF SAN JOAQUIN

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THE PEOPLE OF THE STATE Of CALIFORNIA,

 vs.

ALVIN LARRY DAVIS,

Defendant.

No. STK-CR-FE-2016-0004780
Department Number 9B
TESTIMONY OF
DR. JOHN BUCKLETON

December 18, 2017

The above-entitled matter came on regularly at the date and time above set forth, before the HONORABLE GEORGE J. ABDALLAH, JR., Judge of said Superior Court, for the purpose of a Kelly Hearing.

APPEARANCES OF COUNSEL

GINA DELLA MAGGIORE, Deputy District Attorney, County of San Joaquin, 222 East Weber Avenue, Room 202, Stockton, California 95202, appeared as counsel for and on behalf of the People.

ANNIE C. BELES, Attorney at Law, Beles & Beles Law Offices, 1 Kaiser Plaza, Suite 2300, Oakland, California 94612, appeared as counsel for and on behalf of the Defendant.

Reported by: KELLIE A. GAFF, C.S.R. No. 7567
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THE COURT: Calling the matter of People

versus Alvin Davis.

MS. DELLA MAGGIORE: Gina Della Maggiore on

behalf of the People. Sitting next to me is Eduardo

Rodriguez, DA investigator.

MS. BELES: Annie Beles with Mr. Davis who is

present in custody and present.

THE COURT: We are here today in Mr. Davis' 

matter to conduct what is known as first prong Kelly hearing, 

that is the Court's understanding.

I'm going to state the issue, what I believe is the 

issue for the day, and hear from counsel if you believe it is 

different from what has been raised by this -- the prior 
motions in this matter.

So today the issue is is the STRmix technique in DNA 
analysis a test generally accepted in the forensic science 
community upon consensus drawn from a typical cross-section 
of the qualified forensic science community?

Is that our issue?

MS. BELES: I'm still reciting it.

Yes, Your Honor, I believe that is an accurate -- an 
accurate question with -- considering Kelly and other case 
law I brought up in my motion.

One other preliminary matter.

MS. DELLA MAGGIORE: Before we get there, yes, 

I agree with the Court as long as the Court -- I believe it 

would be the Court's understanding as well that it is not 
simply based on the number of experts or the number of votes,
if you will, that are out there in support of this, it is
rather based on the general forensic scientific community and
the quality of the testimony that you're going to hear
today.

MR. BELES: Huh-uh (negative). I think that
is argument. I'm not going to respond.

THE COURT: So we make a record as to what
occurred at the preliminary hearing with regard to this
evidence. As I understand, it was admitted subject to --

MS. BELES: It was not admitted.

What happened at the preliminary examination was that
the prosecutors and I had discussed the potential of
admitting it at the prelim and having the Kelly argument at a
later date. The Court did not agree with that procedure and,
therefore, this item of evidence was not introduced and no
STRmix, the technology, was discussed at the prelim. It was
simple random match probability DNA testing.

THE COURT: Thank you.

Ready to proceed?

MS. BELES: No.

The preliminary matter is this: In the courtroom, Dr.
Buckleton is one expert that will be testifying and
Mr. Halsing, H-a-l-s-i-n-g, from the Department of Justice,
will also be testifying. I would ask that Mr. Halsing be
excused from the court and excluded from the court while Dr.
Buckleton testifies.

I'm also aware that Ms. Kyo, K-y-o, who testified at the
preliminary hearing regarding what I call the regular DNA
testing is present in the courtroom. I don't think --
because she's not implicated in the STRmix analysis, I don't
think Ms. Kyo is a problem.

I think Mr. Halsing should not be present during Dr.
Buckleton's testimony.

I further request that Dr. Buckleton and Mr. Halsing be
admonished, as we discussed in our motions in limine last
week, they are not to discuss their testimony during the
course of the 402 hearing -- during the course of the Kelly
hearing.

THE COURT: Counsel.

MS. DELLA MAGGIORE: Your Honor, a couple
comments.

I believe Evidence Code Section 777 covers this. I
believe there is case law out there, I'm not aware of that
exact citing, which the Court can exercise discretion in
allowing Eric Halsing to remain.

Dr. Buckleton's testimony is regarding the general
scientific community. He's one of the creators of STRmix.

Eric Halsing's testimony goes to not only some of what DOJ in
California has done with STRmix and how long it has been used
and that it's been validated, but he also talks about case
specific more along the lines of a third prong Kelly. If the
Court would allow them to watch each other's testimony, that
is the People's request.

I also feel it would be appropriate to make an order
that they not discuss their testimony.

MS. BELES: I have concerns about Dr.
Buckleton -- I understand their roles are different. But I believe the safest route and to preserve the independent roles that each of them have is best preserved by them not observing each other's testimony. Certainly as experts if they want to consult at a later time, long after this case, about using transcripts or how -- how things work that may be of scientific benefit, but not in tune with what I believe is my client's due process rights under the United States and California Constitutions.

THE COURT: What will Mr. Halsing's role be?

MS. DELLA MAGGIORE: His role will be to provide evidence that California Department of Justice has basically adopted and gone live and utilizes STRmix in active casework. He'll explain his training. He'll explain the validation process and what California Department of Justice is doing with STRmix. He -- he would go into the various steps that are utilized regarding deconvolution and statistical analysis.

MS. BELES: Well, I certainly do not put on any Clarence Deiro hat.

I would say I think what might be of concern to me is if I cross-examine Dr. Buckleton in one way and I want to cross-examine Dr. Halsing as a clean slate, I can't do that if Mr. Halsing remains in the courtroom during Dr. Buckleton's testimony. One hopes I could be that artful.

THE COURT: There appears to be some case law, the rule under Evidence Code Section 777, in a different way when experts are involved, so I'm going to look at that case.
MS. BELES: Does the Court have a citation?

THE COURT: People versus Valdez 177 Cal.App.3rd and the pinpoint is 687.

I'm still getting accustomed to my new courtroom. I'm afraid my Case Law access is not operating.

We'll take a break until 10:20 -- 10:25.

MS. BELES: Thank you.

MS. DELLA MAGGIORE: Thank you.

(Recess)

THE COURT: Returning to the matter of People versus Alvin Davis.

Did you have a chance to look?

MS. BELES: I did, Your Honor, Valdez 177 Cal.App.3d 680. I note the difference in the sense -- I looked at a couple other cases as well. In that situation in the Valdez case, there were two experts, one on each side, defense expert and a prosecutorial expert. Those experts wanted to be able to watch one another, to respond almost in real time before the defense expert testified about the forensic and serological issue.

There were a couple other cases that I reviewed. There was the Maxi case, 1972 case, that does stand for the premise -- 28 Cal.App.3d 190, that cross experts -- there is some validity to that. But I don't believe we are in that situation because we have experts on the same side, meaning the prosecution, that intertwines with one another inextricably. I'm not impugning bad intent on Dr. Buckleton or Mr. Halsing, but I think to safeguard my client's right to
having an untainted, uneven, implied, not a clean slate
witness is compromised and I object to the two of them being
in the courtroom at the same time.

THE COURT: Ms. Della Maggiore.

MS. DELLA MAGGIORE: Your Honor, it's
discretionary for the Court. 777 states that the Court may
exclude.

I will submit to the Court and respect the Court's
decision.

MS. BELES: Also, if I may --

THE COURT: Yes.

MS. BELES: -- make one more comment.

I don't think I'm -- I think my position is reasonable
to ensure my client's due process rights.

Given my concession that Ms. Kyo is not involved in the
STRmix, I don't have a problem with Ms. Kyo being in the
courtroom. But it is the two experts about the same issue
that is problematic for me and I object.

THE COURT: So Dr. Buckleton who will discuss
the STRmix technique in general and offer a basis for a
finding of reliability and the other gentleman will be
testifying again to what?

MS. DELLA MAGGIORE: As to the same concept,
Your Honor, but specifically to its validation for the state
of California through DOJ.

THE COURT: But not as to this particular
case?

MS. DELLA MAGGIORE: As to this particular
case Eric Halsing will ultimately be coming in to testify as
to that hopefully should we get to the third prong.

THE COURT: Why are we going to the third prong today?

MS. DELLA MAGGIORE: It's my understanding we're not. I'm just stating that to the Court that he does have that information.

MR. BELES: So I would note, first of all, they are present in the courtroom during this whole argument.

Secondarily, I think what I'm hearing Ms. Della Maggiore say is Dr. Buckleton is going to testify to general STRmix's alleged reliability and then Mr. Halsing is going to testify what the California DOJ has done to support whatever Dr. Buckleton says makes it reliability of the validation studies.

MS. DELLA MAGGIORE: Not that he's just testifying generally to STRmix. He's in fact one of the creators. He will testify specifically to what STRmix is.

MS. BELES: Of course.

THE COURT: Both will?

MS. DELLA MAGGIORE: Both will, yes.

THE COURT: Why the duplication?

MS. DELLA MAGGIORE: Because the People feel that there is import to be given to the fact that California Department of Justice is utilizing STRmix and has been trained on it in fact by Dr. Buckleton.

THE COURT: But that you wouldn't go necessarily to the first prong.
MS. DELLA MAGGIORE: However, it could because there has been a validation study that has been performed by the California Department of Justice.

MS. BELES: One -- one of the comments makes me even more concerned.

If Dr. Buckleton is training Mr. Halsing in a scientific manner, I don't want Dr. Buckleton training Mr. Halsing in testifying either.

THE COURT: Well --

MS. BELES: Again, I'm not trying to be derogatory, these are two people being offered as expert witnesses on basically the same issue and they should be independent of one another. And no matter how much it may be interesting how Dr. Buckleton testifies to Mr. Halsing for future testimony, et cetera, I want Mr. Halsing to testify from Mr. Halsing's perspective without knowledge and without hearing what Dr. Buckleton testified to.

THE COURT: Let me ask you this. Let's say I excluded Mr. Halsing, is it?

MS. BELES: Yes.

MS. DELLA MAGGIORE: Yes.

THE COURT: In preparation for trial, would he not be allowed to read the doctor's transcript of his testimony?

MS. BELES: He probably would be, but that would not affect his testimony in this 402 hearing. We are humans, we are not robots, where we are not somewhat swayed by what someone said before the revered inventor of the
actual software who trained the person. I understand that.

I can see probably this transcript will be ordered, Mr. Halsing review it before his trial testimony if either of them are allowed to testify. But I just want this hearing to be clean and concise and without taint.

THE COURT: Matter submitted?

MS. BELES: Submitted.

THE COURT: Submitted?

MS. DELLA MAGGIORE: Submitted.

THE COURT: As the Court pointed out in People versus Valdez, the danger is of tailored testimony or less than candid testimony arising out of the inclusion of various witnesses as they testify.

The Court finds based on the argument of counsel and the offers of proof that -- the notion of tailored testimony, the Court would hope that it is focused between the two so that we can avoid duplication and undue consumption of time. The Court does not find the dangers noted in People versus Valdez exist in the presence of both of the individuals who will testify and, therefore, the request that Mr. Halsing be excluded during the doctor's testimony is denied.

MS. BELES: The only other preliminary matter prior to the testimony is that I spoke with Ms. Della Maggiore and with the Court's permission I would reserve voir dire of both gentlemen's expertise. I would prefer to do just one cross. If I have an objection to their designation as an expert, which is not my strongest point, I will make that objection after the testimony, but I will reserve that.
THE COURT: All right.

MS. BELES: Thank you.

THE COURT: Call your first witness.

MS. DELLA MAGGIORE: Thank you.

People call Dr. John Buckleton to the stand.

JOHN SIMON BUCKLETON,
a witness called on behalf of the People, having been
duly and regularly sworn, testified as follows:

THE WITNESS: I do.

THE CLERK: Thank you.

THE COURT: Good morning.

THE WITNESS: Good morning, sir.

THE COURT: Please state your full name.

THE WITNESS: My full name is John Simon
Buckleton, last name spelled B-u-c-k-l-e-t-o-n.

THE COURT: Thank you.

You may proceed, counsel.

MS. DELLA MAGGIORE: Thank you.

DIRECT EXAMINATION

BY MS. DELLA MAGGIORE: Q. Dr. Buckleton,
please tell us your occupation?

A. I'm a forensic scientist, employment of the New Zealand
government.

Q. How long have you held that position?

A. Since 1983.

Q. And could you please state your prior education as it
pertains to DNA analysis?

A. My formal degrees are a Ph.D in chemistry from the
University of Auckland. I have another, a DSC, British Commonwealth degree, it's called a doctor of science, no equivalent in America, but the highest degree in the British Commonwealth system. Neither of those are in DNA. They precede the DNA era.

My specific exposure to DNA comes from working in the United Kingdom on the team that was actually developing DNA for casework, in the very first inception of it.

MS. BELES: This is becoming nonresponsive to education.

THE COURT: It is, but it's -- inevitable these questions will be asked regarding his experience. I'll allow the question.

MS. DELLA MAGGIORE: Q. What other academic qualifications do you have?
A. Those are my academic qualifications, my highest ones. I have lower ones, BSC and MSC in chemistry from the University of Auckland.

Q. And then could you please tell us your employment record?
A. I've been employed by the New Zealand government since 1983 but that employment is broken. I've had four periods of employment in the United Kingdom and one in the USA in 1995.

Q. Could you please provide us some details as it pertains to United Kingdom?
A. I worked for the Forensic Science Services in the United Kingdom. It's held various different names over that time. And I was employed in resurgent teaching in the field of DNA
1 evidence interpretation.
Q. And when did you do that?
3 That was in the United Kingdom, correct?
4 A. Yes.
5 Q. When?
6 A. '88, '93, '95, and '01.
7 Q. And you mentioned your employment once in the U.S.,
8 could you please tell us about that?
9 A. I worked at North Carolina State University for
10 Professor Bruce Weir on the interpretation of DNA evidence.
11 Q. And so what other -- what further employment have you
12 had?
13 A. I think that's -- that's it.
14 Q. Okay. Who is Professor Weir?
15 A. Professor Weir is a highly respected authority in the
16 area of population genetics.
17 Q. And so what sort of work did you do with him as it
18 pertains to DNA analysis?
19 A. At the time in 1995, we were in the midst of what was
20 then termed "the DNA wars," where it was being argued whether
21 we could estimate the frequency of certain genotypes in the
22 human population. And Professor Weir was the leader in this
23 field and I was working with him on that subject.
24 Q. Have you also published any writings as it pertains to
25 DNA analysis?
26 A. Yes, I have.
27 Q. Please tell us about those.
28 A. I've published, I think, 193 referee'd publications. I
don't have an exact count, about half of those would be on DNA.

Q. When you say "referee'd" --
A. Referee'd is an academic term when you submit a paper for publication and it is viewed by two anonymous referees; if permitted, it is then published.

Q. So then that would be published in what type of -- what type of organizations publish those?
A. There are a number of scientific journals that publish such papers.

Q. Do you -- those also become published -- strike that.
As far as your training of others for purposes of DNA analysis, what can you elaborate on there?
A. I've been training forensic scientists around the world in DNA analysis since 1988. Over the last three years I've been living in the United States and have run something of the order of 70 STRmix training courses in the United States.

Q. Besides about 193 referee'd academic publications you have had, have you also written other papers on the subject of DNA analysis?
A. Yes, I have.

Q. Could you tell us about those?
A. I provided you with I think my CV which lists a number of unreferee'd publications that I consider significant. I've also published a number of books of relevance, one on DNA evidence interpretation.

Q. Where was that book published?
A. CRC Press and, I'm not sure, I think it might be New York Interalia.

Q. In -- would it be 2017 you were also stationed at the University of Washington?
A. Well, living in Maryland, but working for the University of Washington in Seattle.

Q. Let's go back a bit.
Your current employment is with the government in New Zealand; is that correct?
A. Yes.

Q. So what is it -- how was it that you came to the United States I believe you said in 2014?
A. I came to the United States in 2014 to assist with the transition to probabilistic genotyping in the United States.

Q. Still under the employ of the New Zealand government, correct?
A. I --

MS. BELES: I'm sorry, I move to strike the last portion because it assumes fact not in evidence regarding transitioning to probabilistic genotype DNA testing.

It assumes that is occurring.

THE COURT: Overruled.

MS. DELLA MAGGIORE: Q. So if we could go back. If you could answer that last question.

When you came here in 2014 to the United States, you were still under the employ of and currently under the employ of the government of New Zealand, correct?
A. Yes.
Q. What was the purpose for your arriving in the United States in 2014?
A. Various organizations within the United States were starting to purchase STRmix.
Q. Like who?
A. The first U.S. organization to use STRmix was United States Army Criminal Investigation Laboratory.
Q. So that was one of the various organizations who were purchasing STRmix; is that correct?
A. Yes.
Q. Was that your sole and only purpose to come here in 2014 to the United States?
A. It was to support those organizations that were transitioning to STRmix.
Q. Have you been previously qualified to testify as an expert in DNA analysis?
A. Yes.
Q. Where?
A. Within America a number of times and in the United Kingdom, Netherlands, Australia, and New Zealand.
Q. When you say a number of times in the United States, can you give us any certain quantitative amount?
A. Have I given you a list of my testimonies? I thought I had. It appears in my CV.

(People's Exhibit Number 1 was introduced into evidence, a curriculum vitae.)

MS. DELLA MAGGIORE: Having been previously marked as People's Exhibit 1, showing defense counsel the CV.
MS. BELES: Received.

MS. DELLA MAGGIORE: Q. Familiar with what is in People's Exhibit 1?

A. Yes.

Q. What is that?

A. My curriculum vitae.

Q. Is that up to date?

A. Yes.

Q. You prepared that, correct?

A. Yes.

Q. So are you needing to review that to formulate an answer to about how many times you've been qualified as DNA expert?

A. There are eight times in the STRmix era. I was actually qualified on an unrelated set of issues in 1995.

Q. When you say unrelated issues, what do you mean?

A. At that time the issues related to population genetics, not mixtures.

Q. Okay. So at least eight times previously you qualified as an expert as it pertained to STRmix; is that accurate?

A. Yes.

Q. About how many times have you been previously qualified as an expert in DNA analysis and STRmix in the -- between the UK, Australia, and Netherlands?

A. I don't know, a large number.

Q. A larger number than eight?

A. Yes, one in the Netherlands, one in the UK, and a very large number in Australia or New Zealand.

Q. Okay. I know I have focused on your expertise in DNA
If we could go into your training, background, and education as it pertains to STRmix expertise.

Tell us about that, what training, background, or expertise do you have as it pertains to STRmix and its analysis?

A. So the answer is going to be relating to background, not training.

Q. Okay.

A. I'm one of the three creators of STRmix and I've been intimately involved with the development and deployment and testing of STRmix from about 2011.

Q. To the present?

A. To the present.

Q. So you helped create it?

A. Yes.

Q. And why was that?

MS. BELES: Objection, vague.

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. Why was it that you created -- helped to create STRmix?

MS. BELES: Same objection.

THE COURT: The witness appears to understand the question. Overruled.

THE WITNESS: In 2009, the Melbourne laboratory in Australia was closed due to concerns about DNA interpretation. As a consequence of that closure of the laboratory there was created a standardization project across Australia and New Zealand. Collectively Australia and New
Zealand are termed Australasia. I was one of the two people on the project. We were tasked to create software for DNA analysis. A third person has been added to that team which is why I'm one of the three creators.

Q. And so for how long is it, Dr. Buckleton, that you have been engaged in DNA analysis in the forensic world?
A. Since 1988.

Q. And so the People would -- People's Exhibit 1, the curriculum vitae you have, does that accurately represent your training and experience and qualifications as it pertains to DNA analysis and the utilization of STRmix?
A. Yes.

MS. DELLA MAGGIORE: Your Honor, the People at this time would like to admit the CV into evidence.

MS. BELES: For the purposes of the Kelly hearing only, I do not object.

THE COURT: People's Exhibit Number 1 is admitted.

(People's Exhibit Number 1 was received in evidence.)

MS. DELLA MAGGIORE: At this time, the People would like to proffer Dr. John Buckleton an expert in forensic DNA analysis and in STRmix specifically.

MS. BELES: As indicated previously, Your Honor, I preserve to conduct my voir dire, such designation, into one cross-examination.

THE COURT: Why don't you go ahead and continue with your questioning then, I suppose at some point.
you could make a motion to strike.

   MS. BELES: Thank you.

   MS. DELLA MAGGIORE: Q. Dr. Buckleton, what is STRmix?

   A. STRmix is a software program.

   MS. BELES: Could we have a timeout?

   As I was making my objection, I did not get the specific language that the prosecutor made for the area of expertise the expert is in.

   MS. DELLA MAGGIORE: DNA analysis and STRmix.

   MS. BELES: Thank you.

   MS. DELLA MAGGIORE: Q. Dr. Buckleton, what is STRmix?

   A. STRmix is a software program.

   Q. What does it aid in?

   A. It assists the expert interpreting DNA profiles.

   Q. And so does it determine what DNA types could have made up a certain DNA profile and the probability of each?

   MS. BELES: Objection, leading.

   MS. DELLA MAGGIORE: This is an expert.

   MS. BELES: I think -- I don't believe that all leading questions are appropriate of experts. I believe that foundation needs to be laid.

   THE COURT: Matter submitted?

   MS. DELLA MAGGIORE: Submitted.

   THE COURT: Submitted?

   MS. BELES: Submitted.

   THE COURT: Objection overruled.
MS. DELLA MAGGIORE: Q. Again, I want to make sure we had the answer to that. Does STRmix determine what DNA types could have made up a certain DNA profile and the probability of each?
A. Yes.
Q. Is STRmix a form of probabilistic genotyping?
A. Yes.

MS. BELES: Same objection, leading.

THE COURT: It is, but I'm going to allow the question.

MS. DELLA MAGGIORE: Q. Your answer was yes, it is a form of probabilistic genotyping?
A. Yes.
Q. What is probabilistic genotyping?
A. Probabilistic genotyping is a collective noun for a number of methods that interpret simple through complex DNA profiles.
Q. Does STRmix play any role whatsoever in the detection or discovery of a DNA profile?
A. No.
Q. So, in other words, is it -- is it fair to state that STRmix interprets the DNA profile that has been presented to the computer program known as STRmix?

MS. BELES: Objection, leading, Your Honor.

It perhaps --

THE COURT: You are getting into greater detail at this point. This is beyond the preliminary matters that may probably be the subject of leading questions on
direct. So I'll ask -- I will sustain that objection.

MS. DELLA MAGGIORE: Q. Were there certain areas of data ambiguity prior to the creation and implementation of STRmix?

MS. BELES: Objection, vague.

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. What is it that STRmix is capable of doing that possibly prior DNA analyses were not able to do?

MS. BELES: Your Honor, for clarity, I object. No foundation of what the prior DNA testing could do. There has to be a foundation.

I understand the question, but I think the evidence has to be present first.

THE COURT: It does assume that there are limitations that were overcome and we don't know what those are, so sustained.

MS. DELLA MAGGIORE: Q. Previous DNA analyses that have been utilized in the United States, were there certain limitations that you're aware of?

A. Yes.

Q. What are those?

A. Specifically to the state of California, California Department of Justice, used the RMP method -- RMP method. This method was thoroughly reliable and thoroughly effective, but did not utilize all the information present in a DNA profile. By utilizing all the information present in a DNA profile, we enhance the system's ability to differentiate
between true and false standards.

Q. How does it do that?

A. It does it using a method of probabilistic genotyping whereby it assists the probability of the data given various genotype proposals.

Q. And so what would you say was the date of the creation of STRmix?

A. STRmix itself was created in 2011 and was first used in live casework in 2012.

Q. In what jurisdiction?

A. Simultaneously in LA; Australia; and Auckland, New Zealand.

Q. And then where -- where else was it used?

A. I have a list of laboratories, 44 laboratories worldwide, 30 in the United States. The first United States jurisdiction to go live was the U.S. Army Criminal Investigation Laboratory in November 2014.

MS. BELES: Your Honor, if the Court is going to rely upon this, I am objecting as hearsay unless there is a foundation of how Dr. Buckleton knows when laboratories used STRmix. I think there is a hearsay objection to be lodged.

THE COURT: Even with an expert?

MS. BELES: Yes, given People versus Sanchez.

THE COURT: It's not case specific.

MS. BELES: Okay. I'm lodging the objection.

THE COURT: Overruled.
MS. BELES: May it be a standing one?

THE COURT: Yes.

MS. BELES: Thank you.

(People's Exhibit Number 2 was introduced into evidence, a document.)

MS. DELLA MAGGIORE: Q. Dr. Buckleton, I'm going to show you what has been marked People's Exhibit 2. Could you tell us what that is?

A. This is a list of laboratories that are using STRmix in casework and the dates they went live.

Q. And how is it that you are familiar with such laboratories contained in People's Exhibit 2?

A. In some, I'm very directly involved in the training and implementation.

Q. Which ones?

A. Oh, there are 44 on this list.

Q. So which of the 44 were you directly involved with?

A. All right. I'm just going down the U.S. list, if you will forgive me.

I have been directly involved in either training or implementation in all the U.S. laboratories that are currently using STRmix.

Q. So how many of them are there?

A. There are 30 in the United States.

Q. And when you say "directly involved," what does that mean?

A. I have personally trained their staff and/or personally been involved in their implementation and validation.
Q. And when you say personally involved in their implementation and validation, having said validation has taken place, what does that mean for all 30 of those laboratories in the United States as it pertains to STRmix?

A. There are a number of aspects to your question.

MS. BELES: Then I would move, object as compound.

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. When a United States laboratory becomes validated in the use of STRmix, what does that mean?

MS. BELES: Objection, no foundation what validation is. That has not been explained.

THE COURT: That is what is being asked.

MS. BELES: Okay.

THE COURT: Overruled.

THE WITNESS: Validation in the United States is done to the SWGDAM, S-W-G-DAM, 2015 guidelines, and for the Court's information, that actually applies to those labs that went live prior to 2015. The final stage of validation after completing the requirements detailed by SWGDAM are signed off by the technical leader. After that time, the laboratory is then permitted to use the software in casework. My personal involvement in that usually is -- comes at the stage of either review or problem solving during the validation and implementation process.

MS. DELLA MAGGIORE: Q. And so beyond your having been directly involved in the validation of the 30
United States laboratories, what other laboratories have you been directly involved in the training and implementation and validation of?

A. Just may clarify, the 30 U.S. laboratories, I have definitely been involved in the training of all of them and in the validation of many of them.

Outside the United States, I have been involved in the training of all the other laboratories and in the validation of some of them.

Q. Okay. Let's -- let's be specific. Let me go back to the United States.

Could you please tell us your -- those 30 laboratories in the United States that you mentioned previously, if you could list them for us.

THE COURT: Are they listed in the exhibit?

THE WITNESS: Yes, they are listed in the exhibit.

MS. DELLA MAGGIORE: Q. Are they listed in the exhibit?

A. Yes, they are.

Q. Very good.

MS. BELES: To which I'm going to object based on my prior objection of hearsay, just so the Court knows.

MS. DELLA MAGGIORE: Q. And let's be very specific with those labs that you have been involved in the training, implementation and validation process outside of the United States.

A. You would like -- they also appear on this list.
Q. Please briefly tell us how many, where they are located?
A. Okay. Thank you.

There are eight in Australasia and five in the rest of the world, the rest of the world includes Ireland, England, Scotland, and Canada.

Q. And in all of these 44 laboratories that are on People's Exhibit 2, are they all forensic laboratories engaged -- let me ask you that, are they all forensic laboratories?
A. Yes.

Q. You mentioned previously SWGDAM, could you please tell us what that stands for?
A. Scientific working group DNA analysis methods. And in order to make it possible to say it, we usually insert an "I," so S-W-I-G-D-A-M.

Q. SWGDAM?
A. SWGDAM.

Q. Tell us what that entity is?
A. It's an FBI sponsored and organized group of about 70 scientists drawn from north America and invited guests who the FBI utilize to develop guidelines for DNA analysis.

Q. Who makes up that committee, if you will?
A. There are about 70 persons on that and they are drawn from practitioners across North America; and academics and invited guests from the rest of the world.

Q. And so is it fair to state that they are scientists that represent federal, state, and local forensic DNA laboratories in the United States and Canada?

MS. BELES: Leading.
THE COURT: Overruled.

THE WITNESS: Yes.

MS. DELLA MAGGIORI: Q. And so is it also fair to state that they provide the guidelines for the validation of probabilistic genotyping systems?

MS. BELES: Objection, leading.

THE COURT: Overruled.

THE WITNESS: Yes.

MS. DELLA MAGGIORI: Q. And the most recent guidelines as it would pertain to the use of probabilistic genotyping and STRmix, what date would those guidelines have been published?

A. It's the only -- only guidelines. It's not the most recent. It's the original and it's 2015.

Q. And what -- what has basically -- have they made any recommendations regarding STRmix or its simple guidelines that a laboratory must follow?

A. I don't believe STRmix is specifically mentioned in them at all. There are guidelines that labs are expected to follow for the validation of any probabilistic genotyping system. Probabilistic genotyping can be abbreviated in the United States as prob gen or PG if any of you wish to shorten it.

Q. And so could you please explain when you talk about the 30 forensic laboratories in the United States, do you have any familiarity with whether or not those 30 laboratories meet or exceed or something other than what the guidelines set out by SWGDAM?
A. All those laboratories meet or exceed the guidelines set out by SWGDAM.

Q. How about State of California Department of Justice?
A. Yes, it does.

Q. What familiarity do you have with the California Department of Justice as it pertains to STRmix?
A. I've been involved in training I believe six cohorts of their staff and involved in their -- with their validation group in multiple events regarding the validation.

Q. Are there any other scientific working groups or organizations made up of scientists that have likewise, like SWGDAM, formulated guidelines for PG or prob gen?
A. Yes.

Q. Tell us about those.
A. With specific regard to the United States, there are two with published guidelines. They are the International Society of Forensic Geneticists which may be abbreviated ISFG and the President's Council of Advisors on Science and Technology which may be abbreviated PCAST. Those two groups have published guidelines. There is another United States based organization called OSAC, O-S-A-C, that has an advanced draft about which I'm not at liberty to speak.

Q. And so what is the interplay, if you will -- of those two organizations, ISFG and the PCAST, what is the interplay with probalistic genotyping?

MS. BELES: Objection, vague "interplay."

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. So ISFG and PCAST is
it fair to state are given certain guidelines to follow when utilizing PG?

A. Yes.

Q. Who makes up the ISFG?

A. In the specific regard that I'm speaking it's the ISFG DNA commission and that is a group of scientists who are appointed to the commission by invitation. The lead author of the published guidelines is Dr. Michael Cobel who is a United States citizen who works at the National Institute of Science and Technology, abbreviated NIST.

Q. And so is ISFG, does -- does that group work similarly to SWGDAM or does -- do you understand my question?

MS. BELES: Objection, vague.

THE COURT: Did you understand the question?

THE WITNESS: Yes, sir.

THE COURT: Overruled.

THE WITNESS: In the broad sense they are similar. SWGDAM is very much practical and practitioner focused. Where ISFG tended to be little more high level in its recommendations.

MS. DELLA MAGGIORE: Q. What does that mean?

A. SWGDAM very much spelled out the exact experiments it wanted for validation. ISFG did not do that.

Q. What, if any, significance does PCAST have as it pertains to prob gen?

A. PCAST was a very high profile publication, being the president's council, it appeared, I think just drawing on my memory, October 2016. It was not specifically on prob gen,
but it did have an extensive section on that.
I apologize for my accent.

Q. Did -- did ISFG endorse the use of prob gen?
A. Yes.

MS. BELES: I object still as hearsay.

THE COURT: Is this your Sanchez objection, counsel?

MS. BELES: If the Court is taking that as truth, then in order to -- to discuss the Kelly prong, yes, it is still Sanchez.

MS. DELLA MAGGIORE: As far as the People are aware, in Sanchez that is case specific and also would have to pertain to material that would be meant for testimonial purposes.

Furthermore, this is an expert who certainly is involved in and utilizes the guidelines contained in ISFG writings similarly as SWGDAM. This isn't hearsay.

THE COURT: Matter submitted?

MS. DELLA MAGGIORE: Submitted.

THE COURT: Submitted?

MS. BELES: Your Honor, if the Court is taking it for truth, then it is being offered as hearsay. It's not being offered as a basis for an opinion as to whether or not any of these organizations, you know, certified STRmix. Yes, I'm objecting as hearsay.

We submit it

THE COURT: I don't think your objection goes to the question. But with regard to your Sanchez objection,
overruled.

THE WITNESS: May I be reminded of the question, please?

MS. DELLA MAGGIORE: I would like that as well. Let's go back. Can we have the question read back.

(Court reporter read back.)

THE WITNESS: My answer is yes.

MS. DELLA MAGGIORE: Q. Dr. Buckleton, following the creation and development of STRmix, did it go through developmental validation?

A. Yes.

Q. Could you please elaborate on what developmental validation is as it pertains to STRmix?

A. Again, we have followed the developmental validation as outlined by the SWGDAM guidelines. There are a number of requirements and for brevity at this point I will mention I think two of the highlights. One of those is to repeat a large number of the calculations by hand and another is to trial the system with a large number of true donors and known non donors.

Q. And so was that done — was a developmental validation done following the creation and development of STRmix?

A. Developmental validation was done for each of the commercially-released versions of STRmix, so it has been done more than once.

Q. Did you author any research papers as it pertains to the developmental validation of STRmix?

A. Yes.
Q. Could you elaborate on that for us?
A. I was a coauthor in the published developmental validation of STRmix which appears in Forensic Science International Genetics.

Q. What is Forensic Science International Genetics in the regard of the publication that you're talking about?
A. It is a scientific journal.

Q. And are there other published articles that have appeared in various scientific publications contained in the forensic science committee regarding the validation of STRmix?
A. Well, there are 24 publications that relate to STRmix. They are not all specifically on the validation but certainly some of them are.

Q. And so these -- these 24 publications, are those peer reviewed publications?
A. They are all peer reviewed publications.

Q. What does that mean -- what does "peer reviewed" mean in the scientific community?
A. Peer reviewed is your publication is submitted to two anonymous referees selected by the editor. Those referees provide the editor with a report that may require amendments of further work. And if that is done to the satisfaction of the editor, the article is then published.

Q. And those 24 peer reviewed publications that you just mentioned, were those considered to be favorable or not when -- as it pertains to STRmix?

MS. BELES: Objection, vague.
THE COURT: The word "favorable," sustained.

Counsel, let me remind everyone we are at the first prong of this Kelly hearing and what the scope of the issues are. That is why I began the morning reminding everyone and everyone concurring as to the scope of the issues at this hearing.

Next question.

MS. DELLA MAGGIORE: Q. Do those 24 peer reviewed publications endorse the general acceptance of STRmix?

MS. BELES: Objection, A, leading; B, the province of the Court.

THE COURT: Overruled.

THE WITNESS: Those 24 publications outline all the algorithms and usage of STRmix and the underpinnings of the utilization of it. I guess your question was do they endorse; and yes, they do. I'm an author on them all.

MS. DELLA MAGGIORE: Q. But are you the only author?

A. No.

Q. So who are the other authors?

MS. BELES: Objection, compound, 24 publications.

THE COURT: Overruled.

THE WITNESS: I've compiled a list of these publications for you that does have the names of the other authors. But in brief, they constitute the three developers often with other external persons.
MS. DELLA MAGGIORE: Q. Who are those?
A. They range. For instance, there are some FBI authors on one of them and other meritorious scientists around the world.

Q. So if we could begin to talk about at what point in DNA analysis does STRmix enter the picture?
A. In --

Q. At what point is it used?
A. Indeed. The analysis of DNA proceeds exactly as it has for a great many years in the development of an STR profile. The profile is produced by the machine electronically and it is that electronic data that STRmix takes as its import. There are also some inputs from the human operator and then STRmix proceeds with its analysis.

Q. So is it fair to state the DNA gets processed using STR analysis or PCR analysis, but profiles are evaluated using STRmix?
A. Yes.

Q. What is the STRmix model based on?
A. The STRmix model is based on established mathematical principles and models for the behavior of PCR.

Q. So if you could please tell us what is STRmix biological model?
A. The biological model is based on interpreting the quantity and quality of DNA in the profile.

Q. Are there basically two steps in the STRmix biological model, one being deconvolution and the second being statistical analysis?
A. Yes.

MS. BELES: Leading.

THE COURT: We are -- we are going to get into this area which I'm not certain is within the scope of the first prong of the Kelly analysis.

MS. DELLA MAGGIORE: However --

THE COURT: Next question.

MS. DELLA MAGGIORE: Q. Could you tell us what deconvolution is?

A. In STRmix, deconvolution generates a weight for each genotype proposal. Essentially it is attempting to determine those genotypes that best explain the data.

Q. And so what is the process involved in deconvolution?

A. Markov chain Monte Carlo, that might be abbreviated MCMC.

Q. Is that an algorithm?

A. Yes.

Q. How long has it been around for?

A. In its totality it's been around since 1950, but its roots date back to 1908.

Q. What happened in 1908 with MCMC?

A. Dr. Andrey Markov published his first paper on the analysis of Russian poetry. He was seeking to determine whether the next letter was a vowel or consonant based on the previous letter and he developed the Markov chain.

Q. And I believe you said something took place in the 1950s pertaining to MCMC, what is that?

A. Specifically the Monte Carlo aspect was added algorithms
by scientists. So the 1940s, during the production of the
atomic bomb for the second World War, the two were put
together in a Markov chain Monte Carlo or MCMC in the 1950s
and could not be implemented until the advent of fast
computing in the 1970s. From then on, it has been a very
prevalent tool in science.
Q. And so has it been widely accepted by scientists?
A. Yes.
Q. And is MCMC utilized in any other sort of academia or
common everyday subjects?
A. Yes.
Q. Could you please tell us about that?
A. Yes.
MCMC is a -- is one of the dominant tools used for this
type of problem in engineering, molecular genetics, physics,
linguistics, weather predicting, stock market, sports
betting, and my favorite is code breaking.
Q. Why is that your favorite?
A. I think it's just lovely.
Q. Did that assist us in any sort of wars that took place?
MS. BELES: Objection, relevance, Your Honor.
THE COURT: Well, we're talking about reliance
and I suppose the application does bear on the notion of
reliance. Let's -- but as interesting historically, I think
I'll allow the response.
And please, again, Ms. Della Maggiore, keep in mind
where we are in this hearing, that is what is the scope of
the hearing and the issues to be addressed.
THE WITNESS: To answer the question, some of the principles involved in Markov chain Monte Carlo were established by Alan Turing who was instrumental in the second World War in breaking the code for the enigma machine which was the German coding machine used in the second World War. And the code breaking group is often accredited with shortening the war by possibly up to a year and saving a great many lives.

MS. DELLA MAGGIORE: Q. So when it comes to -- so deconvolution in the STRmix model, it -- it simply uses MCMC algorithms; fair statement?

MS. BELES: Leading, Your Honor.

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. What is involved in the deconvolution process in STRmix is MCMC, correct?

MS. BELES: Leading, Your Honor.

MS. DELLA MAGGIORE: I'll ask it a different way.

Q. As far as MCMC algorithms as utilized by STRmix, is that process -- that step generally accepted in the scientific community?

A. Yes.

Q. And then onto another step involved in STRmix, would that be the -- the statistical analysis that is performed?

A. Yes.

Q. What is involved in that step?

A. That is very much standard mathematics, it essentially applied the third lower of probability and follows from
Bayes' theorem of 1763.

Q. And that statistical analysis that STRmix is engaged in, is that generally accepted in the scientific community?
A. Yes.

Q. Have -- the scientific principles utilized in STRmix, have they all been peer reviewed?
A. Yes.

Q. Has the principle of prob gen been around for many years?

MS. BELES: Objection, vague "many years."

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. How long has prob gen been around in the scientific community?
A. Since 1999.

Q. Is it also -- is prob gen being taught at scientific seminars throughout the United States?
A. Yes.

Q. And also all over the world, correct?
A. Yes.

Q. Could you elaborate on likelihood ratios, what is that?
A. The likely ratio is the modern and most powerful -- I apologize for my accent, is the modern and most powerful expert of the weight over evidence.

Q. The utilization of likelihood ratio, is that something generally accepted in the scientific community?
A. Yes.

MS. BELES: Objection, vague and leading.

THE COURT: Overruled.
THE WITNESS: Yes.

MS. DELLA MAGGIORE: Q. STRmix, is it reliable?

MS. BELES: Vague.

Your Honor, I'm sorry, did I not say it loud enough?

Objection, vague. According to whom? How? What does that mean?

THE COURT: Sustained.

MS. DELLA MAGGIORE: Q. In your opinion is STRmix software reliable?

MS. BELES: Same objection.

THE COURT: Reliable as to what, counsel?

MS. DELLA MAGGIORE: As to the way it computes mathematical methodologies.

THE COURT: Have you completed your question?

MS. DELLA MAGGIORE: Yes.

THE COURT: You can answer that.

THE WITNESS: I didn't perceive a question.

THE COURT: Restate it, please.

MS. DELLA MAGGIORE: Certainly.

Q. Is STRmix software reliable as it pertains to the mathematical methodologies that it performs?

A. Yes.

Q. And what do you base that opinion on?

A. Millions of trials.

Q. Anything other than that millions of trials?

A. I wrote --

MS. BELES: Withdrawn.
THE WITNESS: -- a robust basis in science.

MS. DELLA MAGGIORE: Q. And are there any other learned scientific treatises, published papers, books, or other writings that you can cite for us that demonstrate the acceptance of STRmix in the scientific community than what you have already stated?

A. Yes.

Q. What are those?

A. There are a number of authors completely unconnected with our group who are utilizing STRmix and are publishing in the public domain.

Q. Elaborate on that.

A. They appear in the list I gave you.

Q. What list?

A. I'm hoping it's a list I have given you. If not, I shall find it.

Q. Could you, please.

A. I can tell you without needing to refer they are all one group utilizing it in Melbourne, Australia for various experiments they are doing.

Now there are quite a large number of conference presentations being made on the utilization of STRmix.

THE COURT: Were you going to ask specific questions about each of them or can the list be found at a break and you can use the witness's time --

MS. DELLA MAGGIORE: Certainly.

THE COURT: -- to explore the issues before the Court?
Doctor, look for it later and let them ask their questions.

THE WITNESS: Thank you, sir.

MS. DELLA MAGGIORE: Q. In your opinion, Dr. Buckleton, does STRmix reliably deconvolute DNA profiles and provide likelihood ratios that can be used for forensic case lab work?

MS. BELES: Objection, leading.

THE COURT: Overruled.

THE WITNESS: Yes.

MS. DELLA MAGGIORE: Q. Is it your opinion that the science behind it is well established?

A. Yes.

Q. And is it fair to state that what STRmix is doing is -- is improving the ability of forensic labs to confirm or deny the identity of DNA samples, particularly when multiple sources are involved?

MS. BELES: Objection, leading, Your Honor.

THE COURT: But it's a request for an expert opinion, counsel. Why would this be an improper question?

MS. BELES: It's not a question, it is a statement. And because -- I mean I can deal with it on cross, but it seems abundantly clear to me Ms. Della Maggiore is using direct quotations for Dr. Buckleton. So I think what was just said was, number one, quite lengthy and perhaps compound. I didn't make that objection. But secondarily, it is -- it is Ms. Della Maggiore saying it, not the doctor.

So it is -- it is the very opinion that the Court has to
decide whether -- the weight of and on prong one, and so I
mean to ask the question of the witness, not give the answer
to the witness and ask for affirmation is my request.

THE COURT: Submitted?

MS. BELES: Submitted.

THE COURT: Submitted?

MS. DELLA MAGGIORE: Submitted.

THE COURT: Overruled.

THE WITNESS: Yes.

MS. DELLA MAGGIORE: Q. Could you tell us,
Dr. Buckleton, approximately what percentage of North
American laboratories have now purchased STRmix and if any
have gone live and that they are using it or in the process
of validation?

A. Sixty-five percent.

Q. So 65 percent are what?

A. Have purchased.

Q. And of the 65 percent of the North American laboratories
that have purchased STRmix, what percentage has actually
validated it and began to use it in actual casework?

A. I don't have that as a percentage, but 30 laboratories,
all laboratory systems.

Q. Are there other forensic laboratories in North America
who are in the process of validation?

A. Yes.

Q. And are you able to tell us any certain amount of those?

A. Yes, it's about 70.

Q. What laboratory would be -- what laboratory in North
America would be the longest user of STRmix post validation process?

A. The U.S. Army Criminal Investigation Laboratory.

Q. When does that date back to?

When did they began using it after the validation process in actual casework?

A. I think it was 17:00 on the 30th of November, 2014.

Q. Is there --

MS. BELES: I'm sorry, I didn't catch that date, November?


MS. BELES: Thank you.

MS. DELLA MAGGIORE: Q. What would be the next, if you're able to state, longest utilizer of STRmix post validation process?

A. Erie County in New York state.

Q. And is the FBI currently utilizing STRmix?

A. Yes.

Q. Are you familiar with when it was that they began to use it post validation in actual casework?

A. Yes.

Q. When is that?

A. Am I allowed to look at the list?

Q. Would that refresh your recollection?

A. Certainly would.

Q. Please do so.

A. They were the fourth lab in the union to go live and that was on the 1st of December 2015.
Q. So it was the Army, then Erie County, and there is the third, I don't believe we heard who that was?
A. San Diego Police Department.
Q. Were you at all part of their training or validation process?
A. Yes.
Q. How so? What did you do?
A. I physically trained their staff and have interacted with their technical lead numerous times between that date and currently.
Q. And so what year did it occur that they began to use it in actual casework post validation, if you're familiar?
A. The 5th of October, 2015.
Q. As it pertains to the FBI's implementation and use of STRmix, does the FBI comport with the SWGDAM guidelines?
A. Yes.
Q. And are you familiar with the validation date and use of STRmix in actual casework at the Department of Justice California?
Q. When a laboratory is -- I'm going to formulate a different question. One moment, please.
(Pause)
MS. DELLA MAGGIORE: I have no further questions, thank you.
THE COURT: Do you want to start fresh after lunch?
MS. BELES: Whatever the Court wants.
THE COURT: Why don't we do that.
We've had no break this morning.
We'll begin after the lunch hour, 1:30.

THE WITNESS: Thank you, sir.

THE COURT: 1:30.

(Lunch recess)

THE COURT: Ready to proceed, Ms. Beles?

MS. BELES: Yes.

THE COURT: You may do so.

CROSS-EXAMINATION

BY MS. BELES: Q. Good afternoon, Dr.

Buckleton.

A. Good afternoon.

Q. I'm going a bit in chronological order regarding STRmix.

STRmix was developed -- began to be developed in 2009, correct?

A. No, 2011. The lab closure was late '09 and STRmix was developed in 2011.

Q. Okay. Prior to the development of STRmix in 2011, what was your focus in DNA analysis?

A. My focus has been on the interpretation of DNA profiles for the whole -- of the period of '88 until now.

Q. Just to frame our discussion of STRmix, the identification of profiles prior to STRmix was based on random match probability, correct?

A. In California, but not New Zealand.

Q. All right. Were you familiar with RMP prior to your beginning developing STRmix?
A. I'm one of the authors on the foundational paper for RMP.

Q. So you are fully familiar with RMP, correct?
A. Yes, I'm the uncle of RMP.

Q. You're the father of STRmix, fair?
A. I'm one of the three fathers of STRmix.

Q. Understood.

In 2009, when the Melbourne lab closes, you and Mr. Taylor were asked to determine a way to fix the problem that that lab had; is that accurate?

A. Dr. Taylor.

Q. Dr. Taylor, yes?
A. Yes.

Q. Taylor?
A. T-a-y-l-o-r.

Q. In the beginning, you and Dr. Taylor began looking at mathematical solutions to problems with RMP; is that correct?
A. No. RMP was not used in Australasia at that time at all.

Q. At all.

The problem in Melbourne was different than RMP

A. Misuse of software called DNAmix.

Q. Did you -- were you any parent or family member of that DNA software?
A. Yes.

Q. Did that DNA software utilize the MCM theorems?
A. No.

Q. Did it use MC?
A. No.

Q. But that prior software that you were a part of the development of was found to be insufficient to create identifications; is that fair?

A. I'm in no way anything to do with the programming, however, it is based on a paper that I'm a coauthor of in 1997 which arose out of the mathematics developed for the OJ Simpson trial.

Q. Understood.

Let's get those -- let me tease out some of what you just said, especially in terms of your parentage of the software for STRmix.

Is it fair to say that you and Dr. Taylor and Dr. Bright --

A. Yes.

Q. -- developed the mathematics that -- the mathematical algorithms that are the basis for STRmix?

A. Not mathematical algorithms, they have heritage that predates my birth; we applied them.

Q. Understood.

You utilized known mathematical principles and tried to put them in a software program that became STRmix, correct?

A. Yes.

Q. At a very basic level, STRmix is coded by someone other than you and Dr. Taylor and Dr. Bright, correct?

A. No.

Q. Oh.

A. In the particular version that is used in Cal DOJ and in
this case it was coded by Dr. Taylor.

Q. Himself?
A. Yes.

Q. Are you a part of the coding -- were you a part of any of the coding of STRmix software?
A. Only vicariously inasmuch as I worked on algorithms and checked the workings of it.

Q. In terms of development of STRmix by you, Dr. Taylor, and Dr. Bright, that culminated in a product of STRmix in 2011, correct?
A. Yes.

Q. And that product STRmix is a software program, correct?
A. Yes.

Q. And in the old days, you could get it on a floppy drive or CD. Now some way it can be downloaded correct?
A. Not so much. It is installed on people's computers by our installer who is a U.S. company called Niche Vision. I think you say Niche in America.

Q. Tomato, tomato. Thank you.

When you say "it is installed," it is a commercial software, correct?
A. That's correct.

Q. And the agencies that purchase STRmix must pay for it, correct?
A. Yes.

Q. Do you have any financial interest in the purchasing of STRmix?
A. No.
Q. Do you hold a patent for the STRmix program?
A. No.

Q. Is there a patent held for the STRmix program?
A. No.

Q. Do you hold a patent for one of the mathematical theorems that is the basis for STRmix?
A. No.

Q. Do you hold a patent for MC?
A. Maybe.

Q. Maybe.

A. I do have a patent on the application of Monte Carlo to DNA profiles that is not related to STRmix.

Q. That was my question.
A. Yes.

Q. You in fact have prepared a document in relation to the admissibility of STRmix or some of the issues that come up in these admissibility hearings, correct?
A. Yes.

Q. When was that document created?
A. It's live. I'm improving it in real-time.

Q. And you provided it to Ms. Della Maggiore, correct?
A. Yes.

Q. So you do hold a patent on utilization of the Monte Carlo method in DNA, but that has nothing to do with STRmix; am I correct?
A. The Sidney Monte Carlo, but my initial ideas were naive.

Q. Unreliable?
A. Certainly not. Unimplementable.
Q. Okay. So once -- once STRmix becomes a commercially available program, how is that program disseminated to the world community?
A. Speaking of California Department of Justice, they purchase licenses and they are installed places with licensing by remote system on their computers.
Q. And it -- was STRmix marketed to any agencies?
A. STRmix is marketed internationally and across the world.
Q. Are you involved in any of that marketing of STRmix?
A. No.
Q. Are you utilized in any of the marketing materials as quoted, anything like that?
A. I would imagine I am, but I don't read those.
Q. All right.
A. But I would think I would be.
Q. Does Dr. Taylor still have the same role -- does Dr. Taylor have the same role with STRmix as you do at this time?
A. We've never had the same role.
Q. Okay.
A. We are different people with different talents, but he is no longer the programmer.
Q. How about Dr. Bright, is she still involved?
A. We are all still involved, but we all have very different -- we all bring very different things to the table.
Q. So let's talk a little bit about what STRmix does, a very little bit, to move us into the ideas of the community. Does STRmix -- is STRmix best used on mixed sample DNA?
A. No. It's perfectly capable of being used on anything from single source to mixed.

Q. So it is -- is STRmix -- if STRmix is used on single source DNA, does it come up with the same likelihood ratios and would there be a random match probability analysis?

A. It does as long as we have a good template of single source profile.

Q. Understood.

If we have solid single source profile, RMP and STRmix are going to have equally successful results?

A. Yes.

Q. Understood.

Now, is it fair to say that STRmix in the deconvolution process is in your view doing something different than our RMP can do with mixed donor samples?

A. Different -- it's different in detail, but the principles have been applied in RMP. The principles involve the utilization of information in peak height. Previous RMP methods were manual and needed really some substantial differences to be able to extract a major from a profile.

Q. All right. Let me follow up on a couple of those. I think I know. I need it for the record.

In RMP with multiple donor samples, there could be some deconvolution, but you would have to have higher allele peaks in order to do that manually with RMP; is that true?

A. Yes.

Q. What STRmix does is mathematically creates the likelihood ratios without that peak height or with it or
something different?
A. With it.
Q. With it.

Now, does STRmix utilize other bits of information that RMP does not utilize in order to create a likelihood ratio?
A. It utilizes the height information better than is capable of being done manually. It also models stutter. It models s-t-u-ter -- s-t-u-t-t-e-r, better than can be done manually.

Q. All right. So in two -- well, let me ask you this.

In using RMP for a multiple donor sample, would there be a -- automatically be a different result if you utilized STRmix for that same multiple donor sample?
A. The answer is sometimes. So if you have a clean major, then we would get the same or strongly similar answer. But if you're speaking of the minor or a more -- a more difficult deconvoluted sample, then STRmix would be more powerful.

Q. So when an analyst -- when an analyst uses -- strike that. Let me get the language right.

What name would you give to the person who uses the STRmix kind of boots on the ground at the agency, would that be an analyst?
A. I guess so, yes.
Q. So when an analyst is utilizing STRmix, are -- is there certain information that the analyst has to input in order for STRmix to function?
A. Yes.
Q. What are those items of information?
A. If you would permit me to answer your question more holistically. The analyst's function prior to running STRmix involves some artefact management and an assignment of the number of contributors.

Q. Some artefact management and the number --
A. Assignment of the number of contributors. I believe there is a section in that document I sent you that outlines this.

Q. Right. But we're --
A. Getting it on the record.

Q. -- getting it on the record, exactly.

Once --

MS. BELES: Your Honor, do you mind if I'm seated?

THE COURT: Not at all.

MS. BELES: Q. The -- once the analyst receives a profile from wherever, either its own lab, another lab, et cetera, the analyst, he or she, then would enter in that sample, whatever they have. They would enter in an assignment of number of donors and they would enter in some artefacts?

A. That happens prior to the entry.

Q. Okay.

A. It's standard. This is historic, it's not use. It's not a part to STRmix. It's artefact management. We often call it clicking off. And in particular, in the version and use of Cal DOJ, we need the analyst to remove spikes and --

Q. Anything else?
A. -- forward stutter. I believe there is management protocol at Cal DOJ that is very excellent. And Cal DOJ, they ignore two alleles, SE33 and D1. But I would love it if you could just clarify that with Mr. Halsing when the time comes.

Q. Speaking of which, did you speak with Mr. Halsing over the lunch hour about your testimony?

A. No. I'm a little surprised at the question.

Q. I had to ask.

So once -- once the analyst enters in that material, does the artefacts management clicking off, removing spikes for Cal DOJ, and then assigns a number of donors, then it is the program that creates the likelihood ratios, correct?

A. Yes.

Q. And those likelihood ratios, are they reproducible?

A. Yes.

Q. Are they always the same -- for the same sample?

A. As long as we define "same" as within experimental areas. They are not identical.

Q. Sometimes they are a little bit different, but you attribute that to experimental error rate?

A. That is Monte Carlo fate. Monte Carlo, as you well know, is a casino in Europe. Monte Carlo is a numerical simulation and we don't get an identical answer, but they are typically very close to each other.

Q. Okay. So can -- can -- once the analyst introduces the assignment of the number of donors, does the program only contemplate that number of donors?
A. Yes.

Q. So let's talk about the use of STRmix in -- let's just talk about the United States at the moment. Okay?

A. Okay.

Q. So in the U.S., you indicated that the Army got it first, correct?

A. Yes.

Q. And then you listed a couple other places, but one statistic you mentioned during direct I want to clarify. You indicated that 65 percent of what labs utilize STRmix?

A. Purchased. I said purchased.

Q. Purchased?

A. This is an estimate of the number of U.S. laboratories that have purchased STRmix.

Q. You estimate 65 percent of all laboratories in the United States have purchased STRmix software?

A. If you want the exact source of my data, 65 percent of the laboratories that appear on the accreditation list, forensic accreditation list, have purchased STRmix.

Q. It wasn't 65 percent of labs purchased PG software. It was specifically 65 percent of all labs that have purchased STRmix; is that right?

A. Sixty-five percent have that are accredited forensic laboratories.

Q. Okay. So STRmix is not the only PG software, correct?

A. No.

Q. I asked that incorrectly.

Are there other PG software programs?
Q. Approximately how many in the U.S.?
A. Well, in the U.S. is an interesting question.
Q. Let's --
A. Used in the U.S., now, you mentioned hearsay earlier and now you're really getting me to hearsay.
Q. It was found to be okay, so we're going with it.
A. All right.
Q. I'll ask the question.
A. I'm sure that is Your Honor's decision.
Q. We think of the seven using TrueAllele and about two are using Lab new word Retriever.
Q. Okay. So theoretically the same type of software?
A. No.
Q. No.
A. Okay. Lab Retriever is qualitative. TrueAllele on medical may not be similar. I actually genuinely don't know.
Q. Let's talk about if STRmix has had any review by any of the other PG software makers.
Q. Has STRmix been reviewed by any of the people associated with TrueAllele?
A. No.
Q. Any people associated with Lab Retriever?
A. No.
Q. Do you make available to people associated with TrueAllele the STRmix software?
A. We would not make it available; however, they have obtained it nonetheless.
Q. TrueAllele has?
A. We believe Dr. Perlin who is principal of Cybergenetics, the parent company of TrueAllele.

Q. Same question, just to finish out, would you allow the purchase of the STRmix software to anyone associated with Lab Retriever?
A. No, but they have attended our training.

Q. All right. So in direct examination, you discussed the idea of peer review. I want to go one step backward and talk about the PCAST report.
   Okay?
A. Okay.

Q. PCAST report made recommendations about the validity of STRmix, correct?
A. No.

Q. Okay. Why don't you tell us what PCAST said about STRmix?
A. The principal matter in the -- well, PCAST doesn't directly address STRmix, although it is named in there. They speak about prob gen in general. It would be quite improper of them really to make a recommendation on software.

Q. Certainly would.
A. Finding three is the -- is the clause of interest in the PCAST report.
   And part one of three says the community should move rapidly toward more appropriate methods of probabilistic genotyping.
   Clause two of finding three cites that foundational
validity has been established up to three person mixtures
where the minor exceeds twenty percent.

In the addendum to the report, they clarify that and
change the word "minor" to "person of interest."

Q. And that was -- let's go back. I know what you're
talking about. Again, we're making a record here.

Originally PCAST was discussing PGS, probabilistic
genotyping software, and made some recommendations about how
to get better validation of PG software, correct?

A. They make recommendations, yeah, I think they do. I
think that is correct.

Q. Right. One of the issues was -- one of the issues was
validation of STRmix in general, correct?

A. No.

Q. It was not validation?

A. No.

Q. Was it peer review?

A. No.

Q. Okay.

A. I don't think they make any direct reference to STRmix
except on a footnote commenting on New York versus Hillary.

Q. I should have asked those questions about PGS in
general.

Does PCAST make any recommendation about PGS?

A. I don't think they use the acronym "PGS," but, yes, they
do.

Q. Okay. Dr. Buckleton, does PCAST make any
recommendations about probabilistic genotyping software?
A. Yes.

Q. What recommendations does PCAST make?
A. I'm guessing you have it in front of you, I don't. But I think they essentially asked NIST, N-I-S-T, to do studies.

Q. In response to the PCAST analysis of probabilistic genotyping software, did you meet with members of PCAST?
A. Yes.

Q. And did you make recommendations to them about how they should change the language of their original report?
A. I wouldn't phrase it that way, no.

Q. Did you contribute -- or did you contribute to PCAST your ideas of how probabilistic genotyping software might be better in the future?
A. So I've interacted with PCAST by a number of emails and phone conversations and then meeting on I believe November 20th, 2016, at the Eisenhower Executive Building. The particular meeting on the 20th to which you are referring was dominated by Dr. Perlin of Cybergenetics arguing with Dr. Lander of PCAST and using up nearly all the time. At the end of that time, I did have a very cordial and constructive discussion with the three members of PCAST who were present and they outlined between us -- we collectively outlined what they thought we should do so that they would be satisfied that STRmix was valid beyond the limitations they had incorrectly in my opinion suggested.

Q. STRmix or PGS?
A. STRmix. By this time, Dr. Perlin had rather preemptively left the building.
Q. So in that meeting with PCAST, the original meeting with Dr. Perlin, did you agree that empirical testing of PGS software should be done?
A. I agreed it should be done and had already been done. They were insisting on publication and I believe the process has happened properly. You have before you the draft of that publication.
Q. We'll get to that draft, Dr. Buckleton. It's a draft, correct? Correct?
A. Well, it's a draft inasmuch as it is submitted to the journal and is in the refereeing process.
Q. Let's talk about the empirical testing.
   How would one as a scientist not associated with any laboratory that uses STRmix be able to empirically test the efficacy of STRmix?
A. Well, the usual way is as to SWGDAM guidelines as outlined, that has been done multiple times across the world.
Q. Well, no -- perhaps, Doctor, you could explain what you mean by "empirical testing."
   My question went to if STRmix can be empirically tested, can it be empirically tested by someone not associated with STRmix either as a developer or as a user within a lab?
A. Well, it would have to have STRmix. I don't know how you could test something you didn't have any access to. They would need access to it.
Q. Right.
   The only people that have access to STRmix are the developers and the people who have purchased the software,
correct?
A. No.
Q. Who else would have access to STRmix?
A. We have at different times placed versions with different parties.
Q. Such as?
A. Initially we placed a version with NIST. They have now purchased it, but certainly initially we placed it with them.
Q. You gave it to NIST without the licensing fees?
A. Yes.
Q. Why did you do that?
A. The same time we did that with California Department of Justice, we actually gave them a version early on for them to try.
Q. A sample of sorts?
A. I'm not a very commercial person. I don't really think that way.
Q. Okay.
A. These were respected colleagues. We had no intent whatsoever selling STRmix anyway. It was going to be an Australasia product. In fact, Steven Mars from the California Department of Justice is the one that talked my management into releasing it internationally. We linked him a version for his own use and experimentation. And I think we would heavily do that with many other people.
Q. Go back to the original question about the empirical testing that was conceivably recommended -- the empirical testing of STRmix that PCAST mentioned with which you agreed
at a later date. To your knowledge, has there ever been any empirical testing of STRmix?

A. Yes.

Q. And is that by agencies that utilize STRmix?

A. Yes. They've utilized it, also includes those who just purchased and are not in casework, yes.

Q. That isn't why I used "utilize."

Anyone who has STRmix and is either --

A. Experimenting with it or thinking of using it in casework or any other purpose.

Q. But not yet operational?

A. Yep.

Q. Did Dr. Perlin in the perhaps contested meeting with PCAST indicate that he believed that empirical testing was unnecessary?

A. Yes, he did.

Q. And isn't it true that PCAST in their addendum to the 2016 report, which may also have been in 2016, believed the empirical testing to be necessary to excise assumptions or errors in assumptions that might be put into the use of the program?

A. The addendum of PCAST in January '17?

Q. I'm sorry, yes.

A. Yes, they requested or demanded empirical testing be published. That empirical testing in the case of Stonic (phonetic) already happened. They demanded it be published.

Q. Has there been empirical testing published since the PCAST addendum in early 2017?
A. Yes.
Q. Yes?
A. Yes.
Q. What empirical testing was published since PCAST's recommendation early 2017?
A. FBI internal validation which reports a very sizable empirical testing and I believe is in the material that I hope has made its way to you.
Q. So the FBI international validation --
A. Yes.
Q. Just on a -- this is an important point. Just on a definitional level, do you include internal laboratory validations as empirical testing of STRmix?
A. Yes.
Q. In your meetings with PCAST or in their recommendations, was there a different type of empirical testing of STRmix contemplated besides internal testing or internal validation?
A. I think PCAST were keen on a third party validation by NIST the last year.
Q. NIST has conducted a third party empirical testing since the PCAST addendum in early 2017?
A. Well, I no longer work at NIST. I left NIST in December '16, so I have no firsthand knowledge of that. But I believe they have not and have indicated they will not.
Q. Oh.
Okay. Do you need water?
A. No, I'm good. Thank you.
Q. So the -- in terms of published empirical testing, we
have the FBI internal validation. Anything else you can think of?

A. If I could outline to you the situation.

Journals have a policy of not publishing validations. We are very lucky to have got the FBI one published. They, many of them including the Journal of Forensic Sciences, have a policy of not publishing validations. Validations are exceptionally dull reading and they would not want multiple validations published and I think we were lucky to get one.

Now, the draft --

Q. We'll get to the draft.

MS. DELLA MAGGIORE: Could the witness be entitled to answer the question?

THE WITNESS: I'm happy to wait.

THE COURT: Next question.

MS. BELES: Q. I want to pinpoint, in your experience, the forensic journals have a policy of not publishing internal validation studies?

A. General forensic science has an explicit policy of not publishing. Many others have an implicit policy of not publishing.

Q. In your opinion, that is because they are boring on some level?

A. Well, I've been directly told by the editors that is the reason.

Q. Is there any concern about -- in your opinion or your experience, about the publication of internal validations as being biased to that particular user of that particular
product?
A. No, I don't think so. I think it is really quite the opposite. A great many internal validations are in the public domain. I'm certain all of them would be made available for defense to review by any independent scientist they chose. But my experience working with those people doing the internal validations, they are the harshest critic of the software. They are generally looking to test it before putting it into use. I would feel it as really the opposite. There is no bias to slip through some software they felt was inappropriately. They are genuinely testing it to see if it is fit for purpose.

Q. Do people or agencies that have paid -- let me come back one step.

The licensing of STRmix costs in the area of what, 30 to 50,000 dollars?
A. I don't follow that. But I think your number for first license is approximately right. I think it is about 27ish thousand U.S. If that is important, I can obtain those numbers for you. There are three sources of revenue: People pay for training, pay for licensing, and they pay for support hours. Many of those support hours go to assisting validation and implementation.

Q. I'm sorry, Dr. Buckleton. Perhaps I didn't write fast enough. Three sources of revenue: For licensing?
A. Training, licensing, and support.
Q. Got it.

You conduct the training on the STRmix or not?
A. There are about 12 trainers, but I certainly have done a large number of them. At each training event we tend to front with three trainers at most. I would be one of three.

MS. BELES: Your Honor, I'm just checking a note, if I may.

Q. So in speaking about PCAST, in speaking about moving to the validation idea, when you were speaking with the prosecution, it appeared to me that there were vali -- internal validation of labs occurs with really three guidelines, the PCAST, International Society of Forensic Geneticists, and then SWGDAM; is that right?

A. You've named them correctly, but SWGDAM is completely dominant. We all work with the SWGDAM guidelines.

Q. Because SWGDAM guidelines -- you're talking about the 2015 ones, but SWGDAM created guidelines before that, haven't they?

A. Never on validating probabilistic genotyping, but they have been creating guidelines since the early '00s.

Q. Right.

In terms -- you just said something about validating -- validation within the labs. One of the things that you do as a trainer is assist the lab in how to conduct the validation process, correct?

A. Yes.

Q. Of the labs that utilize -- utilize including purchased, going through validation or actually using STRmix in the United States, how many of those did you participate in the validation process?
A. So I am unsure of the number. And you phrased the question as me personally, but we have a team of about 12. Between the 12 of us we would have supported the validation of the majority of U.S. laboratories.

Q. I'm actually asking the personal question. If you can estimate of--

A. I would have been personally involved in I would have thought plausibly a third of those, that would come at the tail end, the troubleshooting end if something needed looking at.

Q. Were you testifying on direct examination, in very short notes I wrote, that you had personal involvement in review and/or I think problem solving or troubleshooting?

A. Yes.

Q. In all American labs?

A. Well, if you count the various processes that I actually set up and the spreadsheets I've set up, then it would be not quite all. I'm sure Cal DOJ did most of it themselves with any vicarious assistance from us.

Q. Vicarious?

A. Assistance from us.

But for many of the others, their involvement is much larger than that.

Q. So did you assist in the validation process for Cal DOJ?

A. Me personally, yes, to a moderate extent; my codevelopers more toward a significant extent.

Q. In terms of the other two working groups, International Society of Foreign Geneticists --
A. Call it ISFG, if that helps you.
Q. -- ISFG has had guidelines in existence for laboratories since when?
A. 2016, I think, but I wouldn't mind checking that.
Q. Do you have something with which to refresh your recollection?
A. I can do that while you're asking the next question, if you want.
Q. Great. I could pause.
A. If we look at the end of my CV --
Q. Process if you want to refresh your recollection for dates, please do, read it silently to yourself, look up at me. We can see if your memory is refreshed.
Is your memory refreshed, Dr. Buckleton?
A. No, I have not found it in the list I was looking at.
Q. Estimate 2016 ISFG created guidelines; is that fair?
A. Yes.
Q. The PCAST guidelines we talked about were in the beginning of this year, correct, the addendum?
A. The addendum came out January 17th.
Q. Well, apparently there is probably other nondisclosure or some other secret.
You mentioned OSAC, tell us what that stands for at the very least
A. Organization of Science Area Committees. And there is no nondisclosure. Simply expected that we don't disseminate it widely in advance of its publication.
Q. Okay. Now, speaking of publications and drafts, I have
been provided and you started to mention a few times a draft
of a paper -- not the right academic word, roll with it for
the moment, a research paper, basically in compiling internal
validations of PGS within over 30 laboratories, right?
A. Thirty-one.
Q. Right.
You are one of its authors, correct?
A. Yes.
Q. And there are an estimated 25, 30 other authors,
correct? I didn't count.
A. I think it's more.
Q. I'm sorry?
A. I think it is more.
Q. Okay. Okay. More in the range of 45 to 50 because I
counted quickly, is that fair, authors?
A. Yes.
Q. Now, this paper was assembled in response to the PCAST
addendum or for some other purpose?
A. To the meeting on the 20th of November with PCAST, this
was what we discussed with them or what I discussed with
them.
Q. But it is -- it is still a compilation -- number one,
it's not published, correct?
A. It is in the process, but it is not actually published.
Q. Number two, it is compilation of internal validation?
A. Yes.
Q. Of each of these labs, correct?
A. Yes.
Q. All of the labs that are contained in this draft conduct internal validation studies, correct?
A. Yes.

Q. These are labs that are in the United States, correct?
A. No.

Q. Not all of them?
A. No.

Q. Were you involved with each of the internal -- internal validation studies that are compiled as part of this draft?
A. I would have been involved in a fraction of them.

Q. A fraction of them?
A. Uh-huh (affirmative).

Q. Okay. This paper -- also one of the ways science works is that you mentioned that you have blind referees -- "referees" the correct word?
A. Yes.

Q. -- look at the paper and it's not just proofreading, it is scientific proofreading, correct?
A. They vary.

Q. In this particular paper of the 45 to 50 authors, I mean that everyone -- strike that whole question. Not strike it, ignore it for the moment.

Isn't it true that in academic or forensic papers such as this, there was a recommendation of review, correct?
A. Yes.

Q. And isn't it true in this draft that the recommended reviewers are the same 45 to 48 people who are listed as the authors?
A. No.

Q. No?

A. No. The editor sends it out to two anonymous referees who are unknown to me but will not be an author.

Q. Oh, it's just the way it printed out.

MS. BELES: Your Honor, may I approach just a moment --

THE COURT: Yes.

MS. BELES: -- to verify some of my facts here.

Q. Dr. Buckleton, this is the draft as I received it. What it indicates on page one suggested reviewers at the bottom. Is it true the beginning of the second page has the same authors?

Does that suggest that those are the suggested reviewers or something different? Is it just the way it printed out?

A. I've not printed this in a particular helpful way for you.

Q. Okay. Are the suggestive reviewers the 45, 48 authors?

A. No, certainly not.

Q. Because perhaps the authors of said paper should not be reviewing themselves?

A. I'm sure they would do a lovely job, but that is not the process.

Q. Aside from that draft and the published FBI internal validation process, are there any other peer review articles of STRmix since the PCAST recommendation of early 2017?

A. No.
Q. Are there any peer review articles about STRmix by people who do not use or did not develop STRmix?
A. No.

Q. Let's just ask about the other -- the crossways peer review. Have you ever reviewed TrueAllele?
A. Yes, I'm the referee on the foundational paper for TrueAllele.

Q. And have you -- did you need to gain access to the TrueAllele software in order to do that?
A. No.
Q. No?
A. No.

Q. Could you explain how -- could you explain how either PGS, TrueAllele, or STRmix could possibly be peer reviewed without access to the software?
A. I was asked to review the mathematics of it --

Q. Okay.
A. -- which I did.

Q. Has anyone, not -- a developer or a trainer or a person who uses STRmix ever peer reviewed the mathematics of STRmix?
A. Plausibly. We've been cloned twice.

How would I answer that question? I have to know what everyone on earth had done.

Q. I'm asking about review, if someone ever conducted a paper or referee'd a paper like you did on TrueAllele, on STRmix?

STRmix is mathematical conclusions?
A. Yes, two separate organizations have cloned us and
published their work.

Q. Okay. Is that reviewing it or cloning?

A. Maybe not getting the cloning?

Q. I'm sorry?

A. It's cloning. Their purpose was to recreate the software and sell it themselves --

Q. Right.

A. -- in one case and make it free ware in another.

Q. So that -- what I'm asking, is cloning the same thing as reviewing?

A. No, I don't think it is probably.

Q. Has anyone other than people who use STRmix or the developers of STRmix ever peer reviewed the mathematics of STRmix?

MS. DELLA MAGGIORE: Objection, relevance.

THE COURT: At this point --

MS. BELES: Did you want a response, Your Honor?

THE COURT: Once again, I began this hearing with consensus of everyone what the scope of the hearing is. Yes, this is not relevant to the scope of the hearing. However, the last good portion of the cross-examination has been not -- irrelevant to the scope of this hearing. Now the People wish to say lack of relevance. I'm going to allow the question.

THE WITNESS: I think the answer is yes, all the 24 publications outlining various aspects of the
mathematics of STRmix have been reviewed by two anonymous referees including the core mathematical paper of, I think, 20 -- of 2014.

MS. BELES: Q. So it is your position there have been 24 publications that have reviewed STRmix's mathematical bases as STRmix, not just a matter on MCMC but as STRmix?

A. There are 24 STRmix publications, all of which have had two anonymous reviewers, that would be 48 reviewers.

Q. I just asked for publication, Dr. Buckleton.

There have been 24 publications that have reviewed the mathematical foundation for STRmix -- for use of STRmix?

A. I and others published 24, all of which have been reviewed.

Q. I and others.

Have you been listed author of every publication that has discussed the mathematics -- the mathematical foundation to STRmix?

A. Yes.

Q. Okay. I'm sure that, Dr. Buckleton, you know that I would ask you about this.

Is -- has STRmix ever been provably wrong on its likelihood ratios?

A. No.

Q. Could you explain what happened in the Hillary case in New York about --

MS. DELLA MAGGIORE: Objection, relevance.

MS. BELES: It's reliability, Your Honor.
THE COURT: I'm sorry?

MS. BELES: Reliability.

The issue before the Court is whether it has been
generally accepted in the forensic science community and is
reliable.

THE COURT: That was not raised this morning
when I saw the consensus from counsel as to the purpose of
the first prong of the Kelly review and the scope of today's
hearing.

MS. BELES: Well, then I -- Your Honor, the
way I wrote it down was, prior to the Court saying it, maybe
I was looking at my own notes not writing down carefully,
scientific method generally accepted as reliable by the
relevant scientific community in the -- upon consensus drawn
from a typical cross-section of the relevant scientific
community. Reliability is certainly a part of prong one.

THE COURT: Do you have the exact cite from
Kelly? That is not what was said this morning. That is
not.

MS. DELLA MAGGIORE: It's not.

THE COURT: Not what counsel indicated this
morning. If we open it up to that, it is a different
hearing.

MS. DELLA MAGGIORE: That is not what Kelly
states. It's limited to whether or not STRmix is
sufficiently established to have gained general acceptance in
its field.

THE COURT: That is not what was indicated
this morning either.

MS. BELES: Well, I think perhaps we -- so --
ookay. Couple things, Your Honor. The Court made a ruling,
allowed me to ask a question but made a comment about what
the parameters were.

There's -- there's aspects of the Kelly case that I do
want to argue. I do not want to do it in front of Dr.
Buckleton. If we want to take little time to refine our
issues because I do think I get to ask about reliability, not
just -- and I do think some of my questions that the Court
said were irrelevant are not irrelevant given the ruling in
Kelly. If we want to talk about this quickly.

THE COURT: Now you raise it?

MS. BELES: Well, I didn't think the Court
thought my questions were irrelevant, that is why I bring it
up.

THE COURT: There was no objection to what the
Court thought -- the Court said.

That is why I began with my -- my very purpose this
morning was to have a consensus as to the first prong of the
Kelly test and what the scope of this hearing was.

MS. BELES: So, Your Honor --

THE COURT: Counsel agreed and now counsel
wishes to expand it greatly, so....

MS. BELES: Your Honor, I don't think I wish
to expand anything greatly from the Kelly case. I made this
clear in my papers. If I was inartful this morning not
adding the reliability issue, it is at page 30 in Kelly.
It's at 17 Cal.3rd 24 pinpoint 70.

"The reliability of a method must be established."

And then it goes further, "One of the prongs requires that it be generally accepted as reliable by this relevant scientific community." It's not just accepted. It is accepted as reliable.

But there is another aspect of Kelly I didn't think I had to bring up this morning, but I don't want to bring it up in front of the witness.

THE COURT: All right. Then, Doctor, if I could ask you to please step down for a period of time.

We'll recall you when this argument is concluded.

(The witness left the courtroom.)

THE COURT: Record reflect, first of all, that the witness has left the courtroom.

MS. BELES: I apologize if I didn't refine it in relation -- I viewed Kelly's first prong as exactly the way I wrote it in my motion and as it is stated at page 30 which is that the proponent of the evidence must establish that the scientific methods utilized be generally accepted as reliable by the relevant scientific community.

The Court also included the consensus idea, that is from People v. Shirley 31 Cal.3rd 18. I just didn't say the idea reliable. I want to make clear to the Court that the Kelly -- one, failure in Kelly was -- part of it is who's testifying and who is saying this is a reliable method and who is saying this is generally accepted. That case was a voice print case. I think it is Agent Nash who testified.
What the Kelly court found is that Agent Nash had too much of a personal bias and then interest in voice print analysis of technology to be relied upon. So -- so that is why I'm asking questions about Dr. Buckleton's involvement in each of these peer reviews; in each of these trainings; in each of these validations -- internal validations of the labs.

I understand the Court may not like that argument at the moment because maybe I should have made it this morning, I apologize for that. But Kelly was based on the idea that the person who is testifying cannot have a personal bias, interest, or motive in the success or lack of success of the procedure, that you have to have an independent expert. I'm going to argue that as well. But I think reliability included in the Kelly first prong is not general acceptance, it has to be generally accepted as reliable.

Secondary aspect, when the Court indicated some of my questions were irrelevant in its opinion, okay, I don't think they are irrelevant given my eventual argument, there is no question what I'm doing here, this is all Dr. Buckleton. Dr. Buckleton made it. Dr. Buckleton peer reviewed it. Dr. Buckleton said that it was part of the validation studies, it was part of the training, and that is not an independent witness make.

I have a copy of Kelly if the Court wants to review it given the dynamics at the moment. It does have highlights on it, but no notes.

It was Lieutenant Nash not agent. I apologize.

THE COURT: So you say you have a copy of
Kelly there?

MS. BELES: I do.

THE COURT: I read it this way: The first prong requires a showing as we discussed this morning.

The third prong would go to reliability of the scientific procedure.

This issue of reliability seems to me goes beyond the first prong.

MS. BELES: I think that prong three discusses the reliability of the process used in this case. I think in prong one it requires a reliability of the generalized process. That is the way I've always read Kelly.

I think that prong three talks about was the process used correctly and reliably so.

I think STRmix has to be a reliable scientific method under prong one as well.

MS. DELLA MAGGIORE: That is not what the case law states.

The Court couched the issue in the absolute correct terms in that it must be shown that the new technique has gained general acceptance in a relevant scientific community and that the expert who is offering that opinion is qualified. That is where it stops. It should not be read to mean that there is some sort of process by which the Court is supposed to evaluate the reliability by therefore getting into whether or not it has been independently peer reviewed or validated. That is not the issue.

THE COURT: I think at some point that Ms.
Beles does have every right to challenge that, the
to the reliability. I just don't think this is the time.

MS. DELLA MAGGIORE: That's correct.

THE COURT: That is the very reason why I
wanted to talk with you both this morning. I brought up the
scope of the first prong. This is a Kelly first prong
hearing. The challenge was -- you're asking me to decide is
this a new technique or is it a breakthrough or a significant
change in methodology when the motion was first made. I
found that defense has a right to -- to challenge that first
prong as to whether it is accepted in the scientific
community.

Whether it is a reliable method, whether each of these
agencies has adopted an unreliable method, I think defense
certainly can challenge that. I just don't think under Kelly
this is the time.

MS. BELES: See --

MS. DELLA MAGGIORE: I believe the Court has
the correct interpretation.

MS. BELES: See, I don't know how that could
happen. I don't know how we can excise reliability of the
novel technique from general -- prong three talks about
whether STRmix is used the way STRmix is supposed to be used,
doesn't talk about reliability. Reliability is embedded in
the general consensus as I wrote it, as I understood all the
case law. I'll -- I've been wrong before, I'll be wrong
again. But general acceptance is not general acceptance that
it is tomfoolery, it is general acceptance. It is accepted
as reliable by the relevant consensus of the typical scientific community. I think reliability is embedded in prong one.

Reliability technique used on this particular case is Mr. Halsing saying -- I mean it may come later as prong three.

The other thing is practically how can I talk about reliability -- how can I make any motion to exclude on reliability issues or on this issue that it's not peer reviewed by anybody that is independent which is clearly within Kelly unless I ask the witness who is here now about reliability?

I mean the Court -- I don't -- if I overstepped or I didn't clarify, I really viewed that reliability was embedded in the general acceptance notion because it has to be generally accepted as reliable. Maybe it's a parenthetical that I -- I certainly wrote it that way. I think that is what it means because generally accepted as balderdash would certainly not get past Kelly prong one.

MS. DELLA MAGGIORE: General acceptance in the relevant scientific community, that is all that prong one requires and such that if it is the forensic science community, it is being generally accepted. It is being used. It is being endorsed. It is being adopted by those people and those experts who understand it, who utilize it, who have put it through testing, who have validated it, who can say that, yes, we the scientific community of forensic labs and all of us scientists out there we generally accept this.
THE COURT: I don't think we're at the point with this witness and on the first prong that you argue you shouldn't have done it, you shouldn't have accepted it, it's not reliable, it's not a good scientific technique, it hasn't had the scrutiny that it should. The fact that these various agencies have accepted it, they are forensic science -- members of the forensic science community. You're challenged with the witness and you're arguing they shouldn't have done it.

Well, if they've done it or not is what we are here to learn today, aren't we? Maybe I'm not making myself clear.

MS. BELES: This is like in Kelly, Lieutenant Nash was intrical to the imprint of voice analysis, intrical in all the training around the world, country. Dr. Buckleton is the same -- is in the same category and we're going to have Dr. Buckleton say I developed STRmix, STRmix is good, people bought it, people are using it, I reviewed it, I've -- I held validation studies. It's all Dr. Buckleton. There has been no independent review. The general acceptance, I can't -- I cannot fathom how that could not involve reliability. If you didn't have reliability, then Sargon Enterprises comes rearing its dragon-like head. I don't think prong one -- I mean we always call it prong one. Prong one I always contemplated the reliability part of that.

Prong three talks about the correct scientific procedure, correct scientific process of STRmix: Number of donors go in, did X, Y, Z happen. Dr. Halsing will talk about it if we get to that point.
THE COURT: If we get to prong three at some point, absolutely you have the right to cross-examine on the issues that you're raising now. I just, again, don't agree that we're at that point.

MS. BELES: No.

THE COURT: The issue raised initially in your papers had to do with whether this was a new technique or whether it was an evolution in the existing technique of DNA analysis. I thought that should come from an expert. That is why we are here today as was my ruling on your initial motion.

Now that we are here, as I said, I wanted to hear from both of you this morning so I would know what everyone understood to be the scope of the first prong hearing.

MS. DELLA MAGGIORE: I understood it to be exactly what comports with all the case law under Kelly. And not only that, this area that she wants to attack, she -- she can attack that. She can bring in cross-examination of this. She could bring in her own witnesses to try to say that this is controversial and you can't trust it. But what we are to deal with here today, the very issue is narrowly defined by court, supported by case law, not just what Ms. Beles thinks that she wants to read into it. It is what the case law says. And to then go off about Sargon, this is not a 402 hearing, this is an admissibility hearing. That is what it is and it is confined to the narrow issue that the Court stated correctly before we began this.

MS. BELES: I brought a motion. I was very
clear that I argued that, well, DNA evidence has been readily accepted as reliable to relevant scientific community; this particular STRmix testing has not. That fails prong one of Kelly Fry. That is the argument I made. I made Sargon in my original argument as well.

THE COURT: I wish you would have said something this morning.

MS. BELES: All I can do -- say is I apologize for that.

Also, if we're only talking about general consensus, I don't -- I'm -- I apologize for that. That's all I can do. But my argument was extremely clear. I'm not bringing up anything new.

I'm talking about peer review, Kelly the case. The time is -- now, whether you call it prong one, you call it 402, it is not time for cross-examination. It is time to say this evidence is not sufficiently reliable and there is not a general consensus or opinion by somebody who doesn't have a personal stake in it, therefore, it must be excluded. That is why I'm here, that is what I'm asking for.

What I'm asking for is exclusion. I wasn't asking for hearing -- to hear the sound of my own voice. I was asking for a hearing because we don't have independent evidence. We have Dr. Buckleton who is inextricably intertwined with every potential validation or peer review. That is part of the Kelly. I apologize I didn't do it this morning. I'm doing it now. That is all I can do. I thought my papers were clear and Sargon is not just some random thing that I'm
saying. I said it throughout my papers. I didn't come in here for ProfMan. I know the Court didn't. I came in to argue this should not be admitted into this case because of Kelly and Fry and Sargon.

If I didn't crystallize it right away, please don't hold it against Mr. Davis.

It is not time for cross-examination. It is a threshold issue. Dr. Buckleton and Mr. Halsing should not be able to testify to STRmix.

THE COURT: What do you mean they should not testify to it?

MS. BELES: It should be excluded because as of the moment we don't have anybody saying this is reliable and relied upon in the scientific community except for the most bias person they could find who is the developer, trainer, educator, and writer about all the STRmix, which is just like Lieutenant Nash in Kelly.

THE COURT: Do you agree that during this hearing this Court must decide whether or not this technique in DNA analysis is generally accepted in the forensic scientific community? Do you agree?

MS. BELES: No, it doesn't have as reliable.

THE COURT: Let's take a break.

MS. BELES: Generally reliable would be, I agree.

THE COURT: Take 15.

(RECESS)

THE COURT: So the issue remains as to the
scope of cross-examination.

So, Ms. Beles, tell me again where are you going with your cross-examination?

MS. BELES: Where I am going with my cross-examination is that the determiners -- the determination of general acceptance and general acceptance of reliability, which is I believe embedded within the first prong of Kelly, is not met because of a lack of independence of the witness, like Lieutenant Nash.

I'll tell you, Judge, I really do not feel good if I did not crystallize this this morning. I apologize for that.

But in rereading, reading over again, and reading Kelly again, I really realize that Dr. Buckleton has some of the same infirmatories as an expert that Lieutenant Nash did in Kelly. My cross-examination was going into what is the peer review, what is the reliability. I was also going off some of the direct that was asked about mathematical techniques. I understand I didn't object to it because I thought that is where we were going.

Final question I was asking in terms of reliability, this is all known, this isn't any secret, there is a specific case that I wanted Dr. Buckleton to explain why there were two different results and whether it was STRmix that was used twice or if -- it's the Hillary case, with two "l's." It was going to be very -- just a couple more questions, couple followups on direct, and I was done.

My argument fundamentally is that even if the Court -- number one, if the Court found that there was acceptance in
the community, the Court was getting it from a source that was not reliable and therefore should exclude it. I also in my papers moved to exclude STRmix entirely because gatekeeping of Sargon. I was actually almost done. But the Hillary case was one aspect and I did not. I did not alert the Court about Lieutenant Nash. I was not implicit. I thought it was argument I could make at the end. I think Kelly stands for the general idea that general acceptance has to be acceptance as reliable. Because general acceptance as not reliable or general acceptance as partially reliable doesn't make any sense for admissibility. Again, apologize not crystallizing the issue when the Court said it this morning. I think reliable is embedded in it.

I think my strongest argument is that of the evidentiary problems with Dr. Buckleton testifying as being so -- his opinion being so interwoven with his personal interest akin to Lieutenant Nash in Kelly.

MS. DELLA MAGGIORE: Yes, Your Honor, I would like to first point out in defendant's motion to exclude STRmix DNA analysis, page 11, line 25, she cites, "The goal is not to decide the actual reliability of the new technique, but simply to determine whether the technique is generally accepted in the relevant scientific community." She goes on to cite this case that I'll give the Court, "If the scientific literature discloses the technique is deemed unreliable by scientists significant either in number or expertise, the Court may safely conclude there is no general acceptance." She cites People v. Barney, 1992 case, 8
Cal.App.4th 789 at 810.

She goes on to cite People v. Kelly, "Ideally resolution of the general acceptance issue would require consideration of the views of a typical cross-section of the scientific community including representatives if there are such of those who oppose or question the new technique."

What I would point out to the Court is that it -- it is -- has now become apparent that defense is not asking questions that are relevant as to prong one. She is rather challenging credibility or some perceived bias that in her mind she believes exists. What she in effect is doing is ignoring the evidence that is before the Court that shows that it has been peer reviewed. It has been peer reviewed by undisclosed referees.

THE COURT: But now you're arguing reliability.

MS. DELLA MAGGIORE: I'm simply stating, Your Honor, that she's ignoring what has been testified to by Dr. Buckleton as -- as far as, yes, there have been peer reviews. She wants to ignore that.

And overall, this is not injurious to her client. She still would be able to cross-examine on this issue before the trier of fact. She -- no one is precluding her from presenting expert testimony or other people from the relevant scientific community to explain contradictory feelings out there in the scientific community.

THE COURT: Ms. Beles.

MS. BELES: So after what was just quoted in
my papers, the sentence in my papers at page 12 reads, "The
gatekeeping role of the Court requires that the proponent of
the evidence make a substantial showing that the proffered
methods are generally accepted as reliable." So I state that
there. Quotation from Kelly at 31 saying, "In determining
the question of general acceptance, courts must consider the
quality as well as quantity of the evidence supporting or
opposing a new scientific technique." I always said
reliable.

I'm not ignoring the testimony. I have a position about
the testimony. And perhaps I might make the argument as to
what is injurious to my client and the Court might make the
ruling, not the prosecution deciding what I'm thinking about
it. I take some issue with that characterization and that
whole way of arguing that she's trying to do something.

So what I'm saying and what I have said from the very
beginning is that I'm moving to exclude STRmix results. The
Court has provided a hearing pursuant to Kelly prong one,
whether you call it 402, we got down that rabbit hole at one
point, it doesn't matter.

I believe general acceptance in a vacuum. Without
general acceptance of reliability is not what Kelly
contemplates. I am using the Kelly case to make an
additional argument about the evidence that has been
presented by the prosecution. I couldn't make the Kelly
argument until -- the Kelly argument I'm making today about
Dr. Buckleton's bias and about the breaths or lack thereof of
peer review and independent discussion of general acceptance,
I couldn't do that until I knew it was going to be Dr. Buckleton and Dr. Halsing, only I couldn't do it until Dr. Buckleton testified. I can't say, I don't know, if Ms. Della Maggiore had told me last week, no, I got another expert, that motion -- that issue would have been moot.

So while I'm trying to make the best argument for my client, it is very clear I'm moving to exclude it. This whole idea of cross-examination, that is the whole point of my motion. I think the Court understands that. I don't want cross-examination. I think as a threshold matter STRmix should not be admissible based on the Kelly problem and the evidence that we heard thus far. We hadn't heard from Mr. Halsing. I don't think we're going to be able to find any peer review, any general acceptance from anybody that doesn't have a stake in it. That is what Kelly stands for in terms of the Lieutenant Nash problem.

THE COURT: The Lieutenant Nash problem, the individual who testified in Kelly, he was found not qualified to give an opinion at all. He was described as a technician lacking the background, training, and experience, and education to offer an expert opinion; isn't that correct?

MS. BELES: It is correct. I think that is where the rubber meets the road. I don't have the rest of the testimony. I think that may be -- may be a sticking point. I understand that. As opposed to hurling insults across counsel table, what she want -- I take responsibility what my argument is, I take responsibility what the law is, without doing any of that.
So I understand that may be the issue at the end of the
argument. Whether or not you -- whether or not the Court
finds that Dr. Buckleton was different in kind and in
expertise than Lieutenant Nash, that is one of my arguments.
As we were discussing it I thought the Court -- now, that Dr.
Buckleton -- now I'm in cross, the Court should know what I'm
doing here because you asked about it this morning and I just
didn't do it. I don't know what else to say.

I ask to be able to complete Dr. Buckleton. It's not
that much more. I ask to be able to ask about the Hillary
case. I'm sure Dr. Buckleton has a response that is minimal
and concise. A couple followup questions from my -- from my
notes and then I was done with Dr. Buckleton. And I would
ask to complete my argument once Mr. Halsing testified who
has actually been present the entire time which I didn't
object to. I'm not asking for remedy, but I would note that.

That is where we are.

THE COURT: Counsel, anything further?
MS. DELLA MAGGIORE: No.
THE COURT: Anything further?
MS. BELES: Submitted.

THE COURT: I looked at Kelly again after your
argument this morning. I feel absolutely that you have and
should have every right and should challenge the reliability
of the test. That is basic.

That is a basic defense attack whether we are talking
about in context of Kelly or not, wouldn't you agree?

MS. BELES: Yes. Yes, sir.
THE COURT: So I cannot agree that this is the
time, this is the vehicle in which to do it.
This is the first prong Kelly hearing that we're
conducting now. As I said, that was my very purpose in
everyone understanding the scope of today's hearing.
Kelly even uses the term "if accepted by a cross-section
of the scientific community, it is therefore reliable."

MS. BELES: I think that begs the question --
I didn't mean to interrupt.

THE COURT: I know you would, but that's
what -- in discussing the acceptance in the scientific
community, that is what the Kelly court indicated. I'm not
so certain it's all not founded on the Fry case which we
don't follow anymore.

MS. BELES: Right.

THE COURT: Nevertheless, if -- I've relied on
your representation. If you're telling the Court you just
have these few questions left and you wish to garner
information which may bear you feel on the overall
credibility of the witness, I'll allow the questions.

MS. BELES: Thank you, Your Honor.

THE COURT: But I want you to understand what
my ruling is with regard to the Kelly issue.
And I'm not making a ruling that the issue of
reliability is open in this hearing in the manner in which
you described, Ms. Beles.

Based on what you indicated and your purpose -- what you
indicated in terms of your further questioning and your
purpose, you may ask the questions.

MS. BELES: Thank you, Your Honor.

THE COURT: If we could have the doctor return.

(The witness returned to the stand.)

THE COURT: Okay. Thank you for your patience.

And, Ms. Beles, you may ask your next question.

MS. BELES: Thank you.

CROSS-EXAMINATION - resumed

BY MS. BELES: Q. You are familiar, Dr. Buckleton, with the Hillary case out of New York, correct?

A. Yes. Yes.

Q. In that case, was there a problem with the STRmix analysis?

A. No.

Q. Okay. Could you explain what happened with the PGS in that case?

A. There was no DNA evidence given at all in the case.

In the Fry hearing for the case --

Q. That is what I meant.

A. -- His Honor ruled this court finds the STRmix has been developed --

Q. Before the Court's ruling, which we will get to, let me ask you, were you involved in the Fry hearing in the Hillary case?

A. Yes.

Q. Did you testify?
A. Yes.

Q. And what year was that?

A. 2016.

Q. Were you the analyst -- was there -- was STRmix utilized to analyze a multiple -- any DNA evidence in the Hillary case?

A. Yes.

Q. Was another PGS used as well?

A. I believe so.

Q. And were -- did the two of them -- the two different PGS, probabilistic genotype software, systems, did they come up with different results?

A. I'm not sure.

Q. Okay. And was STRmix admitted in that case?

MS. DELLA MAGGIORE: I'm going to object to that question.

THE COURT: Sustained.

MS. BELES: Okay.

Q. Did you testify at the trial in the Hillary matter regarding STRmix?

A. No.

Q. You provided a number of articles to the prosecution and then thus probably to me in preparation for this hearing, correct?

A. Yes.

Q. Did you provide any list of questions for the prosecutor prior to this hearing?

A. Yes.
MS. DELLA MAGGIORE: Objection, calls for work product.

MS. BELES: I'm not asking the topic.

THE COURT: Just whether or not they were provided, overruled.

MS. BELES: Q. Did you provide a list of questions?

A. Yes.

Q. That -- let me finish, just to get it out. Did you provide a list of questions for the prosecutor to ask you in this hearing?

A. Yes.

Q. Did you provide a list of questions to me for -- that I should ask of you?

A. No, I don't think I did.

Q. Did you have multiple meetings with Ms. Della Maggiore regarding your testimony in this case?

MS. DELLA MAGGIORE: Objection, relevance.

MS. BELES: Bias, interest, and motive.

THE COURT: Are you going very far with this?

MS. BELES: Not that far, just a number.

THE COURT: That is fine.

For the record, the objection is overruled.

THE WITNESS: One phone call and one meeting.

MS. BELES: Q. You've talked about MCMC being relied upon in the general -- being generally accepted as a mathematical proposition, correct?

A. Yes.
Q. MCMC, current form, has been around for approximately how long?
A. Fortyish -- more than 40ish years. Much more than 40 probably.
Q. And MCMC is generally accepted in the scientific community, correct?
A. Yes.
Q. Oh, the prosecutor asked you if the mathematical methodology that STRmix performs was reliable, you answered yes; do you recall that?
A. Yes.
Q. Ms. Della Maggiore then asked you the basis of your opinion and you indicated millions of trials?
A. Yes.
Q. I think you may have meant -- I inquire, did you mean legal trials or a different type of trial?
A. Different type of trial.
Q. What type of trial did you mean?
A. I think the most specific was false donor trials.
Q. Well, could you explain to us what the word "trial" means within the context of scientific testing?
A. In the context I'm using it, we take a false donor and test it against the mixture and the desirable outcome is indications of exclusion for the false donors.
Q. Meaning if the PGS is working correctly, it should exclude the false donor, correct?
A. The vast majority of them, yes.
Q. Vast majority of the trials, I mean just in one?
That was too conversational.

In a false donor trial, just a single let's run this one time, it is hopeful that the PGS would be able to exclude the false donor as -- as the accurate result?

A. Can I say officially answer yes, as far as gives numerical output, not the word "exclusion."

Q. I understand that.

Okay. There would be a numerical exclusion output a false donor trial, correct?

A. Can I insert the word "indication," numerical indication of exclusion.

Q. Thank you. I want to clarify trial. Thank you.

MS. BELES: Check a few notes, Your Honor. I believe I'm done.

(Pause)

MS. BELES: Q. Prefacing this with a legal argument, in order to make the arguments that I discussed at the break, hypothetically if STRmix were found to be unreliable, would that have a deleterious effect upon your reputation in the scientific community?

MS. DELLA MAGGIORE: Objection, relevance and speculation.

THE COURT: Overruled.

THE WITNESS: Yes, I think so.

MS. BELES: Q. Is it therefore in your interest that STRmix be admitted in as many courts as possible?

A. Again, simply yes.
However, I just do not have that belief structure, I would never seek to deceive a Court.

MS. BELES: Okay. Thank you very much, Dr. Buckleton.

THE COURT: Anything else?

MS. DELLA MAGGIORE: No, Your Honor.

THE COURT: All right. Thank you, Doctor.

MS. DELLA MAGGIORE: People at this time would ask to admit People's Exhibit 2 into evidence.

MS. BELES: I object.

Submitted. I think I said that on the record in the middle.

THE COURT: People's 2 is a list of those members of the forensic scientific community that have adopted the use of the STRmix; is that correct?

MS. DELLA MAGGIORE: Correct.

MS. BELES: Your Honor, it was my memory the testimony indicated they were not all on that list, had gotten to the use, but the testimony would be clear on that than my memory this late in the day.

So I only take issue with the idea of use versus acquired or the word I was using was utilized. Utilize, I would agree that the witness testified to that. Whether or not they were actually using it was a different question in my mind.

THE COURT: Matter submitted?

MS. DELLA MAGGIORE: Submitted.

MS. BELES: Submitted.
THE COURT: People's Number 2 is admitted.
(People's Exhibit Number 2 was received in
evidence.)

THE COURT: Should we have the evening recess?
MS. DELLA MAGGIORE: No, I don't think so.
THE COURT: I need to remember Mr. Davis is in
custody, leaves at 4:15.

MS. DELLA MAGGIORE: Absolutely.
THE COURT: 9:15, 9:30 tomorrow.

Are you traveling back and forth?
MS. BELES: I'm traveling. 9:30?
THE COURT: Makes it easier.
MS. BELES: I can make it right at 9:30. 9:30 it is.

THE COURT: Ms. Della Maggiore, did you have
something else?
MS. DELLA MAGGIORE: Would the Court like me
to utilize the next couple minutes to establish the next
witness?

THE COURT: No.
MS. DELLA MAGGIORE: Wait until tomorrow?
THE COURT: Wait until tomorrow.
MS. DELLA MAGGIORE: Thank you.
THE COURT: Another exhibit, this goes back to
Ms. Beles.

Court is adjourned.

(Court recessed at 4:09 p.m.)
STATE OF CALIFORNIA  
) ss.  
COUNTY OF SAN JOAQUIN  

I, KELLIE A. GAFF, Official Court Reporter  
of the Superior Court of the State of California, do hereby  
certify:  

That I was present in the Superior Court,  
County of San Joaquin, State of California, at the hearing of  
the above-entitled matter, that at said time and place, I  
took down in shorthand notes all the testimony given and  
proceedings had; that I thereafter caused said shorthand  
notes to be transcribed into longhand typewriting by  
computer-aided transcription, the above and foregoing being a  
full, true and correct transcript of all testimony taken and  
proceedings had.

Official Court Reporter, C.S.R. No. 7567
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