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Tyrone Harvin v. State of Maryland, No. 1951, September Term, 2022. Opinion by Ripken, J.

EXPERT WITNESSES – ADMISSIBILITY OF EXPERT TESTIMONY – MARYLAND RULE 5–702 – ABUSE OF DISCRETION

Under *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993) and *Rochkind v. Stevenson*, 471 Md. 1 (2020), whether expert testimony is admissible is not a determination of whether the proposed testimony is correct or incorrect; rather, the question is whether the testimony meets a minimum threshold of reliability.

EXPERT WITNESSES – ADMISSIBILITY OF EXPERT TESTIMONY – MARYLAND RULE 5–702 – ABUSE OF DISCRETION

A trial court's determination as to the reliability of an expert's conclusion will sometimes require the court to consider data and assumptions that the expert has employed in deciding threshold points relating to the methodology. Here, the circuit court was faced with a challenge to the expert's input of data into TrueAllele software. The circuit court did not abuse its discretion in admitting the testimony because there was ample evidence from which the court could properly conclude that the expert's assumptions and parameters for testing did not render the TrueAllele data inadmissible; however, those same assumptions and parameters testified to by the expert are subjects available for exploration via cross-examination.

EXPERT WITNESSES – ADMISSIBILITY OF EXPERT TESTIMONY – MARYLAND RULE 5–702 – ABUSE OF DISCRETION

The inquiry into the admissibility of evidence under Rule 5-702 is a flexible one, and its focus must be solely on the expert's principles and methodology, not on the conclusions that they generate. Here, when faced with a challenge that some of the data generated by TrueAllele may not comport with Appellant's DNA profile, the court heard testimony from the State's expert explaining why TrueAllele might have produced such results and how she interpreted and validated those results into the final analysis. The circuit court determined that the potential discrepancies in the data were not fatal to the admissibility of the TrueAllele testimony. As the circuit court's decision was supported by the record, it acted within its discretion in admitting the State's expert testimony.

EXPERT WITNESSES – ADMISSIBILITY OF EXPERT TESTIMONY – MARYLAND RULE 5–702 – ABUSE OF DISCRETION – PEER REVIEW

Under the *Daubert-Rochkind* standard, one factor that trial courts may consider in evaluating the admissibility of expert testimony under Maryland Rule 5-702 is whether a theory or technique has been subjected to peer review and publication. Here, Appellant challenged the admission of testimony about TrueAllele test results due to an alleged failure to demonstrate that the software had been appropriately validated for use on samples that may include artifacts or bacterial contamination. The record, however, contained evidence of internal validation and multiple peer-reviewed studies, including studies that used samples exhibiting real-world conditions. Thus, the circuit court did not act outside the bounds of reason in determining that the TrueAllele software had been peer-reviewed.

EXPERT WITNESSES – ADMISSIBILITY OF EXPERT TESTIMONY – MARYLAND RULE 5–702 – ABUSE OF DISCRETION

When an expert's scientific testimony rests upon reliable grounds, it should be tested by the adversary process, to include competing expert testimony and active cross-examination, rather than excluding the testimony from jurors' scrutiny for fear that they will not grasp its complexities or satisfactorily weigh its inadequacies. Here, Appellant challenged the admission of the expert's testimony on the TrueAllele test results due to the allegation that the electrophoresis machine producing the data subjected to TrueAllele analysis was improperly calibrated. Appellant's challenge was based on his expert's testimony that the machine required calibration, and his assertion that the State's expert failed to follow laboratory procedures that dictated when recalibration was required. Yet, the circuit court also had evidence from the State's expert that the machine did not require calibration under the circumstances. The circuit court noted that the experts disagreed on whether the machine had been properly calibrated but found that the State's expert properly applied principles and methods required by the department's lab, which made this testimony proper to submit to the jury. As the circuit court was not required to negate the testimony of the State's expert based on the competing explanation of Appellant's expert, the circuit court did not abuse its discretion in admitting the testimony.

Circuit Court for Baltimore City
Case No. 118261014

REPORTED

IN THE APPELLATE COURT

OF MARYLAND

No. 1951

September Term, 2022

TYRONE HARVIN

v.

STATE OF MARYLAND

Shaw,
Ripken,
Harrell, Glenn T., Jr.
(Senior Judge, Specially Assigned),

JJ.

Opinion by Ripken, J.

Filed: September 26, 2024

In June of 2022, a jury sitting in the Circuit Court for Baltimore City found Tyrone Harvin ("Appellant") guilty of raping and murdering an 83-year-old victim in her home. The court sentenced Appellant to life in prison. As part of the case against Appellant, the State introduced DNA evidence analyzed by TrueAllele, a probabilistic genotyping software. Appellant presents the following issue for our review: whether the circuit court erred in concluding that the results of the TrueAllele analysis were admissible under Maryland Rule 5-702.[1] For the reasons to follow, we shall affirm.

FACTUAL AND PROCEDURAL BACKGROUND

In August of 2018, Officer Alesha Salyers ("Ofc. Salyers") of the Baltimore City Police Department ("BPD") was asked to perform a wellbeing check on the resident of an apartment building who had not been seen for several days. After knocking on the door and receiving no answer, Ofc. Salyers requested that a building employee unlock the apartment door. Inside, Ofc. Salyers discovered a bloodied unclothed woman lying on the floor, unresponsive and struggling to breathe. Ofc. Salyers immediately requested that a medic be dispatched to the location. The victim was transported to a nearby hospital, where she later succumbed to her injuries. The state of the victim's wounds indicated that multiple days had passed between the assault on the victim and her discovery by law enforcement.

Inside the victim's apartment, crime scene technicians observed suspected blood on the interior and exterior of the apartment door. They also observed several items scattered around the apartment. Technicians retrieved multiple pieces of evidence from the scene of

[1] Rephrased from: "Did the lower court err in denying Appellant's Motion to Exclude the Results of Trueallele Probabilistic Genotyping?"

the crime, including swabs of suspected blood, fragments of a broken lamp, and used condoms and condom wrappers. An autopsy was performed on the victim. The autopsy revealed that the victim suffered multiple injuries, including to the head, face, torso, and arms. There was also evidence that the victim had been sexually assaulted. A BPD forensic biologist analyzed numerous items, including swabs taken from various areas of the victim's body, as well as "pieces of a condom wrapper, a torn condom wrapper, another condom wrapper, condoms, one condom, swabs of suspected semen, swabs from the exterior of the front door, and a broken lamp." Also analyzed were DNA reference samples from both the victim and Appellant.

Christina Hurley ("Hurley"), a BPD forensic scientist, analyzed 22 DNA swabs taken from items recovered during the investigation. After performing a manual analysis of the DNA profile generated by a swab taken from a torn condom wrapper, Hurley determined that it "yielded a single source male DNA profile" which matched Appellant. Several other swabs contained DNA from a single contributor that matched the DNA profile of the victim. In addition, Hurley examined several samples which contained a mix of DNA from multiple sources. Some of these mixed-DNA samples were of insufficient quality for Hurley to draw any meaningful results or provide a match to a specific individual.

However, Hurley also identified three samples which contained mixtures of DNA sources that she believed could be used to provide reliable matches. These were: (1) a swab taken from the exterior of a condom ("condom A"), (2) a swab taken from the interior of a second condom ("condom B"), and (3) swabs taken from the exterior of a broken lamp

found in the victim's apartment.[2] Hurley believed that although each of the three samples contained a complex mixture of DNA from at least two different contributors, the samples also contained sufficient data to allow a computer program to generate a probabilistic model of the likely DNA profile of the contributors.

Thus, Hurley elected to run the three identified samples through TrueAllele, a probabilistic genotyping software designed to "develop a DNA profile from [an] evidentiary . . . sample" that can then be compared against the known DNA profile of individuals related to a given case. With the assistance of the TrueAllele software, Hurley was able to determine with 99.9% certainty that the primary DNA contributor in two of the three samples was the victim.[3] Hurley was also able to develop a probable genotype for a contributor other than the victim in each of the three tested samples. In all three of those samples, Appellant's DNA matched the inferred genotype generated by TrueAllele.

In a pretrial motion *in limine*, Appellant asserted that the State's use of TrueAllele to aid in DNA interpretation was inadmissible under Maryland Rule 5-702.[4] The circuit court denied the motion, and at trial, the DNA evidence was admitted over Appellant's

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[2] The State asserted that the lamp, which was discovered broken on the floor, had been used to bludgeon the victim.

[3] The sample taken from the interior of condom B resulted in "a partial DNA profile consistent with an indeterminant[] mixture of at least two contributors." Although one of the contributor genotype profiles could be inferred by TrueAllele, and was matched to Appellant, the other contributor could not be determined.

[4] Appellant also argued that introduction of the DNA evidence would violate his right to due process under both the Maryland Declaration of Rights and the federal constitution. This argument was rejected by the court, and Appellant does not reassert it on appeal.

objection. Subsequently, the jury found Appellant guilty of murder in the first degree, felony murder, rape in the first degree, and carrying a deadly weapon openly with the intent to injure. Appellant noted a timely appeal. Additional facts will be incorporated as they become relevant to the issues.

DISCUSSION

I. THE CIRCUIT COURT DID NOT ABUSE ITS DISCRETION IN ADMITTING EVIDENCE DERIVED FROM TRUEALLELE PROBABILISTIC GENOTYPING.

A. Forensic DNA Analysis in General

We begin with a brief discussion of the 'traditional' form of DNA analysis, which has long been recognized by the Supreme Court of Maryland as an important tool in criminal investigations. *See Armstead v. State*, 342 Md. 38 (1996). Deoxyribonucleic acid, or DNA, is comprised of a series of base pairs, which form the 'rungs' of a double-helix structure. *See Young v. State*, 388 Md. 99, 106–07 (2005). The specific position that a gene occupies in the double-helix structure is known as its locus. *Id*. at 107.

> The vast majority of the base pair sequences of human DNA are identical for all people. There are, however, a few DNA segments or genes, called "polymorphic loci," which are highly variable among individuals. The alternative forms of these individual polymorphic gene fragments are called "alleles." It is these polymorphisms that have great significance for forensic DNA analysis because they provide the basis for DNA identification.

Gross v. State, 371 Md. 334, 339 n.1 (2002) (internal citations omitted).

Forensic DNA analysis involves generating a profile based on a DNA sample taken from a potential suspect and comparing it to the profile generated from a sample of DNA recovered at a crime scene. *See Armstead*, 342 Md. at 52. This analysis typically "does not compare every nucleotide of the suspect's DNA with every nucleotide of the sample

DNA," but rather involves determining the specific allele pairs that appear at a series of identified loci in the suspect's genome and comparing those results with the alleles appearing in the corresponding loci of the sample recovered from a crime scene. *See id*. The Supreme Court of Maryland has recognized DNA testing as a "powerful evidentiary tool" and opined that its importance for both exculpatory and inculpatory purposes "cannot be overstated." *Allen v. State*, 440 Md. 643, 658 (2014) (internal quotation marks and citations omitted).

B. The *Daubert* Hearing

Returning to the case at bar, in October of 2021, the circuit court held a two-day hearing ("the *Daubert* hearing") addressing Appellant's motion *in limine*. In the motion, Appellant requested that the court preclude the State's experts from discussing the TrueAllele analysis pursuant to Maryland's *Daubert-Rochkind* standard of evaluating the admissibility of expert testimony. *See Rochkind v. Stevenson*, 471 Md. 1 (2020) (adopting *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993) for the purposes of applying Md. Rule 5-702).

i. The State's expert

During the hearing, the State called Hurley as a witness to testify about her experience using TrueAllele in the course of her work as a BPD forensic scientist. Hurley testified that when her lab receives a new DNA sample from the field, lab technicians first add heat and chemicals to attempt to isolate a purified form of the DNA present in the sample. Next, a technician estimates the total amount of DNA in the sample and amplifies the DNA so the lab's instruments can more easily detect the DNA. These samples, along

with concurrently prepared controls, are then placed in a calibrated electrophoresis machine, or "genetic analyzer[,]" which produces the dataset that can subsequently be used in genetic analysis.

Hurley explained that when performing a DNA analysis, she begins by attempting to draw any conclusions she can from a manual interpretation of the data. Hurley indicated that if a sample included a "complex mixture" of DNA from multiple sources, or if the sample was low quality, meaning that "some of the DNA is not fully detected,"[5] she can elect to input the data into the TrueAllele program to aid her interpretation. Hurley noted that TrueAllele does not play any role in the process of refining DNA or gathering data from a physical sample. Rather, TrueAllele is a "probabilistic genotyping software system." It can evaluate the data generated from the physical DNA sample, and, after tens of thousands of iterative analyses of the dataset, assigns a probability as to each possible allele present at each locus in the sample. The result of this process is that TrueAllele generates electropherograms, which display the presence of possible alleles as peaks on a graph. In this way, TrueAllele can use an imperfect DNA sample or a sample containing a mixture of multiple DNA sources to make an inference as to the likely genotypes present at given loci, as well as estimate the mixture weight for each DNA contributor in a sample. Thus, TrueAllele is a tool used to assist in analyzing DNA evidence when human review

[5] Hurley noted that in the instance where some portions of the DNA cannot be successfully sequenced, the resultant gaps in the data are referred to as "drop out." By contrast, "drop in" occurs when "an allele is present from an unidentified source that you cannot attribute to anything." Hurley agreed that 'drop in' is either "low level contamination" in the sample, or potentially an allele from another individual's DNA present in the sample.

of the raw data might not be possible.

Hurley testified that the BPD lab had been using TrueAllele as part of its DNA analysis procedure since the software was internally validated as effective in 2015. Per Hurley, the validation was conducted in accordance with nationally recognized standards, and the lab tested the TrueAllele software to ensure it was able to produce "reasonable and reproducible[]" results. Hurley also noted that TrueAllele was validated using test DNA samples which included between one and six different contributors, so as to "represent what we typically see in casework from good, pristine samples down to complex mixtures with degraded DNA[.]" As part of BPD's validation, the lab ran the test samples multiple times; the validation data was also shared with a lab at Cybergenetics, the company that owns and licenses TrueAllele, which completed a parallel test producing concordant results. The BPD validation was also externally audited by a third party, and Hurley testified that TrueAllele had been the subject of several peer-reviewed publications.

Hurley also testified that any data inputs are reviewed by two different analysts to ensure that the data quality is sufficiently high to generate usable results, and when an analyst generates TrueAllele results, those results will also be reviewed by a second qualified DNA analyst, as well as subjected to an administrative review. BPD policy dictates that TrueAllele results must be reproducible in order to be reportable, meaning at least two different runs of the program using the same data must show concordant results. The policy states that a maximum of six runs using "the same run conditions" is permissible. Additionally, Hurley noted that the electrophoresis machines that perform the genetic analysis receive yearly calibration and maintenance, in addition to being subjected

to additional recalibration as needed. While Hurley noted that some of the samples in this case included impurities in the DNA, this was not out of the ordinary, as "we do generally see [artifacts] in our samples." Hurley testified that these artifacts could result in pull-up—peaks in the TrueAllele-produced graphs that did not represent actual alleles present in the sample. Although Hurley testified that manual analysis could be used to determine whether or not a peak was a real allele or merely the product of an artifact in the sample, TrueAllele itself "is a continuous biological modeling software so it is assigning a probability to everything[,]" including the possibility that a presumptive artifact in the data is actually an allele from a DNA contributor.

During the hearing, the State introduced evidence concerning the three inculpatory DNA samples Hurley identified using TrueAllele. Hurley's report reflected that when she analyzed the data from the exterior of condom A, the sample appeared to contain a mixture of two contributors—a major female contributor, identified by manual analysis as the victim, and a minor male contributor whose DNA profile could not be identified with manual analysis. Hurley input the data into TrueAllele and instructed it to assume the presence of two contributors, one of whom was the victim. Hurley conducted three runs of the data, which generated a reportable inferred genotype for the minor contributor—that inferred genotype matched Appellant. A match between Appellant and the inferred genotype was between 1.55 million and 259 million "times more probable than a coincidental match to an unrelated individual in the . . . American population[,]" depending on the specific ethnic group.

Using data from the second sample, the swab taken from the interior of condom B,

Hurley was unable to make any definite conclusions using manual DNA analysis. However, Hurley testified that the profile "looked mostly like a single source profile[,]" although with the addition of a third allele at one locus, as well as the presence of an "off-ladder" allele, numbered 10.1, at a locus termed Penta E.[6] Hurley began by entering the data into TrueAllele and instructing the program to assume the presence of two DNA contributors. TrueAllele did not produce any usable results based on two runs under this parameter. Next, Hurley instructed TrueAllele to assume that only a single contributor was present in the sample, essentially informing the program to "look[] for the major contributor" in the sample. Under the single-contributor parameter, TrueAllele was able to produce two successive concordant results—notably, the inferred genotype from both runs matched to Appellant.[7] Although the analysis had produced reportable results, Hurley also elected to run the data through TrueAllele several additional times, instructing the program to assume the presence of two DNA contributors, one of whom was Appellant. This did not produce usable results.

Hurley also applied TrueAllele to data generated from a swab taken from a fragment

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[6] Hurley testified that an "off-ladder allele" or an "off-ladder peak" is an allele that doesn't "fall within one of the bins in [the] associated ladder" and is thus possibly the result of non-human DNA mixed into the sample. Nevertheless, although noting that the 10.1 result "did not fit with the rest of the data," Hurley also agreed that an allele of 10.1 at Penta E could occur within the human genome, and that Appellant does not have a 10.1 allele located at Penta E. Thus, as she could not conclusively determine that the 10.1 peak was contamination that should have been removed from the data prior to TrueAllele analysis, Hurley included it in the data she subjected to probabilistic analysis.

[7] A match between the inferred genotype and Appellant's genotype was between 39.1 trillion and 18.6 quadrillion times more probable than a coincidental match to an unrelated American individual, depending on ethnic group.

of the broken lamp. Like the swab from condom A, the analysis determined that the sample from the lamp contained a mix of DNA from a "major female contributor[,]" identified as the victim, and at least one minor DNA contributor. After inputting the data into TrueAllele and performing three runs, concordant results were achieved, and TrueAllele generated an inferred genotype for the minor contributor. The genotype inferred by TrueAllele matched Appellant; this match was determined to be between 7.35 million and 101 million times more probable than a coincidental match to an unrelated individual, depending on ethnic group.

ii. Appellant's expert

During the hearing, Appellant called Dr. Karl Reich ("Dr. Reich") as an expert witness in forensic DNA analysis. Dr. Reich opined that he did not consider the TrueAllele results reliable. In support, Dr. Reich asserted that TrueAllele has not been subjected to peer review, because employees of the firm that created TrueAllele had been involved in the software's validation testing process. However, Dr. Reich agreed that in a typical peer review process, "the developer is not involved in the review of the manuscript" prior to publication, and that a developer's financial interest should not have any impact on the peer review process. Dr. Reich further noted that as TrueAllele is a proprietary software, he did not have access to its source code, although he agreed that he "underst[ood] the basis for how the software is working[.]" He also opined that TrueAllele did not have a known error rate, but that by the same token, "there isn't a decent error rate for all of forensic DNA testing."

In addition to his concerns with TrueAllele's reliability generally, a significant

portion of Dr. Reich's testimony was concerned with "quality control issues with the samples[.]" Dr. Reich asserted his concern that the presence of pull-up artifacts in the sample potentially could "affect the ability to differentiate authentic DNA fragments . . . from noise and artifact[s] which should be ignored[.]" Dr. Reich noted that the underlying data contained "some degree of pull-up." In Dr. Reich's view, additional allele peaks caused by pull-up artifacts should never occur in a "correctly calibrated instrument" as "they merely complicate the analysis," could "hide or obscure data" and can "add to the time or effort it takes to decide whether [potential alleles are] real or should be . . . eliminated."

Dr. Reich also addressed the sample from the exterior of condom A that indicated the presence of a 10.1 allele at Penta E, which does not appear in Appellant's genome. In Dr. Reich's view, if the presence of the 10.1 allele was an actual allele arising from the genome of a single-source contributor, as opposed to an artifact, Appellant could not be the source of the DNA. Notably, Dr. Reich did not advance an opinion about whether the 10.1 allele was part of the genome, or an artifact that should have been ignored by the analysis. Moreover, he indicated that the results for the sample including the 10.1 allele were not "[c]onsistent with [Appellant's] exclusion" as a DNA contributor.

Although Dr. Reich maintained that TrueAllele produced unreliable results, he allowed that it had been used by the FBI since 2006, that it had been profitably applied by the Innocence Project to exonerate people convicted of crimes, and that it had been upheld

as sufficiently reliable under the *Daubert* standard in multiple states.[8] Dr. Reich strongly agreed that TrueAllele results should "fit with the logic of a human analysis[,]"and confirmed that in his view, Hurley had described using TrueAllele to supplement her manual analysis, and had not substituted its results for her own. Additionally, when asked if he agreed with the practice of instructing the software to assume the presence of certain contributors, or a certain number of contributors, Dr. Reich replied:

> [T]here was a decision made . . . to run the program under certain parameters and that's fair. Do it again under another set of parameters and see what the difference is. Do it again. The computer is free work. . . . So do it as many times as you need before you have a firm grasp of what the best results are.

iii. The court's ruling

Following the *Daubert* hearing, the court issued a detailed written memorandum in which it explained the rationale for denying Appellant's motion to exclude the TrueAllele evidence under Maryland Rule 5-702. In the memorandum, the court addressed each of the enumerated *Daubert-Rochkind* factors in turn.[9] The court determined that the question of

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[8] Dr. Reich noted that he had "been involved" in several cases in which state courts admitted TrueAllele results.

[9] The Supreme Court of Maryland has endorsed a non-exclusive list of factors which trial courts should consider in evaluating the admissibility of expert testimony under Maryland Rule 5-702. *See State v. Matthews*, 479 Md. 278, 310–11 (2022). These factors are:

> (1) whether a theory or technique can be (and has been) tested;
> (2) whether a theory or technique has been subjected to peer review and publication;
> (3) whether a particular scientific technique has a known or potential rate of error;
> (4) the existence and maintenance of standards and controls; and
> (5) whether a theory or technique is generally accepted[;]
> . . .

whether the BPD lab's electrophoresis machine was properly calibrated prior to producing the data which was analyzed by TrueAllele was an issue of fact for the jury to resolve. The court explained that this question, which arose from a disagreement between the experts over whether artifacts or impurities in the data were misidentified as actual alleles, was "classic fodder for . . . cross-examination" rather than a basis for excluding the TrueAllele results entirely. The court determined that TrueAllele had been peer-reviewed, that BPD utilized significant quality control standards, and that Hurley had not unreasonably extrapolated her conclusion from an accepted premise. Likewise, the court found that Hurley had adequately explained her baseline assumptions in using TrueAllele, and the court considered them reasonable. The court also found that TrueAllele had been subjected to validation studies and was known to reach reliable results.

The court noted that Hurley's conclusions, although not developed expressly for the purposes of testifying or in the capacity of a paid consultant, did arise out of her employment as a forensic analysist with BPD, and thus, she had knowledge that she could

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> (6) whether experts are proposing to testify about matters growing naturally and directly out of research they have conducted independent of the litigation, or whether they have developed their opinions expressly for purposes of testifying;
> (7) whether the expert has unjustifiably extrapolated from an accepted premise to an unfounded conclusion;
> (8) whether the expert has adequately accounted for obvious alternative explanations;
> (9) whether the expert is being as careful as he [or she] would be in his [or her] regular professional work outside his [or her] paid litigation consulting; and
> (10) whether the field of expertise claimed by the expert is known to reach reliable results for the type of opinion the expert would give.

Id.

be called to present testimony related to the cases she was assigned. The court did not make an explicit finding that TrueAllele results were or were not "generally accepted[,]" but noted that the courts of several states have allowed TrueAllele results, and further that Appellant's argument focused less on the reliability of TrueAllele in general, but "more on the program's reliability in light of the claim that the electrophoresis machine was uncalibrated."

After completing its consideration of the *Daubert-Rochkind* factors, the court concluded that:

> Hurley did not use an unknown, untested procedure in conducting her analysis. In accordance with the BPD's validation studies, she analyzed samples, made a decision on which samples to run through TrueAllele as well as the number of runs, reached her conclusions, and had those conclusions subjected to technical and administrative review.

The court determined that Appellant's contentions related to the quality of the data and the calibration of the electrophoresis machine went "to weight, rather than admissibility of the evidence." Thus, the court concluded that the TrueAllele results were sufficiently reliable under the *Daubert-Rochkind* standard to be useful to a trier of fact in determining a fact at issue.

C. The Standard of Review

As the Supreme Court of Maryland has stated, the admissibility of evidence under Md. Rule 5-702 is a matter entrusted to the sound discretion of the trial court:

> "[T]he admissibility of expert testimony is a matter largely within the discretion of the trial court, and its action in admitting or excluding such testimony will seldom constitute ground for reversal." *Roy v. Dackman*, 445 Md. 23, 38–39, 124 A.3d 169 (2015). When the basis of an expert's opinion is challenged pursuant to Maryland Rule 5-702, the review is abuse of

discretion. *Blackwell v. Wyeth*, 408 Md. 575, 618, 971 A.2d 235 (2009).

Rochkind v. Stevenson, 471 Md. 1, 10–11 (2020) (adopting the standard outlined in *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993), as the test for determining admissibility under Md. Rule 5-702). A court abuses its discretion when "no reasonable person would take the view adopted by the [trial] court." *Williams v. State*, 457 Md. 551, 563 (2018). "Rather, the trial court's decision must be well removed from any center mark imagined by the reviewing court and beyond the fringe of what that court deems minimally acceptable." *Devincentz v. State*, 460 Md. 518, 550 (2018) (internal quotation marks and citation omitted). A trial court may also abuse its discretion under the *Daubert-Rochkind* framework when it admits expert evidence "where there is an analytical gap between the type of evidence the methodology can reliably support and the evidence offered." *Abruquah v. State*, 483 Md. 637, 652 (2023). Nevertheless, the standard remains a deferential one, as "the law grants a [trial] court the same broad latitude when it decides *how* to determine reliability as it enjoys in respect to its ultimate reliability determination." *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 142 (1999) (emphasis in original); *see also Rochkind*, 471 Md. at 38 (incorporating *Kumho Tire* into Maryland's *Daubert-Rochkind* standard). As the Supreme Court of Maryland has instructed, "it is still the rare case in which a Maryland trial court's exercise of discretion to admit or deny expert testimony will be overturned." *State v. Matthews*, 479 Md. 278, 306 (2022).

D. The Parties' Contentions

Appellant asserts that the circuit court abused its discretion by failing to grant his motion excluding the TrueAllele evidence under Maryland's *Daubert-Rochkind* standard.

Although Appellant does not argue on appeal that TrueAllele is inherently unreliable, he contends that the trial court erred by failing to assess whether the use of TrueAllele was properly applied in this case specifically.[10] Appellant likewise contends that the TrueAllele evidence should have been excluded because some of its outputs were inconsistent with Hurley's manual analysis of the data, and asserts that the State failed to demonstrate that TrueAllele had been specifically tested against data including artifacts and potential bacterial contamination. Last, Appellant contends that the court erred by concluding that the dataset itself was adequate, as it included several artifacts and potential impurities. In so arguing, Appellant does not advance the contention that TrueAllele is *per se* unreliable, merely that the court did not properly exercise its gatekeeping function in this case.[11]

The State disagrees, arguing that the court properly fulfilled its role as gatekeeper under the *Daubert-Rochkind* standard, and did not abuse its discretion in concluding that TrueAllele and its application were sufficiently reliable for the results to be admitted during trial. The State asserts that the court correctly concluded that any disputes between the

[10] Appellant conceded at oral argument that in this case, the challenge to the reliability of the methodology concerned Hurley's application of the procedures rather than the reliability of the TrueAllele system itself. We note that the evidence available to the circuit court demonstrated that TrueAllele evidence has been widely accepted in multiple courts across the country, including in at least one reported appellate case. *See State v. Simmer*, 935 N.W.2d 167 (Neb. 2019).

[11] This Court has previously determined that TrueAllele is "by definition, a less reliable DNA test" than traditional analysis but is "one necessary to resort to by police when the circumstances do not permit a more reliable test." *Morten v. State*, 242 Md. App. 537, 561 (2019). In *Morten*, we found no error in a court's admission of TrueAllele testimony under Maryland Rule 5-702, but nevertheless vacated on other grounds. *See id.* at 570–71, 586–87.

parties' experts were nothing more than "fodder for vigorous cross-examination." Specifically, the State argues that Hurley correctly utilized the TrueAllele software, that any discrepancies between Hurley's manual results and the TrueAllele results did not impact admissibility under the *Daubert-Rochkind* standard, that TrueAllele has been validated using complex DNA samples which include artifacts, and that the court permissibly determined that the question of whether Hurley's electrophoresis machine was properly calibrated could be considered by the jury. Thus, the State contends that the court did not abuse its discretion in concluding that the TrueAllele results were admissible pursuant to Maryland Rule 5-702.[12]

E. Analysis

Under the *Daubert-Rochkind* framework, trial courts evaluate the admissibility of expert testimony by a "flexible inquiry into an expert's reliability, focusing on the expert's principles and methodology as opposed to their conclusions." *Covel v. State*, 258 Md. App. 308, 329 (2023). In so doing, the Supreme Court has urged courts to consider the non-exhaustive list of factors enumerated in *Rochkind*, none of which is determinative. *Rochkind*, 471 Md. at 35–37. Although the Supreme Court has described an expert's methodology as "a critical aspect" of their reliability and the "center" of a *Daubert-Rochkind* analysis, the Court has also noted that the question of "whether an expert's

[12] In the alternative, the State asserts that the TrueAllele results should have been automatically admitted under section 10-915 of the Courts and Judicial Proceedings Article ("CJP") of the Maryland Code, which allows DNA evidence to be automatically admissible under certain circumstances. *See* Md. Code CJP § 10-915. Because we affirm the circuit court's admissibility determination under the *Daubert-Rochkind* standard, we need not reach the State's alternative argument.

methodology is sufficiently reliable to admit the expert's testimony at trial will sometimes require a trial court to consider data and assumptions that the expert has employed in deciding threshold points relating to the methodology." *Katz, Abosch, Windesheim, Gershman & Freedman, P.A. v. Parkway Neuroscience and Spine Inst., LLC*, 485 Md. 335, 376 (2023) ("*Katz Abosch*").

Appellate courts must still "rely on trial courts that conduct *Daubert-Rochkind* hearings to determine where the line between data and methodology is in the specific cases before them, and whether the proffered expert's choices relating to data, assumptions, and other inputs implicate the reliability of the expert's methodology." *Id*. at 378. Moreover, a *Daubert-Rochkind* analysis does "not upend [the] trial court's gatekeeping function. Vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking shaky but admissible evidence." *Matthews*, 479 Md. at 312 (internal quotation marks and citations omitted). At its core, a *Daubert-Rochkind* analysis seeks to determine "not whether proposed expert testimony is right or wrong, but whether it meets a minimum threshold of reliability so that it may be presented to a jury[.]" *Abruquah*, 483 Md. at 655.

In the instant case, we determine that the circuit court did not abuse its discretion in concluding the TrueAllele evidence passed the *Daubert-Rochkind* reliability standard. The court carefully evaluated each of the enumerated factors and concluded based on the evidence that the TrueAllele data, as analyzed by Hurley, was sufficiently reliable to be properly submitted to the jury. We will, however, address each of Appellant's contentions in turn.

i. The TrueAllele parameters

Appellant first asserts that some of the programmatic parameters used in the TrueAllele analysis did not "fit the data[,]" and thus, the circuit court erred by concluding that "the assumptions and parameters Hurley used to engage TrueAllele are fodder for cross-examination, not a basis for excluding TrueAllele." Specifically, Appellant claims that "TrueAllele was unable to generate usable results when it was run with the correct [] number [of] contributors[,]" and argues that "the software only generated results including assuming a single source sample and did not generate *any* results including as a mixture of two people[.]" Therefore, in Appellant's view, the court was required to exclude the TrueAllele data, notwithstanding the fact that Hurley's analysis did not rely upon the runs which utilized the parameters Appellant views as suspect. Upon review of the record, we find no error.

Here, the court heard testimony from Hurley that when analyzing one of the samples, the swab from the interior of condom B, she ran the program under two different parameter sets—alternately asking TrueAllele to assume the presence of two contributors during some runs, and the presence of only a single contributor during others. Hurley stated that although "the profile, as a whole, looked mostly like a one-person profile[,]" which matched closely to Appellant's DNA, there were additional alleles that could indicate the presence of an additional DNA contributor. Therefore, despite achieving reportable results using the single contributor parameter, Hurley "set [TrueAllele] up to run both ways." Because TrueAllele did not return usable results when asked to assume the presence of two contributors, Hurley did not include those outputs as part of her final analysis.

Our reading of the record does not support Appellant's contention that Hurley's use of TrueAllele to query the possibility of a second DNA contributor in a single sample "implicated the reliability of the method" overall. Indeed, Appellant's own expert explicitly *endorsed* this application of probabilistic genotyping, stating:

> [T]here was a decision made . . . to run the program under certain parameters and that's fair. Do it again under another set of parameters and see what the difference is. . . . So do it as many times as you need before you have a firm grasp of what the best results are.

We do not agree with Appellant that Hurley's mere exploration of the possible presence of an additional contributor, which did not affect her ultimate analysis, rendered Hurley's use of TrueAllele unreliable. Here, the court could properly conclude that Hurley's action, which did not generate usable results, did not impact the successful use of TrueAllele in other contexts when she instructed the software to use other parameters.

Nor do we agree with Appellant that the court impermissibly declined to consider Hurley's use of parameters as part of the *Daubert-Rochkind* analysis. To be sure, Appellant is correct that determining the reliability of an expert's conclusion "will sometimes require a trial court to consider data and assumptions that the expert has employed in deciding threshold points relating to the methodology." *Katz Abosch*, 485 Md. at 376. Here, the circuit court found that the evidence did "not demonstrate [that] Hurley extrapolated from an accepted premise to an unfounded conclusion." The court also determined that "the assumptions and parameters Hurley used to engage TrueAllele are fodder for cross-examination, not a basis for excluding TrueAllele." This was not erroneous.

The court did not conclude, as Appellant asserts, that the sufficiency of Hurley's

basis for her opinion or Hurley's application of TrueAllele were *inherently* questions reserved for the jury. Nor did the court incorrectly assert that the assumptions and parameters an expert uses *always* impact the weight rather than the admissibility of evidence. Rather, the court applied its discretion and concluded that in *this* case, Hurley's assumptions and parameters did not render the TrueAllele data inadmissible, although they might also potentially prove fruitful subjects for cross-examination. *See id.* at 378 ("We rely on trial courts . . . to determine where the line between data and methodology is in the specific cases before them, and whether the proffered expert's choices relating to data, assumptions, and other inputs implicate the reliability of the expert's methodology.").

Indeed, as this Court has held, specifically on the topic of TrueAllele's admissibility under Maryland Rule 5-702, "[w]hatever evidence was competent to prove or disprove the very admissibility of the TrueAllele modality as a matter of law should *ipso facto* have been competent for the lesser task of adding to or subtracting from its persuasive weight as a matter of fact." *Morten v. State*, 242 Md. App. 537, 570 (2019). The court acted well within its discretion in declining to exclude the TrueAllele evidence on these bases, but nevertheless permitting cross-examination on those same topics. *See Rochkind*, 471 Md. at 38 ("Vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking shaky but admissible evidence." (quoting *Daubert*, 509 U.S. at 596)).

ii. Consistency between results and underlying data

Appellant also argues that because in his view, Hurley "failed to reconcile the generated results and the underlying data[,]" the court erred by admitting the TrueAllele

evidence. Specifically, Appellant contends that in one location in one sample, the software "ignored three of the four peaks it had identified [at one locus], instead assigning a 100% probability" to a specific allele pair, despite Hurley's subsequent statement that TrueAllele assigns each peak a probability "no matter what." In so arguing, Appellant misunderstands Hurley's testimony. Hurley's comment that TrueAllele assigns peaks a probability "no matter what" was part of a response to a question about whether she was concerned by the potential for TrueAllele to erroneously consider artifacts as part of a DNA profile. Hurley responded that she was not, because, in addition to assigning each part of the inferred profile a probability, TrueAllele would be "evaluating the data as a whole[,]" and was "going to consider everything[,] including any artifacts as . . . potential peak[s]." Hurley subsequently emphasized the steps she took to evaluate the effectiveness of any TrueAllele run.

Appellant also asserts that TrueAllele produced results inconsistent with the underlying data when, in one sample at the Penta E locus, the program determined that the most likely allele pair at the locus was (10, 10), although it had identified peaks of alleles 10.1, 10.3, and 15, as opposed to at 10.[13] In Appellant's view, this was indicative of an unreliable methodology. However, Hurley presented testimony that when she analyzed the Penta E data, she noticed the presence of "an off[-]ladder allele[.]" She testified that the off-ladder peak was "very high" and "did not match or . . . fit with the rest of the data in that profile[,]" which led Hurley to believe that the off-ladder peak was potentially an

[13] For further clarification, see discussion at footnote 6 *supra*.

artifact, that is, "DNA amplified from another source, a non-human source." Hurley subsequently re-ran and re-amplified the sample, which confirmed the presence of the off-ladder peak, and that "the rest of the data fit within th[e] quality parameters[.]" Therefore, Hurley "didn't have any concerns" that TrueAllele wasn't working properly. She also testified that TrueAllele can consider the possibility that not all data present in the sample comes from the same individual and assigns a probability to that situation. Hurley also noted that during analysis of the sample that Appellant asserts generated unreliable data, TrueAllele "was run under the off[-]ladder high contributor option which will expand the bins of the ladder. So that may account for it calling the 10.1 a 10."

In both circumstances, Appellant points to situations where TrueAllele assigned high probabilities to the potential presence of alleles at loci which are inconsistent with Appellant's genetic code. This, in Appellant's view, "should have excluded Appellant as a possible contributor."[14] We disagree. The purpose of the TrueAllele software is to derive probable genetic codes of DNA contributors from samples which are either less than

[14] At oral argument, Appellant's counsel clarified his contention that Appellant should have been excluded, stating that "[Appellant's] alleles did not match . . . at two locations." He argued that Hurley had testified that "if she were doing this analysis on her own, through what is called manual interpretation, that [Appellant] would have been excluded." Appellant asserted that these results indicated he should not have been included as contributing to this particular sample. We note that Hurley's testimony reflected the following: "[I]f I would complete a manual interpretation and say that there is no drop out, and that person's DNA is not there, then I would call that an exclusion." However, she immediately went on to state that "[t]his is a continuous biological modeling software so it is assigning a probability to everything." In our view, this evidence, which was available to the circuit court, demonstrated that there is a distinction in interpreting a DNA profile developed manually by an analyst compared to interpreting an inferred genotype generated by TrueAllele software. It does not reflect an improper application of methodology by Hurley.

pristine, or which represent mixes of DNA from multiple contributors. This process will necessarily involve the generation of results which in some cases do not align with a specific possible contributor; this does not preclude TrueAllele from generating a probability that a given derived genotype matches to the genotype found in a control sample from that contributor. As Hurley testified:

> TrueAllele will have a list of possible inferred genotypes that it has already assigned the probability to each genotype. When it then makes the comparison to the standard, if that person's genotype is present, it will use that probability in the calculation. If it hasn't assigned it a probability, it will assign it an exclusionary probability for that location.

Thus, when TrueAllele generated results incompatible with Appellant's DNA profile, the program did not ignore those results, but instead integrated the data into its final match calculation, adjusting the match probability downward. Therefore, contrary to Appellant's contention that TrueAllele "should have excluded" him due to the software detecting a probable allele inconsistent with Appellant's DNA profile, the program used that data to inform its probability calculations.[15]

The Supreme Court of Maryland has instructed that "the inquiry into admissibility of evidence under Rule [5-702] is 'a flexible one,' and its focus 'must be solely on principles and methodology, not on the conclusions that they generate.'" *Matthews*, 479 Md. at 307 (quoting *Daubert*, 509 U.S. at 594–95). Here, Appellant is correct that the record contains evidence that some of the data that TrueAllele generated did not comport

[15] We note that despite TrueAllele's downward adjustments, a match between Appellant and the inferred genotype was still at *minimum* more than 1.5 million times more likely than a match between the inferred genotype and a coincidental match to an unrelated person.

with Appellant's DNA profile. However, the record *also* contains explanations from Hurley about the reason TrueAllele might have produced such results, the manner in which those results impacted the final probability analysis, and how she interpreted and validated that final analysis.

The circuit court, after considering the testimony of both parties, undertook a thorough analysis of the *Daubert-Rochkind* factors, and concluded that the TrueAllele analysis was "based on sufficiently reliable principles and methods" and that Hurley "properly applied" the principles and methods so that the results could be profitably applied by a jury. Here, the court determined that based on Hurley's explanations, the possible discrepancies in the data were not fatal to the admissibility of the TrueAllele testimony. We cannot conclude that "no reasonable person would take the view adopted by the circuit court." *See Katz Abosch*, 485 Md. at 361 (internal quotation marks and citations omitted). Thus, we cannot say that the court abused its discretion on this point.

iii. Sufficiency of validation process

Appellant next asserts that the TrueAllele results were improperly admitted because the State failed to introduce evidence that the software had been appropriately validated for use on samples that may include artifacts or bacterial contamination. We disagree. Here, the record shows that BPD performed an internal validation, and that this validation process involved testing TrueAllele using samples typical of those generated by the BPD

laboratory, which Hurley stated typically *did* include artifacts.[16] Additionally, the record evidence shows that TrueAllele had been the subject of more than 34 validation studies, including multiple peer-reviewed studies which "use[d] DNA data exhibiting real-world issues developed by a crime laboratory in the course of their usual casework activity." These studies were identified in a declaration from the co-founder of the company that owns and licenses TrueAllele, which Appellant acknowledged was available to the circuit court at the *Daubert* hearing.

Moreover, even had the record lacked such evidence, Maryland's *Daubert-Rochkind* standard does not mandate any single specific type of validation; it is rather a "flexible inquiry into an expert's reliability, focusing on the expert's principles and methodology[.]" *Covel*, 258 Md. App. at 329; *see also Rochkind*, 471 Md. at 37 (noting that a court is granted "the same broad latitude when it decides *how* to determine reliability as it enjoys in respect to its ultimate reliability determination[,]" and a court "may apply some, all, or none of the [enumerated] factors[,]" none of which are individually determinative) (internal citation omitted). Here, the court determined, as part of its broader *Daubert-Rochkind* analysis, that BPD's validation, which was conducted according to nationally recognized standards, weighed in favor of TrueAllele's reliability. This Court does not, and indeed should not, "nitpick an expert's opinion in order to reach a perfect expression of what the basis and methodology can support[.]" *Katz Abosch*, 485 Md. at

[16] Hurley agreed that although TrueAllele had been validated by BPD's internal study, which sought to "represent what we typically see in casework from good, pristine samples down to complex mixtures with degraded DNA[,]" she had not personally reviewed the samples which were used in the internal validation study.

381 (internal quotation marks and citation omitted). Thus, we determine that the court properly exercised its discretion on this point.

iv. The calibration of the electrophoresis machine

Appellant next asserts that the court failed to "perform its gatekeeping role" by declining to exclude the evidence due to Appellant's allegation that the electrophoresis machine producing the data subjected to TrueAllele analysis was improperly calibrated. Appellant's argument features two aspects: first, that the inclusion of artifacts in the data evaluated by TrueAllele indicated incorrect calibration; and second, that the BPD technical manual requires elimination of spectral overlap through calibration of the electrophoresis machine.

Appellant's argument regarding artifacts in the data is premised on the testimony of his own expert, who testified that the presence of additional allele peaks caused by artifacts would not appear in a correctly calibrated machine. However, Appellant's argument ignores that the circuit court had the benefit of more than one explanation on this point—it also had the benefit of Hurley's testimony. The circuit court was not required to negate Hurley's testimony based on the competing explanation of Appellant's expert, because when "an expert's scientific testimony rests upon good grounds, based on what is known, it should be tested by the adversary process—competing expert testimony and active cross-examination—rather than excluded from jurors' scrutiny for fear that they will not grasp its complexities or satisfactorily weigh its inadequacies." *Matthews*, 479 Md. at 322–23 (citing *Ruiz-Troche v. Pepsi Cola of Puerto Rico Bottling Co.*, 161 F.3d 77, 85 (1st Cir. 1998)) (internal quotation marks and citation omitted).

Here, the record contained testimony from Hurley that the presence of artifacts in the data could "potentially" make a sample uninterpretable, and a statement that some samples contained "a lot" of pull-up artifacts. However, Hurley also stated that "[j]ust because artifacts are present in a sample does not necessarily mean it is non-interpretable or shouldn't be used." Likewise, she testified that despite the level of pull-up artifacts in a sample, she "was able to evaluate that data still and deem that sample as an interpretable sample for analysis." Similarly, Hurley testified that she was "not concerned" that the presence of artifacts in the data would invalidate the TrueAllele results for the samples she analyzed.

Appellant also argues that BPD's technical manual states that "spectral overlap . . . must be *eliminated* for proper data analysis[,]" and therefore, Hurley's failure to follow the BPD's technical manual demonstrates that she did not reliably apply the methodology.[17] As the State explained in its brief and during argument, the BPD technical manual does not state that spectral overlap must be eliminated through calibration of the electrophoresis machine. Rather, the level of spectral overlap requiring calibration of the electrophoresis machine is triggered if the pull-ups reach certain thresholds, which, as Hurley explained at trial, concern the intensity of the pull-ups rather than the number of peaks.

In addition, Hurley testified at the *Daubert* hearing that at the BPD, as at other forensic labs, analysts have analytical thresholds they use to differentiate true peaks from

[17] The record does not appear to contain any reference to that provision of the BPD technical manual or its context. Nor does the technical manual itself appear to have been introduced during the *Daubert* hearing.

"background noise." She testified that the lab performs spectral calibration to "minimize"—not eliminate—overlap in pull-ups and true peaks. She stated that if there was a very high level of pull-up—for instance, if there were "large pull-up peaks [overlapping] smaller true peaks"—that would be a cause for concern requiring spectral calibration under the manual. She also testified that the results in this case were "all low level" and were "consistent with what [BPD analysts] see in [their] regular casework[,]" and therefore not at the level requiring spectral calibration outside the normal annual maintenance.

Although Appellant is correct that an "improperly calibrated machine . . . could lead to an inaccurate result[,]" *Cole v. State*, 378 Md. 42, 67 (2003), the question of whether a technician has properly calibrated a scientific instrument so as to produce "an adequate supply of data" is entrusted to the sound discretion of the trial court. *Matthews*, 479 Md. at 316–17. Similar to the contention regarding the data validation, Appellant asserts that the court erred by not making a more explicit determination that the instrument was properly calibrated, and in concluding that "the electrophoresis machine at issue in this case [is] not a basis for excluding the TrueAllele evidence." However, we note that although the quality of data is of course related to the reliability of a conclusion, when conducting a *Daubert-Rochkind* analysis, "a trial court generally should be most concerned about the reliability of an expert's methodology[,]" *Matthews*, 479 Md. at 316, and should avoid "unduly scrutiniz[ing] the quality of the expert's data and conclusion[] rather than the reliability of the methodology the expert employed." *Id.* (quoting *Manpower, Inc. v. Ins. Co. of Pennsylvania*, 732 F.2d 796, 806 (7th Cir. 2013)).

Here, the trial court noted that the experts disagreed whether the machine had been properly calibrated but found that "Hurley . . . properly applied principles and methods required by the BPD's lab" which made this testimony proper to submit to the jury. Thus, the court clearly evinced its understanding of Appellant's contention, but disagreed that it proved fatal to the reliability of the TrueAllele results, particularly due to the record evidence showing that Hurley was able to successfully evaluate the data despite the presence of artifacts. Nor did the court's observation that the topic of the machine's calibration might be explored in cross-examination equate to a ruling that the court either completely discounted Appellant's contention as part of its *Daubert-Rochkind* analysis or believed that such a question was reserved for the jury alone. *See Katz Abosch*, 485 Md. at 378; *see also Morten*, 242 Md. App. at 569–71.

For the reasons articulated above, the circuit court did not abuse its discretion in admitting the TrueAllele evidence under Md. Rule 5-702. *See Rochkind*, 471 Md. at 10.

JUDGMENTS OF THE CIRCUIT COURT FOR BALTIMORE CITY AFFIRMED. COSTS TO BE PAID BY APPELLANT.