# U.S. COURT OF APPEALS
# FOR THE THIRD CIRCUIT

No. 25-1223

UNITED STATES OF AMERICA

v.

HUNTER RYAN ANDERSON,
Appellant

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Appeal from the U.S. District Court, M.D. Pa.
Chief Judge Matthew W. Brann, No. 4:21-cr-00204-001

Before: BIBAS, PORTER, and BOVE, *Circuit Judges*
Submitted Jan. 29, 2026; Decided Mar. 26, 2026

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OPINION OF THE COURT

BOVE, *Circuit Judge*. If you dislike jargon, buckle up. The focus of this appeal is the reliability of probabilistic genotyping software in forensic DNA identification under *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579 (1993) and Rule 702 of the Federal Rules of Evidence.[1]

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[1] Unless otherwise indicated, case quotations omit all internal citations, quotation marks, footnotes, alterations, and subsequent history. Unless otherwise indicated, references to a "Rule" are to the Federal Rules of Evidence.

The underlying criminal case involved a charge of unlawful possession of a firearm. At the request of law enforcement, a private company used software—called TrueAllele—to compare DNA profiles swabbed from the gun and Defendant Hunter Anderson. TrueAllele calculated a likelihood ratio of 11.5 trillion. We explain what that means below, but it was not good for Defendant. He challenged the TrueAllele evidence under *Daubert*. Following a battle of experts, the District Court ruled that the government had cleared the threshold reliability requirement for admissibility of expert evidence under Rule 702. We agree. TrueAllele may not be perfect, but most science is not. TrueAllele's probabilistic genotyping methodology has adequate scientific foundations to be used in federal trials. It is reliable enough. Cross-examination at trial is the appropriate time to address any alleged flaws in TrueAllele's methodology or results.

Defendant's other appellate arguments are without merit. Accordingly, we will affirm.

## I.

The relevant facts are straightforward even if the related science is not. While executing a search warrant, Pennsylvania State Police seized a gun from a bag that also contained Defendant's ID and two loaded magazines. Defendant was in the same bedroom as the bag at the time of the search. He was on parole for a state-law offense at the time.

Police swabbed DNA evidence from the gun. They also collected a DNA sample from Defendant based on a separate search warrant. The Pennsylvania State Police Crime Laboratory found multiple sources of DNA in the gun swab

and could not state "within a degree of scientific certainty" whether there was a match with Defendant's DNA. A501.

Law enforcement sent the DNA evidence and Defendant's sample to Pittsburgh-based Cybergenetics, Corp., which used TrueAllele to do a comparison. TrueAllele concluded that the multi-source mixture of DNA from the gun was 11.5 trillion times more likely to have been created if Defendant contributed to that mixture than if another Caucasian contributed to the mixture. In plain English, TrueAllele's likelihood ratio was strong evidence that Defendant had left DNA on the gun, in a case that turned on whether Defendant possessed that gun.

Defendant moved to exclude the TrueAllele evidence under *Daubert*. After a two day-hearing at which the government offered testimony from the founder of Cybergenetics and Defendant relied on testimony from two experts of his own, the District Court denied the motion in a thorough opinion. Defendant also moved to dismiss the Indictment based on facial and as-applied Second Amendment challenges to § 922(g)(1). The District Court denied that motion as well.

Defendant later pleaded guilty to the § 922(g)(1) charge. His plea agreement preserved his ability to challenge the District Court's rulings relating to the DNA evidence and his Second Amendment motion. At sentencing, the District Court imposed a prison term of 78 months of imprisonment, which the court ordered to run consecutive to Defendant's anticipated state-law sentence for the parole violation. Defendant timely appealed.

## II.

The District Court had jurisdiction under 18 U.S.C. § 3231. We have jurisdiction under 28 U.S.C. § 1291.

In Part III, we review the District Court's application of *Daubert* for abuse of discretion. *Cohen v. Cohen*, 125 F.4th 454, 459 n.2 (3d Cir. 2025). In Part IV, we review the District Court's Second Amendment analysis de novo. *United States v. Harris*, 144 F.4th 154, 157 (3d Cir. 2025). In Part V, we review the District Court's sentence for abuse of discretion. *United States v. Jumper*, 74 F.4th 107, 111 (3d Cir. 2023).

## III.

The government established at the *Daubert* hearing that TrueAllele's probabilistic genotyping methodology was sufficiently reliable to be admissible pursuant to Rule 702. Our holding is a natural extension of existing precedent based on the record before the District Court and the scientific advancements that the record reflects.

We previously held that the government had established the reliability of a DNA-testing methodology that relied on software and statistics but was not as complex as TrueAllele. *See United States v. Trala*, 386 F.3d 536, 541-42 (3d Cir. 2004). The Sixth Circuit has held that a different probabilistic genotyping software, STRmix, is reliable under *Daubert*. *See United States v. Gissantaner*, 990 F.3d 457, 467 (6th Cir. 2021). We agree with substantially all of Chief Judge Sutton's points in *Gissantaner*, as well as the District Court's thoughtful analysis of the issues in this case. We write here to address Defendant's arguments on appeal and underscore some of the

District Court's points regarding TrueAllele's reliability under the relevant standard.

**A.**

The purpose of a *Daubert* hearing is to permit a trial court to address preliminary questions relating to the admissibility of expert evidence under Rule 702. *See In re Paoli R.R. Yard PCB Litig.*, 35 F.3d 717, 743-44 (3d Cir. 1994). In this context, the proponent of the evidence must establish admissibility by a preponderance under Rule 104(a). *See id.* at 744 n.11. This "rigorous gatekeeping function" usually requires trial courts to develop an evidentiary record, through a hearing or otherwise, in support of their findings. *Cohen*, 125 F.4th at 460.

Admissibility under Rule 702 is governed by three issues: expert qualifications, reliability of the methodology, and relevance of the evidence. *See Elcock v. Kmart Corp.*, 233 F.3d 734, 741 (3d Cir. 2000). Reliability is the issue here. The expert does not have to be right. "[T]he evidentiary requirement of reliability is lower than the merits standard of correctness." *In re TMI Litig.*, 193 F.3d 613, 665 (3d Cir. 1999). Some of the factors bearing on reliability are testability, peer review, error rates, existence of standards, and general acceptance of the method. *See United States v. Mitchell*, 365 F.3d 215, 235 (3d Cir. 2004). These are just guideposts. The list is not exhaustive. Determining reliability is not a check-the-box exercise, and we give trial courts significant autonomy to do the necessary work.

**B.**

"DNA testing has an unparalleled ability both to exonerate the wrongly convicted and to identify the guilty." *Dist. Att'y's Off. for Third Jud. Dist. v. Osborne*, 557 U.S. 52, 55 (2009). "The advent of DNA technology is one of the most significant scientific advancements of our era," and "the utility of DNA identification in the criminal justice system is already undisputed." *Maryland v. King*, 569 U.S. 435, 442 (2013). Caution and analytic precision are required, however, because forensic DNA testing "often fails to provide absolute proof of anything." *Osborne*, 557 U.S. at 80-81 (Alito, J., concurring). Some context is necessary to understand why.

DNA is a molecule shaped like a long, twisted ladder. A gene is a strand from a DNA ladder. The rungs of the ladder are called base pairs. DNA base pairs are organized on chromosomes. A person's genotype—that is, his genetic makeup—is governed by the chromosomes and all of the base-pair information those chromosomes contain. Only identical twins have the same genotype.

Zooming in, forensic DNA identification involves analyzing particular locations on chromosomes. Each location is sensibly called a locus. The loci at issue are mostly standardized. A locus usually has two alleles, which are the DNA information from each parent. The focus at a locus is on the content of the DNA base pairs and the number of times the pairs repeat in a sequence. This is one of the distinctive features of each person's DNA. The unit of measure is called a short tandem repeat. An allele has a specific number of short tandem repeats that can be measured and compared to alleles at the same locus from other DNA.

One of the most basic situations for DNA comparison involves an evidentiary sample that contains DNA from only one person. Think of skin cells or blood. In a lab, the DNA is extracted from the biological material. Particular loci are replicated to facilitate the analysis. The loci are then examined and labeled, and the short tandem repeats that help make up alleles at the loci are measured. These measurements can be depicted as a DNA profile in several ways. One is an electropherogram that plots the short tandem repeats and related characteristics.

Sticking with our base case of a single-source DNA sample, scientists would anticipate no more than two alleles at each locus. That is because we expect to see one allele from each parent. One or both of the alleles may not have made it into the sample, however, so lab personnel would not be shocked to see zero or one allele at a locus. But the short tandem repeats in the alleles extracted from the evidence can be compared to the short tandem repeats in alleles at the same locus in another DNA profile to assess the likelihood of a match. Sometimes the comparison can be performed manually when forensic scientists are dealing with a single-source sample.

Things get more complicated when the sample has more than two alleles at a locus. This suggests DNA from multiple people is present. More than one person can leave DNA on a piece of physical evidence by touching it, among other things. It is hardly uncommon. Then we have what is called a multi-source mixture. For example, three alleles at a locus could result from one person contributing two alleles to the mixture and a second person leaving only one allele behind. Or three people could each have contributed one allele. The more alleles at the locus, the more challenging it becomes to figure

out which alleles came from each contributor and how many contributors there were to the sample. There are also other variables that add to the complexity, such as the quantity of DNA from each contributor in the evidentiary sample.

These are the types of complications that left the Pennsylvania State Police Crime Laboratory uncomfortable making comparative findings between Defendant's DNA and the evidentiary DNA mixture from the gun in this case. That is where probabilistic genotyping came in. Law enforcement sent Cybergenetics the DNA profiles that the lab had processed from the gun and Defendant. The company did not handle biological material for the government in this case. Cybergenetics deployed the TrueAllele software to compare the DNA profiles using an algorithm and calculate a likelihood ratio.

A likelihood ratio is a DNA match statistic that compares (1) the probability of a DNA mixture that includes a target's DNA to (2) the probability of the same DNA mixture including DNA from a random person. A positive likelihood ratio supports the first hypothesis involving the presence of the target's DNA. Here, the likelihood ratio was 11.5 trillion. The government's expert explained that this likelihood ratio meant that a match between some of the DNA from the gun and Defendant's DNA is "11.5 trillion times more probable than a coincidental match" between the evidentiary sample and a random person's DNA. A72. This tells us that, "in the abstract and without considering any other evidence in this case, it would be unusual if this DNA contained no DNA contributed from [Defendant]." *Gissantaner*, 990 F.3d at 462.

## C.

Because the defense challenged the TrueAllele evidence, the government had to prove by a preponderance that TrueAllele's probabilistic genotyping methodology was reliable. To resolve the dispute, the District Court played the traditional role of *Daubert* gatekeeper during a two-day hearing. The government established during that process that TrueAllele's probabilistic genotyping is (1) capable of being tested; (2) susceptible to error-rate calculations; (3) governed by standards that can be applied to reduce errors; (4) a product of peer-review scrutiny; and last, but not least, (5) generally accepted in the relevant scientific field of DNA evidence interpretation. These considerations were sufficient to support the District Court's conclusion that the TrueAllele evidence would have been admissible at trial under Rule 702 had Defendant not pleaded guilty.

### 1.

The government established that TrueAllele's testability supported a finding of reliability.

*Daubert* does not require "directed, specific actual testing." *Mitchell*, 365 F.3d at 238. Where a methodology is capable of being tested using scientific methods, that is indicative of an adequately rigorous and reliable design. The fact that TrueAllele's likelihood ratios are probabilistic rather than absolute is not an insurmountable barrier. *See id.* at 236-37; *see also United States v. Mornan*, 413 F.3d 372, 381 (3d Cir. 2005) ("Handwriting experts often give their opinions in terms of probabilities rather than certainties."). The issue is whether the expert's methodology can be "challenged in some objective sense, or whether it is instead simply a subjective,

conclusory approach that cannot reasonably be assessed for reliability." Fed. R. Evid. 702 advisory committee's note to 2000 amendment. Testability based on objective metrics also "assures the opponent of proffered evidence the possibility of meaningful cross-examination (should he or someone else undertake the testing)." *Mitchell*, 365 F.3d at 238.

TrueAllele can be tested. This can be accomplished by creating multi-source DNA mixtures in lab settings for the software to analyze. *See Gissantaner*, 990 F.3d at 463-64. In such a test, a false negative would occur if TrueAllele returned a likelihood ratio suggesting that one of the samples that was actually used in the experiment was not present in the mixture. *See id.* at 464. A false positive would occur if TrueAllele returned a likelihood ratio suggesting that some other DNA, which was not included in the experiment, was a part of the experimental mixture. *See id.* The feasibility of these types of tests was enough to resolve the testability factor in favor of the government.

The defense also had an opportunity to conduct tests. Defense counsel had access to the algorithm that guides TrueAllele's calculations. The government gave defense counsel an opportunity to use a computer running TrueAllele, the DNA profiles from the gun and Defendant, and about 27,000 other DNA profiles from a university research lab. The government also produced to the defense materials relating to the testing of TrueAllele's server, which runs the math to separate multi-source DNA mixtures into individual profiles, and TrueAllele's Visual User Interface (VUIer), which calculates and displays likelihood ratios. These were additional objective materials relevant to the operation of TrueAllele that put the defense in a position to seek to falsify the hypotheses underlying the software's methodology. The

possibility of challenging the hypotheses underlying a methodology is the core issue for testability.

In addition, TrueAllele "has been" tested. *Daubert*, 509 U.S. at 593. Cybergenetics used five unaffiliated probabilistic genotyping programs to compare the DNA profiles from the gun and Defendant. Each of the other programs produced a likelihood ratio that was similar to the ratio calculated by TrueAllele. The government disclosed those results, as well as TrueAllele's calculations, to the defense. At the *Daubert* hearing, the government also identified 42 validation studies relating to testing of TrueAllele.

Despite these disclosures, Defendant argues on appeal that he should have been granted access to TrueAllele's source code so that he could test that too. The District Court rejected Defendant's demand, and some state courts have issued similar rulings when applying their own expert-admissibility standards. *See Anderson*, 673 F. Supp. 3d at 681-82; *see also People v. Wakefield*, 195 N.E.3d 19, 29-30 (N.Y. 2022); *State v. Simmer*, 935 N.W.2d 167, 180-81 (Neb. 2019); *Commonwealth v. Foley*, 38 A.3d 882, 890 (Pa. Super. Ct. 2012). We agree with the thrust of those decisions and are not persuaded by Defendant's non-binding contrary authorities.

Because the issue was whether TrueAllele is capable of being tested based on objective criteria, Cybergenetics was not required to let the defense under TrueAllele's hood by disclosing the source code. Keep in mind that the source code is just a compilation of words and programmer syntax implementing TrueAllele's algorithm. As noted, the defense already had access to that algorithm. Source code is not presumed to be flawless, but the government also produced a log of changes to TrueAllele's source code, including updates

and fixes for software bugs. And the defense could have compared those materials to the readily accessible source code for the other probabilistic genotyping programs that Cybergenetics used to test TrueAllele's likelihood ratio in this case. No further disclosures were required under *Daubert* or Rule 702 in order to establish testability based on the evidence at the hearing.

Finally, we take seriously Defendant's invocation of potential fairness concerns arising from his lack of access to TrueAllele's source code. But *Daubert* is not a criminal discovery device. Courts have long relied upon other mechanisms to ensure fairness in prosecutions. For example, in addition to the general discovery requirements of Rule 16 of the Federal Rules of Criminal Procedure, which apply to information in the possession of the prosecution team, the government has additional, particular discovery obligations with respect to expert witnesses. *See* Fed. R. Crim. P. 16(a)(1)(G); *see also* 18 U.S.C. § 3500; Fed. R. Crim. P. 26.2. The Constitution requires prosecutors to disclose evidence within the possession of the prosecution team that is favorable to the defense, including information that undercuts material factual, expert, and legal theories of the case. *See Dennis v. Sec'y, Pa. Dep't of Corr.*, 834 F.3d 263, 284 (3d Cir. 2016). This obligation mandates disclosure of evidence bearing on the credibility of government witnesses. *See United States v. Scarfo*, 41 F.4th 136, 227 (3d Cir. 2022). District Courts also have tools at their disposal to remedy "stonewalling" by experts in response to cross-examination, including the discretion to exclude the testimony in its entirety. *Mitchell*, 365 F.3d at 246.

In light of these overlapping discovery obligations, and in the context of a record that reveals robust disclosures by the

government, we will not authorize a fishing expedition through TrueAllele's source code under the auspices of *Daubert*. For purposes of testability, what matters is that the challengers of the methodology could run scientific tests to try to show that TrueAllele does not function in the manner that the government's expert described. The defense in this case was as well-positioned to do so as *Daubert* and our related caselaw requires. We therefore agree with the District Court that the government established that TrueAllele is capable of being tested and has in fact been tested, and that additional disclosures were not necessary.

**2.**

The government demonstrated that it is possible to calculate error rates relating to TrueAllele's performance, and that the software's error rates are low. These considerations also favored admissibility.

We focus on false positives when we consider error rates under *Daubert*. *See Mitchell*, 365 F.3d at 240. On this issue, the government's expert relied in part on a 2014 study that he conducted with the Virginia Department of Forensic Science. The study identified a false-positive rate for TrueAllele of 0.005%.[2] At the *Daubert* hearing, the government's expert estimated that the error rate for manual-review comparative DNA analysis by humans was between 2% and 6%. The expert also described how the Virginia study demonstrated that TrueAllele's rate of false positives decreased

[2] *See* Mark W. Perlin, et al., *TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases*, 9 PLOS ONE 3: e92837 1, 12 (Mar. 25, 2014), https://perma.cc/4T76-EBUM.

as the strength of the likelihood ratio increased. When TrueAllele calculated a likelihood ratio expressed in trillions, the rate of false positives was infinitesimally small. In this case, based on the strength of the likelihood ratio, the government's expert estimated an error rate of approximately one in 146 trillion.

Defendant argues that these error rates are inaccurate because, in his view, they fail to account for potential errors by software operators and problems lurking in TrueAllele's source code. Neither argument is compelling. There was no dispute that analysts running TrueAllele have some discretion. They input hypotheses about the number of contributors to an evidentiary DNA mixture and set parameters relating to degradation of the DNA, and they also make decisions about how many times to run the software when doing the comparison. Discretion is not a dealbreaker. In *Mitchell*, we held that a fingerprint identification methodology was reliable under *Daubert* notwithstanding the fact that the process involved "an unspecified, subjective, sliding-scale" and human judgment calls relating to the quality and level of detail in a fingerprint. 365 F.3d at 236. The discretion exercised by TrueAllele analysts is more limited, and the testing process described above would permit the defense to identify outcome-determinative errors whether they result from human or technological problems.

Defendant's second argument regarding the error rate is based on testimony from a defense expert about an average error rate of "six errors per thousand lines of code." A381. Defense counsel described this as the "average rate in the field of software engineering." A157-58. Despite having access to a change log for core aspects of TrueAllele's code, and aided by experts who had been permitted to view TrueAllele's source

code in a different matter, counsel did not tie that "average rate" to the evidence in this case.[3] When defense counsel suggested that such an error could impact a likelihood ratio, the government's expert responded that such an outcome was "hypothetically possible, but extensive testing hasn't produced anything like that claim." A162-63.

We are left, then, with little more than defense speculation that people sometimes make mistakes, source code sometimes contains errors, software sometimes malfunctions, and TrueAllele may suffer from one or more of these issues. These concerns are not substantial enough to undermine reliability under Rule 702. "[T]he various methods of estimating the error rate all suggest that it is very low." *Mitchell*, 365 F.3d at 241. This "strongly" favors reliability under *Daubert*. *Id.*

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[3] In *United States v. Ellis*, a District Court permitted defense experts to review TrueAllele's source code pursuant to a protective order. *See* ECF Nos. 196, 202, No. 19 Cr. 369 (W.D. Pa. Jan. 2022). The case resulted in a guilty plea, and we did not have an opportunity to review that discovery ruling. Defendant retained one of the experts from *Ellis*, and the expert testified at the *Daubert* hearing in this case. While the record in *Ellis* and this case both indicate that the defense expert would have liked even more access to the source code than he received, the expert did not identify any issues at the *Daubert* hearing based on his review in *Ellis* that specifically tied the defense arguments about average rates of source-code error to TrueAllele. Nor did Defendant seek relief from the protective order in *Ellis* in order to present any such issues to the District Court in this case. These circumstances further illustrate the lack of merit to Defendant's blanket demand for TrueAllele's entire source code.

**3.**

TrueAllele's probabilistic genotyping methodology is governed by the type of standards that are a hallmark of a reliable methodology grounded in hard science. We also care about standards because, if properly applied, they can reduce error rates. *See Mitchell*, 365 F.3d at 241. That is true here.

Forensic DNA identification has been governed by standards for decades. Predecessors of the Scientific Working Group on DNA Analysis Methods, which is associated with the FBI, date back to the 1980s. In 2015, this Scientific Working Group published "Guidelines for the Validation of Probabilistic Genotyping Systems." In 2020, the American National Standards Institute and the Standards Board of the American Academy of Forensic Sciences jointly issued a "Standard for Validation of Probabilistic Genotyping Systems." At the *Daubert* hearing, the government offered a written summary from Cybergenetics describing TrueAllele's positions regarding compliance with this Standard. Defendant did not agree with all of those positions, but that tension was to be addressed through cross-examination at a trial.

Defendant challenges the government's standards evidence by arguing that there was no evidence that the Pennsylvania State Police Crime Laboratory followed these standards or was calibrated to use TrueAllele. The problem with that argument is that the lab did not do any probabilistic genotyping. Rather, the lab extracted and amplified the DNA and prepared files depicting short tandem repeats at standardized loci in Defendant's sample and the evidentiary mixture from the gun. Those are separate "wet lab" steps—extraction, amplification, and quantification of short tandem repeats—with an even longer history and separate-but-related

standards, which Defendant did not challenge in his *Daubert* motion. *See, e.g.*, *King*, 569 U.S. at 442-43. Speculation about the state lab's standards and performance, without a basis in the record, is insufficient to overcome the government's *Daubert* showing with respect to probabilistic genotyping.

Defendant also argues that TrueAllele should be subject to additional standards established by the Institute of Electrical and Electronics Engineers. We take no position on the technical and scientific merit of that contention, but it is not a legal basis to exclude evidence. We previously affirmed a *Daubert* reliability finding where the expert was subject to the criticism, by a competing expert, that his field "lacked measurable standards." *United States v. Velasquez*, 64 F.3d 844, 846, 851 (3d Cir. 1995). If a dispute as to the existence of governing standards is insufficient to preclude expert evidence, then Defendant's argument that probabilistic genotyping software should be subject to additional standards must also fail. And it does fail, particularly in light of the extent of the existing standards and the weight of the other factors.

**4.**

TrueAllele has been subjected to peer review and publication. These processes are not "necessary conditions of reliability." *Kannankeril v. Terminix Int'l, Inc.*, 128 F.3d 802, 809 (3d Cir. 1997). But going through the process is another "component of good science." *In re TMI Litig.*, 193 F.3d at 663-64; *see also Gissantaner*, 990 F.3d at 464-65 ("[P]ublication in a peer-reviewed journal alone typically satisfies this *Daubert* inquiry.").

Of the 42 TrueAllele validation studies presented by the government at the *Daubert* hearing, eight of them were subject

to peer review. One of the peer-reviewed studies addressed TrueAllele's efficacy with DNA mixtures involving up to 10 contributors, which are more complex than the mixture swabbed from the gun in this case. Defendant takes issue with the fact that the expert helped author seven of the eight studies. This was another issue to be taken up during cross-examination at trial, and it is of little consequence under *Daubert* or Rule 702. *See Mitchell*, 365 F.3d at 239, 245-46. The important part, confirmed at the hearing, is that the peer reviews were conducted by anonymous independent scientists. This factor provides substantial additional support for TrueAllele's reliability.

**5.**

Probabilistic genotyping is generally accepted, for purposes of *Daubert*, in the field of forensic DNA identification. This is another "important factor in ruling particular evidence admissible." *Daubert*, 509 U.S. at 594.

Courts have previously concluded that probabilistic genotyping software is generally accepted. *See Gissantaner*, 990 F.3d at 466-67 (collecting cases). This is true of TrueAllele in particular, though some of those cases applied expert standards different than *Daubert*. *See United States v. Lockett*, 2023 WL 7181251, at *7 (M.D. La. 2023); *Wakefield*, 195 N.E.3d at 28; *Foley*, 38 A.3d at 888. The District Court agreed with these decisions, and the evidence at the *Daubert* hearing substantiated general acceptance for purposes of this case.

The government's expert testified that TrueAllele had been used in a variety of settings for more than 25 years, including by approximately 400 organizations involved in law enforcement, criminal defense and exoneration work, paternity

testing and kinship analysis, and identification of remains. *See In re Paoli R.R. Yard PCB Litig.*, 35 F.3d at 742 (reemphasizing, post-*Daubert*, relevance of non-judicial uses of the challenged methodology). More than 250 criminal defense teams have used the software. The expert also explained, without contradiction, that the software has been deemed admissible in 37 cases in the United States. Collectively, this was enough evidence to establish general acceptance.

Defendant's citation to the Ninth Circuit's non-precedential discussion of STRmix, a different probabilistic genotyping software, is not enough to overcome that evidence. *See United States v. Russell*, 2024 WL 4054382 (9th Cir. 2024). In *Russell*, the trial judge did not conduct a *Daubert* hearing and therefore lacked the type of record developed by the District Court in this case. The Ninth Circuit held that the error was not harmless based in large part on a draft report from the National Institute of Standards and Technology (NIST).[4] *See id.* at *1. The court noted concern in the NIST's draft about a supposed lack of "established and accepted criteria" for complex mixtures involving low quantities of DNA. *Id.* The final version of the report deleted that concern. *Compare* NIST Draft Report at 82, *with* NIST Final Report at 73. The NIST maintained language in the final report regarding a lack of publicly available data for use in an "external and independent

[4] *See* NIST, *DNA Mixture Interpretation: A NIST Scientific Foundation Review* (June 2021), https://perma.cc/J3MU-6VKL [NIST Draft Report]. The NIST published the final version of the report in 2024. NIST, *DNA Mixture Interpretation: A NIST Scientific Foundation Review* (December 2024), https://perma.cc/6DQR-3B4W [NIST Final Report].

assessment" of probabilistic genotyping, which the *Russell* panel had emphasized from the draft. NIST Final Report at 94; NIST Draft Report at 75. But additional external review of scientific methodologies has never been dispositive of *Daubert* reliability. We look to peer review, which has been conducted on TrueAllele, and general acceptance, which the government established. Therefore, the harmless-error analysis in *Russell* is not persuasive.

Defendant also attacks the District Court's conclusion by pointing to his experts' opinions that TrueAllele is not generally accepted in "the community of computer scientists and software engineers." Br. 44. The contention fails because of the mismatch between the methodology and the field Defendant presses. When evaluating general acceptance, we have defined the relevant scientific community in a narrower fashion and with greater emphasis on the salient features of the challenged methodology. In *Mitchell*, for example, we defined the relevant community as "forensic identification" for purposes of assessing a manual-review latent fingerprint identification process. 365 F.3d at 220-21, 241. The District Court decision that we affirmed in *Trala*, 386 F.3d at 541-42, which involved use of statistics to analyze short tandem repeats, defined the relevant community as "forensic geneticists." *United States v. Trala*, 162 F. Supp. 2d 336, 348 (D. Del. 2001). Requiring the government to establish general acceptance by computer scientists and software engineers would be in tension with the reasoning in those cases.

It is also difficult to discern a limiting principle from Defendant's attempt to bring these additional disciplines into the fold. Using software in scientific pursuits is hardly unique. Scientists may ultimately decide that it makes sense to enhance technical software standards governing probabilistic

genotyping to align more closely with standards thought wise by some computer scientists or electrical engineers. We decline to adopt a rule that weighs in on that debate, and Defendant's argument presumes a threshold for reliability under Rule 702 that does not exist. The government demonstrated that TrueAllele was generally accepted in the relevant scientific community, which was all that was necessary at the *Daubert* hearing.

## IV.

The District Court correctly rejected Defendant's Second Amendment challenges to § 922(g)(1) based on the facts of this case. Under our precedent, because Defendant was serving a term of parole under state law at the time of his federal arrest, his as-applied challenge is foreclosed, which dooms his facial challenge as well. *See United States v. Moses*, 142 F.4th 126, 135 (3d Cir. 2025).

## V.

Defendant's challenge to his sentence is similarly without merit. The District Court correctly calculated a Guidelines range of 77 to 96 months based on an Offense Level of 21 and Criminal History Category VI. Following a careful hearing, the District Court sentenced Defendant principally to a within-Guidelines term of imprisonment of 78 months. The District Court indicated that the prison term should run consecutive to any sentence imposed as a result of the state-law parole violation.

On appeal, Defendant argues that his sentence violated U.S.S.G. § 5G1.3(d), which authorizes sentencing judges to impose a consecutive sentence in order to "achieve a

reasonable punishment for the instant offense." The District Court was aware of the related state proceedings, and the court's stated concerns about Defendant's criminal history and risk of recidivism, among other things, amply supported the decision to require the federal sentence to run consecutively to any state-law sentence. *Setser v. United States*, 566 U.S. 231, 243-45 (2012). We see no abuse of discretion in that decision.

## VI.

The government demonstrated that TrueAllele is reliable enough to be admissible at trial. Defendant's Second Amendment arguments are foreclosed by precedents we lack authority to revisit. His sentencing challenges are meritless. Accordingly, we will affirm.

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