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January 17, 2025

The Hon. Marc C. Lemieux, A.J.S.C.
Superior Court of New Jersey
Monmouth County Courthouse
71 Monument Park
Freehold, N.J. 07728

Re: State of New Jersey v. Paul Caneiro
Case # 18-4915/Indictment # 19-02-0283
Motion to Exclude Evidence

Dear Judge Lemieux:

As this Court is obviously aware, a hearing was recently conducted regarding defendant's motion to exclude scientific evidence pursuant to State v. Olenowksi I, 253 N.J. 133 (2023). Having concluded testimony, the Court has asked for written summations from both the State and the defendant. As such, the State submits the following in support of its position that the evidence produced utilizing the STRmix probabilistic genotyping software should be admitted as reliable under Olenowski I and Daubert v. Merrell Dow Pharmaceuticals Inc., 509 U.S. 579 (1993).

SUMMARY OF TESTIMONY AND STATE'S POSITION

Prior to getting into the legal analysis at issue here, the State felt it best to start with a summary that hits at the heart of the matter. STRmix is not new and, like other advancements in DNA technology since its inception in the late 1980s, offers significant improvements that benefit the criminal justice system as a whole. Mr. Godin, in his oral summation, started off by reminding this Court that, as the proponent of the evidence, the State bears the burden of establishing reliability under the confines of Olenowski I[1]/Daubert[2]. We certainly understand and appreciate that burden. The State would, under normal circumstances, seek to remind this Court that the standard is largely uncomplicated; however, we would be remiss if we failed to acknowledge that, at times, the Court actually reminded us to focus on what the Court actually needed to decide. With that in mind, the State tried its best to be cognizant of the Court's reminder – yet still attempted to address arguments that it knew would be coming by way of the defense experts. In the end, similar to all of the admissibility hearings that have taken place in State and Federal courts in the United States, we are left with the obvious reality that STRmix is reliable and, in fact, a revolutionary advancement in the state of DNA analysis in the United States and throughout the world.

STRmix is the predominant Probabilistic Genotyping software in the United States. On November 19, 2014, a United States

[1] State v. Olenowksi I, 253 N.J. 133 (2023).
[2] Daubert v. Merrell Dow Pharmaceuticals Inc., 509 U.S. 579(1993).

laboratory began using STRmix in casework for the first time when the United States Army lab completed its internal validation of STRmix and began using it in casework. S-140. As of November 10, 2024, 89 laboratory systems are using STRmix in daily casework. Ibid. As this Court knows, despite the arguments that STRmix has not been adequately tested, the above indicates that 89 laboratories have independently, internally validated the software (some, multiple times) with ground truth samples and comparisons to non-contributor profiles. Ibid. Regarding the totality of testing, Dr. Buckleton indicated that they have done "over 9 billion false donor tests." (T6:98-20). He explained that this is comparing a "false donor against a mixture and you're hoping to get them (sic) an exclusionary result." Id. at lines 23-24. He said that, of these 9 billion tests, "I've published over 100 million." (T6:99-13 to 99-15).[3]

While it has been posited that this Court would have to "walk out on a limb if it wants to say that STRmix is reliable," the State would suspect that this Court recognizes that it

[3] T1: 11/12/24 a.m. (Ghannam)
T2: 11/12/24 p.m. (Ghannam and Naughton)
T3: 11/13/24 a.m. (Naughton and Reed)
T4: 11/13/24 p.m. (Reed)
T5: 11/14/24 a.m. (Reed)
T6: 11/14/24 p.m. (Buckleton)
T7: 11/15/24 a.m. (Buckleton)
T8: 11/18/24 a.m. (Thayer)
T9: 11/18/24 p.m. (Thayer and Schlenker)
T10: 11/19/24 a.m. (Coble)
T11: 11/19/24 p.m. (Coble)
T12: 12/2/24 a.m. (Reich)
T13: 12/2 p.m. (Reich)
T14: 12/3 part 1 (Heimdahl)
T15: 12/3 part 2 Heimdahl
T16: 12/4 a.m. (Adams)
T17: 12/4 p.m. (Adams)
T18: 12/6 full day (Martin)
T19: 12/0 full day (Inman)
T20: Summations

actually is the other way around. (T20:35-7 to 35-8). The defense also attempts to warn this Court – stating that "whether or not this Court is opening the flood gates, just know that it's going to be difficult to turn that around once we do it." (T20:90-24 to 91-2). The proverbial "flood gates" have been open since 2017 in neighboring counties; the Court need not worry about bearing that burden, especially in light of the fact that no defense attorney in this State seems to have done anything about it until this case. The persuasive law from across the country and the sheer volume of ground truth testing truly speaks for itself. The Court need not be fooled when Dr. Heimdahl yells "fire" in a crowded theater by misciting a newspaper article in order to mislead the Court into thinking that source-code review has revealed catastrophic errors with STRmix, dismissal of Breathalyzer cases and the overturning of a high-profile conviction. S-191; D-10. Heimdahl and most of the other defense experts have never even bothered to try STRmix. And, cross-examination made clear that Dr. Heimdahl flagrantly mischaracterized these things in this case and in State v. Pickett, 466 N.J.Super. 270 (App. Div. 2021).

That being said, STRmix has consistently been found reliable in State and Federal Courts throughout this Country. Moreover, while no defendant has formally challenged STRmix in New Jersey by way of a Frye or Daubert challenge, STRmix has been used in this State since 2017. T1:33-10 to 33-11. The Union County Prosecutor's Office DNA Laboratory ("UCPO lab") was the 19th lab in the United States to begin using STRmix in casework. S-140.

According to Monica Ghannam, the DNA Technical Leader for the UCPO lab, their laboratory has conducted internal validations of three versions of STRmix, V.2.4.6, V.2.5.11 and V.2.7, which they are currently using. The UCPO lab currently uses STRmix for all of their DNA analyses, including for single-source samples. (T1:42-9 to 42-13). Ms. Ghannam further indicated that analysts from their lab have testified approximately 33 times in State or Federal Court in New Jersey regarding STRmix results, and that these cases range from gun possession to homicides. (T1:43-11 to 43-20); S-7.

The State would note at the outset that, despite the lack of a Frye or Daubert hearing in New Jersey regarding the admissibility of STRmix, our Appellate Division has commented on STRmix software in State v. Price, 2022 N.J. Super. Unpub. LEXIS 691. In Price, the state proffered the aforementioned Monica Ghannam, who testified on the State's behalf. In Price, Ghannam implemented STRmix and explained that swabs taken from a firearm recovered at the scene were compared to the defendant's DNA sample. Id. at 20. On appeal, the defendant challenged the expert testimony that the defendant's DNA was present on the gun. The New Jersey Appellate Division stated:

> Nothing about Ghannam's testimony warrants reversal of defendant's conviction. First, defendant failed to object [to] any portion of her testimony, and we are satisfied the admission of the now challenged portions of her testimony are not "clearly capable of producing an unjust result," as her opinions were clearly relevant, admissible, and nonprejudicial. R. 2:10-2. Indeed, just prior to providing her opinion that defendant's DNA was present on the Glock's magazine Ghannam presented scientific findings indicating it was "approximately 57.4 quadrillion times more likely" that the DNA on the magazine belonged to defendant, rather

> than an unknown individual. That testimony was based on overwhelmingly accurate scientific data, and its admission was not capable of "le[ading] the jury to a result it otherwise might not have reached." McGuire, 419 N.J. Super. at 106-07 (App. Div. 2011) quoting Taffaro, 195 N.J. 454).

State v. Price, 2022 N.J. Super. Unpub. LEXIS 691, *32-33.

Regarding use of STRmix in New Jersey, more recently, in June 2022, the New Jersey State Police Office of Forensic Science DNA Laboratory ("NJSP DNA lab") became the 72nd laboratory in the United States to validate and begin using STRmix in casework. S-140. The NJSP DNA lab conducted an internal validation of and currently uses STRmix V.2.8. S-161A; S-162A. According to DNA Lab Director Jennifer Thayer, analysts from her lab have now testified regarding STRmix results 11 times in this State. (T9:15-8 to 15-12); S-164.

Less than two years after the United States Armed Forces Criminal Investigation Laboratory became the first lab in the United States to begin using STRmix in casework, the President's Council of Advisors on Science and Technology (PCAST) issued a report entitled "Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods (hereinafter, "PCAST report")." S-141. While often cited by the defense in admissibility hearings for purposes of limitations on the range of foundational validity (i.e. coverage and/or factor space) of Probabilistic Genotyping software, the report is largely complimentary of Probabilistic Genotyping. Moreover, by utilizing the report for the purposes of attempting to limit factor space and/or coverage, one must actually presuppose that

the report is valid and, consequently, that STRmix is foundationally reliable. Specifically, in Finding 3: DNA analysis of complex-mixture samples, PCAST indicates "DNA analysis of complex mixtures should move rapidly to more appropriate methods based on probabilistic genotyping." S-141 at 82. Subsection (2), "Probabilistic genotyping" reads as follows:

> Objective analysis of complex DNA mixtures with probabilistic genotyping software is relatively new and promising approach. Empirical evidence is required to establish the foundational validity of each such method within specified ranges. At present, published evidence supports the foundational validity of analysis, with some programs, of DNA mixtures of 3 individuals in which the DNA minor contributor constitutes at least 20 percent of the intact DNA in the mixture and in which the DNA amount exceeds the minimum required level for the method. The range is which foundational validity has been established is likely to grow as adequate evidence for more complex mixtures is obtained and published.

Ibid.

One cannot argue the PCAST report as gospel for purposes of saying certain mixtures are outside the bounds of the conservative limits of PCAST, while also arguing that STRmix is not reliable because the documentation of their software isn't what the software engineers think is proper. Simply put, STRmix works. We actually had the benefit of an in-court demonstration of that courtesy of Mr. Godin during the cross examination of Danielle Reed. See generally T5. It should be noted that PCAST also stated that, "[w]hen further studies are published, it will likely be possible to extend the range in which scientific validity has been established to include more challenging samples… Such studies should be performed by or should include

independent research groups not connected with the developers and with no stake in the outcome." Id. at 81. Clearly, during the hearing, this Court was made aware of the significant efforts undertaken post-PCAST by the developers of STRmix and others to provide significant data and analysis of same, which greatly expands the foundational validity of Probabilistic Genotyping, generally, and STRmix, specifically. Much has been made about the lack of independence regarding much of the peer-reviewed publications addressing STRmix; however, it is certainly fair to say that "independent research groups" were not jumping at the opportunity to spend significant time analyzing all of this validation data.

This Court likely has realized that this analysis is not a small undertaking, especially in light of the fact that defense expert Keith Inman could not come close to completing an assessment of the data underlying the New Jersey State Police laboratory's internal validation – and that data is from just one lab. Inman's own testimony indicating that there was an "enormous amount of data" also flies in the face of the oft-used argument that STRmix has not been tested sufficiently to satisfy the Daubert analysis. (T19:103-12). Inman also confirmed that NJSP invested "… easily thousands of hours, easily, because it was, I mean the validation I think took two to three years and there was at least five or six analysts involved but there was really from the beginning of making the samples, getting the EPG's from each of them, and then putting them through the probabilistic genotyping so it was an enormous amount of work."

(T19:103-19 to 103-25).

When asked about how long it would take for him to also to evaluate the data from the Bode validation, Inman estimated another 6-8 months. (T19:135-9 to 135-13). With that in mind, the State would ask this Court to consider how the Bright et al. 31 lab compilation could ever have been possible without the work of the developers and the scientists from those 31 labs, who authored the compilation publication. Despite consistent arguments regarding the lack of independent review, the State would ask the somewhat-rhetorical question of, "If not them, then who?" The Bright, et al. publication, to be clear, discussed the results of sensitivity and specificity studies on 2,825 mixtures and over 28 million false donor tests. See S-146; (T7:100-1 to 100-2). Dr. Buckleton made clear that this study certainly "meets the request that PCAST made;" in light of this, Dr. Buckleton wrote to PCAST to see if they would acknowledge that it had expanded, and they didn't respond. (T7:100-20 to 101-2). This 31 lab compilation clearly addresses the most relevant of questions… how often STRmix falsely includes… with a high LR… or very strong support." (T7:103-1 to 107-11). The Court also asked a similar question of Dr. Buckleton, referencing the 15 miscodes and whether he was "confident overall that this software, and using this software, that whatever type of miscoding that's happened over time, we've talked about the 15 of them in this exhibit, that none of them were including someone that shouldn't have been included in a particular running of the STRmix, correct?" Dr. Buckleton responded, "[t]hat's correct,

sir, I have no evidence that STRmix has ever created a false inclusion of a large nature." (T7:210-13 to 210-22).

The conclusion reached by the Bright et al. publication "demonstrates a foundational validity of, at least, the STRmix software method for complex, mixed DNA profiles to levels well beyond the complexity and contribution levels suggested by PCAST." S-146 at 23. And, importantly, with respect to the PCAST limit of 20 percent for the smallest contributor, Bright et al. substantiated that "2293 out of the 2825 submitted profiles had at least one component who contributed less than 20% of the sample." Ibid. The State would also note that PCAST made no mention of picograms and also no mention of specific labs – so, essentially, PCAST found Probabilistic Genotyping to be reliable at those stated limits across all labs. This idea of "horizontal validation" will be discussed infra.

One year prior to the 31 laboratory compilation study, the "Internal Validation of STRmix for the interpretation of single-source and mixed DNA profiles" publication was released. S-145. That study, often referred to as the Moretti et al. study, discussed the findings from the FBI Laboratory's internal validation of STRmix. The validation totaled "more than 800 known contributor propositions, nearly 60,000 non-contributor tests, and nearly 100 reference sample comparisons to mixed profiles developed from authentic forensic specimens." Id. at 143. The Moretti study indicated that:

> The implementation of a fully continuous probabilistic genotyping system on December 1, 2015 represents a major step forward in the interpretation of autosomal STR data at the FBI Laboratory. As evidenced by the

> comparative examinations of prepared mixtures and evidentiary profiles from prior FBI cases, the conclusions derived from the results of probabilistic genotyping can be expected to align with properly applied historical methods. The probabilistic approach used by STRmix greatly increases the information that can be used to deconvolute mixtures and estimate evidentiary weight, showing distinct advantages with mixtures with three or more individuals and low-level contributors. Our analysis of findings supports that STRmix reliably applies suitable biological modeling and statistical methods, is sufficiently robust for usage with forensic-type specimens and, as a probabilistic genotyping system, represents a vital enhancement in the field of human identification testing.

Ibid.

A deep dive into redundant criticisms of STRmix reveals an argument that the testing of STRmix only involves "ground truth" samples. This is largely true, yet universally accepted as the only way to validate any software in a given lab. While Standards and Guidelines will be discussed in greater detail infra, the state would note that ANSI/ASB Standard 018, the only United States standard that applies to Validation of Probabilistic Genotyping Systems defines "accuracy studies" as:

> [s]tudies performed to assess the degree of conformity of a measured quantity to its actual (true) value. In probabilistic genotyping, these are studies performed to establish that the calculation made by the probabilistic genotyping system are correctly executed, and that the results obtained produce the expected likelihood ratio for situations where the calculations can be performed manually or with an alternate software program or application. Such situations include profile results from single source samples, 2-person mixtures with unambiguous major and minor contributors, and 2-person mixtures with equal mixture proportions. However, profile results where the ground truth is not known are not suitable for accuracy studies. (emphasis added)."

S-133 at 1. Clearly ASB 018 dictates that the only way to conduct

internal validation is with ground truth samples. This is designed to ensure that the labs know that, for instance, STRmix, is actually providing the correct results.

Interestingly, Nathan Adams cited ASB 018 in his report (and testimony) for the direct opposite idea. While he cited the standard correctly in a footnote, in his "Conclusion" section, Adams wrote, "…STRmix v2.5.11 compliance with the 'accuracy' requirement of ASB Std 018 should be also demonstrated via developmental and internal validation studies involving 'profiles results where the ground truth is not known.'" D-16 at 16. Adams blatantly took a portion of the "accuracy" definition from ASB 018 (fully cited in his report at page 3) and used it to argue the exact opposite of what it says. Despite cross examination on this topic, he would not acknowledge how he misused ASB 018. See generally (T16:118-6 to 119-24).

Regarding accuracy, the State would ask also this Court to compare the results from the traditional analysis originally conducted by the NJSP DNA lab and the STRmix results from Bode. This appears to be another way to test both the reliability of STRmix for samples without ground truth and, additionally, the "horizontal validation" of STRmix across two separate laboratories. See (T7:92-25 to 94-15) (concerning Dr. Buckleton's explanation of horizontal validation). Dr. Buckleton confirmed that STRmix has been validated horizontally, meaning across different labs, and specifically pointed to the Boodoosingh, et al. publication (Number 13 on S-158, list of independent publications). Dr. Buckleton explained that

Boodoosingh:

> was a student at Sam Houston University in Texas and did some work with people none of the developers of STRmix where interpreted data from one lab using the parameters from another and she did this for multiple combinations of different labs. And, again she plotted the answers and if there on the diagonal line you're getting the same answer and so in large measure, that's the answer, You get the same answer if you make data in one lab and run it in another which shows that all the different labs, tied together in that they all support each other in terms of giving the same answers.

(T7:93-9 to 93-25). When asked to explain how that effected the idea of foundational validity or "coverage," Dr. Buckleton explained that, "so scientifically, STRmix has vertical and horizontal transportability and the coverage and our belief in reliability is the sum of all the data. There's no need to focus on microscopic focus." T7:94-1 to 94-10).

The Boodoosingh article, "An inter-laboratory comparison of probabilistic genotyping parameters and evaluation of performance on DNA mixtures from different laboratories," Forensic Science International: Genetics 71 (2024) 103046, substantiated that STRmix is relatively unaffected by differences in parameter settings. Boodoosingh indicated further that a DNA mixture that is analyzed in different laboratories using STRmix will result in different LRs, but less than 0.05% of these LRs would result in a different or misleading conclusion as long as the LR is greater than 50. This article, completely independent of the developers, further substantiates horizontal validation of STRmix.

In light of the above, we turn back to the comparison of case samples from STRmix and traditional DNA analysis in this case. The results from Bode's use of STRmix finds the presence

of [redacted] on the jeans in two locations (E01a – interior thigh above the knee with a LR of 470 sextillion & E01c – exterior front right thigh with a LR of 2.1 septillion). The traditional, manual analysis originally done by the NJSP DNA lab in 2018 also found the presence of [redacted] indicating that she was the "source" of DNA found on the jeans in five separate areas (samples 6-1-2-1; 6-1-3-1; 6-1-5-1; 6-1-7-1 and 6-1-8-1). S-184A. The threshold for source attribution at the NJSP DNA lab was defined by NJSP Forensic Scientist 3 Christine Schlenker as exceeding 1 in 8 trillion. T9:85-9 to 10. It is hard to imagine a better way to prove that the STRmix results are reliable – here, the STRmix results and the traditional results produce the same answer on the exact same items – a pair of jeans found in defendant's basement.

Much was also made about lack of independence in the testing of STRmix, both scientifically and from a software engineering perspective. The State is confident that the Court recognizes the massive amount of testing that been done with STRmix; but, the State would highlight that the detractors, both in this case and in the past, are scientists or software engineers who say that STRmix needs to go further in order to prove the limits (scientific) or to ensure that there aren't more yet-to-be identified bugs (software engineering). All of these statements by the defense experts must be evaluated for credibility against the backdrop that none of these defense experts in this case have ever even used STRmix, with the exception of Mr. Adams, who actually attended one of the STRmix four-day trainings. It is

interesting that the only expert who actually has used STRmix is one of the software engineers. There does not appear to be any evidence in this record to suggest, however, that Adams has ever attempted to use available data to verify that the software works.

Dr. John Buckleton and STRmix have always listened to fair criticisms and made appropriate changes. (T7:13-20 to 13-25). Dr. Buckleton explained how he created the specification document because Mr. Adams "in previous cases has complained that he wanted a centralized specification document, so at his request I made one. So, I wrote out a specification for 2.5.11, which was the version that he was interested in at the time." (T7:12-2 to 12-8). It should be noted that this marked the second time Mr. Adams was afforded the opportunity to review the source code for V.2.5.11. The State will expand upon the irony of that infra. Despite arguments by the defense to the contrary, the State would note that, if Dr. Buckleton did not possess significant training and experience in software engineering, we suspect he would not have been able to essentially translate STRmix's code into this specification document.

That being said, while there are several paid detractors, only one has ever actually run STRmix. This is particularly troubling, in the State's opinion, for the defense DNA experts, Dr. Reich and Keith Inman, especially given the fact that Inman was involved in the creation of a semi-continuous Probabilistic Genotyping software, Lab Retriever (for which Dr. Buckleton wrote the math). (T10:26-10 to 26-11); (T10:43-4 to 43-9). One would

suspect that Inman might think it important, given his experience in the field, to actually try STRmix, a continuous Probabilistic Genotyping software, before coming to critique it. This is especially so because Inman testified that he uses EuroForMix and LikeLTD, two continuous Probabilistic Genotyping software that are predominantly used in Europe, likely because he is a visiting professor/fellow in Europe. (T19:130-12 to 131-3).

The State would submit that EuroForMix (EFM) and LikeLTD were both discussed by Drs. Buckleton and Coble, and neither appears to be drastically different than STRmix. Additionally, comparative testing studies have been done comparing EFM and STRmix. Also, recall that Dr. Coble, when discussing how using a PG software is a far better way to detect errors than source-code review, also discussed how they tested EuroForMix with the five Mix 13 mixtures and found errors. Coble said that they reached out to their colleagues at EuroForMix and notified them of the issues, and they fixed it. EuroForMix then came out with a newer version and they re-ran the mixture and it gave an intuitive result. T10:87-4 to 87-22. The State does not point this out to, in any way, denigrate EuroForMix. This is simply an example of how an error can be discovered and fixed; but, it also highlights the ironic nature that Inman can use EuroForMix without concern, but can testify for a whole morning about the pitfalls of STRmix. The State submits that the opinions of Dr. Inman have little credibility. He had months to evaluate the data from the NJSP DNA lab's validation. His report essentially said nothing other than he did not have enough time to complete

that task. D-18. To add insult to injury, he was then sent Bode's internal validation summary and wrote a second report, indicating that it provided insufficient information for him to evaluate the depths of their validation. D-19. Ultimately, Inman spent a substantial amount of time testifying despite the fact that none of his opinions were contained in any report.

Similarly disturbing was Dr. Reich's testimony criticizing Bode and STRmix. His report for this case was dated February 6, 2024. D-14. Shortly thereafter, on March 12, 2024, unbeknownst to anyone at the time, Reich submitted a certification to the State of Wisconsin, Circuit Court, Manitowoc County in State v. Steven A. Avery, Sr., where he was retained by Avery's post-conviction attorney to provide scientific information regarding the viability of touch DNA testing on certain items of evidence." S-188A. He further certified that it was his opinion that specific evidentiary items "would produce a partial or full DNA profile of they came in contact with an individual's skin or sebum." Ibid. Lastly, he indicated that he has "a qualified representative at my laboratory, Independent Forensics of Illinois, to do the swabbing of the RAV-4. After the swabbing, we shall transmit the swabs to Bode Technology Group, Inc. at 10430 Furnace Road, Lorton, VA 22079 for touch DNA testing. Ibid. On cross examination, he acknowledged that touch DNA would "typically" amount to "low level DNA samples. (T13:26-7 to 26-13). Essentially, Dr. Reich has "never used STRmix," doesn't feel Bode & STRmix are reliable, but he's happy to send evidence there to utilize their version of STRmix. The State submits that this

greatly affects his credibility. (T13:27-15 to 27-16).

Looking at this point through a different lens further highlights the fact that Probabilistic Genotyping and STRmix specifically, is a powerful tool, both for the State and for the defense. In his initial report dated October 26, 2023, S-186, Dr. Michael Coble indicated that "STRmix has been a gamechanger for the field of forensic DNA testing and in my opinion is now the gold standard for DNA interpretation." S-186, page 7. During his testimony, Dr. Coble explained how he first crossed paths with TrueAllele, then STRmix, while working for the National Institute of Standards and Technology (NIST). (T10:20-15 to 20-19); (T10:23-19 to 23-20). NIST, according to Dr. Coble, has a "mission… to conduct research, you know looking at developing new standards and new technologies, whether testing new technologies or developing new technologies." (T10:15-16 to 15-20). NIST does not do criminal casework. (T10:23-14 to 24-1). He has authored 101 peer-reviewed publications. (T10:26-22 to 26-25). He is on the editorial board of the Journal of Forensic Sciences and Forensic Science International: Genetics. (T10:28-4 to 28-7). He is a fellow of the American Academy of Forensic Sciences and a member of the International Society for Forensic Genetics (ISFG). He was a Court-appointed neutral expert in one of the seminal cases involving the admissibility of STRmix, United States v. Gissantaner, 990 F.3d 457, 463 (6th Cir. 2021); (T10:34-20 to 35-25).

Dr. Coble explained how issues in Australia led to the creation of STRmix by Drs. Buckleton, Taylor and Jo-Anne Bright,

and how he was first exposed to STRmix while at an ISFG conference in Copenhagen. A conversation he had with Dr. Buckleton ultimately led to his trip to Australia to learn more about STRmix. He left "very much" impressed with STRmix and returned to the United States with a copy of an early version of STRmix. Shortly thereafter, the US Army lab went live with STRmix in November 2014. See generally (T10:44-3 to 48-20).

Dr. Coble then discussed a pivotal moment, which likely led to the shift in the United States towards the use of Probabilistic Genotyping. He discussed a study that he and Dr. John Butler (also of NIST) prepared for U.S. DNA laboratories "to sort of get a test, get a lay of the land on how the US is doing with mixture interpretation in light of now applying this stochastic threshold." It was called Mix 13, reflective of the year it was created, 2013. (T10:54-23 to 55-3). Dr. Coble discussed how the results from the participating labs were extremely inconsistent and how "a lot of people falsely included this person in the mixture." (T10:58-4 to 58-6). He then discussed the culmination of this – the first technical leader summit with approximately 106 labs participating, which was held at a CODIS meeting in Norman, Oklahoma, and how "people were quite upset." (T10:58-8 to 58-12). Coble made clear that people were very upset (not sure how this was so contrasting to Mr. Godin's John Butler "flak jacket" reference in summation). Coble explained, while sitting in the back of the room sensing the tension, "he opened up his laptop and began to run the mixtures from Mix 13 through STRmix." (T10:58-12 to 58-20). He then

described how he gave a presentation the next day upon the work he did with STRmix and showed them. He said that he explained how using STRmix, despite the obvious and intended complexity of this one mixture, he got a likelihood ratio of zero, so the person (previously falsely included by most), would be excluded – the proper result. (T10:58-21 to 59-5). Coble testified that "this is the utility of using a computer software program that can do this type of interpretation for these types of really complex mixtures." (T10:59-2 to 59-5). The Court should also note that this was approximately 10 years ago. The State believes that this Court should accord great weight to the testimony of Dr. Coble, someone who encountered STRmix as an employee of NIST and was simply trying to investigate and find solutions for the problem that existed in the United States and throughout the world, of complex mixture deconvolution. The connection between Dr. Coble is simple – he tried it and realized, years ago, how well it works. Given his role at NIST, he exposed the DNA community in the United States to the benefits of probabilistic genotyping and, specifically, STRmix.

One critical point worth noting, as the State did in its initial brief, is along the lines of STRmix being the "gamechanger" Dr. Coble described in his report. He highlighted in that report and in his testimony how the power of Probabilistic Genotyping and STRmix can be used to both exonerate those who have been wrongfully convicted and, of significant import, to ensure that innocent persons of interest are excluded from mixtures so that they are never charged in the first place.

Dr. Coble was asked, "if you did not believe in what you saw was (sic) STRmix back in 2013/2014 would you have written about it in the forensic community?" His answer is as follows:

> No, it's certainly it's something that I feel and I still feel to this day feel that it has really that it has really made the field move forward and it has really been helpful, you know Lydell Grant would still be in jail. Now he has some issues that we won't go into but he would still be in jail, never get that exoneration if we didn't use ProbGen. And I think about the number of people that never go to jail because they are excluded from the beginning with this software that you know, otherwise it would have been – oh I don't know inconclusive. I think it has really helped the community and I think it's been a positive thing.

(T10:87-9 to 87-21).

Earlier in his testimony, Dr. Coble first discussed the above TrueAllele exoneration of Lydell Grant, which he explained arose in Texas, where he is the Commissioner of the Texas Forensic Science Commission. (T10:33-11). He explained how Grant was serving a life sentence for murder. At the time the DNA testing was performed, the results were deemed to be inconclusive. So, the DNA was not helpful to the defense or the prosecution. He indicated that, during trial, the DNA expert was asked both whether he (Grant) could be there and whether he could not be there in the mixture. Both answers were "yes." Long after Grant's conviction, the Conviction Integrity Unit asked if the sample could be tested with Probabilistic Genotyping. They used TrueAllele and excluded Lydell Grant, and they were actually able to determine the person of interest who committed the crimes. They searched CODIS and got a hit for someone else. That person later confessed to the crime. See (10T:99-21 to 101-3).

Dr. Coble also described another situation in Texas with a case where the person of interest was determined to be inconclusive. This occurred while the lab was in the middle of validating STRmix. The lab had advised that the validation would be complete in six months. Six months later, the lab was approached about retesting, and the person was excluded. (10T:101-16 to 101-23). While this may seem like a simple example, I am sure that this Court can imagine how Probabilistic Genotyping is a gamechanger for other "stakeholders" like the Innocence Project and Conviction Integrity Units, both of which operate in the State of New Jersey. Excluding an innocent person of interest – in lieu of an inconclusive result – is a "gamechanger" for the criminal justice system.

Finally, during his testimony, Dr. Michael Coble was asked if he would recommend Probabilistic Genotyping. Dr. Coble succinctly and accurately stated, "I basically say there are two types of labs in the U.S. There are labs that are using probabilistic genotyping and there are labs that will soon be using probabilistic genotyping." Coble at p. 82 lines 10-13. With this in mind, the State would point out that the majority of those labs are all using STRmix. At last count, the number is 89 United States laboratory systems. S-140. This "lab system" distinction was also explained throughout this hearing by more than one witness, given the fact that, for instance, the California Department of Justice laboratory is listed one time, yet several different laboratories that use STRmix. Dr. Coble was asked by the Court about the number of laboratories in the

United States. He estimated that 212 laboratories do DNA testing and estimated that 130 or 140 of those have brought on Probabilistic Genotyping software. (11T:84-9 to 84-12).

The above is critically important, not just because it highlights the proliferation of STRmix in the United States, but also because it demonstrates all of the additional testing that has been done in all of these internal validations of STRmix since 2014, when the first laboratory went live. S-140. Much has been made about the distinction between software IV&V and scientific, lab-conducted validations; however, both result in an extreme amount of testing of the software. Neither the State nor Dr. Buckleton are ignoring IV&V and/or IEEE 1012-2016; the State is simply reminding this Court that there is no particular mandate in the United States that Probabilistic Genotyping software conform to any software engineering standards. That being said, given the testimony of Dr. John Buckleton, the State would be disingenuous were it to wholly ignore the importance of adequate testing of software. It is hard to imagine, given the detailed testimony of Dr. Buckleton regarding his intimate knowledge of governing software engineering principles, including IEEE 1012-2016, that STRmix has not adequately tested the software over the course of the last 13 years, since STRmix was created. Similarly, the Court should also not let the defense attempt to downplay the sheer amount of scientific testing that STRmix has undergone throughout its existence. Doing so would seemingly ignore the language from IEEE 1012-2016 itself. IEEE 1012-2016 specifically states that, "[u]se of an IEEE standard is

wholly voluntary. The existence of an IEEE standard does not imply that there are no other ways to produce, test, measure, purchase, market, or provide other goods and services related to the scope of the IEEE standard. Furthermore, the viewpoint expressed at the time a standard is approved and issued is subject to change brought about through developments in the state of the art and comments received from users of the standard." S-136 at 4.

The State would note that STRmix has been tested over the course of approximately 13 years, since it was created by Drs. Buckleton and Duncan Taylor. The software engineers that testified for the defense attack the documentation of STRmix code. They point out how code should be developed from its inception. The issue here, however, is that STRmix was created to solve a problem in Australasia, not to be sold commercially in the United States. The State submits that this is important because it is undisputed that it was not developed initially to be sold to anyone – and, therefore, STRmix has strived for years now to satisfy the critiques of people like Nathan Adams. Dr. Buckleton largely explained this and discussed how he sought to satisfy Adams and others to better *document* STRmix code. Interestingly, when the Court asked Dr. Buckleton to take a step back and provide what he would consider to be STRmix's biggest flaw, he told the Court that it was the documentation. This answer – in the State's opinion – explains why STRmix is reliable. Improvements can certainly always occur; however, nothing postured by the defense affects reliability in the use of

STRmix every day in this Country. Specifically, Dr. Buckleton told Your Honor:

> I think the areas we're currently failing in, or could improve in, relate to the assurance issue I was talking about earlier. So I believe it works, the labs believe it works. I think we are probably deficient on putting sufficient documentation in front of people like Mr. Adams, that he can be confident in it. SO I think our software documentation needs a step up.
>
> We are currently moving large blocks of material from my IEEE-1012 into our ISO-9001 SOP, so that we will now formally be meeting the 1012 requirements.
>
> I don't know, I mean people want an even more remote organization from us to do the IV&V on it. And we're just completely cool with that. I would feel fine if Mr. Godin wanted to do the IV&V on it, we could set him up with the gear. No one seems to want to do it. Well, NIST have said that they won't do it, they won't do IV&V on software. And they're the obvious go to organization. They have a considerable reputation for independence. And they would be – but they do not want to do the IV&V of software for the United States. That (sic) don't want that sort of service rile. They do do it on document evidence. You know recovery of information from computers. They do have a IV&V unit for that. So I don't know why they can't have one for PG.
>
> But no one else has offered. And we have paid people, but if we pay people then it's said that we're paying the,. So we sort of need almost someone to just rock along and say, I've got nothing to do for two years, can I IV&V your software. And that hasn't happened.

(T7:207-12 to 208-24).

Mr. Godin argued in his oral summation that STRmix could pay Dr. Paul Martin to do an IV&V – and they certainly could. But, in reality, someone will still always say that this is not independent because they are paying. Also, the Court should realize what Dr. Buckleton's candid analysis means in relation to arguments made by the defense experts: it works, we just need to do a better job from a software perspective of being able to show

them it works. That, simply doesn't affect reliability – just documentation. The State and STRmix understands and appreciates the arguments; however, documentation simply is not a factor in the Daubert analysis.

The software engineers made largely cosmetic and documentary critiques of STRmix's code. They essentially speculate that there must be more "bugs," and, just like with every piece of software in existence, there probably are. Objectively speaking, the problem with the testimony of Martin, Heimdahl and Adams, is really that they have never found any of them. Adams found them with FST, but never with STRmix. Adams also decided to essentially throw in the towel in this case, electing not to review the code for V.2.8; therefore, Dr. Martin had to step in and do it. This created an interesting scenario as Adams has spent his whole career attacking PG; Dr. Paul Martin has a very diversified and credible software engineering background (Bachelors, Masters and Ph.D. from Johns Hopkins). (T18:10-1 to 10-3).

The State would submit that Adams has some arguments which are, obviously, credible. Dr. Buckleton knows what they are and consistently have been and discussed same in his testimony. These were discussed above. Adams also testified he had 2 issues during his code review – the first was not having the specification document. He asked and they gave it to him. The other issue was, essentially, not being able to step through the code. He said that he told STRmix' lawyer, Blake Gerney, about the issue and he was told there was nothing that could be done

about this. (T16:56-4 to 57-17). Adams said that he called counsel for the defendant. The State never heard a word. STRmix never heard a word. The State and STRmix learned about this approximately 8 months later when we received Adams' report, dated July 31, 2023. D-17. The report reflects that code review occurred on November 1-3, 2022. Ibid. Dr. Buckleton discussed this in his testimony and it is clearly discussed in his report, S-152. Dr. Buckleton said he was awake and on standby with others in case any issues arose. (T7:202-23 to 203-8).

The State is certain that the defense will disagree; however, the State believes that Adams, by no fault of his own, could not step through the code like he wanted. Then, instead of asking for it to be rectified, he decided that he was just going to complain later and make it look like STRmix does not give him the access he needs. This is also consistent with the fact that this was his second review of V2.5.11,; therefore he knew what he was going to find or not find already. (T16:135:3 to 135-7). The State also submits that it found it ironic that Adams regularly uses the GeneMapper software, which creates the electropherograms that are put into STRmix, despite having no concern as to whether they conform to IEEE 1012-2016. He even acknowledged that Genemapper "could be" part of "those catastrophic results" which we warned could occur using STRmix, by virtue of the fact that Genemapper creates the data input into STRmix. (T16:97-7 to 99-10).

Dr. Martin, by contrast, made many of the same documentation critiques. He, however, appeared very candid and

knowledgeable. Interestingly, however, at the end of his direct examination he was asked, "do you have an overall impression on the quality of the code itself?" His answer was as follows:

> I thought it was quite good. Yeah, it complied with most reasonable engineering standards. I didn't see any glaring issues. I thought it was actually professionally developed, nicely commented. Well written. I thought it was a pretty good code.
>
> I thought that they were all written reasonably well. I think that 2.8 was better because it had things like SafeMath and more testing. But outside of the testing issues I thought the code itself looked pretty, pretty professional to be honest with you. And I've seen plenty of unprofessional code.

(T18:66-2 to 66-20). The State submits that this testimony is important; Dr. Martin was the most credible of the defense experts. He doesn't testify in admissibility hearings for a living. Frankly, the State submits that this is why Mr. Godin referenced STRmix paying Dr. Martin to do their IV&V in his summation. He was the only objective defense expert and that was what he said about the source code.

The defense has challenged Dr. Buckleton's expertise in software development. They have pointed to the fact that he last wrote code in 1995, and that Dr. Duncan Taylor wrote the code for the initial versions of STRmix, prior to the contracting of coding to Orbit. This ignores the collaboration between Drs. Taylor and Buckleton in the creation of STRmix and the testimony regarding his input into the code – namely how "we used to talk about how the algorithms should be structured and I've done some work on how to make things fast and we did work on that" and how he "was doing a lot of the early testing." (T6:21-6 to 21-14).

We must be cognizant of the evolution of DNA analysis since its inception. We heard that from Dr. Buckleton, a man educated and skilled in mathematics, statistics, chemistry, forensic biology and software engineering. (T6:11-1 to 13-9). Dr. Buckleton also testified regarding his education and work at the Forensic Science Service in the United Kingdom, where he was in a unit that "was making software" and how he "wrote code from that time '88 consistently up to '94 and I stopped in '95." (6T:13-14 to 13-19). Dr. Buckleton was very candid about how his coding experience essentially ended there, but this Court should not ignore that he had the requisite knowledge to adequately discuss the requisite software engineering principles, and to respond to criticisms of STRmix's code. It must be noted that Dr. Buckleton has always been the person in United States admissibility hearings who has explained criticisms with respect to the code and with respect to the testing, verification and validation of the software. To suggest that he is not qualified simply because he did not actually write the code would certainly make one wonder how the defense experts are qualified, particularly in light of the fact that Nathan Adams has not completed his Master's Degree and that there was zero testimony that any of the defense experts have ever written any code or created a software engineering product.

As to challenges to Dr. Buckleton's candor or credibility, a review of the transcripts would reveal that he was extremely responsive to questions regardless of whether it was on direct or cross examination. This Court could see that Dr. Buckleton was

candid, whether the answer was particularly helpful to the State's case or not. Recall, for instance, how he discussed his belief that Dr. Heimdahl, in the Lewis[4] case, didn't highlight IEEE 1012, but now he has changed his position and does rely heavily on it. Dr. Buckleton specifically stated, "[b]ut what he did say was entirely a gem and is completely correct, is that the key element is to maintain a testing attitude." (T6:115-4 to 115-10). By way of another example highlighting Dr. Buckleton's absolute candor occurred when discussing the substance of Nathan Adams' criticisms. Specifically, he testified that he created the specification document because Nathan Adams, in a previous case, wanted a centralized document. The State asked if Adams found it helpful; Dr. Buckleton stated, "I probably didn't expect him to cheer. He felt I had conflated the concepts of design with specification. And I think I have. I think I have done that. So, specifying something, I want the Mars Lunar Orbiter to fly to Mars and orbit it. That's the specification. Getting down to design is I want it to be able to fire its little rockets in a way that it can aim itself properly. So, he felt I'd got into the design elements. And, I have. I've written out the algorithm in detail." (T7:12-19 to 13-10). These are two examples that occurred on direct examination. As for cross examination, the State submits that he was equally as responsive. Dr. Buckleton described a wide variety of topics regarding the science, as well as the software engineering principles.

Recall also, how Dr. Buckleton, who had witnessed Mr.

[4] United States v. Lewis, 442 F.Supp 3d 1122 (D. Minn. 2020).

Godin's ability to navigate STRmix during his cross examination of Danielle Reed, complemented Mr. Godin when he testified that, "I've got to say that our four day training is pretty effective, Mr. Godin, because you have learned a lot." (T7:189=7 to 189-9). He also answered questions as best he could regarding the STRmix financials. The defense, however, became frustrated that he did not know more. The State submits that was candid. He answered what he knew; for instance, he discussed how Orbit is paid on contract and that is not conditional on the outcomes of testing; and, he even was able to provide the royalty paid to FSSA (Forensic Science South Australia) – specifically, 10 percent of the license sales and 20 percent of the maintenance fees, amounting to approximately "a million US." See (T7:124-1 to 125-25). Dr. Buckleton knows what he knows about STRmix; the defense desperately wanted more. Hence the reliance in oral summation upon the STRmix financials, none of which was discussed in this hearing -- beyond the above.

Despite any commentary to the contrary, Dr. Buckleton is a civil servant and on a salary. As Dr. Buckleton testified, he does not get a percentage of sales and he is "unpromotable" and has been "since he was 38." (T6:47-2 to 47-3). He also stated quite clearly that he understands the impact of STRmix and, particularly, the catastrophic impact that a false inclusion (with a high Likelihood Ratio) would have. Despite arguments that they could never independently test their software, he testified that he would never want "to contribute to an injustice ever" and that for himself and his colleagues, their "actual

motivation is to actually test the software well, try and break it if we can and if we miss something, just honestly report what has happened." (T6:47-1 to 47-9).

He also testified about the origins of STRmix in 2011 and how it was created by himself and Dr. Duncan Taylor after a lab closure in Australia, given the misuse of freeware that had been used. He indicated that, given the cost associated with the Probabilistic Genotyping software, TrueAllele, Australasia could only afford two licenses of TrueAllele; therefore, it was decided that "Duncan Taylor and I would just make some work horse rough thing that would do the two person mixtures and all the harder stuff would be given to TrueAllele." (T6:18-12 to 18-22). Despite that initial thought, he and Dr. Taylor "had a working prototype in two weeks and we were doing four person mixtures within four weeks and it was only limited to that by my own conservatism. I would just put arbitrary limits on it. It was what we call scalable." (T6:20-4 to 20-8).

Dr. Buckleton indicated that, at some point, the powers-that-be in Australia realized that it was "better than TrueAllele and they just changed the policy around." STRmix went live in 2012. The State would again highlight, in light of many of the defense software criticisms, that STRmix was not created to be sold commercially; therefore, at the time of creation, the "stakeholders" were simply the labs in Australasia. Arguments have been made throughout the hearing regarding "requirements." Dr. Mats Heimdahl explained that software requirements are "a statement of what the software ought to be doing… what is the

problem and what does the software have to do to solve that problem." He explained how this might occur and stated that "it might be an engineering team that comes to you and says we need a piece of software that does this for us. If you work in other domains, you might not exactly know what the customers want so you need to go out and talk with them, elicit these requirements, try to understand their problems, their wishes, their likes, their dislikes and then capture that in a requirements document so you can build what the customer wants." (T14:20-7 to 20-24).

The State would argue to this Court that this theory, essentially put forth by all of the defense software engineers, is exactly where they fail to understand that STRmix was not created in a manner similar to how most software is created. Dr. Heimdahl envisions the typical scenario, where a company has an idea and they want to design a way to implement that idea. They then hire someone to write the code to do that. This, obviously, requires the creators of the code to understand what it is that the company wants the software to do. While this theory may be in line with relevant software engineering principles and guidelines, it fails to understand that when Drs. Buckleton and Taylor created STRmix, they knew what the problem was and knew what they wanted the software to do – deconvolute mixtures. While they were the developers, they were also customers and stakeholders, given the fact that, despite the diversity of their experience in other fields, including statistics, software engineering, etc., they were, primarily, forensic DNA analysts.

To this end, it is somewhat unrealistic to evaluate STRmix

in a traditional sense of how most software creations are developed, from inception of an idea to the launch of a commercial product. It is why the arguments regarding consulting stakeholders prior to creating this software are invalid, because doing so would have been impossible. Dr. Heimdahl essentially acknowledged this on cross-examination when he was asked, "[b]ut is it plausible to mandate someone let's say in 2012 that wants to solve a problem in Australia, that they need to come to the United States and consult all relevant stakeholders?" His answer was "No." (T15:21-3 to 21-8).

Dr. Heimdahl, both in his reports and testimony, wants this Court to believe that STRmix is essentially saying to its customers, "just trust me, this is good s**t." (T14:41-1). This flippant argument ignores the years of work that have been put into creating, testing and using STRmix. Dr. Heimdahl's academic approach to software engineering is instructive; however, it is ironic that the man who makes the "just trust us" argument is the same one who authored an amicus brief in State v. Pickett and two reports in this case, essentially asking Court to just trust him. The State submits that when Courts trust him, inaccurate statements make their way into published opinions.

Specifically, in State v. Pickett, 466 N.J.Super. 270 (App. Div. 2021), the Court noted the following information they were supplied with, which they attributed to Drs. Mats Heimdahl and Jeanna Matthews in their *amicus* brief.

- Drs. Heimdahl and Matthews are experts in engineering, testing, and validating computer systems, including forensic evidentiary software. They, together with eight other

> experts in this specific field that they have identified, argue that reliability of the TrueAllele software cannot be evaluated without full access to "executable source code and related documentation," something that no one to date has seen. They contend that doing so is not only prudent, but essential to determining whether TrueAllele operates as Cybergenetics claims, which is fundamental to any fair, legitimate, and impartial assessment of reliability.
>
> - For example, *a source-code review* revealed at least thirteen STRmix coding faults. Drs. Heimdahl and Matthews argue, in one important example, a miscode impacted sixty criminal cases, requiring new likelihood ratios to be issued in twenty-four of them. These errors were not discovered until the source code was independently examined.
> - In FST, alarming discoveries were also made. But the findings did not come to light until a federal judge ordered disclosure of FST's source code. Once that occurred, it was uncovered that a "secret function . . . was present in the software, tending to overestimate the likelihood of guilt." And the functioning of the software did not use the "methodology publicly described in sworn testimony and peer-reviewed publications." *These discoveries led to the overturning of a high-profile conviction.*
> - Drs. Heimdahl and Matthews assert that thousands of faults were discovered in the source code of breathalyzer systems. *They point out that judges in Massachusetts and New Jersey threw out more than 30,000 breath tests in a twelve-month period.* Drs. Heimdahl and Matthews urge us not to ignore these facts.

Pickett, 466 N.J.Super. 270 at 298-299.

Dr. Heimdahl's credibility should be closely scrutinized, given information he provides and/or cites with almost no basis of knowledge. Somehow, his *amicus* brief convinced the New Jersey Appellate Division that *a source-code review* revealed at least 13 STRmix coding faults. The State is not exactly sure whether he was untruthful to the Court, or whether, he just blatantly and negligently failed to investigate certain statements that he has put in writing at least twice. Either way, source-code review has never led to the identification of a miscode or bug in STRmix's software.

In the same vein, the Pickett Court noted that "Drs.

Heimdahl and Matthews argue, in one important example, a miscode impacted sixty criminal cases, requiring new likelihood ratios to be issued in twenty-four of them. *These errors were not discovered until the source code was independently examined.*" While in the amicus brief, to be fair, Drs. Heimdahl and Matthews only wrote the first sentence above, the Court somehow added that "[t]hese errors were not discovered until the source code was independently reviewed." But, given this misstatement, STRmix had no choice but to clear the issue up in its letter entitled, "Incorrect comments relating to STRmix in State of New Jersey v. Corey Pickett. S-138.

However, in his report in this case, Dr. Heimdahl adopted that argument in paragraph 47 of his report, dated July 28, 2023, where he stated, "[n]umerous factors suggest that STRmix™ is likely to contain undetected flaws, including that: (1) flaws have already been discovered in STRmix™ and other PG programs and less complex forensic tools, often only after source code was produced pursuant to judicial orders…" D-10 at 22. Interestingly, Dr. Heimdahl does not clarify that in any meaningful way. But, the testimony, as well as prior written decision regarding STRmix, makes clear that source-code review has never detected any "miscodes" in STRmix' software. The Court can feel free to review the transcript of the Nathan Adams testimony from Illinois v. Morgan, Doty & Edwards (buckleton-x-contd-adams.pdf, page 254) regarding his prior code review of V.2.5.11, the same version used by Bode in this case, when Adams was authorized to discuss this information; same would reveal

that he found no coding errors, bugs or miscodes. (T16:135-3 to 135-7).

The State will not belabor this point much further; however, Dr. Heimdahl's statements regarding source-code faults leading to 30,000 cases being thrown out in Massachusetts and New Jersey is simply not true. Additionally, while source-code review led to errors being discovered in the Forensic Statistical Tool (FST) program, the connection to a high-profile case being thrown out is tenuous at best. Dr. Heimdahl cites only to a New York Times article, "Hasidic Man Convicted of Beating Black Student Gets Verdict Overturned," which does not once mention FST or flaws in its code. Had Dr. Heimdahl read more on the matter, he may have been able to, in some way, substantiate a fairly important point.

The State would submit that Dr. Heimdahl essentially throws a proverbial grenade and walks away, hoping to make this Court fearful of what STRmix is capable of. Despite an occasionally meaningful critique of how STRmix could improve its software documentation, he lost his credibility by mischaracterizing significant facts in order to try and scare this Court. Unfortunately, while some of his documentation arguments may hold weight, STRmix has been thoroughly tested and has never experienced the catastrophic error that Heimdahl and others warn about. The Court is also left with the truth: that source-code review has never detected any miscodes/bugs/coding faults, regardless of the term anyone chooses to use.

Arguments made that STRmix is unreliable with respect to

low-level mixtures presupposes its accuracy and reliability with respect to higher-level contributors – specifically with respect to all of samples that Dr. Karl Reich indicated were reliable results. This argument also flies in the face of the arguments regarding reliability of the software itself. If the software works, then the software works. Nothing changes within the coding or algorithm in STRmix when you input data from an electropherogram. When a smaller number of alleles appear in a sample, nothing changes with respect to the math, the algorithms or how the software deconvolutes mixtures, it just leads to less probative results. Essentially, the State submits, STRmix does exactly what we have seen with traditional results… a likelihood ratio of, say, 450 is not in any way substantially different from a scenario we have encountered in the past with a random match probability of 1 in 450. Any somewhat prepared defense attorney would, I expect, elicit from an analyst (were the State to even use such a result) that there are approximately 8 billion people currently living in the world, and that simple division would indicate that you would expect to be able to find that 17.7 million people could potentially fit that profile. I think it is fair to assume that an attorney, on cross-examination, could do the same thing regarding an LR of 450, particularly if they were to also point out that 450 is within the uninformative range of what some labs utilize. None of this, however, changes that the number 450 is accurate and reliable – it just means it is less probative.

While the State will certainly address the relevant standard

infra, the State would make clear that nothing in Olenowski I tells this Court to ignore Daubert and all of the thoughtful and relevant caselaw throughout the United States. Despite the fact that the Olenowski I Court certainly said that they "decline to embrace the full body of Daubert case law as applied by state and federal courts," they also noted that "caselaw from other jurisdictions… can be persuasive but it not controlling." The State suspects that this Court will certainly take into consideration relevant opinions from other State and Federal courts in both Frye, Kelly and Daubert jurisdictions. A review of same would dictate that STRmix has been found reliable consistently over the course of its 10 years of life in casework in the United States. The State is not aware of any single case where a Court said that STRmix was not reliable – while distinctions have been made about the application of STRmix in a small number of specific cases (based upon the number of contributors being higher than a lab validated), there has never been a wholesale ruling disturbing the reliability of STRmix. And, in this case, the defense software engineers ask this Court to do just that – rule that we cannot trust the software, period. The State submits that the critiques regarding their displeasure with the documentation of STRmix software simply do not change that scientific testing undoubtedly proves that STRmix works exceptionally well. STRmix is not new, and the degree to which it has been tested has been acknowledged time and time again in United States courts.

POINT I

THE STATE SUBMITS THAT THE STRmix EVIDENCE IS ADMISSIBLE PURSUANT TO OLENOWSKI I AND DAUBERT

Opinion testimony by an expert is admissible "[i]f scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue." N.J.R.E. 702. In New Jersey, there are three requirements for the admission of expert testimony:

> (1) the intended testimony must concern a subject matter that is beyond the ken of the average juror; (2) the field testified to must be at a state of the art that such an expert's testimony could be sufficiently reliable; and (3) the witness must have sufficient expertise to offer the intended testimony.

[State v. Kelly, 97 N.J. 178, 208 (1984).] In criminal prosecutions, the conditions of admissibility must be "clearly established" by the party offering the evidence. Windmere, Inc. v. International Ins. Co. 105 N.J. 373, 378 (1987) (citing State v. Johnson, 42 N.J. 146, 171, (1964)).

The introduction or exclusion of evidence is within the sound discretion of the court. State v. Torres, 183 N.J. 554, 567 (2005). Making an admissibility determination might require a N.J.R.E. 104 hearing. Ibid. (citing Harvey, 151 N.J. at 167) .

1. The intended testimony concerns a subject matter that is beyond the ken of the average juror.

The first inquiry in determining admissibility of expert

evidence is whether the testimony addresses evidence that "relates to a relevant subject that is beyond the understanding of the average person of ordinary experience, education and knowledge." State v. Odom, 116 N.J. 65, 71 (1989). If the court determines testimony would help a jury better understand the evidence in determining the facts, the first requirement for admission is met. Ibid. DNA evidence has long been offered in trials using expert testimony and is not in and of itself a novel scientific technique. State v. Marcus, 294 N.J. Super. 267 (App. Div. 1996), certif. denied 157 N.J. 543 (1998); State v. Dishon, 297 N.J. Super. 254 (App. Div. 1996), certif. denied 149 N.J. 144 (1997); Harvey, 151 N.J. 117.

Testimony about the analysis of DNA is based on both scientific and mathematical principles that are well beyond the ken of the average juror, as New Jersey courts have repeatedly held for decades. When, as here, there is newer technology, further inquiry regarding reliability and acceptance may be required. See State v. Doriguzzi, 334 N.J. Super. 530 (App. Div. 2000). Technology relating to forensic DNA analysis remains subject matter beyond the ken of the average juror.

2. The expert's testimony is sufficiently reliable.

In a recent decision, State v. Olenowksi I, 253 N.J. 133 (2023), the New Jersey Supreme Court replaced the previous standard governing the admissibility of testimony based on scientific knowledge and/or technical or other specialized knowledge established by Frye and governed by N.J.R.E. 702. The

Frye standard turned primarily on whether the subject testimony has been generally accepted in the relevant scientific community. In its stead, the New Jersey Supreme Court established a new standard more in line with Daubert v. Merrell Dow Pharmaceuticals Inc., 509 U.S. 579 (1993) and its progeny, with an approach that focuses directly on reliability by evaluating the methodology and reasoning underlying the proposed expert testimony.

Unlike Frye, Daubert requires the trial judge to "determine at the outset … whether the expert is proposing to testify to (1) scientific knowledge that (2) will assist the trier of fact to understand or determine the fact in issue. This entails a preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue." Daubert, 509 U.S. at 592-93. This is a "flexible standard," focused "solely on the principles and methodology, not on the conclusions they generate," and asks the court to find that the expert testimony "rests on a reliable foundation." Id. at 594-95, 597.

Application of this flexible standard allows courts to consider four "nonexhaustive" "Daubert factors:" (1) whether the scientific theory or technique can be, or has been, tested; (2) whether it has been subjected to peer review and publications; (3) the known or potential rate of error as well as the existence of standards governing the operation of the particular scientific technique; and (4) general acceptance in the relevant

scientific community."

In In re Accutane, the New Jersey Supreme Court declined, however, "to embrace the full body of Daubert case law as applied by state and federal courts." 234 N.J. 340, 399 (2018). In practice this means that "caselaw from other jurisdictions" "can be persuasive but is not controlling," with the court holding that "[f]uture challenges in criminal cases that address the admissibility of 'new types of evidence' should be assessed under" New Jersey's Daubert-like standard. Olenowski I, 253 N.J. at 153.

The State would also note that on November 15, 2023, the New Jersey Supreme Court decided State v. Olenowski II, 255 N.J. 529 (2023), which analyzed scientific DRE evidence under the new Olenowski I standard. A review of Olenowski II reiterates that the "our opinions in Accutane and Olenowski I both cautioned that the Daubert factors should not be applied rigidly. Olenowski II, 255 N.J. at 584. The Olenowksi II Court, however, did an analysis of the Daubert factors as they relate to Drug Recognition Expert testimony; however, they chose to reorganize them "for ease of discussion in this particular case." Ibid. They made clear, however, that "[t]he sequence in which we address the Daubert factors here does not reflect their relative importance; all of the bear upon the analysis." They did note and the State would agree, that the "'testability factor', listed by the Court first conceptually, frequently ties in closely with the 'error rate' component of the Court's third factor, particularly in this case." Ibid.

Given the lack of guidance post-Olenowski I, the State has decided that it would be wise to address these factors in the same manner in which the New Jersey Supreme Court addressed them in Olenowski II: (A) adequacy of standards; (B) publication and peer review; (C) testability and error rate; and (D) general acceptance. The Court indicated also indicate that, "[w]e then conclude with an overall assessment." Id. at 585.

The State would also note that, after the aforementioned guidance of in Olenowski I, the evaluation of Drug Recognition Expert (DRE) testimony still needed to be evaluated under the new Daubert-like standard. Therefore, the Court later issued Olenowski II. While this Court certainly does not need the State teach it that procedural history; the State simply points that out because even a cursory review of the ultimate analysis and decision in Olenowski II, makes clear that the Court's opinion is replete with citations and analysis of holdings from Court's throughout the United States.

In fact, the Court noted that "[t]he Public Defender urges that we take note of last year's 2-1 published majority opinion of the Michigan Court of Appeal in *People v. Bowden*, which concluded that a DRE's testimony was inadmissible…" Olenowski II 255 N.J. at 606. Interestingly, the State expects that the defense, given previous arguments, will argue here again that "there is no binding authority on the reliability of STRmix to govern this case." See defendant's pre-hearing brief dated November 4, 2024 at page 19. They continued [n]othing other courts have done is binding in New Jersey, but these other

decisions are not even persuasive if they are not built upon a sufficiently thorough foundation." Id. at 20. They argue that the insufficient "foundation" would be as "now-Justice Fascial explained in Pickett, determinations of reliability of other PGS systems were not even persuasive when they 'entailed no scrutiny of computer science or source code.'" Id. at 20. Interestingly, recall, that we are not asking this Court to consider cases from other jurisdictions that considered "other PGS systems." The United States is replete with cases addressing STRmix; it is largely void of cases involving TrueAllele, likely because it just is not used in many places given the prevalence of STRmix. Now-Justice Fasciale didn't have that luxury in Pickett because Pickett involved TrueAllele; and the State has seen zero cases published where TrueAllele' source code had been reviewed. And, notably, of the numerous cases involving STRmix, many involved "scrutiny of computer science or source code." To that end, this Court knows that Dr. Heimdahl and Nathan Adams have actually testified in several hearings in other jurisdictions to that scrutiny. Of significant note, Dr. Heimdahl and Nathan Adams both testified for the defendant in Lewis and Adams testified in Gissantaner. While the State understands that out-of-state authority is only "persuasive" and "not controlling," it finds it interesting that the Public Defender makes this argument here, yet the opposite in Olenowksi II; asking that Court to consider precedent from other jurisdictions. Olenowski II is replete with analysis of out-of-state cases; the State has no doubt that this Court understands the definition of

persuasive and will evaluate this issue according. Finally, the State would submit, that the Court could easily find STRmix reliable on this record alone.

In the instant case, defendant filed a letter brief dated April 12, 2022 in support of a motion for a testimonial hearing regarding the admissibility of STRmix evidence. As the Court is aware, this challenge was originally filed under the then-relevant Frye standard. As discussed above, the decision in Olenowski I ultimately reversed course in New Jersey in a direction away from Frye and towards Daubert. The State submits that, based upon the totality of the testimony and in light of the relevant caselaw, STRmix meets the admissibility standards imagined by Olenowski I. The Olenowski I Court indicated that "[t]he Daubert factors will help guide trial courts in their role as gatekeepers. But, Daubert's non-exhaustive list of factors does not limit trial judges in their assessment of reliability." Id. at 154. The Court continued, "[t]he same is true for caselaw from other jurisdictions, which can be persuasive but is not controlling." Ibid. Therefore, Olenowski I dictates that "the focus in criminal cases, as in civil cases, belongs on the soundness of the methodology and reasoning used to validate the expert opinion or technique. Given this guidance, an analysis of these factors in light of the requirements under N.J.R.E. 702 and the "Daubert-type" standard envisioned by Olenowski I will follow.

A. ADEQUACY OF STANDARDS

The Gissantaner Court stated that one explanation for the low error rate is the existence of standards to guide the use of STRmix and other probabilistic genotyping software, for the two are "'[c]losely related.'" Gissantaner, 990 F.3d at 466 (quoting Mitchell, 365 F.3d at 241) (brackets in original). In Gissantaner, the Michigan State Police obtained a DNA sample from a gun recovered from the defendant's home, and then "an analyst with the Michigan State Police laboratory took information about the DNA present in the mixture and entered it into STRmix to estimate how much of the DNA came from each person." Because the State Police laboratory operated STRmix and used the program to generate the disputed likelihood ratio for the defendant, the Sixth Circuit appropriately noted the significance of the State Police laboratory's compliance "with the guidelines promulgated by the Scientific Working Group, as confirmed through an audit performed by the FBI." Gissantaner, 990 F.3d at 465. Both Bode and the NJSP DNA lab complied with these SWGDAM guidelines during the validation of STRmix in their respective labs. Same was testified to by Kristen Naughton and Jennifer Thayer.

Further, in Lewis, supra, 442 F.Supp. 3d 1122, the defense challenged STRmix citing an absence of standards, that there is no one standard that governs the foundational reliability of probabilistic genotyping software systems. The Lewis Court held that there are, however, three published guidance documents that specifically pertain to same and noted that STRmix complies with

all published guidance documents specifically directed to software validation for probabilistic genotyping systems. Those guidelines include standards published by the Scientific Working Group on DNA Analysis Methods (SWGDAM), the Forensic Science Regulator, and the International Society for Forensic Genetics (ISFG). Lewis, 442 F.Supp. 3d at 1131. Interestingly, however, the Court did not specifically mention the lone Standard ANSI/ASB Standard 018, "Standard for Validation of Probabilistic Genotyping Systems; however, this document was specifically discussed in this hearing by several witnesses and holds significant weight in the United States DNA community.

The first set of guidelines mentioned above is the 2015 Scientific Working Group on DNA Analysis Methods (SWGDAM)'s "Guidelines of the Validation of Probabilistic Genotyping Systems." S-130. SWGDAM is a consortium of approximately 50 scientists that represent state and local forensic DNA laboratories in the United States and Canada. SWGDAM's guidelines provide developmental validation to be conducted by the manufacturer of the application or the testing laboratory and that developmental validation demonstrates any known or potential limitations of the system and further provides a number of steps in the validation process. Ibid. The Lewis court held that STRmix complies with same. Lewis, R&R, 33-34 (attached as Pa16). Clearly, the Court will recall that various testimony in this matter indicated that the SWGDAM Guidelines are essentially treated as Standards for United States laboratories when validating probabilistic genotyping software.

In addition to pointing out the existence of that standard, Dr. Coble, in his review for this case, also referenced that laboratories also follow the *de facto* "standards" like the aforementioned SWGDAM guidelines for validation of probabilistic genotyping software. Dr. Coble noted that, "[a]lthough the SWGDAM guidelines are not standards, the forensic community treats them as such and follow their guidance. Accredited laboratories, such as Bode and the NJSP laboratory, are audited by their accrediting body (ANAB) to follow the FBI's Quality Assurances Standards. During an audit, the auditors can also examine validation studies and casework performed using STRmix." S-186 at 6. The testimony in this hearing consistently stated that the SWGDAM Guidelines are closely followed by United States labs who validate STRmix. A simple look at the NJSP DNA lab's validation of STRmix V2.8 would reveal a table of contents that tracks their validation with specific references to the requisite section of the SWGDAM Guidelines. See S-162.

The second set of guidelines is "Software Validation for DNA Mixture Interpretation" from the Forensic Science Regulator (FSR), the government official in the United Kingdom who regulates forensic science activities in the United Kingdom's legal system. The FSR Guidance has more detailed requirements then SWGDAM for validation; the Lewis court again found that STRmix complies with same. S-132. Dr. Buckleton said the same during this hearing, discussing both S-132 and S-159, two FSR guidance documents; the first being for interpretation of DNA evidence and the latter being a guideline for software

validation.

Lastly, there is the International Society for Forensic Genetics (ISFG), which published guidelines in 2016 for the validation of software. ISFG is an international "nonprofit scientific society whose aim is to promote scientific knowledge in the field of genetic markers." ISFG Guidance proposes minimum requirements for validation and addresses developmental and internal validation. Again, the Lewis court found that STRmix complies. S-131. Dr. Buckleton indicated that he was involved in creating these guidelines. (T6:39-23 to 40-3). This document, discussed by Dr. Buckleton and Dr. Coble, who chaired the DNA Commission that wrote the ISFG Guidelines, discussed how this guideline addresses software engineering and source code review. (T10:95-22 to 96-3). He discussed that recommendation 7 from the ISFG Guidelines also discusses testing and code review. Coble confirmed that Recommendation 7 says that "the DNA Commission does not consider examination of the source code to be a useful fact-finding measure in a legal setting." (T10:96-25 to 97-3). See S-131 at 194. That Recommendation goes on to state that "[a] rigorous validation study (both developmental and internal) should be sufficient to reveal shortcomings or errors in coding… however, if requested by the legal system, the code should be made available subject to the software provider's legitimate copyright or commercial interests being safeguarded." S-131 at 194. Obviously, both Drs. Buckleton and Coble both testified that they believed that use and testing was the best way to detect errors in the software, not code review. This is

consistent with S-131 and with the fact that the only "miscodes" that have been found (and published) in STRmix were found by STRmix or laboratories in testing and use.

In addition to the aforementioned guidance documents, the State would highlight the lone Standard that applies to United States DNA labs when validating Probabilistic Genotyping systems. This Standard published by the American National Standards Institute (ANSI), along with the American Academy of Forensic Sciences Board (ASB), a Standards Development Organization, is ANSI/ASB Standard 018: Standard for the Validation of Probabilistic Genotyping Systems. S-133. In Standard 018, Section 4, "Requirements," Subsection 4.1.2, indicates that "[d]evelopmental validation studies shall address the following: accuracy, sensitivity, specificity, and precision. These studies shall include case-type profiles of known composition that represent (in terms of number of contributors, mixture ratios, and total DNA template quantities) the range of scenarios that would likely be encountered in casework. Studies shall not be limited to pristine DNA samples but shall include compromised DNA samples (e.g, low template, degraded, and inhibited sample)." S-133 at 3. In ordering certain work to be done, ASB 018 specifically mentions "total DNA template quantities." The State submits that this is exactly what Drs. Buckleton and Coble testified to when discussing the evaluation of the complexity of samples – as opposed to providing a bright-line rule excluding samples with picogram levels outside of the bounds of a lab's internal validation.

In Lewis, an argument from the defense, like that being made by defendant here by way of Nathan Adams, Mats Heimdahl and Dr. Paul Martin, was that STRmix failed to comply with standards set by the Institute of Electrical and Electronics Engineers (IEEE). They argued that STRmix was not sufficiently validated from a software engineering perspective and did not satisfy industry practices for the development and testing of new software. Both Adams and Heimdahl have made this argument before. The Lewis Court held that this argument lacked merit. Instead, the Lewis Court relied on and adopted the findings in the Report and Recommendation from the United States Magistrate Judge (R&R). The District Court recognized the R&R's conclusion that STRmix "complies with all published guidance documents specifically directed to software validation for probabilistic genotyping systems. Those guidelines include standards published by the Scientific Working Group on DNA Analysis Methods, the Forensic Science Regulator, and the International Society for Forensic Genetics." 442 F.Supp. 3d at 1131. Further, the court noted that "the R&R also found that STRmix 'very nearly' complies with the safety-critical software developments published by the Institute of Electrical and Electronics Engineers ("IEEE"), and that strict compliance with IEEE standards is not required because STRmix has been rigorously tested and shown to be reliable." Ibid. (quoting R&R at 37-38, attached as Pa16).

The R&R stated that any lack of strict compliance with the IEEE's higher standard would not render STRmix unreliable. As stated in the R&R, STRmix complies with all three guidance

documents developed specifically for probabilistic genotyping systems and noted there is no requirement that probabilistic genotyping software must comply with IEEE standards. R&R at 37; Pa16. In fact, neither SWGDAM nor ISFG recommendations on validating probabilistic genotyping software require accreditation by any software standardization organization. Buckleton, J.S., et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity,* S-143 at 399. ASB Standard 018 also does require software accreditation by any software standardization organization.

The R&R in Lewis also addressed the two criticisms leveled at STRmix: First, non-compliance with IEEE, or concerns that any non-compliance creates uncertainty as to the limits of the software to produce reliable results; and second, that STRmix could potentially be unreliable in extreme circumstances. Specifically, the R&R stated that same would not amount to a question about reliability in general, noting that the rigorous testing STRmix has been subjected to "shows it works and extremely well" when used in compliance with the post PCAST validation studies. Special Master Report at 31, 33. The District Court agreed and held the arguments did not "overcome the R&R's thorough and well-reasoned analysis leading to the conclusion that the STRmix software has been sufficiently validated." Lewis, 442 F.Supp. 3d at 1131.

Lastly, both Drs. Buckleton and Coble testified regarding the rigors of testing of the software and how this has been done time and time again both by the developers, as well as by 89

separate laboratories in the United States alone. Both Buckleton and Coble agree that testing the software with a sample of known ground truth (i.e. the profiles of the two contributors are known), like laboratories do during their internal validation studies, can identify potential errors in the source code more effectively than reading code." S-186. Along these lines, Dr. Buckleton also points out, "[t]esting and use have discovered all the miscodes detected to date." Buckleton report, S-152 at 8. This was reiterated during the hearing when he confirmed that "no miscodes have been detected by source code review" and that "these miscodes have been identified through use and by users." 7T:206-9 to 21. And, Dr. Buckleton specifically testified that the miscodes they have discovered "haven't affected the DNA evidence because all the – miscodes that we have detected to date all have a minor affect (sic) on the numerical value of the LR, or are in peripheral functionality. We've at no point created a major affect (sic) in the numerical value of the LR. 7T:197-4 to 12.

The State would also highlight that Mr. Adams was "… are you aware of whether there were any miscodes or bugs that affected version 2.5.11, the version that you reviewed?" Adam answered, "Yes. They've disclosed several of them." Adams T:84-8 to 84-13. Interestingly, this answer confirms that he has not found any of these miscodes during his 2 code reviews of V.2.5.11 – in this case and the previous case in Illinois. It should be stressed that this is recognized in the IEEE Guidelines consistently highlighted by Nathan Adams and Dr. Heimdahl. IEEE

Standard 1012-2017 notes, "[t]he dynamics of complex systems and the multitude of different logic paths available within the system in response to varying stimuli and conditions demand that the V&V [verification and validation] effort examines the correctness of the systems for each possible variation in conditions. The ability to model complex, real-world conditions will be limited, and thus the V&V effort examines whether the limits of the modeling are realistic and reasonable for the desired solution. The unlimited combination of system conditions presents the V&V effort with the challenge of using a finite set of analytical, test, simulation, and demonstration techniques to establish a reasonable body of evidence that the system is correct."

This Standard continues, "Use of an IEEE standard is wholly voluntary. The existence of an IEEE standard does not imply that there are no other ways to produce, test, measure, purchase, market, or provide other goods and services related to the scope of the IEEE standard." S-136 at 4. As such, the very document proffered by the defense experts, Dr. Mats Heimdahl and Nathan Adams, in an attempt to discredit STRmix actually holds, explicitly, the opposite. Further, the repetitive attempts by both Dr. Heimdahl and Adams to assert software related issues in STRmix's software have been hailed as unpersuasive by each and every tribunal to whom they have asserted this same argument to. The IEEE is a standard, but unlike those cited above, it does not actually govern the operation of Probabilistic Genotyping software; STRmix has been found by the courts and the scientific

community to comport with all of those that do apply. Despite Dr. Buckleton efforts to comply, there is no mandate. However, the State would remind this Court that he did testify that he believes – despite arguments to the contrary - that STRmix does comply with IEEE 1012-2016. (T6:116-11 to 116-14). The Court should note that Dr. Buckleton testified with a deep understanding of IEEE 1012. When the State highlighted that it did not actually apply to STRmix, he agreed, but he also shared that "[t]here is absolutely nothing wrong with that standard. That standard is outlining basic software assurance principles that were taught to me in 1980 and have been written in an excessively voluminous and detailed document. But they're perfectly sound principles." (T6:113-2 to 113-7). Dr. Buckleton, in answering a question from the Court also indicated that while he "thought our software documentation needs a step up… [w]e are currently moving large blocks of material from my IEEE-1012 into our ISO-9001 SOP, so that we will now formally be meting the 1012 requirements." (T7:207-23 to 208-2).

Again, STRmix complies with the applicable Guidelines and Standard to the DNA labs that use Probabilistic Genotyping/STRmix. None of these condition use upon compliance with software engineering standards and/or IEEE 1012-2016.

B. PUBLICATION AND PEER REVIEW

Another measure of reliability is whether the methodology has been subject to "peer review and publication." Gissantaner,

990 F.3d at 464 and Daubert, 509 U.S. at 593. Publication in a peer-reviewed journal generally satisfies this condition, yet there is no requirement for independent authorship. See Gissantaner 990 F.3d at 464-65. "If experts 'have other scientists review their work' and if the other scientists have the chance to identify any methodological flaws, that usually suffices." Id. at 465 (quoting Mitchell v. Gencorp Inc., 165 F.3d 778, 784 (10th Cir. 1999)).

The 'key' is whether the "theory and procedures have been submitted to the scrutiny of the scientific community." Bonds, 12 F.3d at 559. Again, publication in a peer-reviewed journal typically satisfies this consideration. See Daubert, 509 U.S. at 594. When scientific research is accepted for publication by a reputable journal following the "usual rigors of peer review," that represents "a significant indication that it is taken seriously by other scientists, i.e., that it meets at least the minimal criteria of good science. Daubert, 43 F.3d at 1318. The Gissantaner Court noted that publication of this sort, standing alone, can defeat a Daubert challenge, and went on to say that "[a]t the time of the Daubert hearing in the district court, more than 50 published peer-reviewed articles had addressed STRmix. According to one expert, STRmix is the 'most tested and most ... peer reviewed' probabilistic genotyping software available." Gissantaner, 12 F.3d at 465. The court added, "At least two of the studies were done by individuals unconnected to the development of the software. This plainly suffices." Ibid. As the Court was made aware during this hearing, the depths of peer-

reviewed publications addressing STRmix, just the same as the number of labs using STRmix, and the amount of testing of STRmix, has grown significantly since Gissantaner.

As noted above, this factor does not demand independent authorships – studies done by individuals unaffiliated with the developers of the technology. Bonds, 12 F.3d at 560. There is a reason for this. Peer review contains its own independence, as it involves "anonymously reviewing a given experimenter's methods, data, and conclusion on paper." Mitchell, 365 F.3d at 238. Hence, the review need not be independent of a developer; peer-to-peer is satisfactory. While it was discussed at length by Dr. Buckleton, the Court can also rely on the testimony of Dr. Coble, who was asked about the purpose of engaging in this peer review publication. Coble testified that:

> Well, part of the process of peer review is that you're giving, you're basically presenting your work to peers and depending on the journal, could be as few as two, maybe three people who typically it's a blinded process. So when you submit your paper for publication in a journal, you'll remove any information about the authors, their affiliations and so forth, so the reviewer will get just a paper that has no information about who it's from. And they will give a critical valuation of the paper. They may suggest that this paper is only needs a few minor changes. They may suggest that this paper is not yet ready to be published and reject it and they'll typically will give you feedback, will give critical comments that the author can then go back and redo the paper, add something or take something away, edit in some fashion or form. SO it's a way that you're getting comments from your peers about the work that you've published and then when it's ready to be published, there's at least some confidence that other people have looked at this first and then, you know given their approval.

(T10:27-1 to 24).

As this Court heard, Dr. Coble is an accomplished scientist who devoted a great deal of his career to complex mixture interpretation and has been published in peer-reviewed publications in the area of 100 times. 10T:28-17 to 22. He has also written extensively on Probabilistic Genotyping and STRmix. 10T:81-12 to 16. He has also conducted and published comparative testing between STRmix and other PG software. 10T:81-17 to 23. He also indicated that there are publications that discuss STRmix by way of use and validation of the software and the theory behind what STRmix is doing, noting also that the algorithms used by STRmix have also been published. (T10:83-6 to 83-13).

In addition to the list of articles referred to in Gissantaner, in Lewis another list of peer-reviewed publications related to STRmix was held ample. That list is inclusive of many of the same works cited in Gissantaner, and that list has since grown. The Special Master appointed in Lewis affixed a list of relevant articles to his report, which included affiliated and non-affiliated peer-reviewed publications. See Special Master's Report at 46-48, Lewis, 442 F.Supp. 3d 1122.

Of note, the defense in Lewis expressly argued that the listed articles were insufficient and could not be used to sustain the State's burden that STRmix had been subjected to sufficient peer review and publication. They argued that the listed articles were insufficient because the majority of them were authored by people with an interest in the outcome of their research, reviews and publications. Further, the defense argued that included in that list were some articles that did question

STRmix's reliability in certain ways. The Lewis court held that, while important, the arguments failed to undermine STRmix's general acceptance and reliability. Lewis, 442 F.Supp. 3d 1122; see [Docket No. 115] ("R&R") at 44.

Dr. Coble addressed this argument in this case – finding it lacked merit. While detractors like to argue a lack of "independent peer review" because most of the peer-reviewed articles discussing STRmix include at least one of the developers, Dr. Coble, in his report and less specifically during testimony, indicated that while this "has been highlighted by some as an issue… I personally do not find this to be problematic for a number of reasons." S-186 at 3. Dr. Coble explains these three enumerated reasons:

> First, most crime laboratories are unable to publish their internal validation studies in peer-reviewed journals since the results would be considered "no longer novel" once the first paper was published. In my experience as an author and as a member of the editorial boards of *Forensic Science International: Genetics* and *The Journal of Forensic Sciences*, journals will typically publish one developmental validation paper from the developer, and then one "internal validation" from a forensic laboratory. If the next 80 laboratories submitted their internal validations to a journal for publication, the journal would be overwhelmed with essentially the same information and have no room to publish other interesting studies (and potentially lose readership). Thus, forensic journal no longer considers STRmix validations as novel research.
> Second, many laboratories performing casework are generally too busy with the number of cases to analyze, having little time for the laboratory to conduct independent research for peer-reviewed publication. A publication like Bright et al. (2018) "Internal validation of STRmix: A multi laboratory response to PCAST." *Forensic Science International: Genetics* 34:11-24 is an excellent example of independent peer-review. To me, the most important information in that paper is the fact that the **DATA** used in this study was

> from 31 independent laboratories and the trends observed in aggregate from differing kits, instruments, mixture proportions, etc… confirm the expectation one would observe with low-level mixtures. It matters little to me in this example that some of the authors are from the developers of STRmix.
> Finally, many research laboratories will need to purchase and receive training in STRmix before they can produce independent peer-reviewed publications in the literature. It is much easier for academic and research laboratories to use open-source and freely available tools in the forensic domain since there is no cost with these tools. Therefore, it may take some time before a stream of independent researchers are publishing in this area (although there are at least 21 publications that are independent of the developers).

S-186 at 3-4.

In Gissantaner, supra, STRmix cleared the bar of peer review. At the time Gissantaner was heard in the District Court, more than 50 published peer-reviewed articles had addressed STRmix. Gissantaner also referred to the Special Master report in Lewis and cited a list produced by the prosecution of 47 peer-reviewed articles on DNA mixture interpretation, most relating to Probabilistic Genotyping and which mentioned or discussed STRmix. Key articles that were mentioned included Bright et al. 2018 and Moretti et al. 2017. See Pa14 and Pa15. The Gissantaner Court also noted that according to one expert, STRmix is the "most tested and most…peer to peer reviewed" Probabilistic Genotyping software available; the court highlighted that at "least two of the studies were done by individuals unconnected to the development of the software" holding that this plainly suffices. Gissantaner, 990 F.3d at 465 (citing Bonds, 12 F.3d at 559-60); cf. Gross v. Comm'r. 272 F.3d 333, 340-341 (6th Cir. 2001).

To reiterate, there is a plethora of decisions that document the various peer-reviewed studies that have validated the STRmix software and its low rate of error. See, e.g., Gissantaner, 990 F.3d at 465 ("When examining 'false inclusions,' one peer-reviewed study concluded, based on an analysis of the DNA of 300,000 people who were known not to be in a mixture, that STRmix had accurately excluded the non-contributors 99.1% of the time," and observing the software gave low-confidence estimates in cases of false inclusion); Lewis, 442 F.Supp. 3d at 1128-29 (relying on a government study compiling data from thirty-one laboratories, which "show[] persuasively that STRmix is capable of producing accurate results with extremely low error rates: STRmix not only works, it seems to work extremely well, at least when used in the manner it was used in these studies"); United States v. Washington, No. 8:19CR299, 2020 U.S. Dist. LEXIS 105447, 2020 WL 3265142, at *3 (D. Neb. June 16, 2020) (relying on same government study and citing Lewis) (attached as Pa20); United States v. Pettway, No. 12-CR-103S, 2016 U.S. Dist. LEXIS 145976, 2016 WL 6134493, at *2 (W.D.N.Y. 2016) (overruling Daubert objection to STRmix based in part on testimony "STRmix and its underlying principles have been peer-reviewed in more than 90 articles").

The list of peer-reviewed publications from independent and affiliated authors is touted as ample in Lewis, Gissantaner and other holdings as noted above, and some of those publications has been utilized throughout this hearing. Further, a more recent case out of the Court of Appeal of California stated that:

> The scientific and mathematical principles behind STRmix are well established and widely accepted in the scientific community, and STRmix has been the subject of numerous peer-reviewed articles published in scientific journals. In addition to those articles already mentioned, we granted the Attorney General's request to take judicial notice of the following peer-reviewed scientific literature: (1) Buckleton et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity* (March 2009) vol. 64, No. 2, Journal of Forensic Sciences 393; (2) Coble & Bright, *Probabilistic genotyping software: An overview* (Jan. 2019) vol. 38, Forensic Science International: Genetics 219; and (3) Bright et al., *Internal validation of STRmix: A multi laboratory response to PCAST* (May 2018) vol. 34, Forensic Science International: Genetics 11.

People v. Davis, 75 Cal. App. 5th 694, 717 (2022).

The California court specifically noted testimony given by one of STRmix's creators, John Buckleton. Buckleton testified that he had authored or co-authored 24 peer-reviewed articles published in scientific journals that "endorse[d]" the STRmix method and the mathematical principles it utilizes, some of which specifically involved validation of the method, including an article on the developmental validation of STRmix. He explained that, prior to publication, two anonymous "referees" (i.e., scientists) reviewed the articles to ensure the information was consistent with the standards of the respective journals. Id. at 715. This "referees" approach ensures that the developers of the software cannot simply tout their respective creations as reliable, etc. without the software being independently verified by neutral experts prior to publication in a respected scientific journal. Ibid.

This Court is aware that Dr. Buckleton and STRmix have received plenty of criticism over the course of STRmix's

existence. It appears to the State that Dr. Buckleton and STRmix seem to listen to these criticisms – legitimate or not. Despite Daubert requiring "peer review," not independent peer review, Dr. Buckleton has, for ease of review, adapted his collection or list of peer-reviewed publications. During the hearings, he testified about this list and how he has broken these publications down into degrees of "independence." A quick review of this list, S-129 and S-129A, reveals that articles 1-14 were written by Drs. Buckleton, Bright and Taylor only; articles 15-95 were written by Buckleton, Bright or Taylor and other(s); and 96-111 are written wholly without the aforementioned developers. He lists one article, # 112, as mildly critical and then he lists 113 through 124 as "Using STRmix for other research." Clearly, this reflects sufficient peer review and publication under Olenowski I and Daubert.

Lastly, and importantly, Dr. Buckleton testified about an additional list that he created recently, S-159, "outlining a list of tests of various software, but in all cases including STRmix performed by people who are not associated with the STRmix group in any way." (T7:60-12 to 60-23). Dr. Buckleton explained that the publications on this list compare STRmix with other fully continuous Probabilistic Genotyping software such as Hamiltonian Monte Carlo (HMC), EuroForMix and TrueAllele. Dr. Buckleton was asked if these comparisons were favorable, and he stated that they were not criticisms. See (T7:61-1 to 61-25).

The peer-reviewed articles referenced above in Gissantaner, coupled with referenced publications listed within the Lewis

case, as well as the reference section of the Special Master's report at 48-50, have been held ample on numerous occasions across the country. It should also be noted that relevant peer-reviewed articles pertaining to STRmix are referenced in the validation summaries produced by the UCPO lab and the NJSP lab, as well as Bode. Based on the great volume of peer review and continued publication in reputable journals, the sought-after additional "measurement of reliability" has been met and exceeded via repeated scrutiny within the relevant community. This was found ample and more than legally sufficient at the time of the Gissantaner and Lewis decisions, and the list of accredited peer-reviewed publications has only grown more robust since.

The State submits that there is absolutely no doubt that STRmix has been subjected to peer review, not to mention independent peer review.

C. TESTABILITY AND ERROR RATE

1. THE SCIENTIFIC THEORY OR TECHNIQUE CAN BE AND HAS BEEN TESTED

The case law is clear that it is important that a methodology be testable – otherwise, it remains only theory and completely devoid of science. United States v. Gissantaner, 990 F.3d 457, 463 (6th Cir. 2021). Stated another way, without testability, there can be no way to show that the challenged methodology "works." The State would note that this "methodology" approach in Gissantaner is consistent with Olenowski I's focus on "soundness of the methodology and

reasoning used to validate the expert opinion or technique." Olenowski I, 253 N.J. at 154. Importantly, at the center of this inquiry is whether the methodology "can be 'assessed for reliability,' not whether it always gets it right." Gissantaner 990 F.3d at 464 (quoting Fed. R. Evid. 702 advisory committee's note to 2000 amendment). When the dispute focuses on the "'adequacy of the [theory's] testing' or about the 'accuracy of [a theory's] results,' generally speaking, [the arguments] provide grist for adversarial examination, not grounds for exclusion." Ibid. (quoting United States v. Bonds, 12 F.3d 540, 558-59 (6th Cir. 1993)). Thus, validation of the software becomes paramount to the analysis under this prong.

The Court has heard significant testimony that STRmix absolutely can and has been tested. It has been repeatedly validated. Using lab-created mixtures in which actual contributors of DNA samples are known, scientists have tested STRmix to gauge the reliability of the technology. Gissantaner, 990 F.3d at 463. STRmix has been through developmental validation by software developers and through internal validation by the dozens, and dozens of individual laboratories have adopted its use, including the United States Army Laboratory, the Federal Bureau of Investigation, Bode Technology, the Union County Prosecutor's Office Forensic Laboratory and the New Jersey State Police Office of Forensic Sciences. During the Olenowski hearing, the State called Monica Ghannam, Kristen Naughton and Jennifer Thayer, from the UCPO DNA lab, Bode Technology and the NJSP DNA lab, respectively. Each of these witnesses discussed

the validation process that occurred before they were able to begin using STRmix in actual cases. In addition to these three forensic laboratories, whose internal validations were introduced (UCPO has validated, to differing extents, three versions of STRmix). The defense also introduced several other Internal validation summaries from additional labs who are currently using STRmix.

The Court also heard significant testimony regarding 89 laboratory systems that are currently using STRmix in daily casework. S-140. Each of these laboratories that have STRmix software up and running went through an internal validation process. Notably, internal validation procedure was cited as the most compelling justification for the admission of a forensic tool. See Daubert 509 U.S. at 590 (expert testimony must encompass "scientific knowledge" that is "supported by appropriate validation- i.e., 'good grounds,' based on what is known"); Williams v. Illinois, 567 U.S. 50, 95 (2012).

As referenced earlier, on September 20, 2016, the President's Council of Advisors on Science and Technology (PCAST) published a report that did hold some criticism for Probabilistic Genotyping programs, especially in circumstances that included multiple contributors and where the minor contributors contributed lesser amounts of DNA to the mixture. S-141. Thereafter, on January 6, 2017, they published an addendum to same. S-142. In the addendum, the President's Council of Advisors stated that "the validity of specific PG [probabilistic genotyping] software should be validated by testing a diverse

collection of samples within well-defined ranges" and that "[w]hen considering the admissibility of testimony about complex mixtures (or complex samples), judges should ascertain whether the published validation studies adequately address the nature of the sample being analyzed (e.g., DNA quantity and quality, number of contributors, and mixture proportions for the person of interest)." Id. at 9.

Countless defendants across the country have relied on this "criticism" in attempts to discredit STRmix (as well as TrueAllele). These attempts have been misguided and unsuccessful largely because of repeated validation, as well as the fact that, in response to the suggestions of PCAST, additional studies were undertaken to establish that the software is reliable beyond that which PCAST suggested. It appears to the State that, over 8 years ago, PCAST set a seemingly arbitrary limit; however, it is important to point out what they did not do – they did not tie that 3-contributor/20-percent standard to any given laboratory's internal validation. They also did not mention picograms, specifically referencing "DNA quantity and quality." Id. at 9. ASB Standard 018 defined "case-type profiles" as "exhibiting features that are representative of a plausible range of casework conditions for mixtures and single source samples." S-133 at 1.

But regarding the limit that was set and their pronouncement that "the range in which foundational validity has been established is likely to grow as adequate evidence is obtained and published," it is clear that this range has, in fact, grown significantly. See S-141 at 82. Before discussing the responses

to PCAST, the State would simply state the obvious in this regard. At the time that the PCAST report was issued, STRmix was being used in 11 laboratories. S-140. That number has grown to 89 laboratories, which ultimately amounts to an enormous amount of additional testing, both in sensitivity and specificity testing, but also in real-world casework. Ibid.

While the amount of data available over 89 laboratory validations is significant, it must also be considered in conjunction with the analysis of this data, which has been performed and published for, at minimum, 32 of those laboratories. Two studies, Bright et al. and Moretti et al., published responses to the PCAST criticism. See S-146 & S-145. The studies tested the accuracy of STRmix when used to analyze well over 2,000 known source DNA mixtures with varied numbers of contributors (from 3-6) and with different levels or degrees of contribution, just as the PCAST addendum suggested. See Moretti et al., *Internal validation of STRmix for the interpretation of single source and mixed DNA,* S-145, and Bright, J.-A., et al., *Internal validation of STRmix; A Multi laboratory response to PCAST,* S-146.

Those studies' findings were discussed at length in United States v. Lewis, supra, 442 F. Supp. 3d 1122. The procedural history in Lewis is also important for this Court to note; the fact that the court appointed a neutral Special Master, who provided a 50-page report, entitled "Special Master's Report on the Scientific Foundations of STRmix," prior to United States Magistrate Judge David T. Schulz issuing his Report and

Recommendation, shows the lengths that the court went to in order to reach its conclusion regarding the reliability of STRmix under a Daubert analysis. The Lewis matter went before a United States District Judge for a ruling on the defendant's objection to Magistrate Judge Schultz's January 6, 2020 Report and Recommendation [Docket No. 115] ("R&R"). Ultimately, in Lewis, the defendant's objection was overruled and the Report and Recommendation was adopted. Both opinions cited heavily to the court-secured expert, who authored a report. The opinion of the court-appointed independent Special Master, Dr. William Thompson, was based on a review of the Lewis case and the arguments presented for both admission and exclusion of the DNA evidence obtained via STRmix software. Lewis, 442 F.Supp. 3d at 1127. Dr. Thompson's role as a Special Master was to advise the court on the issues of scientific reliability.

Dr. Thompson reviewed the transcripts and exhibits from the first two days of testimony in the hearing and personally attended the third day, during which he had the opportunity to ask questions of the witnesses. It should be noted that the witnesses for the State were the head of the Midwest Regional Forensic Laboratory (MRFL – which conducted the tests at issue) and Dr. John Buckleton. The defense called Dr. Mats Heimdahl and Nathan Adams; the defense also called Dr. Dan Krane, who is the President, CEO, and Senior Analyst at Forensic Bioinformatics, Inc. (where Nathan Adams is employed). See R&R at 5-7.

The Special Master's report indicated that the aforementioned Bright and Moretti studies showed "persuasively

that STRmix is capable of producing accurate results with extremely low error rates: that STRmix not only works, it seems to work extremely well, at least when used in the manner it was used in these studies." Id. at 1129. The State intends to proffer testimony that the analysis conducted on the evidence in the instant matter did, in fact, utilize STRmix software in the same manner as those studies. STRmix was able to distinguish contributors from non-contributors with a "high level of accuracy." Ibid. The Special Master went on to state that "given the scope of the study, it seems likely that any serious, systemic problems with the program would have been detected. While it is conceivable that undetected problems might still exist or might occur under highly specific circumstances, the findings suggest that such problems, if they do exist, could not be very common." Special Master's Report at 31. The State submits that this analysis strikes to the very heart of the matter in this case. Interestingly, the Special Master's reliance upon that "any serious, systematic problems with the program would have been detected" was after he considered the testimony of Dr. Heimdahl and Nathan Adams, two of the three software engineers in this case. It appears that Dr. Thompson wondered the same thing that the State wonders now – where are all of these bugs/miscodes that Adams, Heimdahl and, to a lesser extent, Martin so strongly suspect "must exist" within STRmix?

That being said, even if there were such issues, or in situations where there are questions that can relate to complete and total accuracy in the scientific practice and/or in the

theory at issue, that is not the standard by which admissibility or reliability is judged. The issue is whether a method can be "assessed for reliability, not whether it always gets it right." United States v. Bonds, 12 F.3rd 540, 559 (6th Cir. 1993). Disputes about the adequacy of testing or the accuracy of a theory's results are the crux of cross-examination, not grounds for exclusion. Bonds, 12 F.3d. at 558-559; United States v. Baines, 573 F.3d 979, 989-90 (10th Cir. 2009). In essence, it appears to the State that the findings of the Special Master, relying on the aforementioned robust research studies of Bright and Moretti, negates or refutes in their entirety the claims made thus far by the defense experts in the instant matter.

Even where independent experts disagree on the adequacy of testing, it does not mean the theory is untestable. In Gissantaner, the Court of Appeals stated that the District Court identified "shortcomings" in STRmix, *but said that* even "serious deficiencies" in testing do not render a method untestable. Gissantaner, 990 F.3d at 468; see also Bonds, 12 F.3d at 559. At stake is "scientific validity," not "scientific precision." Bonds, 12 F.3d at 558. They held that "attempt[s] to refute the [government's] theory and methods with evidence about deficiencies in both the results and the testing of the results," amounts to a "conce[ssion] that the theory and methods can be tested." Id. at 559. The Gissantaner court noted that "[a]lthough the independent experts in this case disagreed about the adequacy of the testing, that does not mean the theory is untestable or even that it has not been tested." 990 F.3d at 468. The same

holds true here. STRmix can be tested. STRmix has been tested. This holds true from both a scientific and software engineering perspective.

The 2019 article, as evidenced by its title, *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity,* also discussed the Bright, et al. internal validation data generated from 31 laboratories using or validating STRmix. S-143. The 2019 publication noted that the Bright study was conducted to specifically address the points raised within the PCAST Report and Addendum. The Bright study was a massive compilation of results from 31 laboratories and their own independent validation studies. The project included 2,825 mixtures. Those mixtures included samples with three, four, five, and six donors, and samples where the contribution proportions of each donor varied and covered a wide range. The Bright study concluded that this combined dataset from the 31 laboratories "demonstrate[d] a foundational validity of, at least, the STRmix software method for complex, mixed DNA profiles to levels <u>well beyond</u> the complexity and contribution levels suggested by PCAST." S-143 at 397. (emphasis added). These efforts, "representing a substantial resource commitment, were a collation of the validation studies from 31 laboratories and demonstrate that there is support for interpreting a minor contributor much less than 20%, and in fact down to 0% (present but not observed), of the total DNA present in the mixture. As the template tends toward 0, the LR tends to approximately 1." Ibid. So while even PCAST considered validity proven for the use

of PG for up to three-person DNA mixtures where the minor contributor is greater than 20% of the mixture (amended to the POI being 20% in the Report addendum) and for two-person mixtures where the minor profile is greater than 10%, the 2019 publication highlights the marked expansion of STRmix's scope of validity established in the massive internal compilation study.

The Moretti study dealt with the assessment and internal validation of STRmix for casework usage at the Federal Bureau of Investigation Laboratory. Lab-specific parameters and more than 300 single-source and mixed-contributor profiles were examined. Simulated specimens with constructed DNA mixtures, to include two- three-, four-, and five-donor mixtures with varying contribution proportions were examined. These samples were used in more than 6,000 tests, comparing hundreds of known contributors and non-contributors to same. The Moretti study concluded that STRmix is "sufficiently robust for implementation" in forensic laboratories. The study cited to the likelihood ratios reflected in the study and the fact that they were found to be reflective of "intuitively correct estimates." S-145 at 126-144.

The Bright and Moretti studies conducted are just two that focused on the reliability of Probabilistic Genotyping at a low template. "STRmix has been extensively tested on profiles generated from optimum template levels down to extinction. Trials have been undertaken where the minor contributor is not observable, at 0%. The results have demonstrated that STRmix reliably reports that a profile is close to uninformative with

respect to whether a person of interest, at zero template and hence not there, is a contributor or not." S-143 at 400; *citing* Taylor, D., *Using Continuous DNA Interpretation Methods to Revisit Likelihood Ratio Behavior,* Forensic Sci Int Genet 2014;11:144-53; Taylor, D., Buckleton J., *Do Low Template DNA Profiles have Useful Quantitative Data?,* Forensic Sci Int Genet 2015;16:13-6; Taylor, D., Buckleton J., *Testing Likelihood Ratios Produced from Complex DNA Profiles,* Forensic Sci Int Genet 2015;16:165-71.

The State would submit that these studies address the reliability of STRmix in many different laboratories. Each lab has limits to the number of samples that it can create and test during internal validation; however, when studies look to validations from over 30 labs, it becomes even clearer that STRmix is extremely reliable, hence, why validations from laboratories like the UCPO lab and those moved into evidence by the defense are relevant. These peer-reviewed studies and the depths of internal lab validations strike head-on at the argument made that the results produced by Bode cannot be considered reliable because some of samples were at or below the threshold of internally validated minor contributor ratios that Bode tested during validation. The State will specifically address the specific samples infra and explain why this is contrary to any bright-line rule that the State has ever come across. To put it simply, however, STRmix does not take the pilot out of the airplane. See T6:86-24 to 89-3 (Dr. Buckleton answering the Court's question regarding the importance of a scientist making

visual observations before STRmix input). Electropherogram review, template amounts and peak heights are important, and guide whether there is sufficient evidence to test in STRmix.

The State would also submit that common sense would dictate that it is impossible to test all scenarios. But, putting common sense aside, Dr. Michael Coble also addresses this argument in his report by stating, "I tend to agree with my former NIST colleague Dr. John Butler that, 'It is impossible to mimic everything that might be seen in casework or in samples processed through a laboratory in the future. Remember that validation simply confirms that the STR kit, instrument or software is 'fit-for-purpose' and works within the range of conditions defined by the validation experiments conducted.'"[5] It should be noted that Dr. Butler wrote the textbook and other materials that the defense utilized during the hearing. Coble explains in his report and will testify that, even if these samples were at or below what Bode validated, "[a]ll of these samples gave sufficient template rfu and strong LR's (Likelihood Ratios) when compared to Paul Caneiro." See generally (T11:18-5 to 18-15) (testifying about the importance of not using an arbitrary threshold).

The testimony in this hearing made clear that STRmix has been tested. The software was tested and validated in development. It should be noted that over the course of 8 years since the PCAST report, it has been clearly established that the

[5] Butler J (2008) Debunking some urban legends surrounding validation within the forensic community. Profiles in DNA: https://projects.nfstc.org/workshops/resources/literature/debunking%20validation

software has been proven *far more capable* then what PCAST conservatively said at the time. The software has been tested in each laboratory that uses it, as well as validated in each laboratory that has it up and running. There are 89 labs in the United States who have tested, validated and implemented STRmix for casework.

Finally, with regard to testability, the State would also highlight that there was testimony that many of these STRmix calculations have been checked "by hand" or excel, leading to further confidence in the results. Drs. Buckleton and Coble both testified regarding Steven Myers, from the California Department of Justice DNA laboratory system and how he replicated many of these calculations by hand. (T7:52-17 to 53-4); (T10:46-15 to 47-5). Notably, however, is the fact that this was confirmed by Keith Inman, who previously worked at the California DOJ laboratory system. Inman confirmed that Mr. Meyers (sic), "what he did do was duplicate or replicate in Excel what the software was supposed to do… it's, it was very valuable. But yes, what the confirmed is that what the software said it was doing, he could do." (T19:143-4 to 143-18). As such, the testimony of Drs. Buckleton and Coble was corroborated by defense expert Keith Inman.

The State submits that STRmix certainly can be and has been tested extensively.

2. <u>KNOWN OR POTENTIAL ERROR RATE</u>

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This factor focuses on the rate of error involved in using the methodology and "whether the scientific community has established standards that forensic scientists can use to mitigate the risk of error." Gissantaner, 990 F.3d at 465; see also Daubert, 509 U.S. at 594. So, for example, if the identified methodology has a high error rate, and lacks standards and guidelines to minimize these risks, this would be of concern. Gissantaner, 990 F.3d at 465. In other words, the government, using STRmix to match a defendant to DNA on a piece of evidence, can do so only if the results are the "product of reliable principles and methods" under R. 702, so if STRmix has a high error rate, if it has trouble "avoid[ing]" "false positives," and if there are no standards or guidelines to avoid or lessen these risks then it should not be used. Bonds, 12 F.3d at 559; Mitchell, 365 F.3d at 241. Clearly there is a need to avoid false positives and have guidelines to minimize risk of same. The State submits that the testimony throughout this hearing displayed that the software has been validated and tested time and time again without issue. This Court heard testimony from several State's DNA experts that described their validation and use of STRmix in casework without ever identifying any substantial error, no less the catastrophic type where someone is falsely included with a high likelihood ratio or very strong support. Also, despite testimony from five defense experts offering predictions about how these errors could occur, this Court heard zero examples or instances of any significant errors

throughout the life of STRmix.

The question posed by the Gissantaner Court was how often does STRmix falsely suggest a suspect matches a DNA sample? The court there held that evidence suggests the answer to that question is not often, stating that when examining "false inclusions," one peer-reviewed study concluded, based on an analysis of the DNA of 300,000 people who were known not to be in a mixture, that STRmix had accurately excluded the non-contributors 99.1% of the time. Just under 1% of the time, in other words, it gave a likelihood ratio suggesting that someone was included in the mixture who was not actually included in it. But, notably, most of these very infrequent false inclusions, were also associated with low likelihood ratios meaning that, under STRmix's own estimates, the confidence that the person was included was low. The court further noted that a likelihood ratio of 100 to 1 is more likely to produce a false inclusion than a likelihood ratio of 1 million to 1. Gissantaner, 990 F.3d at 465-66. Taken together this would mean that, even if a false inclusion were to occur, virtually no weight would be accorded to it. Ibid. One explanation for the low error rate is the existence of standards to guide the use of STRmix and other probabilistic genotyping software, for the two are "'[c]losely related.'" Id. at 466 (quoting Mitchell, 365 F.3d at 241 (brackets in original). The Scientific Working Group on DNA Analysis Methods (SWGDAM), a national association of forensic laboratories sponsored by the FBI, is one such group that has produced guidelines governing the use of this kind of software.

Ibid. These independently-authored guidelines, and others similar to it that are discussed later, also assist in assuring the error rate remains low.

There have been arguments proffered that STRmix has no known error rate associated with Likelihood Ratios (hereinafter LR) and, more broadly, the percentage of time the LR leads to false inclusion or exclusion. Arguments have been made that this makes the software faulty or that it therefore fails under Daubert. As to the applicability of this argument regarding the precise nature of the LR, the courts have dealt with the absence of ground truth. See, e.g. Lewis, 442 F.Supp. 3d 1122. While there is no publication with a precise error rate for false inclusion/exclusion, John Buckleton, one of the creators of the STRmix software established that it is immeasurably small, putting it at "somewhat less than one over the LR". See Special Master's Report at 33-34, Lewis, 442 F.Supp. 3d 1122. The Special Master in Lewis went on to say that the defense raised legitimate issues as to whether validation research has gone far enough, but deemed concerns about potential error rates as "somewhat hypothetical." Special Master's Report at 39. Further, the Special Master found that false inclusions were rare and when occurred, occurred only as often as would be expected due to similarity amongst the different profiles involved. Id. at 33. Dr. Coble supports this very conclusion in his discussion of "known or potential error rate," describing this "false inclusion" scenario as being better described as a "fortuitous match;" he indicates that this is simply due to the rare scenario

when a non-contributor "may share several alleles with the person of interest in the mixture." (T10:85-22 to 86-16). He added that "[t]his is especially true for those very low level, trace contributors in a mixture." Ibid. Dr. Coble indicates simply that, "[i]t is my opinion that these are not 'errors' of the software." Ibid. Coble added that such "fortuitous matches" are not a concept new to probabilistic genotyping. (T10:93-2 to 93-5).

Coble also was asked during his testimony about how you evaluate errors in probabilistic genotyping systems like STRmix. He discussed these "fortuitous" situations that some like to call errors. He, again, explained how these are not errors, just "an example of genetics, biology…" when you're only looking at two or three markers, you may find by random chance people who could give a profile that "matches" with the person of interest, but they're not that contributor. So, that to me, is not a true error." 10T:86-9 to 16. He described what would be an error that we want to avoid – a false inclusion… with a high LR… putting the wrong person into a mixture with a high LR. He said he has seen "nothing that would be at that level, at that high quadrillions type statistics." See (10T:88-1 to 88-13).

Dr. Buckleton also testified regarding the error rate. He stated that "what the Court is often wanting to know is the rate of false inclusions and that's not an error in STRmix. That's caused by the biological processes of having the correct alleles and we can give you estimates of that and it's a different for every sample. So, really bad mixtures, five person mixtures with

low peaks have a high false inclusion rate and really tidy single source samples have an enormously low false inclusion rate." (T7:107-18 to 108-1). He further explained that, as a rule of thumb, that is proven valid, you will not get LR of one hundred more than once in a hundred false donors and you will not get an LR of a thousand more than once in a thousand false donors. He said that this has specifically been tested. (T10:108-6 to 108-15) (essentially the same as explained in Lewis, 442 F.Supp. 3d 1122, "somewhat less than one over the LR"). This is consistent with what he explained in his report, S-152, that "STRmix will produce an LR greater than x from about 1 in x false donors… this is the most concise expression of error rate available." S-152 at 25.

The Lewis court went on to note that the absence of a precisely-calculated error rate because there is not precise ground truth is not the same as saying there is no known error rate. This was based on the fact that the Lewis Court held that the error rate for false inclusion is known and acceptably small. Rate of error can be and is estimated by checking how often the program assigns highly incriminating LRs to profiles of non-contributors. While errors were possible, they held that the STRmix internal validation study established it as acceptably small. Lewis, 442 F.Supp. 3d at 1130; see also, R&R at 42. The Special Master in Lewis, in line with the above-comments by Dr. Coble in this regard, stated that "while there were a few instances in which STRmix produced results that falsely linked non-contributors to the mixtures, these misleading results were

rare and occurred no more often than would be expected by chance due to adventitious (coincidental) similarity between DNA profiles of different individuals." Special Master's Report at 8. In other words, the rate of false inclusions was approximately what would be expected if STRmix performed its function flawlessly." Lewis, 442 F. Supp 3d at 1130; Special Master's Report at 8; R&R at 42.

The Magistrate Judge in Lewis also stated "that the error rate of STRmix is likely to be quite low in most cases. Large studies in which millions of non-contributor profiles were compared with DNA profiles of thousands of mixed DNA samples showed that STRmix very rarely produced strongly incriminating findings against a noncontributor. Statistical analyses suggest that, in the aggregate, the LRs produced by STRmix are properly calibrated and do not overstate the value of incriminating evidence. This evidence strongly supports the claim that STRmix is 'foundationally valid.'" Lewis, 442 F.Supp. 3d at 1130; see R&R at 42.

Moreover, the New Jersey Supreme Court has stated that "[t]he fact that a possibility of error exists does not preclude a conclusion that a scientific device is reliable." Romano v. Kimmelman, 96 N.J. 66, 80 (1984). As such, the possible existence of mere hypothetical or potential errors is not determinative. To the contrary, the proven continued reliability of the software has been firmly established through continuous testing and study. These types of dispute amongst experts was specifically discussed in Gissantaner when the court noted that

"[a]lthough the independent experts in this case disagreed about the adequacy of the testing, that does not mean the theory is untestable or even that it has not been tested." 990 F.3d at 468. Thus, the State submits that disputes about the adequacy of testing or the accuracy of a theory's results are the crux of cross-examination, not grounds for exclusion. Bonds, 12 F.3d at 558-559; Baines, 573 F.3d at 989-90. This is exactly why the type of arguments made by the defense – that the samples cannot be considered reliable because Bode did not internally validate below the weight and percentage of certain minor profiles, as well as the fact that the victims and defendant are related – these are issues that should be left for cross-examination and the jury.

Lastly, of note is that STRmix is designed to err on the side of caution in multiple ways. In forensic science, a tendency to underestimate the evidential weight is called "conservativeness," and STRmix incorporates features to drive the LR toward a conservative lower result. Buckleton, J.S., et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity*, S-143 at 398. As the Gissantaner Court observed, "STRmix also accounts for small amounts of DNA when it creates profile summaries. Because less DNA in a sample creates more uncertainty, STRmix generates lower likelihood ratios for low-quantity DNA mixtures than it otherwise would. The software also errs in the direction of the innocence of criminal suspects by making conservative estimates about the probability of a genetic pattern occurring." 990 F.3d at 467.

Dr. Buckleton specifically discussed in Court at least three layers of conservatism that are built into STRmix. He discussed the inherent conservativeness of the population genetic modelling used, the coancestry coefficient data and the lower 99 percent bound on sampling uncertainty on the Monte Carlo effect. (T7:87-2 to 87-14). While these are all very technical aspects of STRmix, they all serve to err on the side of the defendant, offering the most conservative conclusions. He also indicated that use of the Unified LR would be another layer that labs have the ability to use to add further conservatism, allowing allocation for relatedness. (T7:87-16 to 87-20).

Given the materials utilized in this hearing and the testimony from Drs. Buckleton and Coble, the State would submit that the error rate of STRmix is established and it is low. This has been shown in developmental validations, internal validations and independent studies. This was reflected in the testimony of Monica Ghannam, Kristen Naughton and Jennifer Thayer. Dozens of labs, testing hundreds of thousands of known samples, have repeatedly demonstrated this. The system is designed to err on the side of caution, to be conservative and the testing has shown that the conservativeness has produced a statistically negligible error rate. Further, it has been shown that, on the rare occasion that there would be a false inclusion, the software essentially self-edits and discounts it by producing a low or non-informative Likelihood Ratio (LR). This is the correct result given the biological phenomenon of allele sharing – which, of note, is not unique to STRmix – it has always been the reality

of DNA analysis and comparison. The scientific community, as established by the volume of accredited forensic laboratories who have tested and, thereafter, adopted it, as well as the courts who have repeatedly and, thus far, unanimously held it to be legally sufficient firmly establish that STRmix results are reliable and admissible.

D. GENERAL ACCEPTANCE

General acceptance in the relevant community is the fourth non-exhaustive Daubert factor. The New Jersey Supreme Court concluded that Daubert's focus on methodology and reasoning, one that had been previously applied in civil cases in New Jersey, is a superior approach to use in criminal cases as well. "Under Daubert and In re Accutane, trial courts directly examine the reliability of expert evidence by considering all relevant factors, not just general acceptance. Focusing on testing, peer review, error rates, and other considerations better enables judges to assess the reliability of the theory or technique in question. Courts are also in a better position to examine novel and emerging areas of science." Olenowski, 253 N.J. at 152 (citations omitted). Adopting a Daubert-type standard for criminal cases was also held to be consistent with the New Jersey Rules of Evidence. "Like the federal rule, N.J.R.E. 702 does not require a finding of general acceptance before expert testimony can be admitted." Ibid. But STRmix amply satisfies this prong despite the New Jersey Court's alteration of the weight that it

should be assigned. While not a prerequisite for admission, general acceptance remains germane to the analysis. The State would submit that Gissantaner and Lewis provide the pinnacle of guidance to this Court; however, it cannot be understated that numerous courts throughout the United States have similarly recognized the general acceptance of STRmix. Gissantaner held that STRmix had garnered wide use in forensic laboratories across the country. At the time, the court noted that more than 45 laboratories used it, including the FBI and many state law enforcement agencies. It should also be noted, however, that since the Gissantaner opinion, the list has grown to 83 laboratories at the most recent count. The Gissantaner Court highlighted that STRmix is the "market leader in probabilistic genotyping software." Gissantaner, 990 F.3d at 466-467. The Gissantaner Court continued:

> Consistent with this reality, numerous courts have admitted STRmix over challenges to its general acceptance in the relevant scientific community. *See United States v. Lewis*, 442 F.Supp. 3d 1122, 1155 (D. Minn. 2020) ("[T]here is no doubt that STRmix has gained general acceptance."); *United States v. Washington*, No. 8:19CR299, 2020 U.S. Dist. LEXIS 105447, 2020 WL 3265142, at *2 (D. Neb. June 16, 2020) ("Authority and evidence demonstrate that STRmix is generally accepted by the relevant community.") (Attached as Pa20); *People v. Blash*, No. ST-2015-CR-0000156, 2018 V.I. LEXIS 86, 2018 WL 4062322, at *6 (V.I. Super. Ct. Aug. 24, 2018) (Attached as Pa24); *People v. Muhammad*, 326 Mich. App. 40, 931 N.W.2d 20, 30 (Mich. Ct. App. 2018); *People v. Bullard-Daniel*, 54 Misc. 3d 177, 42 N.Y.S.3d 714, 724-25 (N.Y. Co. Ct. 2016); *United States v. Christensen*, No. 17-CR-20037-JES-JEH, 2019 U.S. Dist. LEXIS 24623, 2019 WL 651500, at *2 (C.D. Ill. Feb. 15, 2019) ("STRmix has been repeatedly tested and widely accepted by the scientific community.") (Attached as Pa25); *United States v. Oldman*, No.18-CR-0020-SWS, 2018 U.S. Dist. LEXIS 232762, ECF No. 227 at *16 & n.5 (D. Wyo. Dec. 31, 2018) (collecting cases) (Attached as Pa26); *United*

> *States v. Russell*, No. CR-14-2563 MCA, 2018 U.S. Dist. LEXIS 232864, 2018 WL 7286831, at *7-8 (D.N.M. Jan. 10, 2018) ("[STRmix's] analyses are based on calculations recognized as reliable in the field.") (Attached as Pa27); *United States v. Pettway*, No. 12-CR-103S (1), (2), 2016 U.S. Dist. LEXIS 145976, 2016 WL 6134493, at *1 (W.D.N.Y. Oct. 21, 2016) (discussing "exhaustive[] research[]" concluding that "the scientific foundations of the STRmix process are based on principles widely accepted in the scientific and forensic science communities")(Attached as Pa21). The Second Circuit determined that the scientific community accepted a different (but similar) DNA-sorting software, Forensic Statistical Tool, even though just one laboratory had used it. *Jones*, 965 F.3d at 156, 162.

Id. at 466.

In addition, more recent case law ruling STRmix as admissible under a Daubert analysis includes: United States v. Washington, No. 8:19CR299, 2020 U.S. Dist. LEXIS 105447, 2020 WL 3265142 at *3 (D. Neb. June 16, 2020) (relying on same government study and citing Lewis); Whittley v. State, 2022 Tex. App. LEXIS 6336, *19-20 (stating STRmix software has achieved general acceptance through its use in multiple laboratories and its admission in various jurisdictions over challenges to its general acceptance in the relevant scientific community and citing Gissantaner) (attached as Pa28); People v. Davis, 75 Cal. App 5th 694, 717 (2022) (ample evidence supporting a finding of general acceptance).

The aforementioned holdings come from other jurisdictions because there has yet to be a Daubert/Olenowski I hearing in New Jersey on STRmix probabilistic genotyping software. The Court here should still look to these cases for guidance. In Pickett, 466 N.J. Super. at 303, our Appellate Division reviewed a discovery motion on a competing but related probabilistic

genotyping software system where the defendant sought access -- at a Frye hearing -- to proprietary information solely to challenge the reliability of the science underlying novel DNA analysis evidentiary software and expert testimony. The Court held that an appropriate review required that they independently scrutinize the record, including the comprehensive and amplified declarations of the experts, which in the instant matter would include the reports and testimony of the expert witnesses, as well as the scientific validation studies, peer-reviewed publications, and judicial opinions. See In re Commitment of R.S., 339 N.J. Super. 507, 531 (App. Div. 2001) (noting that when matters involve "novel scientific evidence in a criminal proceeding, 'an appellate court should scrutinize the record and independently review the relevant authorities, including judicial opinions and scientific literature'") (quoting Harvey, 151 N.J. at 167). The Pickett court further cited Lewis v. Harris, 188 N.J. 415, 436 (2006), which noted that New Jersey courts are "not bound by . . . the precedents of other states, although they may provide guideposts and persuasive authority[.]" Pickett, 466 N.J. Super. at 305.

As cited above, the New Jersey Supreme Court has held that the general acceptance and reliability of scientific evidence can be established by expert testimony, authoritative scientific literature, or persuasive judicial opinions. Harvey, 151 N.J. at 170 (quoting Kelly, 97 N.J. at 210). In Harvey, the Supreme Court looked to other jurisdictions in the context of a Frye hearing where "at the time of the R. 104 hearing, both the State

and the defense were unaware of any judicial opinion discussing a new form of scientific evidence, specifically in that case regarding polymarker evidence." Id. at 175. The court cited Wilkerson v. Pearson, 210 N.J. Super. 333, 336 (Ch. Div. 1985), which held that absence of judicial opinions demonstrating acceptance by other courts of a particular type of scientific technique should not, by itself, foreclose a finding of general scientific acceptance and reliability. The Harvey Court concluded:

> At the time of the *Rule* 104 hearing, both the State and the defense were unaware of any judicial opinion discussing polymarker evidence. See *Wilkerson v. Pearson,* 210 N.J. Super. 333, 336, 509 A.2d 818 (Ch.Div.1985) (holding that absence of judicial opinions demonstrating acceptance by other courts of particular type of scientific technique should not, by itself, foreclose finding of general scientific acceptance and reliability). Before the *Rule* 104 hearing, however, a New York court had admitted polymarker evidence. *People v. Morales, N.Y.L.J.,* Oct. 26, 1994, at 34 (N.Y.Cty.Ct.1994), *aff'd,* 227 A.D.2d 648, 643 N.Y.S.2d 217, *appeal denied,* 677 NE.2d 301 (1996). In *Morales,* experts from the Center for Blood Research Laboratories, Yale University School of Medicine's Department of Genetics, and the Office of the Chief Medical Examiner for New York testified in support of admission of the evidence. Curiously, the witness from the New York Medical Examiner supporting the admission of the polymarker evidence was Dr. Shaler, the same expert who testified against admission of polymarker evidence in the present case. The New York court concluded that "the People have met their burden in establishing that the PCR tests at issue here are sufficiently established to gain general acceptance in the scientific community and satisfy the standard of reliability." *Ibid.*
>
> Since defendant's trial in the present case, at least six other courts have held that polymarker testing is scientifically reliable. *United States v. Beasley,* 102 F.3d 1440, 1448 (8th Cir.1996), *cert. denied,* 520 U.S. 1246, 117 S. Ct. 1856, 137 L. Ed. 2d 1058 (1997) (holding that DQ Alpha and polymarker testing are sufficiently reliable under *Daubert* and have

> achieved general acceptance within relevant scientific community); *United States v. Shea*, 957 F. Supp. 331, 338 (D.N.H.1997) (finding PCR testing, including polymarker testing, reliable under *F.R.E.* 702); *United States v. Lowe*, 954 F. Supp. 401, 418 (D.Mass.1996) (finding that polymarker and another PCR-based test, D1S80, are sufficiently reliable under *Daubert*); *Brodine v. State*, 936 P.2d 545, 550-51 (Alaska.Ct.App.1997) (finding polymarker testing generally accepted in scientific community); *People v. Pope*, 284 Ill. App. 3d 695, 220 Ill.Dec. 309, 314, 672 N.E.2d 1321, 1326 (1996) (finding that DQ Alpha and polymarker typing are generally accepted in scientific community under *Frye*); *Keen v. Commonwealth*, 24 Va. App. 795, 485 S.E.2d 659, 664 (1997) (rejecting defendant's challenges to the polymarker test). In *Pope, supra*, the Illinois Court of Appeals found polymarker testing generally accepted in the scientific community even when the *Frye* hearing in that case involved the testimony of only one witness, the State's expert. *Pope, supra*, 220 Ill.Dec. at 314, 672 N.E.2d at 1326. Admission of the polymarker test in other jurisdictions supports our conclusion that the trial court correctly admitted the evidence in the present case.
>
> We thus conclude that the trial court did not err in admitting expert testimony on the results of the polymarker test. We are satisfied that the polymarker technology is scientifically reliable and that Cellmark conducted the tests in accordance with established procedures.

Harvey, 151 N.J. at 175-176. Consistent with Harvey, the overwhelming amount of case law from various courts around the nation holding that STRmix has met the mark on general acceptance should be considered by this Court.

Of note, this prong is a standard of general NOT universal acceptance. Bonds, 12 F.3d at 562. What matters is if the relevant scientific community accepts the software. Gissantaner citing Daubert, 509 U.S. at 594. For a technology that is widely used, controversies over its use in a given case usually will be left to the jury. See United States v. Jones, 965 F.3d 149, 160 (2d Cir. 2020). While the above examples of cases from around

the United States highlight the multitude of findings that STRmix is "generally accepted," it bears repeating that this general acceptance neither equates to nor is it predicated on unanimity.

The Gissantaner case dealt with this legal premise as the defense argued that there was still controversy regarding the acceptance of STRmix's reliability amongst a subset of computer scientists in cases with low copy or small amounts of DNA. The Gissantaner court held that criticism did not mean STRmix missed the mark on general acceptance. 990 F.3d at 469. The Lewis Court also explained that where there is a discrepancy in opinion, "[a]s a general rule, the factual basis of an expert opinion goes to the credibility of the testimony, not the admissibility, and it is up to the opposing party to examine the factual basis for the opinion in cross-examination." Lewis, 442 F.Supp. 3rd at 1128; see also United States v. Finch, 630 F.3d 1057, 1062 (8th Cir. 2011) (internal quotations and alterations omitted).

Courts consistently make clear that general acceptance does not require unanimity or uniformity or that it be without critique. Notably, New Jersey courts have also stated that there is no requirement that results "are beyond all legitimate debate." Marcus, 294 N.J. Super. at 287. In fact, the Marcus Court noted that it is "commonplace in our courtrooms for juries to hear conflicting expert opinions regarding the precise significance of scientific tests," but this did not deem the science unreliable. Ibid.

Also, as stated previously, the general acceptance of

probabilistic genotyping software has led to its use for exculpatory purposes. See Erik Ortiz, "A Texas jury found him guilty of murder. A computer algorithm proved his innocence," https://news.yahoo.com/prison-murder-computer-algorithm-helped-105609137.html; Jason Hanna & Nick Valencia, "Thanks to a new DNA analysis, a Georgia man is exonerated of rape and freed from prison after 17 years;" https://www.cnn.com/2020/01/10/us/georgia-kerry-robinson-released/index.html. As illustrated by these cases of exoneration, the probabilistic genotyping software advancement is being used in all settings and by proponents on all sides. The Gissantaner Court noted that the key developer of STRmix is a civil servant in New Zealand. Further highlighted was the fact that any revenue from sales of the software go to a government agency, which the court noted, by all appearances "seems as focused on sparing the innocent as on convicting the guilty. What inculpates one day may exonerate the next with DNA-sorting evidence." 990 F.3d at 468. As indicated earlier, the Court heard compelling testimony from Dr. Coble regarding the power that Probabilistic Genotyping, generally, and STRmix, specifically, have to both exonerate and to exclude the innocent before they are ever charged based upon inconclusive DNA evidence and/or a flawed identification.

Recently, the standard of admissibility for scientific evidence in New Jersey was altered leaving behind the former methods of demonstrating acceptance and reliability derived from the test first articulated in Frye, wherein the proponent of

scientific evidence had to establish general acceptance via:

> (1) by expert testimony as to the general acceptance, among those in the profession, of the premises on which the proffered expert witness based his or her analysis;
>
> (2) by authoritative scientific and legal writings indicating that the scientific community accepts the premises underlying the proffered testimony; and
>
> (3) by judicial opinions that indicate the expert's premises have gained general acceptance.

Harvey, 151 N.J. at 170 (citing Kelly, 97 N.J. at 210). The burden was on the proponent to "clearly establish" each of these methods. Ibid. (citing State v. Williams, 252 N.J. Super. 369, 381 (Law Div. 1991)).

While replaced, the Frye test remains important, as it closely relates to the fourth non-exhaustive factor listed in the New Jersey Courts' new Daubert-like standard set forth in Olenowski I. General acceptance remains highly probative and relevant and, therefore, should be considered along with the other factors. Under Frye, New Jersey case law held that the results of scientific tests were "admissible at a criminal trial only when they are shown to have 'sufficient scientific basis to produce uniform and reasonably reliable results and will contribute materially to the ascertainment of the truth." Romano, 96 N.J. at 80 (citing State v. Hurd, 86 N.J. 525, 536 (1981)). Again, in order to be scientifically acceptable, there was no requirement for "unanimous belief or universal agreement in the total or absolute infallibility of the technique,

methodology or procedures that underlie the scientific evidence." Ibid.; see also State v. McGuire, 419 N.J. Super. 88, 133 (App. Div. 2011), certif. den. 208 N.J. 335 (2011); State v. Chun, 194 N.J. 54, 91-92 (2008). Instead, reliability of such evidence could "be demonstrated by showing that the scientific technique has gained general acceptance within the scientific community." Ibid. (citing State v. Johnson, 42 N.J. 146, 170-71 (1964)); see also Marcus, 294 N.J. Super. at 287 (the scientific technique or procedure must be accepted as scientifically reliable). Here, the DNA evidence offered is generally accepted in the scientific community.

"Unlike many other evidentiary issues, whether the scientific community generally accepts a methodology or test can transcend a particular dispute." Harvey, 151 N.J. at 167 (citing People v. Miller, 173 Ill.2d 167 (1996), cert. denied 520 U.S. 1157 (1997)). In fact, when "determining the general acceptance of novel scientific evidence in one case, the court generally will establish the acceptance of that evidence in other cases." Ibid. (citing Jones v. United States, 548 A.2d 35, 40 (D.C.1988)). In Marcus, the Appellate Division held that the trial court properly admitted results of a method of DNA analysis, reasoning that "[a]lthough there is no reported appellate decision in New Jersey dealing with the admissibility in a criminal trial . . . there is overwhelming authority in other jurisdictions sustaining the admissibility of such evidence." Marcus, 294 N.J. Super. at 282-83. The method of DNA analysis used in that case was "clearly established by

authoritative scientific literature, the overwhelming weight of judicial authority throughout the country, and the testimony of experts at the Frye hearing[.]" Id. at 291.

Bode and the NJSP laboratory have been accredited and have been conducting DNA testing and analysis for many years. After completing their respective validations of STRmix, both laboratories went live in their implementation of the STRmix probabilistic genotyping software. As is clear from the plethora of cited cases and peer-reviewed scientific literature, the instant matter is NOT one of the first to utilize STRmix and generate results using likelihood ratios. "Probabilistic genotypes have been recognized by regulatory bodies such as the Scientific Working Group on DNA Analysis Methods [(SWGDAM)] in its 2010 Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories and the American National Standards Institute (ANSI) in the 2011 article Data Format for the Interchange of Fingerprint, Facial & Other Biometric Information' as a valid approach to DNA interpretation and reporting." People v. Wakefield, 47 Misc.3d 850, 853 (NY Supreme Court 2015). As referenced earlier, SWGDAM is a "forensic DNA advisory group to the FBI director that is comprised of forensic scientists who serve as DNA technical leaders or CODIS administrators in their laboratories." Id. at n.1 SWGDAM further issued a document entitled "Guidelines for the Validation of Probabilistic Genotyping Systems" in June 2015. S-130.

Furthermore, the previously mentioned 2016 PCAST report indicated that "probabilistic genotyping software programs

clearly represent a major improvement over purely subjective interpretation." S-141 at 79. As noted earlier, while the PCAST report indicated careful scrutiny would be required in determining use and admissibility, it noted that "[t]he two most widely used methods (STRmix and TrueAllele) appear to be reliable within a certain range, based on the available evidence and the inherent difficulty of the problem." Id. at 80. The PCAST report had suggested that the methods utilized by programs including STRmix were "reliable for three-person mixtures in which the minor contributor constitutes at least 20 percent of the intact DNA in the mixture and in which the DNA amount exceeds the minimum level required for the method." Ibid. That report resulted in the many additional validation studies cited earlier. Those studies, previously referenced, highlighted that even though the previous software and/or reporting methods were found to be sound, their actual capability for detection, reporting use and accuracy far exceeded the PCAST-cited limitations. See Moretti, T.R., et al., *Internal validation of STRmix for the interpretation of single source and mixed DNA* profiles, Forensic Science International: Genetics, 29:126-144 (2017), S-145, and Bright et al., *Internal validation of STRmix: A multi laboratory response to PCAST* (May 2018). S-146.

The State submits that based upon a review of scientific and legal writings and judicial opinions throughout the country that the use of probabilistic genotyping, including STRmix specifically, has been found to be generally accepted and is no longer novel. According to Dr. John Buckleton, STRmix is

currently in laboratories in all eight of the state and territory labs in Australia and labs elsewhere including the United States Army Criminal Investigation Laboratory, FBI, DNA Labs International, the Federal Bureau of Alcohol, Tobacco, Firearms and Explosives, as well as labs in New York, California, Idaho, Michigan, Texas, Arizona, Oregon, Wyoming, Connecticut, Illinois, Florida, Kansas, Indiana and the Union County Prosecutor's Office. An updated list of laboratories was supplied including 89 laboratories. S-140.

Again, currently there are no published or unpublished cases addressing the admissibility of STRmix in New Jersey in the context of a Daubert hearing. However, as noted earlier the New Jersey Appellate Division did comment on testimony given in State v. Price, 2022 N.J. Super. Unpub. LEXIS 691. There, the state proffered expert testimony garnered from STRmix software and the Price Court described same as "overwhelmingly accurate scientific data." Price, 2022 N.J. Super. Unpub. LEXIS at *33. Pa10.

Given the redundant criticisms arguing that the majority of the opinions voiced regarding STRmix by way of peer-reviewed literature come from the developers of STRmix and "those associated with the developers," the State would be remiss if it failed to note the consistent conclusions reached by Dr. Coble in this and other cases. In the past decade, the use of probabilistic genotyping software for DNA Interpretation has become rapidly adopted by forensic laboratories all over the world. Dr. Coble was asked by the Court about the number of laboratories in the United States. He estimated that 212

laboratories do DNA testing and estimated that 130 or 140 of those have brought on Probabilistic Genotyping software. 11T:84-9 to 84-12. Coble indicated in his report that, most importantly, "[t]here are also potentially countless individuals who have been spared from being wrongfully convicted using probabilistic genotyping software today… For example, DNA profiles too complex to interpret in the past were determined to be 'inconclusive.' Juries may therefore have to rely on less reliable methods such as eyewitness testimony." S-186 at 7.

There are a plethora of cases from multiple jurisdictions around the country concluding that the software is clearly accepted in the relevant scientific community. There are also a myriad of publications from the scientific community itself discussing the validity and, hence, tacit acceptance of STRmix. There are scientific organizations from around the world that have published guidelines on the use of STRmix software; those guidelines are necessarily predicated on acceptance of STRmix. Lastly, while there might be those who dispute the wide level of acceptance, the case law clearly marks such dissent as fodder for cross examination. With its widespread use and its status as a market leader in DNA testing and analysis, STRmix is clearly accepted in the relevant scientific community.

OVERALL ASSESSMENT

As suggested by Olenowski II, the State submits that a review of the aforementioned factors in their totality is

important to an overall assessment of reliability. That being said, there can be no doubt that STRmix is reliable given the sheer amount of testing which has determined that it is fit for casework. In reality, probabilistic genotyping is just another in a line of many advancements which have occurred since the advent of DNA in 1988, discussed by Dr. Buckleton, who was in the epicenter of that transformative moment. As this Court heard, STRmix was not the first continuous probabilistic genotyping system; however, it is undoubtedly the preeminent in the United States. Since the PCAST report was issued in 2016, the number of labs using STRmix has grown eight-fold, from 11 to 89 laboratory systems. The defense will undoubtedly highlight the testimony of the software engineers that testified; however, their criticisms are regarding documentation of the software. None have ever pointed to a specific scenario, despite millions of data points being available, where STRmix has had a catastrophic or even minimal effect on the life or liberty on any one person. They warn, they make predictions and they attempt to scare the Court into ignoring all of the evidence and testing which shows that STRmix works and it works well.

Mr. Godin stated in summation that "in the last 30 years Dr. Buckleton has been involved in producing exactly one software; STRmix. That does not make him an expert in the field of software engineering." (T20:21-11 to 21-14). His expertise in software engineering compares very well, in the State's estimation, to Mr. Adams, who only has a Bachelor's Degree. Creating but 1 software that has helped revolutionize DNA mixture

interpretation in the world is not too shabby in the State's opinion. But, this also truly begs the question of -- what have any of the defense experts created? The State submits that the governing body of caselaw, the peer reviewed publications and the testimony make abundantly clear that STRmix has simply made it possible for each and every DNA lab to deconvolute complex mixtures in a much more uniform and reliable manner. STRmix meets the Olenowksi I/Daubert standard regarding reliability and should be admitted. Finally, the State will turn to a discussion of reliability as applied in this case.

POINT II

STRMIX WAS RELIABLY APPLIED

1. Coverage

Fifteen evidentiary DNA samples were submitted to Bode and assigned to Forensic DNA Analyst Danielle Reed for testing and analysis. Reed utilized STRmix on thirteen of the aforementioned samples. (T4:17-18 to 19-20). The results of Reed's DNA analysis are summarized as follows:

1. **E01a-Jeans, interior thigh above knee.** Number of contributors (hereinafter, "NOC"): three. Only contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer and [redacted] visually excluded from suitable contributors.
    - Contributor 1: [redacted] 82%, 4038 RFU

- Contributor 2: Paul Caneiro, 17%, 844 RFU
- Contributor 3: Unknown, 1%, 50 RFU

Likelihood Ratio for [redacted] Assuming a mixture of three, this mixture DNA profile obtained is at least 470 sextillion times more likely to occur if it originated from [redacted] and two unknown, unrelated contributors than if it originated from three unknown, unrelated contributors.

Likelihood Ratio for Paul: Assuming a mixture of three, this mixture DNA profile obtained is at least 3.7 quintillion times more likely to occur if it originated from Paul and two unknown, unrelated contributors than if it originated from three unknown, unrelated contributors.

2. **E01c-Jeans, exterior front right thigh.** NOC: one. Contributor 1 is suitable for comparison. Keith, Jennifer, [redacted] and Paul visually excluded.

   - Contributor 1: [redacted] 100%, 2300 RFU

   Likelihood Ratio for [redacted] Assuming one contributor, this DNA profile obtained is at least 2.1 septillion times more likely to occur if it originated from [redacted] than if it originated from an unknown, unrelated individual.

3. **E02b-Glove 1, interior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer and [redacted] visually excluded from suitable contributors.

   - Contributor 1: [redacted] 94%, 1325 RFU
   - Contributor 2: Paul Caneiro, 6%, 91 RFU

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 1 septillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 43 thousand times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

4. **E03a-Glove 2, exterior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer and [redacted] visually excluded from suitable contributors.

   - Contributor 1: [redacted] 59%, 1922 RFU
   - Contributor 2: Paul Caneiro, 41%, 1325 RFU

   Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 100 quadrillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

   Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 45 quadrillion times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

5. **E03b-Glove 2, interior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. None of the reference profiles could be visually excluded from the suitable contributors.

   - Contributor 1: [redacted] 86%, 600 RFU
   - Contributor 2: Paul Caneiro, 14%, 100 RFU

   Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 750 quintillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

   Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 400 thousand times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

   Likelihood Ratio for Jennifer: Assuming a mixture of two, this mixture DNA profile obtained is 480 times more likely to occur if it originated from two unknown, unrelated individuals than from Jennifer and one unknown, unrelated individual.

   Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is 37 thousand times more likely to occur if it originated from two unknown, unrelated individuals than from Jennifer and one unknown, unrelated individual.

   Likelihood Ratio for Keith: Assuming a mixture of two, this

mixture DNA profile obtained is 630 times more likely to occur if it originated from two unknown, unrelated individuals than from Jennifer and one unknown, unrelated individual.

6. **E04a-Glove 3, exterior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer and [redacted] visually excluded from suitable contributors.

   - Contributor 1: [redacted] 97%, 6519 RFU
   - Contributor 2: Paul Caneiro, 3%, 216 RFU

   Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 980 sextillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

   Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 200 million times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

7. **E05a-Glove 4, exterior.** NOC: three. Only contributor 1 is suitable for comparison. Keith, Jennifer, [redacted] and Paul visually excluded from the suitable contributor.

   - Contributor 1: [redacted] 94%, 2447 RFU
   - Contributor 2: Unknown, 4%, 109 RFU
   - Contributor 3: Unknown, 2%, 56 RFU

Likelihood Ratio for [redacted] Assuming a mixture of three, this mixture DNA profile obtained is at least 720 sextillion times more likely to occur if it originated from [redacted] and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals.

8. **E06a-Glove 5, exterior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer, and [redacted] visually excluded from the suitable contributors.
   - Contributor 1: [redacted] 95%, 6066 RFU
   - Contributor 2: Paul Caneiro, 5%, 313 RFU

   Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 870 sextillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

   Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 21 thousand times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

9. **E06b-Glove 5, interior.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer, and [redacted] visually excluded from the suitable contributors.
   - Contributor 1: Paul Caneiro, 58%, 784 RFU
   - Contributor 2: [redacted] 42%, 563 RFU

Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 49 billion times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 19 quadrillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

10. **E07a-Glove 6, exterior.** NOC: two. Contributors 1 and 2 are suitable for comparison. None of the reference profiles could be visually excluded from the suitable contributors. Inclusionary LR's for all reference profiles but the only combination possible was for [redacted] and Paul.

- Contributor 1: [redacted], 62%, 256 RFU
- Contributor 2: Paul Caneiro, 38%, 159 RFU

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 48 billion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for Paul: Assuming a mixture of two, this mixture DNA profile obtained is at least 1.9 thousand times more likely to occur if it originated from Paul and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for Keith: (Keith was put in contributor number 2 spot). Assuming a mixture of two, this mixture DNA profile obtained is at least 9 thousand times more likely to occur if it originated from Keith and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for [redacted] was put in contributor number 2 spot). Assuming a mixture of two, this mixture DNA profile obtained is at least 85 times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for Jennifer: (Jennifer was put in contributor number 2 spot). Assuming a mixture of two, this mixture DNA profile obtained is at least 2.6 thousand times more likely to occur if it originated from Jennifer and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

11. **E09a-Swab, reddish stain, south side kitchen island.** NOC: one. Contributor 1 is suitable for comparison. Keith, Jennifer, [redacted] and Paul were visually excluded from the suitable contributor.

- Contributor 1: [redacted] 100%, 1788 RFU

Likelihood Ratio for [redacted] Assuming one contributor, this DNA profile obtained is at least 34 quintillion times more likely to occur if it originated from [redacted] than if it originated from an unknown, unrelated individual.

12. **E10a-Swab, reddish stain, lower kitchen cabinet.** NOC: two. Contributors 1 and 2 are suitable for comparison. Combination possible. Keith, Jennifer and Paul were visually excluded from the suitable contributors.

- Contributor 1: [redacted] 73%, 1300 RFU
- Contributor 2: [redacted] 27%, 4913

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 71 septillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 45 septillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

13. **E11a-Swab, reddish stain, pullout drawer below sink.** NOC: two. Only contributor 1 is suitable for comparison. Keith, Jennifer, [redacted] and Paul were visually excluded from the suitable contributor.

- Contributor 1: [redacted] 99%, 13,797 RFU
- Contributor 2: Unknown, 1%, 91 RFU

Likelihood Ratio for [redacted] Assuming a mixture of two, this mixture DNA profile obtained is at least 990 sextillion times more likely to occur if it originated from [redacted] and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.

(T4:37-7 to 106-11).

Two additional samples were tested and analyzed by Reed without the use of STRmix. Sample E01b, the interior waistband of the jeans, consisted of a partial profile, including at least one male. The sample was ultimately deemed inconclusive as there was too little data to conduct an analysis. (T4:29-21 to 30-21). Sample E02a, the exterior of glove one, was analyzed without the use of STRmix. The results of the analysis reflected two contributors, including a major female contributor who matched the DNA profile of [redacted] A random match probability was calculated for same, which amounted to 1 in 14 octillion in the United States population. No conclusions could be drawn on the minor contributor. (T4:30-22 to 34-21).

In addition, testimony was provided by Kristen Naughton, Director of Validation and Quality Control at Bode, regarding Bode's internal validation of STRmix. Dr. Buckleton testified as to the purpose of an internal validation in the context of probabilistic genotyping software. (T6:71-20 to 71-24; 79-7 to 83-3). Essentially, each lab that purchases STRmix must conduct its own internal validation in order to ensure that the software works within the lab and to determine how the software is going to perform within the lab. Ibid.

Along those lines, Dr. Buckleton explained the related concept of coverage, a term which refers to "what the internal validation covers." (T6:83-9 to 83-10). The idea being that the lab is meant to perform testing with known ground truth on a variety of different types of DNA samples that it would expect to

encounter in casework, including samples with varying ratio proportions, template amounts, degradation and number of contributors. (T6:96-3 to 97-3); (T2:52-3 to 52-6); (T8:72-25 to 73-7). ANSI/ASB Standard 018, Validation of Probabilistic Genotyping Systems section 3.2, sets forth the requirements:

> Data exhibiting features that are representative of a plausible range of casework conditions for mixtures and single-source samples. These features include masked/shared alleles and stutter, degradation (including different degradation levels for different contributors to a mixture), allele and locus drop-out, and PCR inhibition.

See S-133. Labs try to test as wide a variety of samples as possible. However, the reality is that a lab cannot test every possible scenario that might exist. (T2:51-23 to 52-6; 99-12 to 99-14); (T8:73-11 to 73-14).

> I tend to agree with my former NIST colleague Dr. John Butler that, 'It is impossible to mimic everything that might be seen in casework or in samples processed through a laboratory in the future. Remember that validation simply confirms that the STR kit, instrument or software is fit for purpose and works within the range of conditions defined by the validation experiments conducted.'

See S-186 at 7. Defendant's expert, Dr. Reich, agreed: "[I]t's too many." (T13:45-14 to 45-18).

While Dr. Buckleton acknowledged "a modern belief that [] [a lab's internal validation] has to cover everything . . . the high end [and] . . . the low end" and that "if you haven't covered it, it's nothing[,]" he testified that coverage is, in fact, broader and encompasses the totality of testing that has been done. "STRmix has vertical and horizontal transportability and the

coverage and our belief in reliability is the sum of all the data." (T7:94-7 to 94-9). Dr. Coble agreed, acknowledging that the totality of developmental data, in conjunction with internal validation data, constitutes coverage. (T11: 17-15 to 17-25).

Defendant claims the State has not proven that STRmix was reliably applied to the aforementioned 13 evidentiary samples, complaining that Bode did not analyze enough samples in its internal validation study similar to the evidentiary samples in the present case. Specifically, defendant takes issue with the evidentiary samples where the minor contributor comprises a lower percentage of the mixture (below 5 percent) and/or contributed less total DNA to the mixture (less than 25 picograms) than Bode's internal validation demonstrated. In support of this claim, the defendant points to Section D of the internal validation summary, which lists the most minor contributor to a mixture as comprising 5% and/or contributing 25 picograms of total DNA. The State submits that defendant's argument is without merit.

At the outset, the State would note that only three of the 13 evidentiary samples reflect a minor contributor who comprised approximately 5% or less of the mixture: E02b (6%), E04a (3%), and E06a (5%). In each of these samples, there is a likelihood ratio that reflects inclusionary support for the defendant as the minor contributor.[6] Of the remaining 13 samples where there is inclusionary support for the defendant, his contribution to the

[6] There are other samples among the 13 whereby a minor contributor comprises less than 5% of the mixture: E01a, E05a, and E11a. However, those minor contributors were deemed not suitable for comparison.

mixture is well above 5%.

That being said, testimony was provided establishing that Bode's internal validation study did, in fact, test below the 5%/25 picogram metric. Naughton testified to multiple samples in the internal validation study whereby the minor contributor comprised less than 5% of the mixture and/or contributed less than 25 picograms of total DNA. (T2:119-19 to 120-16; 120-24 to 124-15; T3:25-6 to 26-25).

Specifically, Naughton testified to a sample in Section D of the internal validation that consisted of a four-person mixture wherein the most minor contributor comprised 3% of that mixture. (T2:118-5 to 119-18). Although this sample was not reflected in the internal validation summary, it was nonetheless contained within the underlying data of Bode's internal validation.[7]

Naughton further testified to two samples contained in section L of the internal validation summary; in each sample the minor contributor comprised less than 5% of the mixture. The first sample—TRN1777-0961-E02—consisted of a three-person mixture where the most minor contributor comprised 4% of the mixture. The second sample—TRN1777-0962-E02—consisted of a three-person mixture where the most minor contributor comprised 1% of the mixture and contributed 8 picograms of DNA. (T3:47-7 to 49-19; 49-20 to 53-1).

Further, Naughton testified that Bode conducted N+1 testing as part of its internal validation study. (T3:31-21 to 32-15; 34-

[7] Same was provided to the defense via discovery well in advance of the hearing.

18 to 37-7). N+1 testing involves adding a contributor to a mixture who is not physically present in the mixture. For example, an analyst will run a two-person mixture through STRmix as a three- person mixture, thereby "adding" a contributor at 0%. (T6:99-16 to 100-25); (T10:102-12 to 102-25). Buckleton explained, "[Y]our N+1 tests are actually testing zero for your coverage. And they do reasonably well. So we've actually tested the lowest possible contributor which is zero." (T:100-4 to 100-7). Thus, by including N+1 testing, Bode essentially tested down to a zero percent contributor.

Despite the aforementioned evidence, the defendant complains that these samples are insufficient. He argues 1) Bode did not include enough of these types of low-level mixture samples in its internal validation, and 2) the low-level mixture samples Naughton testified to are insufficient because no results accompanied them. Notably, these same arguments were made by the defendant in United States v. Gissantaner, 990 F. 3d at 469, and ultimately discounted by the Sixth Circuit on appeal.

The facts and analysis in Gissantaner are akin to those in the present case. Gissantaner dealt with an evidentiary DNA sample taken from a firearm whereby STRmix was utilized to link the defendant to the firearm. Id. at 460. The evidentiary sample consisted of a mixture of three contributors with the third and most minor contributor comprising 7% of the mixture and contributing 49 picograms of DNA. Id. at 462. Utilizing STRmix, a DNA analyst from the Michigan State Police laboratory ran a comparison between the evidentiary sample and the defendant's DNA

profile. Ibid. A likelihood ratio of 49 million was generated in favor of inclusionary support for the defendant as the third contributor. Ibid. Defendant moved to exclude the evidence on grounds that it was unreliable under Rule 702. Id. at 460. A Daubert hearing was held, after which the district court ruled the evidence inadmissible. Ibid. On appeal, the Sixth Circuit reversed, holding the STRmix evidence to be admissible. Id. at 470.

Akin to the defendant's argument in the present case, the defendant in Gissantaner questioned the reliability of the Michigan State Police lab's use of STRmix, claiming that the lab's internal validation did not test STRmix at low contribution and weight levels. Id. at 469. The district court's concern was that the lab's "[internal] validation summary did not mention mixtures similar to the one here—in which the minor contributor donated a small absolute amount of DNA (49 picograms) and a small percentage of the DNA in the mixture (7%)[.]" Ibid.

Holding that the Michigan State Police lab reliably applied STRmix, the Sixth Circuit noted that the lab's internal validation did include sufficient samples similar to the evidentiary samples in the case before it. "It tested a mixture in which one contributor gave just 4% of the DNA (less than the 7% here) and another mixture in which the minor contributor gave only 26 picograms of DNA (less than the 49 picograms here)." Id. at 467. The Sixth Circuit also considered the fact that the lab "produced supplemental data showing that its internal validation included a lab-created mixture of 3.2% and 32 picograms and an

adjudicated-case mixture of 4% and 10 picograms." Ibid. Significantly, these low-level mixture samples, which the Sixth Circuit clearly found sufficient enough to rely on, are approximately equal in number to those in Bode's internal validation that were proffered by the State.

The defendant in Gissantaner also criticized the Michigan State Police lab's internal validation insofar as the "laboratory ran tests on similar mixtures, [but] did not include the likelihood ratios or the false-positive rates from those tests." Id. at 469. The Sixth Circuit discounted that argument as well, explaining that "Rule 702 does not require unstinting perfection in presenting test results[,]" id, at 469, and further admonished that "these concerns were for the jury, not the court." Ibid. Insofar as the defendant in the present case makes an identical argument, attacking the sufficiency of Bode's internal validation samples based on a lack of testing results, the State submits that such an issue goes to the weight of the evidence rather than admissibility. Ibid. Disagreements over the adequacy and/or accuracy of testing "provide grist for adversarial examination, not grounds for exclusion." Id. at 464 (internal citations omitted).

In holding that the Michigan State Police lab reliably applied STRmix, the Sixth Circuit also relied on the fact that other laboratories had validated STRmix at low levels. Id. at 467-468; 469.

> The Michigan State Police laboratory has ample company in concluding that STRmix works at low levels of DNA. A peer reviewed article compiling data from the internal validations of 31 independent laboratories indicated

> that STRmix had been validated with mixtures involving a minor contributor who supplied a small percentage of a mixture. The FBI's internal validation, also subjected to peer review, included mixtures in which the minor contributor contributed less than 7% and fewer than 49 picograms to the sample.

Id. at 467. See also id. at 469 ("As shown, however, the [Michigan State Police] laboratory did validate STRmix at these [low] levels, and so did the FBI.") (emphasis added). Thus, in determining that STRmix was reliably applied, the Sixth Circuit not only took into consideration the Michigan State Police lab's internal validation, but it also relied on validations from other labs which tested STRmix at low levels. This inclusive analysis is in line with Dr. Buckleton's concept of coverage as being both vertical and horizontal.

Furthermore, the above Gissantaner analysis cuts against the defendant's argument that a lab can never reliably perform DNA analysis on an evidentiary sample where the minor contributor is below that for which the lab validated. Although Dr. Reich insisted that such a bright line rule exists, (T13:64-22 to 65-1), there is simply no support for that proposition in any of the case law or authoritative documents. Nor could he identify any such documentation on cross examination. (T13:63-18 to 65-13, 65-24 to 66-25). ANSI/ASB Standard 018, Validation of Probabilistic Genotyping Systems section 3.2, supra, sets out the requirements to be used by laboratories for the validation of probabilistic genotyping software. Strikingly absent from that document is any mention of Dr. Reich's alleged bright line rule. See S-133.

The only bright line rule that appears in the case-law with

regard to coverage is with respect to the number of contributors to a mixture. In other words, the case law is clear that a lab should not utilize STRmix on a DNA sample where the number of contributors is above that for which the lab validated.

Most recently, this concept was addressed in United States v. Ortiz, 2024 U.S. Dist. LEXIS 102951 (Decided June 10, 2024). The defendant in Ortiz "[d]id not question STRmix satisfying Rule 702 as a product of reliable principles and methods." Ortiz, 2024 U.S. Dist. LEXIS *9-10. The defendant also did not challenge "the foundational validity for mixtures up to five contributors or the computer algorithms and biological models that undergird STRmix's probabilistic analysis. Instead he challenges the process by which STRmix was applied to a complex DNA mixture that likely contained six contributors, given that STRmix had not been subjected to developmental validation for six-person mixtures by the developer or the internal validation by the SDPDCL (San Diego Police Department Crime Laboratory)." Id. at *12-13. Ultimately, the district court indicated that the lab's internal validation determined that STRmix may only be used where the number of contributors is five or less. Id. at *8. Based upon the testimony, the court believed that the number of contributors of the disputed evidentiary sample was six; therefore, the court held that the "[g]overnment has failed to demonstrate that STRmix's analysis remains reliable for six-person samples. Id. at *30 (emphasis added).

Here, however, the 13 evidentiary samples Bode tested are comprised of no more than three contributors, with some

containing only one or two donors. (T4:8-15 to 9-2). As such, these samples are not complex in terms of the number of contributors and are well within the bounds of Bode's internal validation. Moreover, the defendant does not dispute the reliability of Bode's DNA analysis with respect to the findings on the major contributors. (T13:50-20 to 63-10; 67-1 to 67-20; 79-8 to 80-22; 81-3 to 90-9). Rather, he takes issue with the low-level minor contributor(s), arguing that Bode's DNA analysis with regard to same is unreliable due to a deficiency in testing. As noted and cited above, however, Bode's internal validation tested sufficiently similar samples to the ones in the present case. Moreover, numerous validations across the country have established that "STRmix works at low levels of DNA." Gissantaner, 990 F. 3d at 467. As such, the State submits that STRmix's vertical and horizontal transportability, in conjunction with Bode's internal validation study, clearly reflect that STRmix was reliably applied in the present case.

Rather than the (non-existent) bright line rule proffered by the defendant, Dr. Coble offers a more fulsome and case specific means to determine whether STRmix can be (or has been) reliably applied to a given DNA sample; namely, an assessment of the totality of data within a sample, to include a review of the electropherogram and peak heights, as well as the STRmix output reports and, importantly, the amount of template RFU of a given donor. (T10:88-19 to 89-4; 91-16 to 91-20; 105-19 to 112-17); (T11:55-7 to 55-21).

RFU stands for "Relative Fluorescent Units" and is the unit

of measurement that corresponds to peak height in an electropherogram. (T1:70-9 to 70-18); (T7:109-14 to 109-16); (T10:106-4 to 106-7). Dr. Coble explained the correlation between template DNA, peak height and RFU:

> Generally, when peak heights, which are generated by the amount of DNA (template) amplified in the PCR reaction, are large, then the information content is also high, and the LR statistic tends to be a very high value. When peak heights are low, there is a chance that data may be missing (partially or completely) in the profile making the information content low, and the LR statistic trends to a value of one (uninformative). This trend was observed in the Bode validation study for various mixture combinations[.]

See S-186 at 8. See also (T10:107-6 to 107-8) ("There's a correlation [ ] between the quantity of DNA and the peak height that you observe in the electropherogram."). The State would also highlight that Dr. Reich, realizing it or not, actually made the same point, substantiating that STRmix works with low level samples. The colloquy was as follows:

> Q. And if you saw like no data in that electropherogram or not enough data in your experience you wouldn't run it through a probabilistic genotyping software, correct?
> A. Well, you could because if you put something in, you'll always get a number out, but it would be very close to one or zero."

(T19:139-9 to 139-15).

Along these lines, Dr. Coble's testimony made clear that just because a minor donor contributed a lower percentage of DNA than that for which the lab validated does not mean that DNA analysis of that minor contributor is unreliable. In fact, a low contributing donor could still have donated enough template RFU

to generate a relatively strong likelihood ratio, and vice versa. (T11:55-7 to 55-21).

Samples E04a and E03b are instructive. In sample E04a, the minor contributor comprised only 3% of the mixture, but the estimated template RFU was 216, which is above Bode's analytical threshold. The likelihood ratio for that minor contributor was relatively strong: 200 million in support of inclusion. (T10:108-17 to 111-20). Conversely, in sample E03b, the minor contributed comprised 14% of the mixture but the template RFU was only 100. The likelihood ratio for that minor contributor was 400 thousand in support of inclusion, a lower likelihood ratio than in the previous sample where the template RFU was higher. Reed also testified that in her experience there are times when template RFU is relatively high, even though the percentage of contribution is relatively low. (T4:11-20 to 11-23).

Overall, in terms of assessing the reliability of STRmix as applied, both Drs. Buckleton and Coble stressed the importance of a having a trained DNA analyst assess of the totality of the DNA sample, both prior to and after running the sample through STRmix. (T6:87-15 to 88-14; T10:91-16 to 92-2; 92-15 to 93-1; 105-19 to 106-16; 110-8 to 111-3). Essentially, the analyst engages in a two-part review. First, the analyst examines the data available on the front end, prior to running a sample through STRmix, to determine whether that sample is even suitable for STRmix. This will include a review of the electropherogram and peak heights. The analyst will attempt to determine the number of contributors, and will ensure that there are results at

the minimum number of locations required by the lab's internal validation and SOPs. If these criteria are not met, then the sample will not be run through STRmix. (T4:7-24 to 11-23; T9:68-7 to 69-9; 78-79-5).

Dr. Buckleton described how this visual assessment could result in a decision not to run a sample through STRmix: "Let's say you had a whole lot of low peaks, they weren't clean. There was noise and there may be . . . three, four or five donors and I'm not sure. I might say, this one's just too hard, too much risk of things being misrepresented." (T6:88-10 to 88-14). Notably, Reed did just that with respect to sample E01b. Based on her visual observations of the electropherogram, which showed a partial profile including at least one male, she ultimately decided not to run the sample through STRmix, instead deeming the sample inconclusive as there was too little data to conduct an analysis. (T4:29-21 to 30-21).

If, on the other hand, a sample is deemed suitable for analysis, and thereby run through STRmix, the analyst will conduct a second review, that being an examination of the STRmix output reports. Specifically, the analyst will compare the data in the STRmix reports to the electropherogram and assess whether the STRmix results are intuitive. The analyst will also review the primary and secondary diagnostics in the STRmix reports to ensure that nothing went wrong with the run. (T4:11-13-16); See also (T10:88-19 to 89-8; 91-11 to 91-25). This second level of review ensures that any problems that occurred during the STRmix run are visible to the analyst.

Such was the case with sample E02a. Reed initially deemed E02a suitable for comparison and ran it through STRmix. However, upon examining the output, she noticed that the results were not intuitive and that there appeared to be a problem with the deconvolution. Therefore, she did not utilize STRmix for that sample. (T4:30-22 to 32-3). It bears noting that Reed, a trained DNA analyst since 2005, (t3:135-3 to 135-7), engaged in this type of fulsome analysis for each of the 15 samples. The only two that gave her pause were the aforementioned samples, for which she did not utilize STRmix. (T4:108-6 to 109-7).

In support of his claim that the State's evidentiary samples reflecting a low-level minor contributor should be excluded, defendant proffered testimony by way of Dr. Reich suggesting that low likelihood ratios are inherently unreliable. What the defendant's argument fails to acknowledge is that the behavior of the likelihood ratio is dependent upon the quantity of DNA a donor contributes to a sample. When the template of a true contributor is at a "relatively 'high' quantity[,]" the likelihood ratio will be relatively strong; and conversely, in a very low-level sample where there is a "trace" amount of template, the likelihood ratio trends toward a value of one (uninformative). See S-186 at 4. Thus, low likelihood ratios are not wrong; they are simply reflective of the low amount of data (template) available.

This trend was demonstrated in section A of Bode's internal validation, (t2:103-18 to 104-9), S-147, and is further reflected in the 13 evidentiary samples. Notably, the likelihood ratio of

the minor contributor is higher for the samples in which the minor contributor donated a larger amount of template RFU: E01a (844 RFU, LR 3.7 quintillion); E03a (1325 RFU, LR 45 quadrillion); and E06b (784 RFU, LR 49 billion). Conversely, the likelihood ratio of the minor contributor is lower for the samples in which the minor contributor donated a smaller amount of template RFU: E02b (91 RFU, LR 43 thousand); E03b (100 RFU, LR 400 thousand); E04a (216 RFU, LR 200 million); E06a (313 RFU, LR 21 thousand); E07a (159 RFU, LR 1.9 thousand).

The aforementioned samples depict the likelihood ratio behaving exactly as would be expected, further demonstrating that STRmix works. The defendant's argument conflates probative value with reliability. As was the case for past 30 years, when traditional DNA analysis was utilized and a low random match probability ("RMP") was calculated, cross examination is the mechanism to challenge the probative value of the low statistic, not exclusion.

Finally, the State would be remiss if it did not address the testimony of Danielle Reed with respect to sample E06b. That sample was determined to contain two contributors, both of whom were suitable for comparison. The deconvolution report reflected contributor one as comprising 58% of the mixture with a template RFU of 784. Contributor two comprised 42% of the mixture with a template RFU of 563. Reed examined the deconvolution report and visually excluded Keith Caneiro, Jennifer Caneiro and [redacted] from both the contributor one and contributor two spots. She then ran comparisons for [redacted] and the defendant.

The STRmix likelihood ratio reports that were subsequently generated reflected a likelihood ratio of 49 billion supporting inclusion for defendant in the contributor one spot, and a likelihood ratio of 19 quadrillion supporting inclusion for [redacted] in the contributor two spot. (T4:88-12 to 91-18).

In court, the defense ran a comparison of Keith Caneiro's DNA profile to the mixture. The output reflected a likelihood ratio supporting inclusion for Keith in the contributor two spot. The question became: why would STRmix reflect inclusionary support for Keith when he was visually excluded from both the contributor one and two spots. The answer soon became clear. It was not an error of STRmix but rather a human error on Reed's part. Reed explained, and clearly demonstrated, that Keith should not have been visually excluded from the contributor two spot. Thus, had she run a comparison of Keith's profile at the time, the likelihood ratio would have reflected inclusionary support as was demonstrated in court by the defense. (T5:20-17 to 67-5).

Significantly, inclusion of the defendant in the contributor one spot remained unchanged. (T5:66-18 to 67-6; 115-22 to 119-6). What's more, upon Dr. Buckleton's review of the sample, he concluded that the only two contributors who could be in the two-person mixture together were Paul and [redacted] (T7:21-17 to 21-24). Although both he and Reed acknowledged that if the sample were run as a three-person mixture there could be support for all three contributors being in the mixture together, Reed stood by her call as to the number of contributors being two; Dr. Buckleton agreed that the sample consisted of two contributors.

(T7:78-1 to 78-5).

New Jersey State Police

In addition to the aforementioned evidentiary samples for which Bode performed DNA analysis, two additional evidentiary DNA samples were submitted to the New Jersey State Police DNA laboratory for DNA analysis. They were assigned to DNA analyst Christine Schlenker. The results of Schlenker's DNA analysis are summarized as follows:

1. **6-1-4-1 Jeans, staining front right shin[8].**

   NOC: two. Contributors 1 and 2 are suitable for comparison.

   - Contributor 1: Unknown male A, 93.82, 1569 RFU
   - Contributor 2: Unknown, 6.18%, 103 RFU

(T9:79-20 to 81-20; 84-2 to 84-5). Schlenker testified that when she ran this sample through STRmix, she ran a simultaneous comparison to the defendant's profile. (T9:80-12 to 80-19). The STRmix output report reflected that the defendant was placed into the contributor two spot, but nonetheless a likelihood ratio strongly supporting exclusion was generated.[9] (T9:81-21 to 82-16).

Schlenker further testified that per the lab's protocol,

[8] These are the same jeans that were submitted to Bode and reflected in Bode samples E01a, E01b and E01c.

[9] Anytime a comparison is run, the reference sample will be placed into a "contributor spot" regardless of whether there is inclusionary or exclusionary support for that contributor. STRmix places the contributor into the spot in which it best fits.

when there is a deconvoluted profile with data at seven or more locations, a visual comparison can be done with a reference sample. If the reference sample cannot be visually excluded, then the lab can issue an RMP without running a comparison through STRmix. (T9: 71-12 to 79-15; 83-2 to 83-6). That is what Schenkler did with regard to contributor one.

Specifically, when examining the deconvoluted profile of contributor one, Schlenker observed that there were results at 7 or more locations. (T9:82-17 to 83-8). She then conducted a visual comparison of contributor one's profile to the reference profile of [redacted]. (T9:84-5 to 84-7; 84-13 to 84-13 to 84-17; 85-6 to 85-7). [redacted] could not be visually excluded. (T9:84-4 to 84-7; 84-18). As such, Schlenker calculated an RMP. The RMP was one in 2.73 septillion, exceeding the source attribution threshold of one in eight trillion, which led to [redacted] being identified as the source of the profile for contributor one. (T9:84-5 to 84-7; 85-6 to 85-10).

Schlenker testified that she ran comparisons of the remaining reference profiles ([redacted], Keith Caneiro, Jennifer Caneiro and Sean Edson) through STRmix. (T9:85-11 to 21). STRmix placed each of the above reference profiles into the contributor two spot, but ultimately generated likelihood ratios supporting exclusion for Keith, Jennifer and Sean, and an uninformative likelihood ratio for [redacted]. (T9:87-2 to 89-15).

(T9:70-24 to 71-21).

2. **41-1-1 Inside collar scraping of long sleeved shirt.**

NOC: two. Contributors 1 and 2 are suitable for comparison.

- Contributor 1: Paul Caneiro, 79.62%, 343 RFU
- Contributor 2: Unknown, 20.38%, 88 RFU

(T9:89-16 to 89-20; 91-8 to 91-10; 91-11 to 92-24). Schlenker testified that when she input sample 41-1-1 to STRmix, she also ran a simultaneous comparison to the defendant's profile. (T9:92-10 to 92-12). The STRmix output report reflected that the defendant was placed into the contributor one spot (t9:92-10 to 92-11) and that a likelihood ratio of 110 million supporting inclusion was calculated. (T9:93-11 to 93-18).

Schlenker testified that she ran comparisons of the remaining reference profiles (Jennifer, [redacted], [redacted], Keith and Sean) through STRmix, and that each was placed into the contributor two spot. (T9:93-22 to 95-25; 94-23 to 95-2). Once again, likelihood ratios supporting exclusion were generated for Keith, Jennifer and Sean; and an uninformative likelihood ratio was generated for [redacted]. (T9:95-13 to 97-14).

2. Relatedness

Defendant claims that the samples for which STRmix was utilized are not reliable because they include relatives, and neither Bode nor the New Jersey State Police lab included studies on relatives in their internal validations. While the defendant appears, in his brief, to apply this argument to all of the State's evidentiary DNA samples, it is noteworthy that during the

hearing, the defendant's DNA experts did not have an issue with the evidentiary samples that were robust. In fact, Dr. Reich agreed that the robust samples were reliable. (T13:50-20 to 63-10; 67-1 to 67-20; 79-8 to 80-22; 81-3 to 90-9). Nonetheless, the State submits that defendant's argument is without merit.

The State recognizes that allele sharing, which occurs more frequently among family members, can be challenging in terms of DNA analysis. (T6:84-12). However, allele sharing among related individuals is not novel to STRmix. Rather, "this is a 'genetics' issue[.]" See S-186 at 11. Moreover, although allele sharing among certain types of related individuals can cause underestimation of the number of contributors to a mixture, (t6:84-12), which can lead to a false exclusion, (t7:164-9 to 165-14), the State emphasizes that none of the evidentiary samples in this case involve those types of challenging mixtures.

Dr. Buckleton identified "certain mixtures of relatives" which cause problems: triads. (T6:84-12 to 84-14; 90-21 to 90-22). Triads are comprised of either "two parents and a child, two children and a parent, or three siblings." See S-128 at 4, 25. The issue with triads is that they can appear to be two-person mixtures when, in reality, they consist of three donors. (T6:91-12 to 91-15). On the other hand, dyads, "mixtures of two close relatives[,]" do not present problems. See S-128 at 25.

In the present case, none of the evidentiary samples constitute triads. In fact, most are two-person mixtures of a biological uncle and niece. In many, if not all of the samples where there is inclusionary support for the defendant and [redacted]

each being in the mixtures individually, there is also inclusionary support for the two of them being in the mixtures together. In some of those samples, the remaining family members were even able to be visually excluded.

In sample E03b, a two-person mixture, none of the family members could be visually excluded. However, when run through STRmix, the only two family members who were assigned likelihood ratios with inclusionary support were the defendant and [redacted]; the remaining family members were assigned exclusionary likelihood ratios.

Sample E07a constituted a two-person mixture where none of the family members could be visually excluded. When run through STRmix, likelihood ratios supporting inclusion were assigned to all of the family members. However, when run in pairs, the only two contributors that could be in E07a together were the defendant and [redacted].

Although the defendant attempted to discredit Reed's analysis with regard to her call on the number of contributors for certain samples such as E06b and E07a, essentially claiming that the samples could have contained a third donor, there was absolutely no evidence supporting that proposition. However, even if Reed did underestimate the number of contributors, and one of the other family members (Keith, Jennifer or [redacted] was also in the mixture, said mixtures would still not constitute the problematic triad because the defendant and [redacted] are not siblings or parent/child. Moreover, a third contributor would not negate the defendant's presence in the mixture.

Finally, the State submits that the Court need look no further than to the testimony of the trained and seasoned DNA analysts, who implemented STRmix in each of their respective laboratories, to be satisfied that STRmix works reliably. Monica Ghannam testified that her level of satisfaction with all three versions of STRmix she implemented and utilized since 2017 at UCPO lab is "very high." She summarized her confidence in STRmix by highlighting its transparency and ability to be checked:

> [A]ll of the information that is used to generate that likelihood ratio is available to us in those STRmix reports. And an analyst can go back and evaluate it for themselves to make sure that what we expect, if we did have any expectations about a profile, we can see how STRmix evaluated it. And it's all open to us. There's no hidden information, if you will, that an analyst would need to truly evaluate a sample.

(T1:109-8 to 109-24). Similarly, Jennifer Thayer testified that she has been satisfied with the work product generated from the use of STRmix at the NJSP lab, and that STRmix has increased the lab's ability to interpret complex mixtures. (T9:15-14 to 15-24). Kristen Naughton also testified that, based on her training and experience, she found STRmix to be accurate, reliable and well-suited for its use at Bode. Based on the foregoing testimony of the individuals who actually utilize STRmix in real-life casework on a daily basis, the State respectfully submits that this Court can be satisfied that STRmix is reliable, and was reliably applied in the present case.

Based upon the testimony, exhibits and the governing law, the State submits that, under the Olenowski I/Daubert standard,

it has met its burden of showing that STRmix is reliable and was used reliably in this case. Thus, for the foregoing reasons and authorities cited in support thereof, the State respectfully requests that the DNA evidence be admitted at trial.

Respectfully submitted,

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