



Summer Newsletter

Better Justice Through Better Science™

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Cybergenetics News

Twenty-five years of forensic innovation

Twenty-five years ago, Cybergenetics revolutionized forensic DNA science. Crime laboratories were putting out highly informative evidence data, but couldn't interpret much of what they saw. Mixtures of several people, small amounts of DNA, and other complex data were left unreported. So science left justice without forensic facts.

TrueAllele® technology changed all that. Using Bayesian probability modeling, a computer could explain complex DNA data, instead of discarding it. Cybergenetics and others validated the technology, establishing TrueAllele accuracy. Automated interpretation of DNA evidence freed analysts from the burden of tedious subjective data decisions.

In August, Cybergenetics Chief Scientist Dr. Mark Perlin [lectured at the University of Cape Town \(UCT\)](#). He discussed the ideas behind the TrueAllele revolution. The system is driven by data, and modeled by mathematics, to find the right scientific answer. Cybergenetics was the first to invent accurate probabilistic genotyping, the first to validate, and the first to bring this powerful science into a courtroom.

TrueAllele can help Africa



- Informative**
 - Accurate
 - Unbiased
- Automated**
 - Few analysts
 - Large population
- Effective**
 - Solve crime
 - Prevent rape

How does TrueAllele work? How is it tested? How do experts explain its results in court? What impact has the innovation had on criminal prosecution and defense, exonerating innocent people, and mass disasters? Why do limited data-discarding alternatives fail? Why do courts

accept TrueAllele as reliable evidence?

The answers show why TrueAllele is the only real option for helping Africa. Its informative DNA results are accurate and unbiased. With true automation, just a few analysts can serve a large population. Effective DNA mixture technology can solve crime and help prevent rape. This [fifty-minute UCT talk](#) explains the TrueAllele solution.

Cape Town Talk

[New Indiana Innocence Project honors Cybergenetics](#)

A new state-wide Indiana innocence project was launched in Indianapolis on August 17. Cybergenetics Dr. Mark Perlin was there to accept the *INIP Hero 2024* award from the Indiana Innocence Project (INIP).



INIP Director Frances Watson and INIP Board Member Roosevelt Glenn made award presentations. They spoke about the Glenn and Darryl Pinkins exonerations, and the role of Cybergenetics TrueAllele Technology. After a combined [40 years in prison](#) for a crime they did not commit, Cybergenetics *pro bono* advanced TrueAllele science [reexamined old DNA evidence](#) and set them free.

INIP's Hero awards recognized [CBS 48 Hours](#) Producer Judy Rybak and Dr. Perlin as "the catalysts and examples of the need to raise awareness and dollars to tackle [innocence] cases." Rybak and Perlin are part of what INIP

calls "historical heroes" of the Indiana Innocence Project. Watson and Glenn gave the *Glenn & Pinkins Award of Honor* to the Herbert Simon Family Foundation, which funded the INIP launch. Twenty exonerees lined up in front of the Dallara IndyCar Factory stage. Glenn celebrated his move "from the penitentiary to the boardroom."

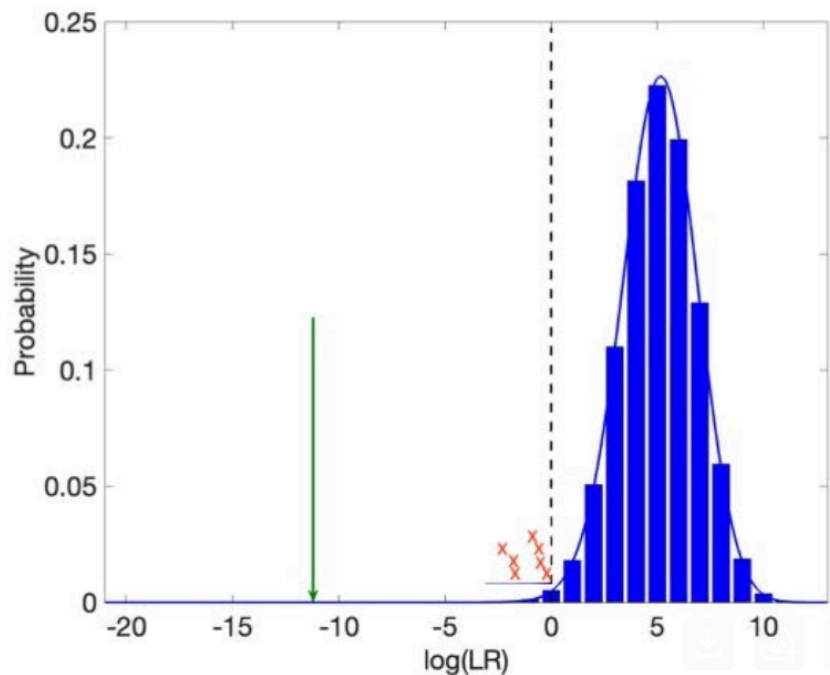
Innocence Talk

TrueAllele Court Acceptance

US v. Mills – The government argues against science

Scientists seek truth, advocates argue. In a recent federal case, an assistant US attorney (AUSA) attempted to undermine validated TrueAllele science. His Daubert motion mistakenly claimed that the computer too often excludes criminals. His argument ignored DNA science. A likelihood ratio (LR) match statistic's magnitude matters, and bigger numbers have lower error rates. The AUSA presented irrelevant weak match statistics from a [validation study](#), discounting the strong exclusionary match statistic in the case.

The following figure from a [Cybergenetics MAAFS conference presentation](#) shows the trial lawyer's error. The x-axis scales DNA match statistics logarithmically; a strong inclusionary LR stat of ten billion is at +10, while a strong exclusionary one over ten billion is at -10. The blue bell curve centered around +5 gives expected inclusionary match statistics for the true person who left his DNA on the firearm. The green arrow shows the defendant's exclusionary DNA stat of -10, far to the left of the actual perpetrator's blue bell stats. The AUSA argued that the red cross values near 0 were somehow relevant. The figure shows this was wrong.



Cybergenetics Dr. Mark Perlin prepared [a thorough response](#) that fully rebutted the lawyer's unfounded argument. "The Court *denied the government's motion* to preclude the evidence," finding [TrueAllele to be admissible](#) under the Daubert reliability standard. "The Court exercised its discretion *not to hold an evidentiary hearing*." The science was clear.

Expert Declaration

[US v. Anderson – A defendant argues against science](#)

In a Central Pennsylvania Daubert hearing in federal court, a defender brought in experts and arguments but couldn't keep out the TrueAllele computer results. The state crime laboratory found "no interpretable results due to the complexity of the mixtures." But TrueAllele's math can look more deeply into the DNA data to find the right answer. Cybergenetics' computers easily solved the four-person mixture. A DNA match statistic of over a trillion connected the defendant to the weapon.

The defense argued about computer source code. They argued about scientific reliability. They refused to test the TrueAllele software Cybergenetics provided on DNA data. Scientists test, advocates argue. Dr. Mark Perlin testified at a Daubert hearing in December 2022 about the TrueAllele testing. In April 2023 [the court wrote](#), "TrueAllele has been tested and validated, subjected to peer review, and broadly accepted in the field of

forensic science,” finding it to be admissible. This year the defendant accepted a plea agreement.

IV. CONCLUSION

Weighing the evidence presented against the relevant *Daubert* reliability factors, the Court finds TrueAllele's DNA identification methodology and the match statistic reported in this case sufficiently reliable to warrant admission. Anderson will be permitted to contest this evidence at trial through cross examination and the testimony of rebuttal witnesses; he cannot, however, keep the evidence from the jury. The *Daubert* motion is denied.

Daubert Decision

Ohio v. Carter – TrueAllele meets *Daubert* reliability standard

Cybergenetics analyst William Allan testified about TrueAllele’s scientific reliability in a Cleveland, Ohio Daubert hearing in March 2024. Allan spoke about validation studies that have tested TrueAllele reliability, known error rates, peer review publication, and the technology’s general acceptance in forensic science. In May 2024, [Judge Burnside denied](#) the “Defendant’s motions *in limine* to prohibit the admission of any TrueAllele evidence.”

50. The Court finds that testimony regarding TrueAllele analyses is based on reliable scientific, technical or other specialized information. Evid. R. 702(3). TrueAllele is derived from well-established mathematical principles and is objectively verifiable, as evident in the multiple validation studies conducted on TrueAllele. TrueAllele was observed to yield an accurate result. The program was observed to have very low error rates on both single source and mixture DNA. The error rates remained low even when the number of DNA contributors increased.

51. The Court finds that TrueAllele has been extensively tested. The State presented the Court with eight published validation studies as well as over thirty additional unpublished internal validation studies in which TrueAllele was tested on both single source and mixture DNA. The validation studies included analysis of DNA mixtures of up to ten contributors. The validation studies also tested TrueAllele using low template DNA. TrueAllele was

Daubert Decision

DNA Data Delivers Justice

Ohio v. Myers – Ignoring data could not stop exoneration



The crime was horrific – a railroad spike murder near an abandoned railroad track in Xenia, Ohio. But was the death-row defendant's DNA on the spike? If not, could that forensic fact have changed the verdict? The judge held a post-conviction hearing to decide.

The crime lab had found the DNA data to be uninterpretable, reporting "Due to the limited data obtained, no conclusions can be made on the minor alleles." But using all the data, TrueAllele forged ahead to statistically exclude the defendant with a "one over a billion billion" match statistic. Creatively, the prosecutor argued that since old, failed ways of looking at DNA data don't work, the data itself must be unreliable. No new science allowed. [The judge did not agree](#) with this specious reasoning. He wrote:

"Herein lies the crux of this case: is one DNA method reliable enough to undermine another? More specifically, is the Defendant's newly discovered DNA evidence -- which purportedly excludes the Defendant's presence at the crime scene - sufficiently reliable to undermine the integrity of the trial verdict? The short answer is "yes." Advances in DNA technology over more than 25 years are unrefuted."

"The newly discovered evidence [gives] a strong probability that the jury would have reached a different verdict had the new evidence been available at trial. The new [TrueAllele] evidence clearly supports the

Defendant's trial defense that another male committed the offense, and that the Defendant was not present. The DNA evidence makes this defense exponentially more credible. The Defendant's motion for a [new trial must be granted](#)."

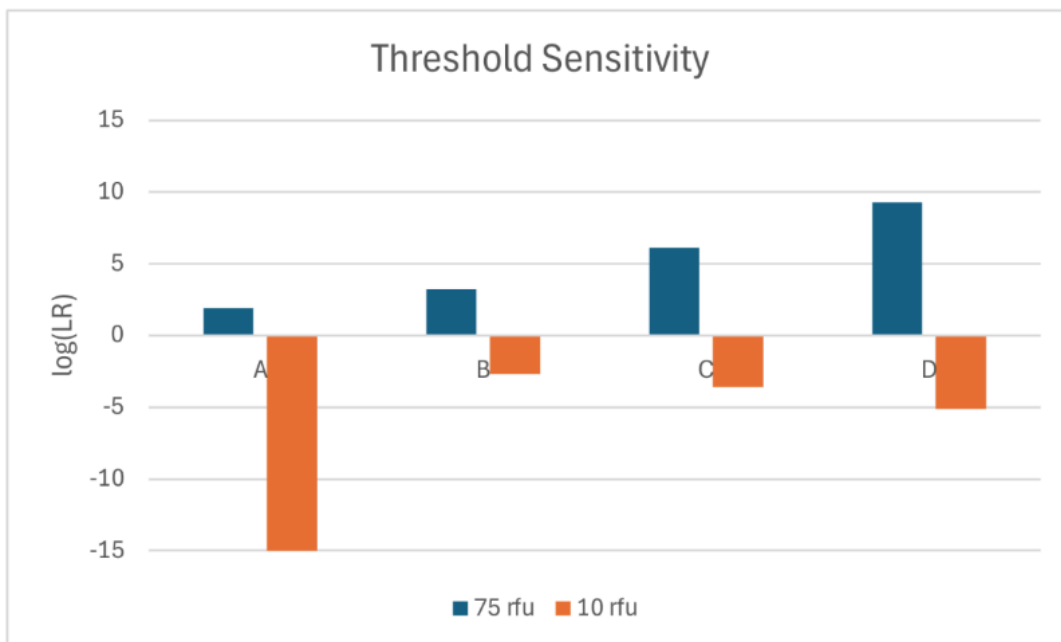
Grant of New Trial

TrueAllele v. Other Software – Choosing data changes answer

Suppose a lawyer could pick a DNA match answer to support their case. Need to convict? Have your expert choose their lab data in a way that gives a large inclusionary match statistic. Need to acquit? Have them select data differently to report a small exclusionary match statistic. Same data, different answers.

Other software can do this. In [New York v. Hillary](#), a higher 50 rfu threshold discarded low-level DNA data, leading STRmix™ software to statistically include the defendant. But a slightly lower 30 rfu threshold retained potentially exculpatory data to statistically exclude him. Fortunately, Cybergenetics assisted Legal Aid *pro bono* in explaining the science to the judge, and helped acquit an innocent man.

In a June *Journal of Forensic Sciences* paper "[A Tale of Two Systems](#)," Dr. Susan Greenspoon and her colleagues at Virginia's Department of Forensic Sciences compared two probabilistic genotyping (PG) systems. Cybergenetics TrueAllele has Bayesian math that uses all the DNA data, without data thresholds or choices, giving reproducible answers. But other software is sensitive to data input. For example, STRmix depends on thresholds and other choices for input. Human data choices can change its LR match statistic.



The above bar chart (adapted from the paper's Figure 4 underlying data) shows inclusionary STRmix match statistics at a higher 75 rfu threshold with less DNA input (blue). But when STRmix sees more data at a lower 10 rfu cutoff (orange), the log(LR) stat flips and turns exclusionary. These DNA mixtures contained 2 to 4 contributors, including a highly degraded item with only partial data. Human review and TrueAllele gave exclusionary results for the item, based on the observed evidence. STRmix gave conflicting answers, depending on the user's input data choices.

JFS Article

Solving Cold Cases

*Wisconsin v. Doxtator – TrueAllele helps solve
1963 cold case*



On a black night in June 1963, a white car pulled up to an Enco gas station along an old Wisconsin highway. Oshkosh station owner Wayne Pratt went over to help. The station lights were out. Pratt's wife found his dead body under a blanket, stabbed over 50 times.

The case went cold. There was no physical evidence or eyewitness. Investigators questioned 75 people and administered 25 lie detector tests.

The case reopened in 2012. DNA testing of old items by the local crime lab was inconclusive. In 2015 and 2023, a private forensic lab retested the items. The degraded low-level DNA was a mixture of different people. Too complex to interpret, the testing was again inconclusive.

In April 2024, Cybergene received the lab's DNA data from the blanket. Unlike less capable forensic software, the company's powerful TrueAllele technology could handle all the evidence data. TrueAllele computing easily unmixed the degraded low-level three-person mixture into three evidence genotypes.

[TrueAllele made the DNA identification](#). Comparing the blanket's evidence genotypes with DNA from suspects, the computer found an answer. Cybergene's June report statistically connected deceased suspect William Doxtator to the blanket. Sixty years after the murder, [TrueAllele helped close the unsolvable DNA case](#).

Forensic Magazine

[Pennsylvania v. Schuback – TrueAllele aids murder conviction](#)



In January 2017, Pennsylvania man Robert Baron was reported missing. Six years later, his remains were found. Based on evidence from a car, police suspected Justin Schuback. Could DNA show whether Schuback had been inside the car?

The state lab tested DNA from the car's steering wheel and an inner door handle. But there was too little DNA for the lab to interpret. Cybergenetics was contacted to conduct a more intensive computer review of the lab's DNA data using their accurate and objective TrueAllele technology. TrueAllele's math used all the data.

TrueAllele [statistically connected Schuback](#) to the car through shared DNA. In May, Cybergenetics William Allan testified at the Lackawanna County trial. The jury found Justin Schuback [guilty of first-degree murder](#), robbery, and burglary. These charges carry an automatic life sentence. TrueAllele intervention helped close the cold case.

[Trial Page](#)

Conferences



Cybergenetics speaks with hundreds of crime investigators at conferences, conventions, and trade shows about how TrueAllele technology and services can help them solve their toughest cases.

SEPTEMBER

- *Arizona Homicide Investigators Association (AHIA)*
 - Location: Phoenix, AZ
 - Dates: September 9-12
- *International Symposium on Human Identification (ISHI)*
 - Location: San Antonio, TX
 - Dates: September 23-26
 - Poster Presentations:
 - [Getting more from less: low-level DNA mixtures on cartridges](#)
 - [Defeating opposition experts using science in a recent case example](#)
 - [Different TrueAllele users, same DNA answer: a multi-center proficiency study](#)

OCTOBER

- *Illinois Homicide Investigators Association (ILHIA)*
 - Location: Itasca, IL
 - Dates: October 15-17
- *Regional Organized Crime Information Center (ROCIC)*
 - Location: Hilton Head Island, SC
 - Dates: October 27-30

Stop by our trade booth to learn how TrueAllele technology can help you solve your most complex DNA cases.

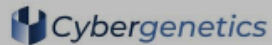
Free Screening

Data-driven DNA forensic science: TrueAllele® computation

Computational Forensics
University of Cape Town South Africa



Mark W Perlin, PhD, MD, PhD
Pittsburgh, PA USA



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This talk shows the ideas behind the TrueAllele revolution. The system is driven by data, and modeled by mathematics, to find the right scientific answer. Cybergenetics was the first to invent accurate probabilistic genotyping, the first to validate, and the first to bring this powerful science into a courtroom.



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Free TrueAllele Screening

Contact Cybergenetics today, making the impossible routine™



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