**How Courts Understand
DNA Evidence**

**Cyril H. Wecht Institute of Forensic Science and Law
Annual Symposium: Topics for the 21st Century
Pittsburgh, Pennsylvania
October 2025**

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

Cybergenetics

Cybergenetics © 2003-2025

DUQUESNE UNIVERSITY

I. Science v. Law

DNA evidence
    PCR technology
    STR data

Simple DNA (one person), simple interpretation
Complex DNA (mixtures), complex interpretation

DNA match statistics
    CPI - simplify data (threshold to qualitative)
    TA/LR - explain data (account for quantitative)
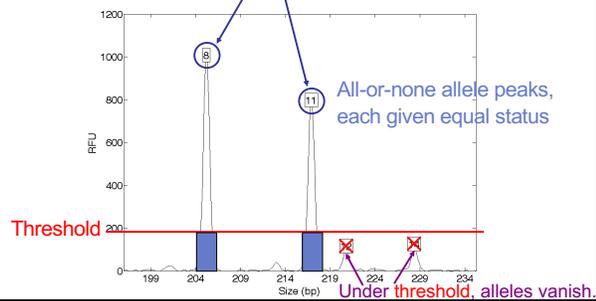
September 2025 – Three Cases

Threshold: simplify the data

Over threshold, peaks are labeled as allele events

All-or-none allele peaks,
each given equal status

Threshold

Under threshold, alleles vanish.

TrueAllele: explain the data

Account for quantitative data

One person's allele pair

Explain the peak pattern

Better explanation has a higher likelihood

Another person's allele pair

(chart: RFU vs Size (bp), peaks labeled 8, 11, 12, 14; x-axis: 199, 204, 209, 214, 219, 224, 229, 234; y-axis: 0, 200, 400, 600, 800, 1000, 1200)
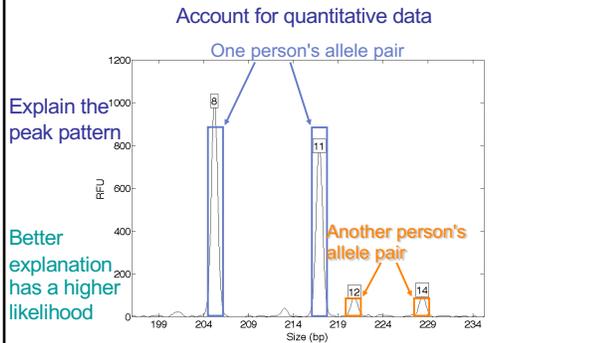
II. Pennsylvania v. Ralph Skundrich

What is a DNA match statistic?

CYRIL H. WECHT, M.D., J.D., CORONER
ALLEGHENY COUNTY CORONER'S OFFICE
DIVISION OF LABORATORIES
FORENSIC SCIENCE SECTION REPORT

2002. Sexual assault of college student
   DNA mixtures: t-shirt and jeans
2011. County lab generated DNA data
   Combined probability of inclusion (CPI)
2013. TrueAllele® likelihood ratio (LR)
2014. Trial testimony – DNA match statistics
   Sentence: 75-150 years

2023: PCRA Petition

Post-Conviction Relief Act

Ineffective assistance of counsel
   Crime lab (CPI): 100,000's (5 zeros)
   Cybergenetics (TA): quadrillions (15 zeros)

Argument: Counsel didn't question TrueAllele reliability nor request its source code

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2023: Appellate Court

Reversed. Arguable merit?

"The TrueAllele DNA match was evidence of a completely different magnitude." – Appellate Ruling

15 zeros - 5 zeros
= **10 orders of magnitude**
= **10 billion ratio**

What is going on?
How is that possible?

Five Rocks

Orange Rock
1¢

Blue Rock
1¢

Green Rock
1¢

White Rock
1¢

Pink Rock
1¢

Count = 5
Value = 5¢

Five Rings

Ring 2
$10,000

Ring 1
$5,000

Ring 3
$15,000

Ring 4
$25,000

Ring 5
$10,000

Count = 5
Value = $65,000

Five Relics

Koh-i-Noor
$500 million

Hope Diamond
$350 million
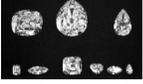
Cullian Diamond
$400 million

De Beers Centenary
$100 million

The Pink Star Diamond
$71.5 million

Count = 5
Value = $1.3 billion

Rocks v. Relics

Count: 5 every time
Same rock statistic

Value: billion dollars / 10 cents

11 zeros - 1 zero (¢)
= **10 orders of magnitude**
= 10 billion ratio

Different rock statistics
Forensic DNA needs **probative value**, **not counts**

TrueAllele prediction rule

An Information Gap in DNA Evidence Interpretation

Mark W. Perlin[1]*, Alexander Sinelnikov[2]   PLoS one 2009

Slide 1

JOURNAL OF **FORENSIC SCIENCES**

PAPER

J Forensic Sci, November 2011, Vol. 56, No. 6
doi: 10.1111/j.1556-4029.2011.01859.x
Available online at: onlinelibrary.wiley.com

CRIMINALISTICS

Mark W. Perlin,[1] M.D., Ph.D.; Matthew M. Legler,[1] B.S.; Cara E. Spencer,[1] M.S.; Jessica L. Smith,[1] M.S.; William P. Allan,[1] M.S.; Jamie L. Belrose,[2] M.S.; and Barry W. Duceman,[3] Ph.D.
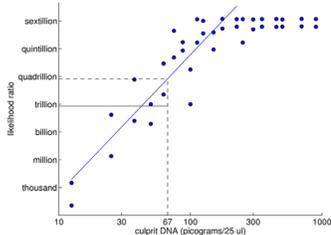
Validating TrueAllele® DNA Mixture Interpretation*,†

Slide 2

JOURNAL OF **FORENSIC SCIENCES**

PAPER

J Forensic Sci, November 2013, Vol. 58, No. 6
doi: 10.1111/1556-4029.12223
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New York State TrueAllele® Casework Validation Study*

Slide 3

CPI counts inclusion tests

Confused courts for 20 years on countless DNA mixtures

J Pathol Inform

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Research Article

Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information

Mark William Perlin[1]

[1]Cybergenetics, Pittsburgh, USA

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Science answers the court

Why was "The TrueAllele DNA match evidence
of a completely different magnitude"?

Because the lab's CPI and TrueAllele measure entirely
different things – **count v. value**

Value matters – *how much* identification information
is the probative reliable match statistic.

Count does not. *How many* tests were done is
incidental, a nonprobative unreliable match statistic.

Opening the door to the past

Court is concerned about unreliable DNA match statistics

Thus, all the state's past CPI crime lab cases –
incorrect & inconclusive – must be reopened & corrected.

TrueAllele automation can help audit and remedy
these past DNA evidence interpretation failures.

Cybergenetics

JUSTICE
THROUGH
SCIENCE

III. Maryland v. Darius Williams

When is a DNA match statistic reliable?

2020. Fatal stabbing
        DNA mixtures: victim fingernails
2021. Baltimore lab reported DNA result
        TrueAllele® likelihood ratio (LR)
2025. *Daubert* hearing
        Judge admitted TrueAllele

Match statistic result

Baltimore lab's TrueAllele analysis

Template	MW	logLR	DNA (pg)
3 ng	8%	8.62	240

419 million

Argument: TrueAllele results "out of scope"
10:1:1 3-person mixture (in case) not done
NIST Report 2024 "Factor space"

TrueAllele reliability

Validation studies
8 peer-reviewed publications
• up to 10-person mixtures
• down to under 1% contributor
36 additional laboratory studies

Admissibility rulings
51 US challenges – 49 wins
Frye, *Daubert*, *Spencer*, etc.

Forensic DNA standards

Standards Groups
SWGDAM (FBI), ASB (AAFS)

Probabilistic genotyping (PG)
Reliability based on scientific testing

Additive
• 10 validation axes
• 10 axis gradations
→ 10 + 10 + ... + 10 = 10x10
= 100 experiments

Compliance based on testing axes
under similar conditions

TrueAllele Studies and SWGDAM Guidelines

Guideline	Description	Study
3.2.1, 4.1.13	Sensitivity	4, 5, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43
3.2.1.1	Type I errors (False exclusions)	16, 21, 22, 23, 24, 27, 28, 32, 34, 36, 37, 39, 40, 42, 43
3.2.1.2	Sensitivity range of LR values expected for contributors	4, 5, 7, 8, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 31, 32, 33, 34, 35, 36, 37, 39, 40, 43
3.2.2, 4.1.13	Specificity	7, 8, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 43
3.2.2.1	Type II errors (False inclusions)	16, 18, 19, 20, 21, 22, 23, 24, 27, 28, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 43
3.2.2.2	Specificity range of LR values expected for non-contributors	12, 15, 16, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 31, 32, 33, 34, 35, 36, 37, 39, 40, 43
3.2.3, 4.1.13	Precision	2, 5, 7, 8, 9, 11, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 31, 32, 33, 34, 35, 36, 37, 39, 40, 43
3.2.3.1	Range of LR values expected between multiple analyses (σ_w)	5, 7, 8, 13, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 27, 28, 31, 32, 33, 34, 35, 36, 37, 39, 40, 43
3.2.3.2	Reducing the variability of LR variation (e.g., increasing MCMC iterations)	15, 16, 18, 28, 29, 31, 33, 34, 37, 39, 42
3.2.4, 3.2.4.1, 4.1.1	Case-type samples (reliable evaluation)	5, 6, 7, 9, 10, 13, 17, 19, 25, 27, 31, 33, 37, 38, 40, 43
3.2.5	Control samples	1, 9, 25
3.2.6	Accuracy	2, 4, 5, 6, 8, 9, 13, 15, 17, 19, 21, 24, 26, 27, 29, 31, 34, 35, 38, 39, 40, 43
3.2.6.1, 4.2	Comparison with manual review	1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 19, 25, 29, 31, 33, 35
3.2.6.2	Comparison of allele calling of raw data (.fsa) files	1, 17
4.1	Data from kits, instruments, and analysis software used in casework	1, 3, 4, 5, 7, 8, 9, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 43
4.1.1	Known contributor samples	4, 8, 9, 12, 14, 15, 16, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43
4.1.2, 4.1.2.1	Hypothesis testing with contributors and non-contributors	4, 6, 9, 11, 12, 13, 17, 18, 19, 25, 26, 28, 29, 31, 32, 37, 38, 39, 40, 42, 43
4.1.3	Variable DNA typing conditions	9, 16, 18, 19, 22, 24, 28, 31, 32, 36, 37, 40, 43
4.1.4	Allelic peak height	3, 9, 16, 18, 19, 22, 24, 28, 30

NIST Report 2024

"Factor space"

Multiplicative
- 10 validation axes
- 10 axis gradations
- $\rightarrow$ 10 x 10 x ... x 10 = 10^{10}
  = 10 billion experiments

Anticipate every possible evidence item

Not done in science

Impossible to do (centuries of testing, $billion)
Unnecessary (bracket by easier & harder items)
19 scientists objected to NIST; 0 agreed
No standards follow this unworkable suggestion

Comments on NIST Report NISTIR 8351-DRAFT
"DNA Mixture Interpretation: *A NIST Scientific Foundation Review*"
https://doi.org/10.6028/NIST.IR.8351-draft

Mark W. Perlin, PhD, MD, PhD
Cybergenetics, Pittsburgh, PA
August 9, 2021

Introduction

I invented reliable genotyping of mixed or low-level deoxyribonucleic acid (DNA) evidence over twenty years ago [1]. My computer-based "probabilistic" genotyping (PG) approach has been widely adopted and tested by the forensic science community. Unlike ineffective human-based "deterministic" mixture interpretation methods, Cybergenetics' TrueAllele® PG system is accurate, objective, impartial, validated, reproducible, sensitive, specific, automated, and thorough. TrueAllele computing can use all short tandem repeat (STR) data, and consider all genotype combinations to explain the data, statistically accounting for polymerase chain reaction (PCR) amplification variation and artifacts.

Report on *Williams* Motion to Exclude

Mark W. Perlin, PhD, MD, PhD
Chief Scientist and Executive
Cybergenetics, Pittsburgh, PA
September 26, 2025

Re: *Daubert* Motion to Exclude TrueAllele in *State of Maryland v. Darius Williams*

Expert qualifications

I hold degrees in Chemistry (BA), Mathematics (PhD), Medicine (MD) and Computer Science (PhD). I was senior research faculty in Computer Science at Carnegie Mellon University. I have led successful and novel bioinformation automation projects, such as building the first DNA contig map of human chromosome 11 at a hundredth of the cost of competing groups. I founded Cybergenetics (Pittsburgh, PA) in 1994 to commercialize my bioinformation inventions. I have testified in court about 100 times.

My 22-page Curriculum Vitae is attached (Attachment A). Also attached is a Declaration I wrote describing the scientific reliability and judicial acceptance of Cybergenetics' TrueAllele® technology for accurate computer interpretation of complex DNA evidence (Attachment B).

From my Comments & Report

An analogy may help. Is a particular car make and model reliable? The manufacturer extensively tests the car before making it available for sale. Independent testing groups (e.g., Consumer Reports) release their findings. The consumer tries out the car by driving it. But nowhere does the government require the owner to test out every possible driving condition (road surface, visibility, speed, curves, rain or snow or sunshine, temperature, humidity, number of passengers, age of driver, weight of car, engine RPM, standard or automatic transmission, type of brakes, number of pistons, body composition, rear camera, city vs. country, highway vs. local road, etc., etc., etc.) before letting them take their car on a similar road. That would be ludicrous. As is NIST's resource-intensive "factor space" proposal.

2015 Baltimore TrueAllele validation

Is the case item typical?
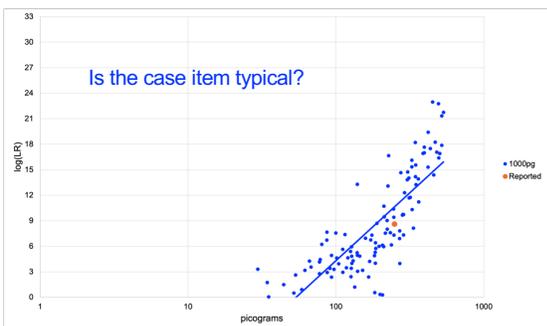
IV. Missouri v. Lance Shockley

Whether to test DNA evidence?

2005. Fatal shooting of police officer
Evidence collected, not tested
2009. Murder trial – jury convicted
Judge imposed death sentence
2025. *Post-conviction* motion
Judge denied DNA testing

PCRA request for DNA testing

10 evidence items

A crime scene cigarette butt
Paper and plastic shotshell wadding
Latent fingerprints
A cell phone

Motion for DNA testing denied

Rejected PCRA theories:
Database, Confession, Redundancy

I. There wasn't "a reasonable probability that the outcome of the trial would have been changed by the discovery of DNA from another person."

II. That "touch DNA analysis was reasonably available to him at the time of trial."

Forensic science disagrees

Four forensic science *amicus curiae* briefs

IN THE COURT OF APPEALS FOR THE SOUTHERN DISTRICT OF MISSOURI
STATE OF MISSOURI

STATE OF MISSOURI,	)	
Appellee,	)	
	)	
v.	)	SD39099
	)	
LANCE C. SHOCKLEY,	)	
	)	
Appellant.	)	

AFFIDAVIT OF DR. MARK W. PERLIN

I, the undersigned individual, being duly sworn and under oath, depose and state as follows:

My name is Mark Perlin and I am over twenty-one years of age, of sound mind and body, and am capable of making the statements contained in this Affidavit as I have personal knowledge of the matters set forth herein:

Forensic Magazine article

Forensic
On the Scene and In the Lab

NEWS   ARTICLES   SUPPLIERS GUIDE   DNA HUB   RESOURCES   WEBINARS   EVENTS

🏠 > All News > DNA Matters: Lance Shockley Set to Die

DNA Matters: Lance Shockley Set to Die

October 08, 2025 | Mark Perlin, M.D., Ph.D. Chief Scientist and Executive

DNA Matters

*Editor's Update: Lance Shockley
on Tuesday, Oct. 14, 2025, follow
prison in Bonne Terre.*

On Oct. 14, 2025, Missouri is set
lethal injection. The circumstanti
comprehensive DNA testing was
decided that it never will be.

In 2005, Sergeant Carl Graham w

The article begins …

"On October 14, 2025, Missouri is set to execute Lance Shockley by lethal injection. The circumstantial evidence is compelling, but comprehensive DNA testing wasn't done—and the courts have decided that it never will be."

Point I response

Why new DNA evidence could have changed the trial outcome

DNA changes case outcomes
        For prosecutors and for defenders

Pennsylvania v. Joshua Huber

Texas v. Lydell Grant
        Database search identified Jermarico Carter
        Confessed when confronted with DNA evidence

Indiana v. Darryl Pinkins and Roosevelt Glenn
        Redundancy of three brothers

Point II response

Effective touch DNA analysis was not reasonably available at the time

DNA testing has two parts:

    (i) laboratory data <u>generation</u>

    (ii) subsequent <u>interpretation</u> of the data

    In 2009, TrueAllele was the only effective touch DNA interpretation method

Pennsylvania v. Kevin Foley

FBI Popstats software **CPI**   = **13 thousand**
Cybergenetics **TrueAllele LR** = **189 billion**
Frye hearing, TrueAllele admitted, testimony

First-ever use of effective PG DNA interpretation
• Friday, March 20, 2009, Foley jury convicted in Pennsylvania
• Monday, March 23, 2009, Shockley's trial started in Missouri

Shockley would **not have known** about TrueAllele

The FM article ends …

"DNA matters. Society submits uncertain samples for DNA testing. Computers consider millions of possibilities, weighing probability and deriving scientific truth. The data decides who left their DNA and who did not.

"But there is no uncertainty in the Courts of Missouri. Only one possibility is left. As sure as the sun will set on October 14, pentobarbital will course through Lance Shockley's veins. And as he departs, so too will the vain hope of DNA truth."

DNA testing denied

The Missouri courts have a local rule that allows them to reject any amicus brief. All four DNA briefs were rejected.

Lance Shockley was pronounced dead at 6:13 p.m. on Tuesday, October 14, 2025, following a lethal injection at the state prison in Bonne Terre.

V. Truth v. Justice

"Truth is what a judge decides." – Berkeley Law professor

V. Truth v. Justice

"Truth is what a judge decides." – Berkeley Law professor

No. *Science* is the only effective path to truth.
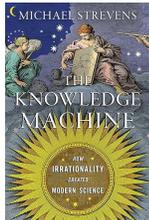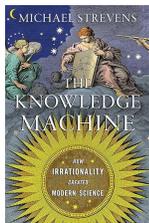
Empirical testing of hypotheses by experiments and data.

V. Truth v. Justice

"Truth is what a judge decides." – Berkeley Law professor

No. *Science* is the only effective path to truth.

Empirical testing of hypotheses by experiments and data.

Justice is the fairness that law can deliver.

Denying science denies justice

More information

http://www.cybgen.com/information

- Courses
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http://www.youtube.com/user/TrueAllele
TrueAllele YouTube channel

Cybergenetics

perlin@cybgen.com

JUSTICE THROUGH SCIENCE