Cybergenetics

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TrueAllele® Investigative Database
DNA Match Report

April 24, 2026

TO: LIEUTENANT
POLICE DEPARTMENT #4
TOWN, STATE ZIP

METHODS:

- The DNA data profiles referenced in this report were previously developed and addressed in documentation issued by LAB.
- The DNA data profiles referenced in this report were previously developed and addressed in documentation issued by the Police Department #4.
- The TrueAllele® Casework system processed each evidence item in independent replicate computer runs to infer possible DNA contributor genotypes from the samples.
- The National Institute of Standards and Technology generated the population allele frequencies.
- The DNA match statistics herein were calculated using VUIer™ version 3.3.8343.1R20b (26-Aug-2022) at a theta value (co-ancestry coefficient) of 1%.
- The evidence items or match comparisons described herein were requested for reporting by the Police Department #4.

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Date	April 24, 2026

Barcode	BHAA0127815
Agency	Police Department 4
Casenumber	2023-PD4
Category	Biological/Saliva
Sampletype	Swab
Description	Syringe
Samplename	BHB2454-4070-E-01a1.1_1

Barcode	BHAA0034195
Agency	Police Department 4
Casenumber	2023-PD4
Category	Biological/Saliva
First	William
Last	Pike
Samplename	BHB2232-2111-R-01a1.1_1

Match	
Likelihood Ratio	276 sextillion
log LR	+23.44
Error Rate	one over 19.5 septillion
log ER	-25.29

Likelihood ratio statement
A match between evidence item BHAA0127815 and William Pike is 276 sextillion times more probable than coincidence.

Error rate statement
For that likelihood ratio value, the chance of some other person matching the evidence as strongly is one over 19.5 septillion.

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Date	April 24, 2026

Barcode	BHAA0034198
Agency	Police Department 4
Casenumber	2023-PD4
Category	Biological/Saliva
Sampletype	Swab
Description	Swab of Baggie
Samplename	BHB2231-2103-E-01a1.1_1

Barcode	BHAA0034195
Agency	Police Department 4
Casenumber	2023-PD4
Category	Biological/Saliva
First	William
Last	Pike
Samplename	BHB2232-2111-R-01a1.1_1

Match	
Likelihood Ratio	32 quintillion
log LR	+19.51
Error Rate	one over 535 quintillion
log ER	-20.73

Likelihood ratio statement
A match between evidence item BHAA0034198 and William Pike is 32 quintillion times more probable than coincidence.

Error rate statement
For that likelihood ratio value, the chance of some other person matching the evidence as strongly is one over 535 quintillion.

TrueAllele® Casework Method

Computer interpretation of DNA evidence

A definite genotype can be determined when a person's DNA produces unambiguous data. However, when the data signals are less definitive, or when there are multiple contributors to the evidence, uncertainty arises. This uncertainty is expressed in the resulting genotype, which may describe different genetic identity possibilities. Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect.

The DNA identification task can thus be understood as a two-step process:

1. objectively *inferring genotypes* from evidence data, accounting for allele pair uncertainty using probability, and
2. subsequently *matching genotypes*, comparing evidence with a suspect relative to a population, to express the strength of association using probability.

The match strength is reported as a single number, the likelihood ratio (LR), which quantifies the change in identification information produced by having examined the DNA evidence.

The TrueAllele Casework system is a computer implementation of this two-step DNA identification inference approach. The computer objectively infers genotypes from DNA data through statistical modeling, without reference to a known comparison genotype. To preserve the identification information present in the data, the system represents genotype uncertainty using probability. These probabilistic genotypes are stored on a relational database. Subsequent comparison with suspects provides evidentiary identification information.

Over forty TrueAllele validation studies have been conducted to establish the reliability of the method [1]. Nine of these studies have been published in peer-reviewed scientific journals, on both synthetic [2, 3, 4, 5, 6] and casework [7, 8, 9, 10] data. There are related papers on data analysis validation [11] and error reporting [12]. TrueAllele has been empirically tested and complies with six national standards for validating probabilistic genotyping systems and other performance criteria, e.g., [13, 14].

References

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