

DNA Analyst Training Laboratory Training Manual

Protocol 7.01 Interpretation



This laboratory protocol (or part thereof) has been provided as an example of a laboratory SOP, courtesy of the Illinois State Police. It has been included for training and example purposes only.

PRESIDENT'S
DNA
INITIATIVE



STATISTICS

All probative inclusionary statements will be accompanied by a statistical evaluation. Statistics will be limited to a full mixture calculation of all peaks at or above 150 RFU at the core loci only. All peaks in stutter position greater than 150 RFU will be included in this calculation.

APPLYING POPULATION FREQUENCY DATA TO STR RESULTS

1. All probative inclusionary statements will be accompanied by a statistical evaluation.
2. The allele frequency data for all STR loci for the Black, White and Hispanic populations are listed in [pdi lab pro 7.02](#), Allele Frequency Data. The Black, White and Hispanic populations were compiled by the FBI Laboratory. The minimum allele frequency at a given locus for each population is calculated as $5/2N$, where N = the number of individuals in the database. The FBI Hispanic database is separated into Southeastern and Southwestern Hispanics. The frequency of the probative samples will be calculated for both databases and the most common overall frequency will be reported as the Hispanic profile frequency.
3. The frequency of probative samples can be calculated using the Popstats program in the CODIS software and/or the ISP mixture calculator software. The formulas for individual loci are:

Heterozygote: use $2pq$.

Homozygote: use $p^2 + p(1-p)$; where $p = 0.01$.

3 Banded Patterns: use $2pq$, where p and q are the two most common allele frequencies.

The product rule is used to calculate the combined frequency for the profile. This calculation is made by multiplying together the individual frequencies for each locus.

4. The frequency will be truncated to 2 significant digits, (no profile frequencies will be rounded). Example: 1,490,000,000 = 1.4 billion.

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