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Technical specification of forensic personal identification

法医学个体识别技术规范

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Table of Contents

Preface	I
1 Scope	1
2 Normative references	1
3 Terms and Definitions	1
4 Abbreviations	2
5 General Requirements	2
6 Inspection Procedure	2
7 Likelihood Calculation	3
8 Expert Opinion	4
9 Identification documents	4
Appendix A (Normative) Cumulative Individual Identification Capability Calculation	5
References	6

Foreword

This document is in accordance with the provisions of GB/T 1.1-2020 "Guidelines for standardization work Part 1: Structure and drafting rules for standardization documents" Drafting.

Please note that some of the contents of this document may involve patents. The issuing organization of this document does not assume the responsibility for identifying patents.

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This document was drafted by: Institute of Forensic Science, Fudan University, Sichuan University, Sun Yat-sen University, Beijing Municipal Public Security Bureau, Supreme People's Procuratorate Procuratorial Technology Information Research Center of the People's Procuratorate.

The main drafters of this document are: Li Chengtao, Zhang Suhua, Hou Yiping, Sun Hongyu, Liu Yacheng, Xie Jianhui, Li Yuanyuan and He Xiaodan.

Technical specifications for forensic individual identification

1 Scope

This document specifies the general requirements for individual identification of forensic

biological specimens, and provides test procedures, likelihood calculations, and identification opinions. and identification documents.

This document is applicable to laboratories conducting individual identification activities of forensic biological specimens.

2 Normative references

The contents of the following documents constitute the essential clauses of this document through normative references in this document.

For referenced documents without a date, only the version corresponding to that date applies to this document; for referenced documents without a date, the latest version (including all amendments) applies to This document.

GA/T 1162 Specification for the collection, storage and submission of forensic biological specimens
GA/T 1163 Analysis and application of human DNA fluorescent marker STR typing results
SF/T 0069 Forensic evidence identification laboratory management specification
SF/T 0134 Technical specification for nucleic acid extraction from forensic biological samples

3 Terms and definitions

The following terms and definitions apply to this document.

3.1 [Source. GA/T 1972-2021, 3.68]

By testing and identifying the genetic markers of biological samples/specimens, it is determined whether the biological samples/specimens are derived from the same individual.

3.2 Individual identification ability discrimination power; DP

The probability that two individuals are randomly selected from the survey population and that their genetic marker phenotypes are different.

Note. See formula (1) for calculation. $DP=1-\sum_{i=1}^n P_i^2$ (1) Where.

n --- the number of phenotypes of a certain genetic marker;

P_i --- the frequency of the i-th phenotype in the population; $i=1$ P_i^2 --- The probability that two unrelated individuals randomly selected from the survey population will have the same phenotype at a certain locus purely due to chance.

3.3

The probability of obtaining a specific genetic marker phenotype when the biological

sample is assumed to be derived from a random individual in the investigated population.

Equal to the estimated frequency $P(X)$ of the genetic marker phenotype in the survey population.

Note. The PM value calculation for autosomal single genetic marker phenotype of homozygous (AA) is shown in formula (2), and the PM value calculation for heterozygous (AB) is shown in formula (3).

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