

Second edition  
2022-10

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# Information technology — Biometric data interchange formats —

## Part 14: DNA data

*Technologies de l'information — Formats d'échange de données  
biométriques —*

*Partie 14: Données ADN*



Reference number  
ISO/IEC 19794-14:2022(E)

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Published in Switzerland

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## Foreword

ISO (the International Organization for Standardization) and IEC (the International Electrotechnical Commission) form the specialized system for worldwide standardization. National bodies that are members of ISO or IEC participate in the development of International Standards through technical committees established by the respective organization to deal with particular fields of technical activity. ISO and IEC technical committees collaborate in fields of mutual interest. Other international organizations, governmental and non-governmental, in liaison with ISO and IEC, also take part in the work.

The procedures used to develop this document and those intended for its further maintenance are described in the ISO/IEC Directives, Part 1. In particular, the different approval criteria needed for the different types of document should be noted. This document was drafted in accordance with the editorial rules of the ISO/IEC Directives, Part 2 (see [www.iso.org/directives](http://www.iso.org/directives) or [www.iec.ch/members\\_experts/refdocs](http://www.iec.ch/members_experts/refdocs)).

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Any trade name used in this document is information given for the convenience of users and does not constitute an endorsement.

For an explanation of the voluntary nature of standards, the meaning of ISO specific terms and expressions related to conformity assessment, as well as information about ISO's adherence to the World Trade Organization (WTO) principles in the Technical Barriers to Trade (TBT) see [www.iso.org/iso/foreword.html](http://www.iso.org/iso/foreword.html). In the IEC, see [www.iec.ch/understanding-standards](http://www.iec.ch/understanding-standards).

This document was prepared by Joint Technical Committee ISO/IEC JTC 1, *Information technology*, Subcommittee SC 37, *Biometrics*.

This second edition cancels and replaces the first edition (ISO/IEC 19794-14:2013), which has been technically revised. It also incorporates the Amendment ISO/IEC 19794-14:2013/Amd. 1:2016.

The main changes are as follows:

- [Clause 6](#) and [Annex A](#) have been technically revised to enable the standardized interchange of DNA profile search results;
- [Annex B](#) has been technically revised to reflect the revised data interchange format;
- New [Annexes E, F](#) and [G](#) have been added.

A list of all parts in the ISO/IEC 19794 series can be found on the ISO and IEC websites.

Any feedback or questions on this document should be directed to the user's national standards body. A complete listing of these bodies can be found at [www.iso.org/members.html](http://www.iso.org/members.html) and [www.iec.ch/national-committees](http://www.iec.ch/national-committees).

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## Introduction

Forensic molecular genetics has evolved from a rapidly developing field with changing technologies into a highly recognized and generally accepted forensic science. Forensic genetics using deoxyribonucleic acid (DNA) profiling comprises a number of important applications. Examples are the investigation of biological stains to obtain evidence for the presence of an alleged perpetrator at a crime scene by comparing the genetic profiles from crime scene samples of human origin, to those available at DNA databases administered by law enforcement agencies. These also include the identification of unknown corpses in the context of both natural death and crime, immigration, paternity testing and disaster victim identification (DVI).

This document is based on DNA data from forensic DNA typing techniques that are commonly used, namely short tandem repeat (STR) profiling and other DNA typing techniques that are standardized by scientific bodies for the purpose of discriminating between individuals.

The purpose of this data interchange format is to enable the exchange of DNA data from different systems, not to impose any constraints on the specific DNA typing system/technique to be used. Where existing DNA data exchange formats have been referenced in the preparation of this document, these formats are listed as references.

Standard profiling systems exploit the non-coding parts of DNA that are referred to as “junk DNA”. The coding regions, which are richer in information pertaining to specific genetic traits of an individual, are deliberately avoided in order to maintain the privacy and civil rights of the donor. In addition, national data protection and privacy legislation can impose special security safeguards, such as (but not limited to) encryption of data transfers and/or storage.

This document supports XML (Extensible Markup Language) encoding, to support a spectrum of user requirements. [Annex A](#) specifies the schema against which XML-encoded DNA data XML documents are required to validate. It also contains a sample DNA data XML document. [Annex B](#) addresses the conformance testing methodology. [Annex C](#) lists some examples of DNA analysis kits. [Annex D](#) lists the names of DNA loci. [Annex E](#) lists interoperability test data for kinship searching in the form of pedigrees. In [Annex F](#), there is a description of interoperability tests at Level 3 (semantics). By means of the sample inclusion and comparison rules listed in [Annex G](#), a target can be identified among a number of candidates.