SLOVENSKI STANDARD
SIST-TS CEN ISO/TS 5798:2023

01-februar-2023

Diagnostični preskusni sistemi in vitro - Zahteve in priporočila za odkrivanje koronavirusa (SARS-CoV-2) z metodami amplifikacije nukleinskih kislin (ISO/TS 5798:2022)

In vitro diagnostic test systems - Requirements and recommendations for detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by nucleic acid amplification methods (ISO/TS 5798:2022)

In-vitro-Diagnostika-Systeme - Anforderungen und Empfehlungen für Qualitätsverfahren für den Nachweis des Coronavirus 2 des Schweren Akuten Respiratorischen Syndroms (SARS-CoV-2) mittels Nukleinsäureamplifikation (ISO/TS 5798:2022)

Systèmes d'essai pour diagnostic in vitro - Exigences et recommandations pour la détection du coronavirus 2 associé au syndrome respiratoire aigu sévère (SARS-CoV-2) par des méthodes d'amplification des acides nucléiques (ISO/TS 5798:2022)

Ta slovenski standard je istoveten z: **CEN ISO/TS 5798:2022**

ICS:

11.100.10	Diagnostični preskusni sistemi in vitro	In vitro diagnostic test systems

SIST-TS CEN ISO/TS 5798:2023 **en,fr,de**

TECHNICAL SPECIFICATION

SPÉCIFICATION TECHNIQUE

TECHNISCHE SPEZIFIKATION

CEN ISO/TS 5798

November 2022

ICS 11.100.01

English Version

In vitro diagnostic test systems - Requirements and recommendations for detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by nucleic acid amplification methods (ISO/TS 5798:2022)

Systèmes d'essai pour diagnostic in vitro - Exigences et recommandations pour la détection du coronavirus 2 associé au syndrome respiratoire aigu sévère (SARS-CoV-2) par des méthodes d'amplification des acides nucléiques (ISO/TS 5798:2022)

In-vitro-Diagnostika-Systeme - Anforderungen und Empfehlungen für Qualitätsverfahren für den Nachweis des Coronavirus 2 des Schweren Akuten Respiratorischen Syndroms (SARS-CoV-2) mittels Nukleinsäureamplifikation (ISO/TS 5798:2022)

This Technical Specification (CEN/TS) was approved by CEN on 21 November 2022 for provisional application.

The period of validity of this CEN/TS is limited initially to three years. After two years the members of CEN will be requested to submit their comments, particularly on the question whether the CEN/TS can be converted into a European Standard.

CEN members are required to announce the existence of this CEN/TS in the same way as for an EN and to make the CEN/TS available promptly at national level in an appropriate form. It is permissible to keep conflicting national standards in force (in parallel to the CEN/TS) until the final decision about the possible conversion of the CEN/TS into an EN is reached.

CEN members are the national standards bodies of Austria, Belgium, Bulgaria, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Norway, Poland, Portugal, Republic of North Macedonia, Romania, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Türkiye and United Kingdom.

EUROPEAN COMMITTEE FOR STANDARDIZATION
COMITÉ EUROPÉEN DE NORMALISATION
EUROPÄISCHES KOMITEE FÜR NORMUNG

CEN-CENELEC Management Centre: Rue de la Science 23, B-1040 Brussels

Ref. No. CEN ISO/TS 5798:2022 E

Contents

Page

European foreword

The text of ISO/TS 5798:2022 has been prepared by Technical Committee ISO/TC 212 "Clinical laboratory testing and in vitro diagnostic test systems" of the International Organization for Standardization (ISO) and has been taken over as CEN ISO/TS 5798:2022 by Technical Committee CEN/TC 140 "In vitro diagnostic medical devices" the secretariat of which is held by DIN.

Attention is drawn to the possibility that some of the elements of this document may be the subject of patent rights. CEN shall not be held responsible for identifying any or all such patent rights.

Any feedback and questions on this document should be directed to the users' national standards body. A complete listing of these bodies can be found on the CEN website.

According to the CEN-CENELEC Internal Regulations, the national standards organizations of the following countries are bound to announce this Technical Specification: Austria, Belgium, Bulgaria, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Norway, Poland, Portugal, Republic of North Macedonia, Romania, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Türkiye and the United Kingdom.

Endorsement notice

The text of ISO/TS 5798:2022 has been approved by CEN as CEN ISO/TS 5798:2022 without any modification.

TECHNICAL SPECIFICATION

ISO/TS 5798

First edition
2022-04

In vitro diagnostic test systems — Requirements and recommendations for detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by nucleic acid amplification methods

Systèmes d'essai pour diagnostic in vitro — Exigences et recommandations pour la détection du coronavirus 2 associé au syndrome respiratoire aigu sévère (SARS-CoV-2) par des méthodes d'amplification des acides nucléiques

Reference number
ISO/TS 5798:2022(E)

ISO copyright office
CP 401 • Ch. de Blandonnet 8
CH-1214 Vernier, Geneva
Phone: +41 22 749 01 11
Email: copyright@iso.org
Website: www.iso.org

Published in Switzerland

Contents

Page

Foreword

ISO (the International Organization for Standardization) is a worldwide federation of national standards bodies (ISO member bodies). The work of preparing International Standards is normally carried out through ISO technical committees. Each member body interested in a subject for which a technical committee has been established has the right to be represented on that committee. International organizations, governmental and non-governmental, in liaison with ISO, also take part in the work. ISO collaborates closely with the International Electrotechnical Commission (IEC) on all matters of electrotechnical standardization.

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 ISO documents 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).

Attention is drawn to the possibility that some of the elements of this document may be the subject of patent rights. ISO shall not be held responsible for identifying any or all such patent rights. Details of any patent rights identified during the development of the document will be in the Introduction and/or on the ISO list of patent declarations received (see www.iso.org/patents).

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.

This document was prepared by Technical Committee ISO/TC 212, *Clinical laboratory testing and in vitro diagnostic test systems*, in collaboration with Technical Committee ISO/TC 276, *Biotechnology*.

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.

Introduction

Coronaviruses are enveloped RNA viruses that are broadly distributed in the animal kingdom. They have been identified in humans, other mammals, and birds. Coronaviruses were named because the spike proteins known to facilitate viral attachment and cell entry appear like a halo on the virus surface when viewed under an electron microscope. Coronaviruses are roughly spherical with a diameter ranging from 118 nm to 136 nm. The coronavirus genome, which ranges from 26 kb to 32 kb, is the largest among all RNA viruses, including RNA viruses that have segmented genomes. Until 2019, six coronaviruses have been associated with human diseases:

— severe acute respiratory syndrome-related coronavirus (SARS-CoV),

— Middle East respiratory syndrome coronavirus (MERS-CoV),

— human coronavirus 229E (HCoV-229E),

— human coronavirus OC43 (HCoV-OC43),

— human coronavirus NL63 (HCoV-NL63), and

— human coronavirus HKU1 (HCoV-HKU1)[1].

In 2019, a cluster of patients presenting with a respiratory disease were shown, by sequencing, to be infected with a novel coronavirus[2]. The coronavirus associated with this cluster was subsequently named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses[3]. SARS-CoV-2 is the seventh coronavirus known to infect humans. The disease caused by SARS-CoV-2 was designated as coronavirus infectious disease 2019 (COVID-19) by the World Health Organization (WHO)[4].

The host range for SARS-CoV-2 is not yet fully defined. SARS-CoV-2 is a beta-coronavirus. The receptor for SARS-CoV-2 is the angiotensin-converting enzyme 2 (ACE2). ACE2 is a cell-surface, zinc-binding carboxypeptidase involved in regulation of cardiac function and blood pressure. It is expressed in epithelial cells of the lung and the small intestine, which are the primary targets of SARS-CoV-2, as well as the heart, kidney, and other tissues.

SARS-CoV-2 replicates in the upper and lower respiratory tracts and is transmitted by droplets and aerosols and most likely other contact with asymptomatic and symptomatic infected persons. The basic reproduction number (R_0) of the original variant is between 2 and 3, but significantly more contagious variants have developed. The median incubation period is 5,7 (range 2 to 14) days[5]. Similarly to SARS and MERS, superspreading events have been reported, with a dispersion parameter (kappa) estimated at 0,1. Most infections are uncomplicated, and 5 % to 10 % of patients are hospitalized mainly due to pneumonia with severe inflammation. However, complications include respiratory and multiorgan failures. Risk factors for the complicated disease increase with age and include hypertension, diabetes, chronic cardiovascular and chronic pulmonary diseases, and immunodeficiency.

Clinical management of COVID-19 and control of infections and spread of SARS-CoV-2 require effective and efficient in vitro diagnostics. There are a number of tests and kits in use for the detection of SARS-CoV-2 and the number of methods will continue to increase. Acceptable design, development and establishment of quality SARS-CoV-2 diagnostics based on nucleic acid detection methods is critical to ensure COVID-19 infection control. Establishing indices for conducting comprehensive quality evaluation of these methods and kits both during development and in routine application will ensure the accuracy of the test results and support epidemic prevention and control. This document provides requirements and recommendations to consider for the quality practice of SARS-CoV-2 nucleic acid amplification methods.

In vitro diagnostic test systems — Requirements and recommendations for detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by nucleic acid amplification methods

1 Scope

This document provides requirements and recommendations for the design, development, verification, validation and implementation of analytical tests for detecting the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) using nucleic acid amplification. It addresses pre-examination, examination and post-examination process steps for human specimens.

This document is applicable to medical laboratories. It is also intended to be used by in vitro diagnostic developers and manufacturers, as well as by institutions and organizations supporting SARS-CoV-2 research and diagnostics.

This document does not apply to environmental samples.

2 Normative references

There are no normative references in this document.

3 Terms and definitions

For the purposes of this document, the following terms and definitions apply.

ISO and IEC maintain terminology databases for use in standardization at the following addresses:

— ISO Online browsing platform: available at https://www.iso.org/obp

— IEC Electropedia: available at https://www.electropedia.org/

3.1
severe acute respiratory syndrome coronavirus 2
SARS-CoV-2
virus that causes coronavirus infectious disease 2019 (COVID-19)

3.2
specimen
primary sample
discrete portion of a body fluid, breath, hair or tissue taken for examination, study or analysis of one or more quantities or properties assumed to apply for the whole

Note 1 to entry: The Global Harmonisation Task Force (GHTF) uses the term specimen in its harmonized guidance documents to mean a sample of biological origin intended for examination by a medical laboratory.

Note 2 to entry: In some countries, the term “specimen” is used instead of “primary sample” (or a subsample of it), which is the sample prepared for sending to, or as received by, the laboratory and which is intended for examination.

[SOURCE: ISO 15189:2012, 3.16[6] modified — Note 2 to entry was removed and Note 3 to entry was renumbered as Note 2 to entry.]

3.3
sample
one or more parts taken from a *primary sample* (3.2)

EXAMPLE A volume of serum taken from a larger volume of serum.

[SOURCE: ISO 15189:2012, 3.24[6]]

3.4
reverse transcription
RT
process of making complementary DNA [*cDNA* (3.6)] from an *RNA* (3.20) *template* (3.22), using the enzymatic activity of a reverse transcriptase associated with one or more oligonucleotide primers under a suitable set of conditions

[SOURCE: ISO 16577:2016, 3.180[7], modified — Replaced "DNA" with "complementary DNA (cDNA)".]

3.5
deoxyribonucleic acid
DNA
polymer of deoxyribonucleotides occurring in a double-stranded (dsDNA) or single-stranded (ssDNA) form

[SOURCE: ISO 22174:2005, 3.1.2[8]]

3.6
complementary DNA
cDNA
single-stranded *DNA* (3.5), complementary to a given *RNA* (3.20) and synthesised in the presence of reverse transcriptase to serve as a *template* (3.22) for *DNA* amplification

[SOURCE: ISO 20395:2019, 3.5[9]]

3.7
analytical specificity
capability of a measuring system, using a specified measurement procedure, to provide measurement results for one or more measurands which do not depend on each other nor on any other quantity in the system undergoing measurement

Note 1 to entry: Lack of analytical specificity is called analytical interference (see ISO 18113-1:2009, A.3.2).

[SOURCE: ISO 18113-1:2009, A.3.4[10]]

3.8
limit of detection
LOD
measured quantity value, obtained by a given measurement procedure, for which the probability of falsely claiming the absence of a component in a material is 0,05, given a probability of 0,05 of falsely claiming its presence

[SOURCE: ISO/IEC Guide 99:2007, 4.18[11], modified — "β, given a probability α" was replaced by "0,05, given a probability of 0,05" and Notes 1 to 3 to entry were deleted.]

3.9
verification
provision of objective evidence that a given item fulfils specified requirements

[SOURCE: ISO/IEC Guide 99:2007, 2.44[11], modified — EXAMPLES 1 to 3 and Notes 1 to 6 to entry were deleted.]

3.10
validation
confirmation, through the provision of objective evidence, that the requirements for a specific intended use or application have been fulfilled

Note 1 to entry: The word "validated" is used to designate the corresponding status.

[SOURCE: ISO 9000:2015, 3.8.13[12], modified — Notes 1 and 3 to entry were deleted and Note 2 to entry was renamed Note 1 to entry.]

3.11
amplicon
specific *DNA* (3.5) fragment produced by a DNA-amplification technology, such as the *polymerase chain reaction (PCR)* (3.12)

[SOURCE: ISO 13495:2013, 3.3.1[13]]

3.12
polymerase chain reaction
PCR
enzymatic procedure which allows in vitro amplification of *DNA* (3.5) or *RNA* (3.20)

[SOURCE: ISO 22174:2005, 3.4.1[8], modified — "or RNA" added to the end of the definition and "in vitro" has been unitalicized in accordance with the ISO House Style.]

3.13
reference material
material, sufficiently homogeneous and stable with reference to specified properties, which has been established to be fit for its intended use in measurement or in examination of nominal properties

[SOURCE: ISO/IEC Guide 99:2007, 5.13[11], modified — Notes 1 to 8 to entry and EXAMPLES 1 to 5 were deleted.]

3.14
pseudo-virus
virus or virus-like particle that can integrate the envelope glycoprotein of another virus to form a virus with an exogenous viral envelope, and the genome retains the characteristics of the retrovirus itself

3.15
digital PCR
dPCR
procedure in which nucleic acid *templates* (3.22) are distributed across multiple partitions of nominally equivalent volume, such that some partitions contain *template* and others do not, followed by *PCR* (3.12) amplification of target sequences and detection of specific *PCR* products, providing a count of the number of partitions with a positive and negative signal for the target template

Note 1 to entry: Nucleic acid target sequences are assumed to be randomly and independently distributed across the partitions during the partitioning process.

Note 2 to entry: The count of positive and negative partitions is normally based on end point detection of *PCR* products following thermal cycling, however real-time *qPCR* (3.16) monitoring of *PCR* product accumulation is additionally possible for some dPCR platforms.

[SOURCE: ISO 20395:2019, 3.10[9]]