FINAL
DRAFT

INTERNATIONAL STANDARD

ISO/FDIS 5058-1

ISO/TC **276**

Secretariat: DIN

Voting begins on:
2021-08-13

Voting terminates on:
2021-10-08

Biotechnology — Genome editing —

Part 1: Vocabulary

Reference number
ISO/FDIS 5058-1:2021(E)

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Published in Switzerland

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Foreword

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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).

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This document was prepared by Technical Committee ISO/TC 276, *Biotechnology*.

A list of all parts in the ISO 5058 series can be found on the ISO website.

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

Genome editing technology is a fast-growing and rapidly advancing global bioscience field with applications in many biotechnology sectors. Genome editing is used to modify the nucleic acids of a genetic code, which can be composed of DNA or RNA, in a site-specific manner. Modifications can include insertion, deletion or alteration of nucleic acids. The technology operates by biochemical principles generally applicable to every kind of cell. Examples of genome editing technology applications with global significance include human cell-based therapeutics, agriculture, microbial based therapeutics, synthetic biology and biomanufacturing.

While genome editing technology is being actively utilized, there is a need for international standardization in terms and definitions for this field, so as to enhance interpretation and communication of concepts, data and results.

This document has been developed to provide a unified standard set of terms and definitions that serve the needs of biotechnology stakeholders and act as a reference for genome editing technology. Standards in the field of genome editing are intended to harmonize and accelerate effective communication, technology development, qualification and evaluation of genome editing products. This document is expected to improve confidence and clarify scientific communication, data reporting and data interpretation in the genome editing field. Specific requirements for the application of genome editing technologies in agriculture and food are not included. For specific requirements, users can consult standards developed by appropriate ISO Technical Committees, e.g. ISO/TC 34/SC 16 *Horizontal methods for molecular biomarker analysis*, or ISO/TC 215 *Health informatics*.

This document provides a vocabulary that standardizes the use and meaning of terms associated with genome editing. This document is organized into categories and sub-categories as follows:

- genome editing concepts (see 3.1);
- genome editing tools (see 3.2):

  - general (see 3.2.1);
  - CRISPR specific (see 3.2.2);
  - meganuclease specific (see 3.2.3);
  - megaTAL specific (see 3.2.4);
  - TALEN specific (see 3.2.5);
  - ZFN specific (see 3.2.6);
- genome editing outcomes (see 3.3).

Terms within categories are listed alphabetically. The sub-category “General” contains terms that apply to all types of genome editing tools. Additional sub-categories contain terms specific to the sub-category of genome editing technology: “CRISPR specific”, “Meganuclease specific”, “megaTAL specific”, “TALEN specific” and “ZFN specific”. An alphabetical list of all terms is given in the index. Definitions follow English word order wherever possible.

It is also recognized that genome editing is a rapidly developing and evolving biotechnology, and additional terms and definitions will be needed as genome editing technologies mature.

Biotechnology — Genome editing —

Part 1: Vocabulary

1 Scope

This document defines terms related to genome editing technology.

This document is applicable to general use of genome editing across species.

2 Normative references

There are no normative references in this document.

3 Terms and definitions

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

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

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

3.1 Genome editing concepts

3.1.1
gene editing
techniques for *genome engineering* (3.1.3) that involve nucleic acid damage, repair mechanisms, replication and/or recombination for incorporating site-specific modification(s) into a gene or genes

Note 1 to entry: Gene editing is a subclass of *genome editing* (3.1.2).

Note 2 to entry: There are various genome editing tools (see 3.2).

3.1.2
genome editing
techniques for *genome engineering* (3.1.3) that involve nucleic acid damage, repair mechanisms, replication and/or recombination for incorporating site-specific modification(s) into a genomic DNA

Note 1 to entry: *Gene editing* (3.1.1) is a subclass of genome editing.

Note 2 to entry: There are various genome editing tools (see 3.2 and Figure 1).

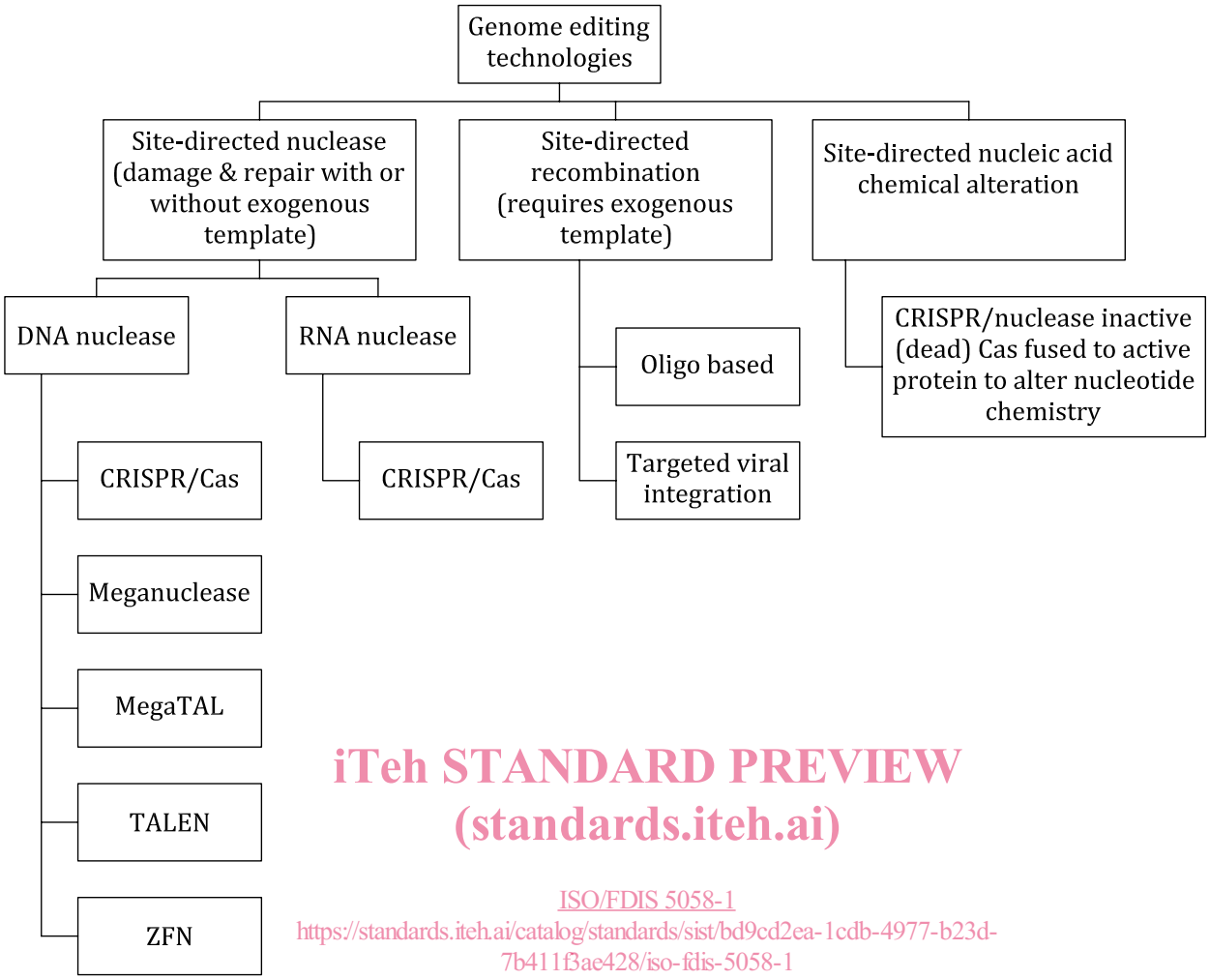

Figure 1 — Examples for genome editing technologies/tools

3.1.3
genome engineering
process of introducing intentional changes to genomic nucleic acid

Note 1 to entry: *Gene editing* (3.1.1) and *genome editing* (3.1.2) are techniques used in genome engineering.

3.1.4
off-target
genome editing off-target
genomic position and/or nucleic acid sequence distinct from the *target* (3.1.6)

EXAMPLE Off-target binding, off-target cleavage, off-target edit, off-target sequence change.

Note 1 to entry: An off-target edit is an example of an *unintended edit* (3.3.7).

3.1.5
specificity
genome editing target specificity
extent to which an editing agent or procedure acts only on its intended *target* (3.1.6)

Note 1 to entry: When using this term, the procedure is defined, intended target is defined, action or outcome is measured and reported, and limits of detection are reported.

3.1.6
target
genome editing target
nucleic acid sequence subject to intentional binding, modification and/or cleavage during a *genome editing* (3.1.2) process

Note 1 to entry: See also *off-target* (3.1.4), *Cas nuclease target site* (3.2.2.2), *meganuclease target site* (3.2.3.4), *megaTAL target site* (3.2.4.3), *TALEN target site* (3.2.5.4) and *ZFN target site* (3.2.6.6).

3.2 Genome editing tools

3.2.1 General

3.2.1.1
repair template
nucleic acid sequence used to direct cellular DNA repair pathways to incorporate specific DNA sequence changes at or near a *target* (3.1.6)

3.2.1.2
site-directed DNA modification enzyme
enzyme capable of modifying DNA at a specific sequence

EXAMPLE *Site-directed nuclease* (3.2.1.3), site-directed adenosine deaminase.

3.2.1.3
site-directed nuclease
sequence-specific nuclease
enzyme capable of cleaving the phosphodiester bond between adjacent nucleotides in a nucleic acid polymer at a specific sequence

3.2.2 CRISPR specific

3.2.2.1
Cas nuclease
CRISPR associated nuclease
enzyme that is a component of CRISPR systems that is capable of breaking the phosphodiester bonds between nucleotides

EXAMPLE Cas3, Cas9, Cas12a, Cas13, CasX.

Note 1 to entry: Some but not all Cas nucleases interact with a *gRNA* (3.2.2.4). See also *crRNA* (3.2.2.3), *sgRNA* (3.2.2.7) and *tracrRNA* (3.2.2.9).

3.2.2.2
Cas nuclease target site
nucleotide sequence comprising the *PAM* (3.2.2.5), in most cases, and a region that hybridizes to the target sequence specific guide of a Cas *RNP* (3.2.2.6)

3.2.2.3
crRNA
CRISPR RNA
polyribonucleotide that includes sequence complementarity to the *target* (3.1.6) and a sequence that interacts with a Cas protein and optionally *tracrRNA* (3.2.2.9)

Note 1 to entry: crRNA is a component of g*RNA* (3.2.2.4) or a complete gRNA, depending on the CRISPR system.

Note 2 to entry: In some CRISPR systems, a portion of the crRNA will base-pair with the tracrRNA (e.g. Cas9). Other CRISPR systems lack tracrRNA (e.g. Cas12a/Cpf1). In systems that do not require tracrRNA, the gRNA is called a “CRISPR RNA” or simply “crRNA”.

3.2.2.4
gRNA
guide RNA
polyribonucleotide containing regions sufficient for productive interaction with a *Cas nuclease* (3.2.2.1) or variant to direct interaction with the specific *target* (3.1.6)

Note 1 to entry: See *crRNA* (3.2.2.3), *tracrRNA* (3.2.2.9) and *sgRNA* (3.2.2.7).

Note 2 to entry: For Cas9-type proteins, the natural gRNA comprises a crRNA that imparts sequence specificity and the tracrRNA that interacts with and activates the protein. This is sometimes referred to as a "dual guide". Other Cas proteins can have different gRNA structures.

Note 3 to entry: sgRNA for Cas9 proteins are non-naturally occurring polyribonucleotides where the crRNA and tracrRNA are fused with an artificial linker.

Note 4 to entry: In some cases, chemical modifications of the polyribonucleotide are used, such as modifications to the phosphodiester linkages, bases or sugar moieties. These can include substitution of DNA (2′-deoxy) or 2′-methoxy nucleotides for RNA nucleotides, etc.

3.2.2.5
PAM
protospacer adjacent motif
short nucleotide motif in the targeted region of nucleic acid required for guided *Cas nuclease* (3.2.2.1) or variant binding

Note 1 to entry: PAMs are distinct from, but in close proximity to, nucleic acid sequence targeted by g*RNA* (3.2.2.4).

3.2.2.6
RNP
ribonucleoprotein
complex comprising protein bound to RNA

Note 1 to entry: In the context of CRISPR-based *genome editing* (3.1.2), RNP refers to the complex of Cas protein(s) and g*RNA* (3.2.2.4).

3.2.2.7
sgRNA
single-guide RNA
fusion of *crRNA* (3.2.2.3) and *tracrRNA* (3.2.2.9)

Note 1 to entry: See g*RNA* (3.2.2.4).

3.2.2.8
target strand
CRISPR target strand
single-stranded nucleic acid sequence that is complementary to the g*RNA* (3.2.2.4) of a Cas protein or variant

3.2.2.9
tracrRNA
trans-activating CRISPR RNA
polyribonucleotide that base-pairs with the *crRNA* (3.2.2.3) and interacts with a *Cas nuclease* (3.2.2.1) to enable sequence-specific interaction of the *target* (3.1.6)

Note 1 to entry: tracrRNA is an optional component of g*RNA* (3.2.2.4).