

---

---

**Biotechnology — Genome editing —**  
**Part 1:**  
**Vocabulary**

*Biotechnologie — Édition génomique —*  
*Partie 1: Vocabulaire*

STANDARDSISO.COM : Click to view the full PDF of ISO 5058-1:2021



STANDARDSISO.COM : Click to view the full PDF of ISO 5058-1:2021



**COPYRIGHT PROTECTED DOCUMENT**

© ISO 2021

All rights reserved. Unless otherwise specified, or required in the context of its implementation, no part of this publication may be reproduced or utilized otherwise in any form or by any means, electronic or mechanical, including photocopying, or posting on the internet or an intranet, without prior written permission. Permission can be requested from either ISO at the address below or ISO's member body in the country of the requester.

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

Published in Switzerland

# Contents

	Page
Foreword.....	iv
Introduction.....	v
<b>1 Scope.....</b>	<b>1</b>
<b>2 Normative references.....</b>	<b>1</b>
<b>3 Terms and definitions.....</b>	<b>1</b>
3.1 Genome editing concepts.....	1
3.2 Genome editing tools.....	3
3.2.1 General.....	3
3.2.2 CRISPR specific.....	3
3.2.3 Meganuclease specific.....	5
3.2.4 megaTAL specific.....	5
3.2.5 TALEN specific.....	6
3.2.6 ZFN specific.....	6
3.3 Genome editing outcomes.....	7
<b>4 Abbreviated terms.....</b>	<b>8</b>
<b>Bibliography.....</b>	<b>9</b>
<b>Index.....</b>	<b>10</b>

STANDARDSISO.COM : Click to view the full PDF of ISO 5058-1:2021

## 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](http://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](http://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](http://www.iso.org/iso/foreword.html).

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](http://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 in and clarity of 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.

STANDARDSISO.COM : Click to view the full PDF of ISO 5058-1:2021

# 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 and Figure 1).

##### 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).

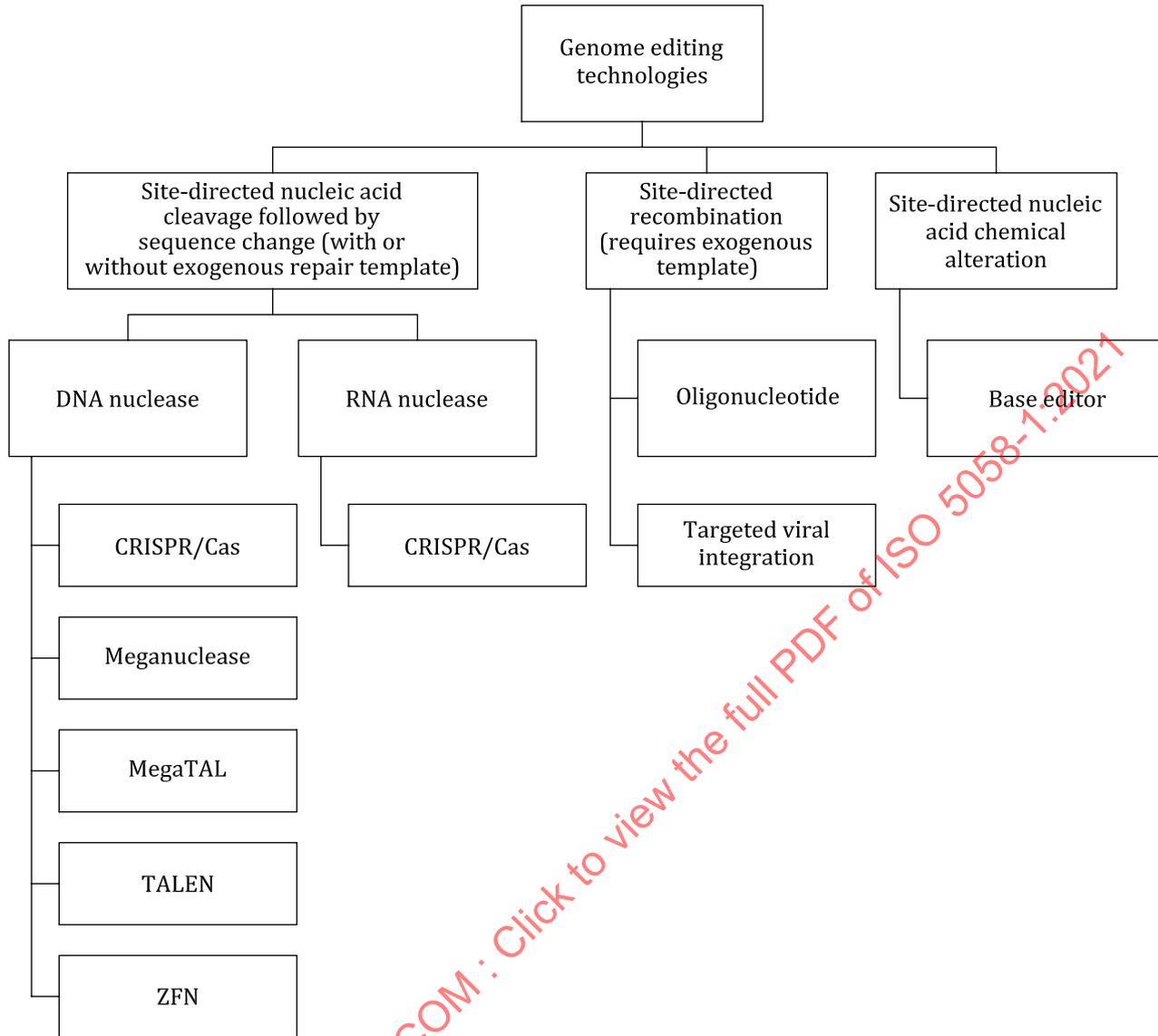


Figure 1 — Examples for genome editing technologies/tools

**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, the intended target is defined, the 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* (3.2.6.5).

**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 gRNA (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 gRNA (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 gRNA (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 gRNA (3.2.2.4).

### 3.2.2.8

#### target strand

CRISPR target strand

single-stranded nucleic acid sequence that is complementary to the gRNA (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 *gRNA* (3.2.2.4).

**3.2.3 Meganuclease specific****3.2.3.1****meganuclease**

variant of the LAGLIDADG subtype of homing endonucleases engineered to recognize a 15 to 40 base pair DNA *target* (3.1.6) different from the site recognized by the parent endonuclease

Note 1 to entry: The LAGLIDADG consensus sequence represents an alpha helix that serves as a dimerization interface and key component in the DNA cleavage site in this family of meganucleases.

**3.2.3.2****meganuclease linker**

natural or artificially derived polypeptide sequence that links two LAGLIDADG domains to one another to form a single polypeptide chain

Note 1 to entry: The LAGLIDADG consensus sequence represents an alpha helix that serves as a dimerization interface and key component in the DNA cleavage site in this family of *meganucleases* (3.2.3.1).

**3.2.3.3****meganuclease single chain**

*meganuclease* (3.2.3.1) composed of two LAGLIDADG domains joined by either a natural or artificially derived polypeptide linker in order to be expressed as a single polypeptide chain

Note 1 to entry: The LAGLIDADG consensus sequence represents an alpha helix that serves as a dimerization interface and key component in the DNA cleavage site in this family of meganucleases.

**3.2.3.4****meganuclease target site**

DNA sequence recognized by *meganucleases* (3.2.3.1)

Note 1 to entry: Meganuclease target sites are 15 to 40 base pair DNA sequence consisting of two equal length half sites separated by a 4 base pair middle sequence (also known as “central 4”). Cleavage occurs at the junction of the half sites and the middle site on each DNA strand leaving a 4 nucleotide 3' overhang.

**3.2.4 megaTAL specific****3.2.4.1****megaTAL**

artificial chimeric nucleases composed of an array of transcription activator-like (TAL) effector (TALE) DNA binding domains, a *megaTAL linker* (3.2.4.2) and a *meganuclease* (3.2.3.1)

**3.2.4.2****megaTAL linker**

amino acid sequence that links an array of TAL DNA binding domains and a *meganuclease* (3.2.3.1)

**3.2.4.3****megaTAL target site**

intended DNA binding site of a *megaTAL* (3.2.4.1), encompassing the DNA sequence targeted by both the TAL array and the *meganuclease* (3.2.3.1)

### 3.2.5 TALEN specific

#### 3.2.5.1

##### RVDs

##### repeat variable diresidue

two amino acid sequence in TAL repeats that imparts DNA binding specificity

#### 3.2.5.2

##### TALEN

##### transcription activator-like effector nuclease

artificial nuclease composed of an endodeoxyribonuclease fused to DNA-binding domains of TALEs<sup>[1]</sup> that cleave DNA at a defined distance from TALE recognition sequences

Note 1 to entry: A TALEN can refer to a pair of TALE-FokI fusion proteins that dimerize on opposite strands of DNA adjacent to a *target* (3.1.6) for cleavage.

#### 3.2.5.3

##### TALEN linker

polypeptide sequence that links an array of TAL DNA binding domains and an endodeoxyribonuclease, typically FokI

#### 3.2.5.4

##### TALEN target site

DNA sequence recognized by *TALENs* (3.2.5.2)

Note 1 to entry: Typical TALEN target sites are recognized by a pair of TALENs and contain a central spacer region flanked by upstream and downstream sequences that are each recognized by one TALEN. This pair is designed in such a way that two TALEN nuclease domains dimerize to cleave DNA within the spacer region.

### 3.2.6 ZFN specific

#### 3.2.6.1

##### zinc finger

Cys2His2 zinc finger

DNA binding domain that folds via coordination of zinc into a compact structure consisting of two beta strands and one alpha-helix ( $\beta \beta \alpha$ )

Note 1 to entry: Zinc finger DNA binding domains typically contain 28 amino acids.

#### 3.2.6.2

##### ZFN

##### zinc finger nuclease

chimeric protein consisting of an array of *zinc fingers* (3.2.6.1) linked to a DNA cleavage domain

Note 1 to entry: FokI is prevalently used as the DNA cleavage domain bound to a zinc finger.

Note 2 to entry: Binding of two ZFNs to a pair of appropriately spaced DNA target sites enables nuclease domain dimerization and DNA cleavage between the targets.

#### 3.2.6.3

##### ZFN linker

polypeptide sequence that links an array of *zinc finger* (3.2.6.1) binding domains and a DNA cleavage domain

Note 1 to entry: FokI is prevalently used as the DNA cleavage domain bound to a zinc finger.

**3.2.6.4****ZFN recognition helix**

seven residue positions within a *zinc finger* (3.2.6.1) that are most directly responsible for its DNA binding preference

Note 1 to entry: The seven residues comprise the first six residues of the alpha helix, along with the residue immediately preceding the N-terminal of the helix. They are typically referred to as positions +1 to +6 (within the alpha helix) and position (-1) (immediately preceding the helix).

**3.2.6.5****ZFN target site**

DNA sequence recognized by a pair of *ZFNs* (3.2.6.2)

Note 1 to entry: Typical ZFN target sites contain a central spacer region flanked by DNA sequences that are each recognized by an array of *zinc fingers* (3.2.6.1) oriented such that the ZFN nuclease domains dimerize and cleave within the spacer.

**3.2.6.6****ZFP****zinc finger protein**

DNA binding protein consisting of a tandem array of multiple *zinc fingers* (3.2.6.1)

**3.3 Genome editing outcomes****3.3.1****edit**

DNA edit

RNA edit

epigenome edit

DNA, RNA or epigenome edit

modification to nucleic acid sequence resulting from the application of *genome editing* (3.1.2) components

EXAMPLE Insertion, deletion, substitution, deamination, methylation, demethylation.

Note 1 to entry: Genome editing components can include a nuclease and *repair template* (3.2.1.1).

**3.3.2****HDR****homology-directed repair**

mechanism of recombinational DNA repair<sup>[2]</sup> where repair is templated by a polynucleotide with regions corresponding to sequences flanking the *target* (3.1.6)

EXAMPLE Single-stranded DNA oligonucleotide templated HDR.

Note 1 to entry: *Repair templates* (3.2.1.1) can be exogenously introduced to achieve sequence changes in *genome editing* (3.1.2) approaches.

**3.3.3****indel**

InDel mutation

sequence change caused by the insertion and/or deletion of nucleotides

**3.3.4****intended edit**

designed modification to a *target* (3.1.6) resulting from the application of *genome editing* (3.1.2) components

Note 1 to entry: See *edit* (3.3.1).

Note 2 to entry: Genome editing components can include a nuclease and *repair template* (3.2.1.1).

### 3.3.5

#### MMEJ

##### microhomology-mediated end joining repair

mechanism of DNA end-joining repair<sup>[3]</sup> where the DNA ends are rejoined to each other using short regions of homology flanking the initiating double-stranded break to align the ends for repair

Note 1 to entry: MMEJ repair of DNA breaks in *genome editing* (3.1.2) approaches can result in deletion between pairs of microhomology regions.

Note 2 to entry: Short regions of homology for MMEJ are typically 2 to 25 base pairs.

### 3.3.6

#### NHEJ

##### non-homologous end joining

mechanism of DNA end-joining repair<sup>[3]</sup> in which DNA ends are joined in a homology-independent manner

Note 1 to entry: NHEJ repair of DNA breaks in *genome editing* (3.1.2) workflows can result in *indel* (3.3.3) formation.

### 3.3.7

#### unintended edit

modification to nucleic acid at an *off-target* (3.1.4) resulting from the application of *genome editing* (3.1.2) components

Note 1 to entry: See *edit* (3.3.1).

Note 2 to entry: Genome editing components can include a nuclease and *repair template* (3.2.1.1).

## 4 Abbreviated terms

DNA	deoxyribonucleic acid
CRISPR	clustered regularly interspaced short palindromic repeats
RNA	ribonucleic acid
TAL	transcription activator-like
TALE	transcription activator-like effector