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Biotechnology — Gene delivery systems —

Part 2: Quantification methods for viral vectors

Biotechnologie — Systèmes de transfert de gènes —

Partie 2: Méthodes de quantification des vecteurs viraux

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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 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).

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This document was prepared by Technical Committee ISO/TC 276, *Biotechnology*, Subcommittee SC 1, *Analytical methods*.

A list of all parts in the ISO 16921 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

Modern biotechnology relies on the ability to manipulate genes and genomes in living systems. Gene delivery systems are foundational to genome engineering. Gene delivery technology is evolving rapidly with numerous types of gene delivery systems providing a comprehensive set of tools and capabilities for in vitro or in vivo targeted delivery.

The ISO 16921 series consists of multiple parts to provide common understanding, guides, analytical methods and, data reporting for characterizing these emerging biotechnology tools. ISO 16921-1 specifies Vocabulary related to gene delivery systems. This document (ISO 16921-2) focuses on quantification of one type of gene delivery system, viral vectors.

Viral vectors are engineered viruses for delivering the desired genetic payload into target cells. Viral vectors are powerful molecular biology tools and have been increasingly used in broad biotechnology applications and products. Various types of viral vectors are used as advanced gene therapies, as vaccines, and as critical reagents for cellular therapies. They have also been increasingly used in genome editing applications. Viral vector titer (titre) is central to all applications. Robust measurements for the quantification and reporting of viral vector titer are important for the industry. This document provides general guidance for viral vector titer as well as aspects of functional analysis including method selection, sample preparation, measurement, qualification and validation, data analysis and reporting.

Biotechnology — Gene delivery systems —

Part 2: Quantification methods for viral vectors

1 Scope

This document specifies minimum requirements for quantifying viral vectors in terms of physical titer and their associated activity. This document specifies key considerations for quantification methods for viral vector titer as well as activity, including method selection, measurement process, data analysis, and reporting.

2 Normative references

The following documents are referred to in the text in such a way that some or all of their content constitutes requirements of this document. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

ISO 16921-1, *Biotechnology — Gene Delivery Systems — Part 1: Vocabulary*

ISO 20395, *Biotechnology — Requirements for evaluating the performance of quantification methods for nucleic acid target sequences — qPCR and dPCR*

3 Terms and definitions

For the purposes of this document, the terms and definitions given in ISO 16921-1 and the following 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
direct particle counting
counting method in which one signal is (or several signals are) detected for each single event

Note 1 to entry: Each single event represents a single viral particle in an idealized measurement

3.2
indirect particle counting
counting method during which a signal (or a set of signals) is measured from a population of viral particles and that signal is then related to viral titer based on a measurement-specific mathematical model (e.g. calibration curve)