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Interested committees:

Title: Draft BS ISO 20397-3 Biotechnology - Massively parallel sequencing. Part 3: General requirements and guidance for metagenomics.

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Introduction

This draft standard is based on national and international discussions. Your comments on this draft are invited and will assist in the preparation of the consequent standard.

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Template for comments and secretariat observations

Date: xx/xx/20xx	Document: ISO/DIS xxxx
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1	2	(3)	4	5	(6)	7
MB	Clause No./ Subclause No./Annex (e.g. 3.1)	Paragraph/ Figure/Table/Note	Type of comment	Comment (justification for change) by the MB	Proposed change by the MB	Secretariat observations on each comment submitted
	3.1	Definition 1	ed	Definition is ambiguous and needs clarifying.	Amend to read '...so that the mains connector to which no connection...'	
	6.4	Paragraph 2	te	The use of the UV photometer as an alternative cannot be supported as serious problems have been encountered in its use in the UK.	Delete reference to UV photometer.	



DRAFT International Standard

ISO/DIS 20397-3

Biotechnology — Massively parallel sequencing —

Part 3: General requirements and guidance for metagenomics

ICS: 07.080

ISO/TC 276/SC 1

Secretariat: **ANSI**

Voting begins on:
2024-09-16

Voting terminates on:
2024-12-09

This document is circulated as received from the committee secretariat.

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Foreword

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

A list of all parts in the ISO 20397 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

Massively parallel sequencing (MPS) is a high-throughput analytical approach to nucleic acid sequencing utilizing massively parallel processing, that allows whole genomes, transcriptomes, and specific nucleic acid targets from different organisms to be investigated in a relatively short time.

Metagenomics approaches are extremely powerful strategy in large-scale genomics applications as a way to study the taxonomic and functional composition of microbial communities from environmental, agricultural, and clinical primary samples/samples. Metagenomics does not require to isolation of single bacterium from complex microbial mixtures, but catalogs by sequencing all genes and genomes from mixtures. It has great advantages to identify new species, including microorganisms that are difficult to cultured under typical laboratory conditions.

Metagenomics, whole genomic DNA is prepared from primary samples, regardless of its microbial composition and is characterized by whole genome sequencing. The assignment of resulting DNA fragments, individual reads or assembled sequence contigs, to individual taxonomic groups or known genome sequences is carried out by sophisticated bioinformatic tools. The analysis is not only traditional MPS pipeline, but more focus on identification of functional composition of a microbial community based on the assignment of protein-coding open reading frames to functional categories, such as protein domain families or Gene Ontologies. Consequently, analysis of whole genome sequencing (WGS) metagenomics data sets involves a large statistical component, as sequence data must be evaluated based on relative abundances rather than on absolute presence/absence data.

