DIN ISO 20397-3:2026-10 (E)

Biotechnology - Massively parallel sequencing - Part 3: General requirements and guidance for metagenomics (ISO 20397-3:2025)

Contents

Page

Foreword ... **iv**

Introduction ... **v**

1 Scope ... **1**

2 Normative references ... **1**

3 Terms and definitions ... **1**

4 Principle ... **4**
4.1 General ... 4

5 Sampling strategy ... **5**
5.1 General ... 5
5.2 Primary sample type ... 6
5.3 Primary sample stabilization and storage ... 6
5.4 Primary sample transportation ... 6
5.5 DNA/RNA isolation ... 7
5.6 DNA/RNA sample quality ... 7

6 Nucleic acid library preparation ... **7**

7 Design and review process including sequencing strategy and assessment ... **7**
7.1 General ... 7
7.2 Short read ... 7
7.3 Long read ... 8
7.4 Hybrid assembly ... 8
7.5 Sample preparation and library construction ... 8
7.6 Assessment ... 8

8 Database construction ... **9**
8.1 General ... 9
8.2 Public database ... 9
8.3 Self-build database ... 9

9 Bioinformatics analysis ... **10**
9.1 General ... 10
9.2 Identification list of microorganisms ... 11

10 Validation and verification ... **11**
10.1 General ... 11
10.2 In silico sequence control for bioinformatics pipeline evaluation ... 11
10.3 Real sample control for pipeline evaluation ... 11

11 Evaluation ... **12**

12 Test report ... **12**
12.1 General ... 12
12.2 Test report content ... 12

Annex A (informative) **Checklist for NA sample quality assessment before library construction** ... **13**

Annex B (informative) **Methods for sample stabilization and storage** ... **14**

Annex C (informative) **Bioinformatics pipeline** ... **15**

Bibliography ... **17**