RNA and DNA sequencing and bioinformatic services through a third-generation long-read sequencing platform

Summary

Profile type	Company's country	POD reference
Technology offer	**Italy**	**TOIT20250401015**
Profile status	**Type of partnership**	**Targeted countries**
PUBLISHED	**Research and development cooperation agreement** **Commercial agreement with technical assistance**	• **World**
Contact Person	**Term of validity**	**Last update**
Enrico FRANZIN	**4 Apr 2025** **4 Apr 2026**	**4 Apr 2025**

General Information

Short summary

An Italian biotech company provides RNA and DNA sequencing services and detection of base modifications through the Oxford Nanopore third-generation platform, enabling long-read sequencing unlike traditional technologies. Based on customer needs, bioinformatic analyses of data produced from other platforms are also provided.
The SME is both looking for partners to target European grants in healthcare and life sciences or customers interested in RNA, DNA sequencing and/or epigenetic analyses.

Full description

An Italian biotech company based in Rome provides RNA and DNA sequencing services through a third-generation sequencing platform, enabling long-read sequencing unlike traditional technologies. This methodology allows for the (1) accurate quantification and characterization of full-length transcripts (RNA-Seq), (2) identification of single nucleotide and structural DNA variations (DNA-Seq), and (3) detection of base modifications (i.e. DNA Methylation).
The long-read RNA-seq allows for the accurate quantification and characterization of full-length transcripts, which is crucial to unambiguously identifying splice variants and fusion transcripts. Starting from 100k cells or 500 ng of total RNA, we can perform a complete workflow producing ready-to-use material for publication.
With the same platform the SME also offers complete Whole Genome Sequencing, starting from either pellet of cells or extracted DNA, to produce raw data and Genome-Wide Association Study (GWAS) reports. Whole genome sequencing provides an extensive overview of single nucleotide variant (SNV) and structural variation (SV). This long

reads technology additionally allows for the sequencing of telomeres, centromeres, and highly variable regions.
In addition, validated methods are available to define RNA Seq and DNA methylation dynamics with or without an in-vitro stimulation to investigate the molecular effects on cells or tissues.

Lastly, using just 1ug of DNA or 500K cells, the company can provide whole genome DNA methylation profile, investigating differentially methylated sites and their enrichment for DNA-binding proteins. To date, the SME can detect 5-methylcytosine (5mC), 5-hydroxymethylcytosine (5hmC), and N6-methylcytosine (6mA) base modifications. The latter was recently discovered to also be present in the human genome. Base modifications are important epigenetic mechanisms that regulate gene expression, and the used sequencing platform directly identifies base modifications at single nucleotide resolution without any chemical steps, such as bisulfite conversion.
The company offers state-of-the-art tools for data management of raw big data generated from biological samples and bioinformatic pipelines for the analysis and interpretation of multi-omics results.

The technological and knowledge value underlying the services offered is the result of years of scientific research in the laboratories of the Department of Systems Medicine at the University.

Advantages and innovations

The team has a strong multidisciplinary composition as it is composed of physicians, biotechnologists, and a bioinformatician, covering the diverse areas of expertise required to generate, analyze, and interpret data. Long-read technology through the Nanopore Oxford platform offers several advantages, including reducing assembly fragmentation, accurately resolving repetitive sequences, enabling the detection of structural variants, and improving metagenomic analysis by allowing better species resolution.
Thus, the ability to explore transcriptomics, genomics, and epigenomics has broad applications, ranging from agri-food to health sciences. These approaches can be used, for example, to assess the effects of an intervention or identify biomarkers of a disease.

Technical specification or expertise sought

Stage of development

Already on the market

IPR Status

No IPR applied

IPR Notes

Sustainable Development goals

- **Goal 3: Good Health and Well-being**

Partner Sought

Expected role of the partner

Possible applications range from the agri-food sector to the health science to investigate RNA- DNA whole sequence and DNA methylation dynamics to investigate the effect of an intervention.

Type of partnership

Research and development cooperation agreement

Commercial agreement with technical assistance

Type and size of the partner

- **SME 50 - 249**
- **University**
- **SME <=10**
- **SME 11-49**
- **R&D Institution**

Dissemination

Technology keywords

- **06003002 - Gene Expression, Proteome Research**
- **06003001 - Bioinformatics**

Market keywords

- **04015 - Gene Expression, Proteome Research**
- **04014 - Bioinformatics**

Targeted countries

- **World**

Sector groups involved