# Article information:

Approaching complete genomes, transcriptomes and epi-omes with accurate long-read sequencing | Nature Methods
<https://www.nature.com/articles/s41592-022-01716-8>

# Article summary:

1. Long-read sequencing has improved dramatically in the past decade, allowing for the first complete human telomere-to-telomere (T2T) genome to be published.

2. Long reads are intrinsically more suited to resolving repetitive sequences like long terminal repeat (LTR) retrotransposons or long interspersed nuclear elements (LINEs).

3. Improvements to biotechnology and bioinformatics have been necessary for this revolution, with signal-level analysis, epigenomics and epitranscriptomics being key techniques.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article is generally reliable and trustworthy, as it provides a comprehensive overview of the current state of accurate long-read sequencing technology and its applications. The article is well researched and provides evidence for its claims, such as citing the publication of the first complete human telomere-to-telomere (T2T) genome based entirely on long reads1 and discussing how using the T2T genome as a reference improves the analysis of globally diverse samples2. The article also discusses how long reads have substantially improved the genome, transcriptome and epigenome sequences in many other humans and non-human species4,5,6,7.

The article does not appear to be biased or one-sided in its reporting; it presents both sides of the argument fairly by discussing both early challenges with long read sequencing technology as well as its current successes. It also acknowledges that improvements to biotechnology and bioinformatics have been necessary for this revolution.

The article does not appear to contain any unsupported claims or missing points of consideration; all claims are backed up by evidence from relevant studies cited throughout the text. Additionally, all potential risks associated with long read sequencing technology are noted in detail throughout the text.

In conclusion, this article is reliable and trustworthy due to its comprehensive coverage of accurate long read sequencing technology and its applications without any bias or unsupported claims present in its reporting.

# Topics for further research:

* Long read sequencing technology accuracy
* Long read sequencing technology applications
* Long read sequencing technology challenges
* Long read sequencing technology biotechnology
* Long read sequencing technology bioinformatics
* Long read sequencing technology risks

# Report location:

<https://www.fullpicture.app/item/abdc9748fc5b0b06531d2324cd828013>