# Article information:

The complete sequence of a human genome
<https://www.science.org/doi/epdf/10.1126/science.abj6987>

# Article summary:

1. The Telomere-to-Telomere (T2T) Consortium has released a complete 3.055 billion–base pair sequence of a human genome, T2T-CHM13.

2. This sequence includes gapless assemblies for all chromosomes except Y, corrects errors in the prior references, and introduces nearly 200 million base pairs of sequence containing 1956 gene predictions.

3. The completed regions include all centromeric satellite arrays, recent segmental duplications, and the short arms of all five acrocentric chromosomes, unlocking these complex regions of the genome to variational and functional studies.

# 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 is based on research conducted by the Telomere-to-Telomere (T2T) Consortium which is composed of experts from various fields such as bioinformatics, systems biology, molecular biology and genetics. The article provides detailed information about the research conducted by the consortium and its findings which are backed up by evidence from other sources such as previous research papers and studies.

The article does not appear to be biased or one-sided as it presents both sides of the argument equally and objectively. It also does not contain any promotional content or partiality towards any particular viewpoint or opinion. Furthermore, it does not make any unsupported claims or missing points of consideration that could lead to misinterpretation or misunderstanding of the findings presented in the article.

The article also mentions potential risks associated with this research such as incomplete assembly due to underrepresentation of repetitive sequences in bacterial artificial chromosomes (BACs). It also acknowledges that some gaps in GRCh38 are unsolvable due to incompatible structural polymorphisms on their flanks and that many other repetitive and polymorphic regions were left unfinished or incorrectly assembled.

In conclusion, this article is reliable and trustworthy as it provides detailed information about the research conducted by the T2T Consortium along with evidence from other sources to back up its claims. It also does not appear to be biased or one-sided as it presents both sides of the argument equally without making any unsupported claims or missing points of consideration that could lead to misinterpretation or misunderstanding of its findings.

# Topics for further research:

* Telomere-to-Telomere Consortium
* GRCh38 assembly
* Bacterial Artificial Chromosomes
* Structural Polymorphisms
* Repetitive Sequences
* Genome Assembly Challenges

# Report location:

<https://www.fullpicture.app/item/4375b66a9f1e2eae4a1e7e65693ff0a6>