

## Hi-C: Quick genome sequencing cracked Zika mosquito genome, more advances likely

Ten years ago, a team of scientists published the [first genome of \*Aedes aegypti\*](#)—the infamous mosquito that spreads Zika, dengue fever, and yellow fever. It was a valiant effort, [but also a complete mess](#)...But [now], a team of scientists led by [Erez Lieberman Aiden](#) at the Baylor College of Medicine announced that they had finally [knitted those pieces into a coherent whole](#)....

This milestone is about more than mosquitoes. The team succeeded by using a technique called Hi-C, which allows scientists to assemble an organism's genome quickly, cheaply, and accurately. To prove that point, the team used Hi-C to piece together a human genome from scratch for just \$10,000; by contrast, the original Human Genome Project took \$4 billion to accomplish the same feat.

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But [Erich Jarvis](#) from Rockefeller University, who is leading one of these dauntingly ambitious projects, says the future lies in pairing Hi-C with new sequencing technologies that can read longer stretches of DNA. That would provide higher-quality pieces for Hi-C to then stitch together.

[Read the original source [here](#)]

**The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [The Game-Changing Technique That Cracked the Zika-Mosquito Genome](#)**

**For more background on the Genetic Literacy Project, read [GLP on Wikipedia](#)**