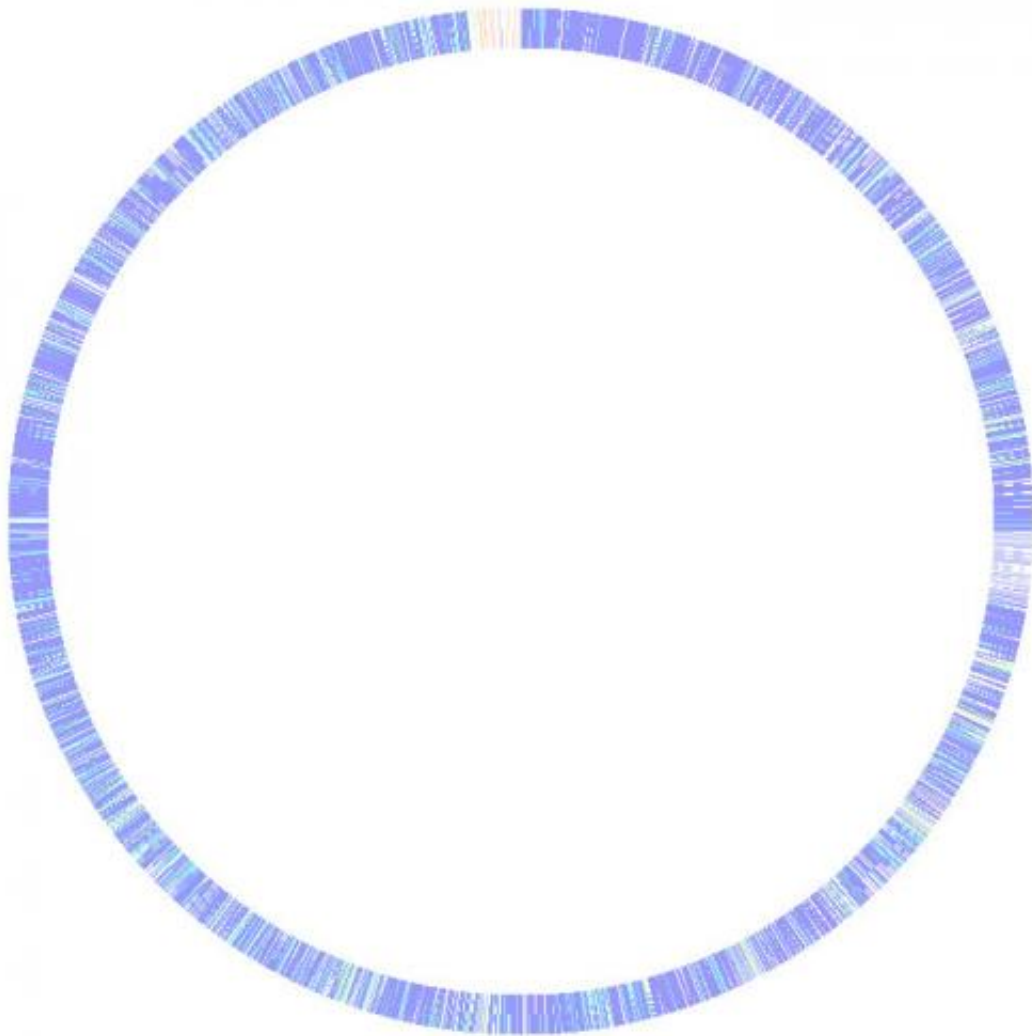


# Scientists sequence complete genome of *E. coli* strain responsible for food poisoning

September 1 2014, by Catherine Hockmuth

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UC San Diego bioengineers have completed the genome sequencing of a particularly harmful strain of *E. coli* that has been tied to outbreaks of food poisoning. The circular map shows the completed sequence with lighter color regions representing gaps in a 2001 sequencing of the strain that have now been

completed with current technology. Credit: The Systems Biology Research Group at UC San Diego.

(Phys.org) —Researchers at the University of California, San Diego have produced the first complete genome sequencing of a strain of *E. coli* that is a common cause of outbreaks of food poisoning in the United States. Although the *E. coli* strain EDL933 was first isolated in the 1980s, it gained national attention in 1993 when it was linked to an outbreak of food poisoning from Jack-in-the-Box restaurants in the western United States.

Their paper published online Aug. 14 in the journal *Genome Announcements* reports the full, complete sequence with no gaps. Their analysis includes so-called jumping genes that can move around the same genome, sometimes causing damage to individual genes or enabling antibiotic resistance.

"With a [complete genome sequence](#), we can now pinpoint the precise location of all such elements, which might help to track and treat future outbreaks," said Ramy Aziz, the senior author on the paper. Aziz led the research as a visiting scientist working in Bernhard Palsson's Systems Biology Research Group at UC San Diego Jacobs School of Engineering. Aziz is also a professor at Cairo University in Egypt.

The [genome sequence](#) for this historical strain was first published in 2001, but there were many gaps in the genome that could not be closed with the sequencing technology available to scientists in 2001. Given the importance of this strain as a major cause of [food poisoning](#), Palsson's Systems Biology Research Group recently sequenced its genome using a combination of sequencing data from instruments made by Pacific Biosciences and Illumina.

"New sequencing and assembly methods are enabling a full expose of pesky pathogens; there is no place to hide genetic characteristics anymore. The full genetic delineation of multiple pathogenic strains is likely to not only improve our understanding of their characteristics, but to find and exploit their vulnerabilities, said Palsson, the Galletti Professor of Bioengineering at UC San Diego.

**More information:** Paper:  
[genomea.asm.org/content/2/4/e00821-14.full.pdf](https://genomea.asm.org/content/2/4/e00821-14.full.pdf)

Provided by University of California - San Diego

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