

# MEGA evolutionary software re-engineered to handle today's big data demands

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A Temple University-led research team has released a new version of their popular MEGA (Molecular Evolutionary Genomics Analysis) software, one of the most highly downloaded and widely used tools used by scientists worldwide to harness large-scale DNA sets for comparative studies.

At its core, MEGA is a powerful bioinformatics tool designed to help researchers identify key patterns among the diversity and complexity of life on Earth, and unravel the mysteries of human evolution, health and disease coded within the genome.

The [MEGA7 edition](#), developed by Temple University professor Sudhir Kumar, Glen Stecher and Tokyo Metropolitan University professor Koichiro Tamura, represents the most sophisticated, powerful and advanced version yet, designed to extend its use to ever more complex and large DNA analysis datasets.

"We've done a significant upgrade of MEGA, which was necessary to speed up the data-crunching time and memory usage with 64 bit processors, and much larger memory space to handle gigabytes of data, so now people can analyze an ever larger amount of sequences," said Kumar, who directs the Institute for Genomics and Evolutionary Medicine at Temple.

For Kumar, making the software freely available to the [scientific community](#) is a key to propelling worldwide evolutionary discoveries.

"MEGA has been freely available for over 20 years for any use, spanning research, teaching and industry. We enable people throughout the world, including developing nations, to use fundamental technologies that are needed to address these burgeoning sequence databases.

"Everyone in the world should be able to use evolutionary and genomics tools to analyze the wealth of information that is being produced relating the genomes of humans to pathogens, to disease to traits, to uncover our similarities and differences. It will take all of our global efforts to do so. The most important thing is to develop user-friendly, sophisticated software for use by all."

MEGA has one of the largest user-bases, and has been downloaded more than 1.1 million times across 184 countries. The latest improvements are only likely to increase its usage in the scientific community, MEGA is cited in more than 10,000 publications annually, making it one of the most cited bioinformatics tools in teaching and research for those uncovering the secrets of the complex, 4 billion year [evolutionary history](#) of life on Earth.

**More information:** *Molecular Biology and Evolution*,  
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