

## UC San Diego Scientists Share in \$57 Million Study of Model Genomes

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Researchers at the University of California, San Diego are among the teams of scientists nationwide charged with building a comprehensive catalog of two animal genomes. The four-year, \$57 million project - Model Organism Encyclopedia of DNA Elements, or modENCODE - involves smaller teams conducting research to support the greater overall task. It is intended as an important adjunct to ENCODE, an even larger effort to generate a similar catalog for the human genome.

James W. Posakony, professor of biological sciences at UC San Diego, and Bing Ren, assistant professor of cellular and molecular medicine at UC San Diego's Ludwig Institute, are part of a consortium awarded \$9.1 million over four years to map all the transcriptional regulatory elements of the fruit-fly genome.

The goal of the modENCODE research, like that of the larger project it supports, is creating a "parts list" of all elements of the genome crucial to biological function. What the UC San Diego scientists learn from their modENCODE work on fruit flies will help colleagues elsewhere apply their results to their maps of the human genome.

In contrast to the human genome, which has about three billion base-pair elements, the simpler organisms have about 150 million base-pairs, making them easier to study and catalog.

"Right now," Posakony said, "we're very good at reading the parts of the genome that code for proteins. But the protein-coding parts are only a small, even a tiny, minority of the typical animal genome. Much of the rest of the sequence - the part we don't understand so well - is rich in regulatory elements: the bits of the genome containing instructions for when, and in what tissues, the genes are to be expressed."

The consortium that includes UC San Diego has as its goal to identify all those regulatory sequences in the fruit fly, said Posakony. "From this, we hope to develop the ability to actually decode the regulatory elements so that - given a new genome sequence - we could not only recognize its regulatory bits, but we could also 'read' their code to determine what instructions they give to the genes."

The modENCODE project awards were announced by the U.S. National Human Genome Research Institute (NHGRI). Scientists have been working on preliminary ENCODE research since 2003.

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