

# Rat Genome Database

## Disease Centric Rat Gene Initiative

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### ABSTRACT

The rat is an ideal whole organism model for human disease. It has become the most widely studied experimental animal model for biomedical research and since 1966, more than 500,000 research articles reporting the use of rats have been published. In addition, more than 200 inbred strains of rats have been developed, most selected for specific disease characteristics. The infrastructure for using the rat as a model organism to identify disease genes already exists. The Rat Genome Database houses genetic and genomic data on genes, SSLPs, ESTs, sequences, QTLs, maps and strains. A comprehensive RH map of the rat as well as a Virtual Comparative Map for rat, human and mouse are also available. Analysis tools such as RH Mapper, Metagene, Genome Scanner and the VC Map Tool have been created for researchers to analyze rat data. The Rat Genome Sequencing Project is now underway and the amount of available genome sequences will increase in the months to come. To build on the resources already available and to develop new resources for disease gene identification, the Bioinformatics Research Center is launching the Disease Centric Rat Gene Initiative. This initiative is a worldwide effort to collect, annotate, and curate all the genes associated with each disease identified as having a profound impact on the human population. The program will involve the Rat Genome Database, Sequence Annotation Pipelines,

Microarray Analysis and Electronic Knowledge Retrieval techniques to integrate disparate data for disease gene identification. A secondary goal of the initiative is to captivate the interest of the rat research community and to provide a forum to expedite the identification of new genes potentially important in disease. Although this initiative focuses on the rat, through homology and comparative mapping techniques, results and findings can be promulgated to mouse and human.

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### REFERENCES

[1] Rat Genome Database web site: <http://rgd.mcw.edu>.