



Putative-Gene Classification. The figure depicts the functional classification of putative genes identified in a 1.02-Mb region on the long arm of human chromosome 19. Analysis of the completed sequence between markers D19S208 and COX7A1 revealed 43 open reading frames (ORFs) or putative genes. (An ORF is a DNA region containing specific sequences that signal the beginning and ending of a gene.)

Thirty of these putative genes were found to have sequence similarities to a wide variety of known genes or proteins, including some involved in transcription, cell adhesion and signaling, and metabolism. Many appear to be related functionally to such known proteins as the GTP-ase activating proteins or the ETS family of transcription factors. Others seem to be new members of existing gene families, for example, the mRNA splicing factor, or of such pseudogenes as the elongation factor Tu.

In addition to those that could be classified, 13 novel genes were identified, including one with high similarity to a predicted ORF of unknown function in the roundworm *Caenorhabditis elegans*. [Source: Adapted from graph provided by Linda Ashworth, LLNL]

clones (from anywhere in the human genome) that relate to susceptibility genes, for example, DNA repair. These clones will be characterized and provided for sequencing and at the same time contribute to understanding the biology of the chromosome, the genome, and susceptibility factors. The mapping team also collaborates with others using the chromosome 19 map as a resource for gene hunting.

Functional Genomics

The functional genomics team is responsible for assembling and characterizing clones for the Integrated Molecular Analysis of Gene Expression (called IMAGE) Consortium and cDNA sequencing, as well as for work on gene expression and comparative mouse

genomics. The effort emphasizes genes involved in DNA repair and links strongly to LLNL's gene-expression and structural biology efforts. In addition, this team is working closely with Oak Ridge National Laboratory (ORNL) to develop a comparative map and the sequence data for mouse regions syntenic to human chromosome 19 (see p. 32).

Informatics and Analytical Genomics

The informatics and analytical genomics group provides computer science support to biologists. The sequencing informatics team works directly with the DNA sequencing group to facilitate and automate sample handing, data acquisition and storage, and DNA sequence analysis and annotation. The

