

# DRAGON: Database Referencing of Array Genes ONline

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## **Abstract**

**Motivation:** Microarray technology allows the detection of the expression of thousands of genes simultaneously. The large data sets generated by microarray experiments promise to increase in size and complexity as genome sequencing projects extend our knowledge base. Therefore, the development of bioinformatics tools that aid in the analysis of microarray data sets is crucial to understanding microarray results and to the further development of microarray technology.

**Results:** We have developed “Database Referencing of Array Genes ONline” or “DRAGON”. DRAGON is a database that consists of information derived from publicly available databases including UniGene, SWISS-PROT, TrEMBL, Pfam, Transfac, OMIM and Interpro. DRAGON rapidly supplies information pertaining to a range of the biological characteristics of a majority of the genes in any microarray data set. The subsequent inclusion of this information during the analysis of microarray data allows for deeper insight into gene expression patterns. We have analyzed publicly available microarray data sets with DRAGON to demonstrate its use.

**Web Site:** [www.kennedykrieger.org/pevsnerlab/dragon.htm](http://www.kennedykrieger.org/pevsnerlab/dragon.htm)

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