Using the proprietary high-content linguistics tool MedScan we compiled a comprehensive database of molecular networks by extracting the information from scientific literature. MedScan is capable of extracting functional associations between proteins, small molecules, and pathways, recognizes types of regulatory mechanisms involved, effects of regulation and experimental conditions. The resulting database stores 900,000 relationships between mammalian proteins and chemicals including facts about protein interactions, promoter binding, modification and protein regulation. Different approaches towards reconstructing individual pathways or cascades from this database and reconstructing networks from microarray data will be described. Our visualization software is capable of systematically mining this database for small network motifs that are robust in regard to the effects induced at the gene expression levels. We have also developed a Bayesian framework for integration of microarray data and binary gene-to-gene regulatory relationships. The approach allows the reduction of expression pattern complexity and finds the minimal set of regulatory proteins that are responsible for differential expression of other genes.