• 計畫中文名稱	建立以微陣列及知識爲基礎的人類疾病及基因之線上資料庫		
• 計畫英文名稱	Microarray and Knowledge-Based on-line Database on the Relationship of Human Diseases and Genes		
• 系統編號	PC9308-1844	• 研究性質	基礎研究
• 計畫編號	NSC93-2320-B038-043	• 研究方式	學術補助
• 主管機關	行政院國家科學委員會	• 研究期間	9308 ~ 9407
• 執行機構	台北醫學院醫學資訊研究所		
• 年度	93 年	• 研究經費	920 千元
• 研究領域	基礎醫學類, 資訊科學--軟體		
• 研究人員	李元綺,邱泓文,徐建業		
• 中文關鍵字	--		
• 英文關鍵字	--		
• 中文摘要	查無中文摘要		
• 英文摘要	The relationship of genes and diseases has gained more and more attention. However, most of the genetic disorders featured on the gene-disease relationship database are limited and incomplete. It lacks of an overview of whole genome expression profiling in respect of a disease or tumor. After release of human genome sequences and the development of new technologies, such as microarray, we will be able to detect the genome alteration of a tumor. Here we present an on-line database featuring human diseases and related genes, which includes powerful Serial Analysis Gene Expression (SAGE) database, Online Mendelian Inheritance in Man (OMIM) database, PubMed/Medline literature database, and above all, for the first time, we have included published microarray results. While not yet complete, continued growth of data from cancer microarray bring us ever closer to a complete human disease. All the microarray datasets used in this database have been re-generalized using Minimum Information About Microarray Experiments (MIAME) in MicroArray Gene Expression Markup Language (MAGE-ML) format. This on-line database provides an exhausted analysis of the detailed relationship of genes and diseases by a variety of microarray algorithms and can be access in a user-friendly fashion with multiple search entries. The associated group of genes has been displayed with detailed annotation and further analyzed for the upstream and downstream relationship in biochemical pathways, gene-ontology assignment distribution and promoter network. The results can be visualized with three-dimension animation with user-centric interphase. The database is built and aimed for unraveling the networks of events, which undoubtedly is a challenge for some time to come, and will be a fundamental resource in future		

	pathology.