十一、研究計畫中英文摘要：請就本計畫要點作一概述，並依本計畫性質自訂關鍵詞。

（二）計畫英文摘要。（五百字以內）

Keywords：ChIP database, transcription regulation, binding site, phylogenetic footprinting.

Identification of transcription factor binding sites is a major challenge to the understanding of gene expression regulation. Understanding the regulation of gene expression requires a complete knowledge of the regulation process and all related elements. We have designed and developed a system to predict transcription factors from gene groups by a computational approach combined with other published methods and tools (Huang et al. 2004). One of the drawbacks is the high false positive rate of prediction. To overcome this problem, we propose in this project to create a ChIP database and develop methods that integrate our system with new experimental techniques and related knowledge to improve accuracy of transcription factor binding site prediction. The proposed database collects various types of ChIP experimental results, integrates the tools used in analysis or representation of the ChIP data and will provide a useful interface for the database users. The creation of a ChIP database will be a significant contribution to experimental verified knowledge on transcription factor binding. The database knowledge will help to construct a more accurate prediction model. We will then use the database to develop methods to predict transcription factor binding sites using real binding profiles from the ChIP database and an integration of new computational approaches. Inputted co-expressed genes will be clustered by the new approach and then used to discover conserved features in their upstream regions. Structural information such as phylogenetic conservation and the presence of CpG-islands will be used to improve the precision of prediction. We will also design into the system a process that analyzes genome active regions in order to present chromosomal structural effects. Finally, biological functional analysis display of target genes will provide information on the biological regulation of gene function by transcription binding factors.

The construction of the ChIP database system and the development of the proposed approach are expected to improve the accuracy of transcription factor binding site prediction. In addition, an accurate binding model should be developed that will reveal the real basis of cellular regulation mechanisms.