

# The Construction of the Knowledge Base on Apoptotic Molecular Interactions

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## Abstract

*For the purpose of an analysis of apoptotic molecular interactions, we have developed the knowledge base on apoptosis, which consists of molecular interactions concerning apoptosis reported in experimental papers. We have collected about 80 entries, where one entry is corresponding to one molecule, and each entry contains their interaction information.*

## 1 Introduction

Apoptosis, which is accompanied with an active proteolysis and nucleosome level DNA incisions, is a characteristic form of cell death [1]. The apoptotic dying cells will be absorbed into other living cells and their bio-material, for instance an amino acid or a nucleotide, seems to be recycled within those living cells. This type of cell death plays important roles in tissue and organ development in ontogenesis and homeostasis of living body. It is also known that apoptosis relates to some diseases such as autoimmune disease, virus infection or cancer. Furthermore many drugs such as anticancer agents take effect via induction of apoptosis in the target cells.

With such a background the studies on apoptosis have become popular and recently many experimental facts have been reported. The authors propose the findings of new apoptotic related genes or molecules and the determination of relationships among those specific molecules. They also suggest that the cell death mechanism like apoptosis has been incorporated and diversified into animals during their evolutionary history but its main system has been conserved from *C.elegans* to *H.sapiens* [3].

Therefore in order to understand its whole mechanism it is very important to analyze apoptotic pathways in the viewpoint of molecular interactions in different species. However, there are few comparative and systematic studies, because no computerized database exists for available knowledge on apoptosis. To achieve this, we have developed the new knowledge base focusing on interactions among those apoptotic molecules, like BRITE [2] database.

## 2 Knowledge base

Fundamentally our knowledge base is made as a flat file format and contains about 80 entries, where each entry corresponds to each apoptotic molecule, and contains information about interactions to other apoptotic molecules, and links to other sequence databases or reference papers, to assist a detail analysis. An example of our knowledge base is shown in Fig.1.

Our knowledge base is not yet made available as a WWW service, but we plan to incorporate these data into BRITE and open to the public.

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ENTRY      BAG1
NAME       BAG-1
           Bcl-2 associated athanogene 1
           glucocorticoid receptor-associated protein RAP46
CLASS      protein
FAMILY     Bcl-2
RELATION
TO         BCL2; Bcl-2
TYPE       direct;bind;enhance
MEDLINE    95136360
AUTHOR     Takayama S, Sato T, Krajewski S, Kochel K, Irie S, Millan JA,
           Reed JC
TITLE      Cloning and functional analysais of BAG-1: a novel Bcl-2-binding
           protein with anti-cell death activity
JOURNAL    Cell, 80:279-284, 1995
SPECIES    Mus musculus; mouse
DBLINKS
           SWISSPROT:BAG1_MOUSE
           SWISSPROT:BAG1_HUMAN
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Figure 1: the sample of knowledge base entry

### 3 Analysis

In this knowledge base, each molecular interaction is represented as a link between two entries. This is an advantage for analysis of the apoptosis, when we consider that the molecular network is important to understand the cell death mechanism. We are trying some analytical works such as, 1) search homologues against known genomes, 2) make an orthologous table of apoptotic molecules, 3) compare two pathways, to make sure if there exists a biologically similar path, within the same species, 4) do the same thing but among several species, for example from *C.elegans* to *H.sapiens*, 5) compare pathways against other biological networks.

### Acknowledgments

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### References

- [1] Kerr, J.F., Wyllie, A.H., Currie, A.R., "Apoptosis: a basic biological phenomenon with wide-ranging implications in tissue kinetics," *Brit. J. Cancer*, 26:239-257, 1972.
- [2] Tsukamoto, N. and Kanehisa, M., "A WWW Tool for Organizing Knowledge of Biomolecular Reaction Pathways," *Proc. Genome Informatics Workshop 1995*, Universal Academy Press, 158-159, 1995.
- [3] Yuan, J., Shaham, S., Ledoux, S., Ellis, H.M., Horvitz, H.R., "The *C.elegans* cell death gene *ced-3* encodes a protein similar to mammalian interleukin-1 beta-converting enzyme," *Cell*, 75:641-652, 1993.