

# “Piment” and “Macaroni”: Nervous System Protein Database

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## 1 Introduction

We recently conducted a systematic molecular phylogenetic analysis for evolutionary study of the nervous system (Tomiki and Saitou, unpublished). We collected amino acid sequence data and related information of synthases, receptors and transporters for neurotransmitters, and those for ion channels. Receptors, transporters and ion channels are important proteins for neurotransmission. We constructed nervous system protein databases to support molecular phylogenetic analysis. The two databases, “Piment” and “Macaroni”, help us to analyze molecular phylogenetic analysis of proteins in neurotransmission and approach the answer about the evolution of nervous system.

## 2 Method and Results

### 2.1 Database Construction

We retrieved the amino acid sequences of synthases, receptors and transporters for neurotransmitters, and the sequences of ion channels from SWISS-PROT and TrEMBL [1]. The amino acid sequences were integrated into the web-based SQL databases (PostgreSQL [2]), the database for ion channels and the database for synthases, receptors and transporters of neurotransmitters. We named the former one “Piment” [3] and the latter one “Macaroni” [4], after the overall molecular shape of the voltage-gated potassium channel and GPCR respectively.

The two databases share the same tables, because of easy maintenance. Ligand-gated channel is categorized into both ion channel and receptor. If the two databases use different tables independently, administrators, namely ourselves, of the databases must input data of ligand-gated channel two times. The five tables are shared by the two databases, and each table has relationships to other tables. Categories in the databases are based on the bibliographies [5, 6, 7, 8, 9], and amino acid sequences are categorized by molecular phylogeny.

### 2.2 Database Operation

Database users can get amino acid sequences which they want via multi FASTA format, can conduct multiple alignment, and can construct phylogenetic trees, by easy operation. Database operation is written in the figure legend in Figure 1.

## 3 Discussion

Macaroni database helps us to analyze molecular phylogeny of neurotransmitter receptors [11]. From the analysis, we revealed how functions of receptors have changed through evolution by domain changes and amino acid substitutions. We plan to integrate other neuroscientific data into our two databases and hope them to become pivotal databases in neuroscience research.

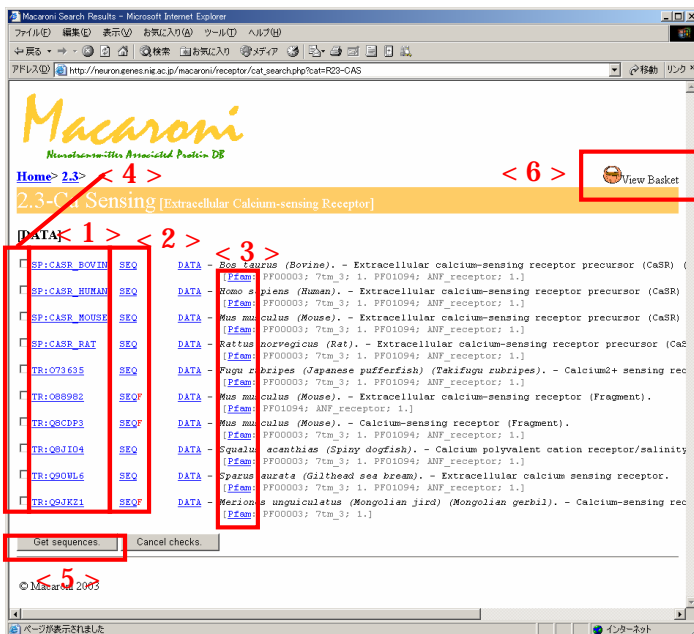


Figure 1: Features of Macaroni.

Each protein data is linked to SWISS-PROT or TrEMBL on GenomeNet [10] (<1> in Fig. 1). Amino acid sequence data of each protein is also linked to SWISS-PROT or TrEMBL on GenomeNet (<2>). If amino acid sequence data is fragment, red "F" is shown (<2>). Domain composition of each protein can be easily known by Pfam through direct link (<3>). Users can easily retrieve amino acid sequence data of proteins in Macaroni. After checking boxes of proteins of which one wants to get sequences (<4>) and clicking the "get the sequences" button (<5>), users can retrieve sequences of checked proteins. The sequences can store in virtual basket of the Macaroni site (<6>), and users can convert to some sequence formats, or do multiple alignments and construct phylogenetic tree by ClustalW on GenomeNet or DDBJ.

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