# Acknowledgement

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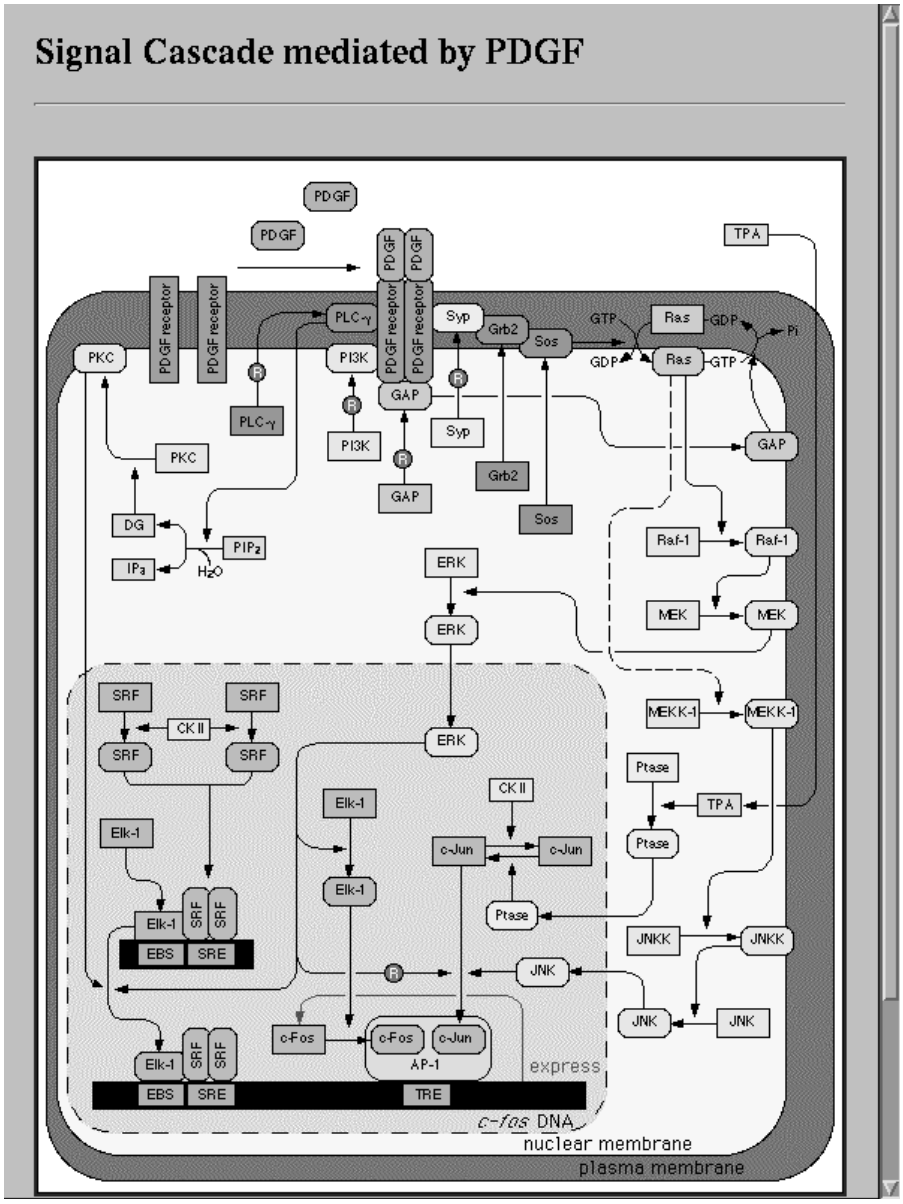


Figure 1

# An integrated database SPAD(Signaling PAthway Database) for signal transduction and genetic information

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## Abstract

Signaling transduction is suggestive of classic symphonies. Organism, like all the great composers it created, depend on masterful variations of themes.

Many studies have rapidly increased our understanding of molecular mechanisms that mediate intercellular signaling transduction. To date, many components in signaling transduction have been identified and mechanisms of the control have been modeled. However, it is important to realize how, in the cell, components are regulated in a total system.

We have been developed an integrated database SPAD(Signaling PAthway Database) based on WWW(World Wide Web) to understand the overview of signaling transduction (http://www.grt.kyushu-u.ac.jp/eny-doc/spad.html). SPAD is classified into the four categories based on extracellular signal molecule (Growth factor, Cytokine, Hormone and Stress) that initiate the intracellular signaling pathway. SPAD compiled the protein-protein interaction, protein-DNA interaction and DNA sequence information. We adopted HTML(HyperText Markup Language) and HTTPD(HyperText Transfer Protocol Daemon) to make WWW server on Sun Workstation. As shown in Figure 1, the system provides a user friendly integrated interface for signaling transduction pathways. DNA sequence information of each gene was reconstructed from GenBank entries. Protein information was linked to SWISS-PROT in GenomeNet WWW server. Reference information of each element was linked to MEDLINE in NCBI.

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