

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

Naoko Tateishi<sup>1</sup>

Haruki Shiotari<sup>1</sup>

Satoru Kuhara<sup>1</sup>

tateishi@grt.kyushu-u.ac.jp haruki@grt.kyushu-u.ac.jp kuhara@grt.kyushu-u.ac.jp

Toshihisa Takagi<sup>2</sup>

Minoru Kanehisa<sup>3</sup>

takagi@ims.u-tokyo.ac.jp kanehisa@kuicr.kyoto-u.ac.jp

<sup>1</sup> Graduate School of Genetic Resources Technology, Kyushu University

<sup>2</sup> Human Genome Center, Institute of Medical Science, The University of Tokyo

<sup>3</sup> Institute of Chemical Research, Kyoto University

## 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 PAtchway 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.

<sup>1</sup>立石直子、塩足春樹、久原 哲：九州大学大学院農学研究科遺伝子資源工学、〒812 福岡市東区箱崎 6-10-1

<sup>2</sup>高木利久：東京大学医科学研究所ヒトゲノム解析センター、〒108 東京都港区白金台 4-6-1

<sup>3</sup>金久 實：京都大学化学研究所、〒611 京都府宇治市五ヶ庄

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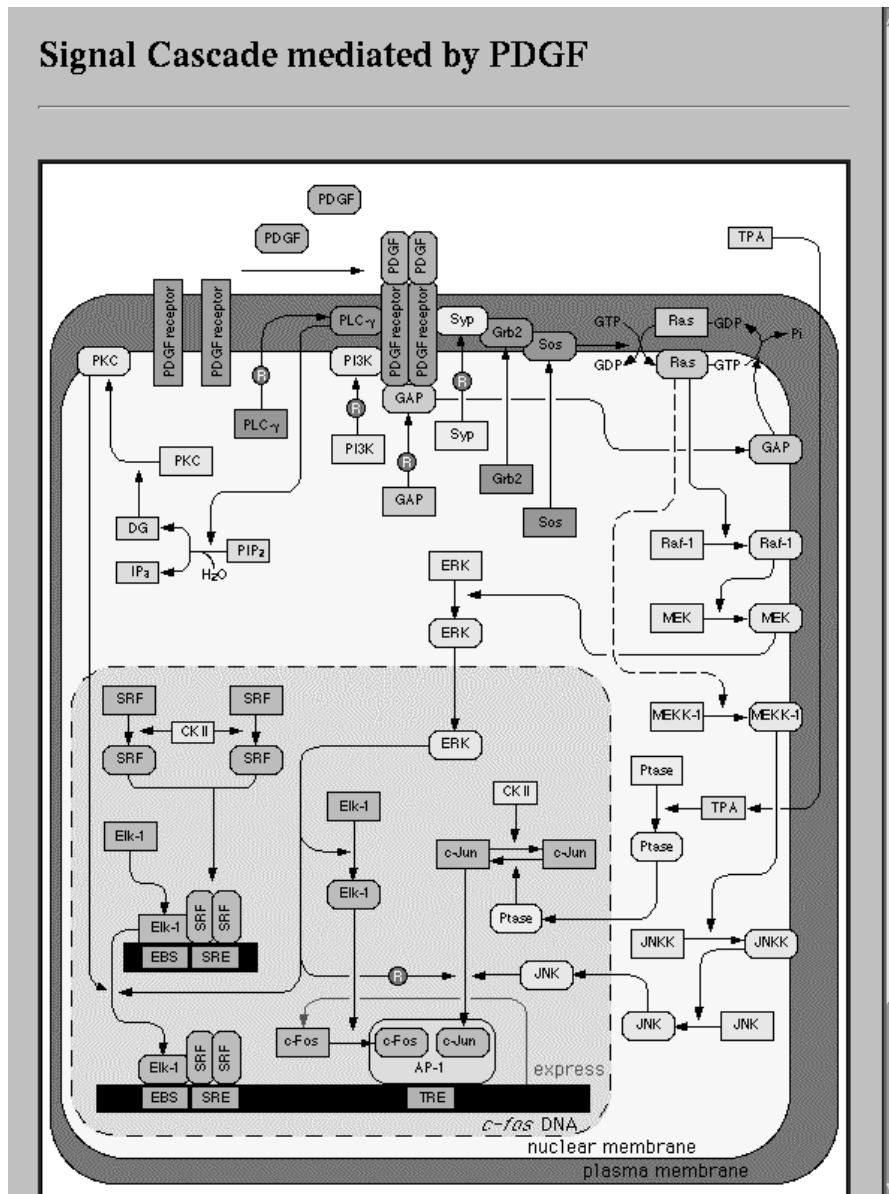


Figure 1