

An Important Tool For Identifying Proteins That Interact

SUNY Stony Brook



Virtually every biological process — including DNA replication, cell growth, key metabolic reactions and disease states — depends upon protein-protein interactions at the cellular level.

In the late 1980s two Stony Brook University School of Medicine researchers, Stanley Fields and Ok-Kyu Song, developed a way to use the yeast transcriptional activator protein for the GAL4 gene to easily detect the interaction of proteins within a cell. This method — the “yeast two-hybrid system for determining protein-protein interactions” — was first published in *Nature*. Initial funding for the research was provided by the National Science Foundation.

“*Transcription is the process through which genetic information is copied from DNA to RNA, ultimately producing a functional peptide or protein. The DNA-binding domain and activation domains from GAL4 are separately fused to the proteins being studied.*”

If the proteins of interest interact, the two domains are brought together and transcription results. This transcription can be easily identified through the use of a marker gene. The system can also be used to discover compounds that

inhibit specific protein interactions.

Understanding and detecting proteins that interact is a fundamental area of inquiry in biology. The yeast two-hybrid system provides an elegant and useful method for carrying out this research. The technology has been licensed nonexclusively to more than one hundred companies, including large pharmaceutical companies and a wide range of biotechnology companies. As a result, hundreds of scientists around the world have used this method, in both corporate and university laboratories.

This story was originally published in 2007.

To see available technologies from research institutions, click [here](#) to visit the AUTM Innovation Marketplace.

Share your story at autm.net/betterworldproject

[#betterworldproject](#)