Studying cell signaling networks enables:

1. Identification of genes and proteins associated with a specific disease
2. In-depth and contextual understanding of the mechanisms of the disease
3. Understanding of how to therapeutically intervene in the disease processes
4. Prediction of drug targets

Our new Cell Signaling Network Protein Profiling Microarray enables you to measure changes in expression levels of multiple key signaling proteins in one or more pathway(s) in a single experiment.

Applications

- Perform drug discovery
- Assess drug efficacy and/or toxicity
- Reveal signaling and potential cross-pathway effects of drug candidates
- Assess exposure to environmental factors (for example, toxins, infectious agents, or radiation).
- Differential profiling of pathway proteins in normal versus diseased tissue
- Compare protein expression in various systems
- Study various changes in pathway events

Systems Biology has emerged as an effective approach to studying complex interactions within biological systems.

By studying entire networks or pathways, we can better understand the underlying structure of cell signaling networks and how changes in these networks may affect the flow of biological information. Comprehensive maps of protein networks will lead to identification of nodal signaling protein motifs and open up avenues for better therapeutic intervention strategies.
Our Comprehensive Service

This is a comprehensive Cell Signaling Network Protein Profiling Service. Just send us your cell sample(s) and we’ll perform all the necessary functions from sample assay to data analysis. Our comprehensive service includes: assistance with project designs, synthesis of a custom phosphopeptide binding – peptide microarray, all on-chip binding reactions, detection of the bound proteins using a suitable method, array image scan, and data analysis.

Workflow

Select your KEGG pathway or pathway(s) of interest. We can detect all pathway proteins containing an SH2 binding domain. Our µPepArray Pro web tool contains panels of phosphotyrosine peptide probes specific for each of the pathway proteins. The PepArray™ microfluidic chip technology enables the total customization of content on each individual microarray to suit your needs. Data analysis is performed with our SVM-PEPARRAY software, the online KEGG & DAVID databases and other tools.

Peptides are synthesized on-chip, not pre-synthesized and spotted. We can synthesize a completely custom one-of-a-kind cell signaling microarray specifically for your experiment delivering results that cannot be achieved with an off-the-shelf assay. With the ability to program new sequence designs on the fly, you can quickly revise microarray design and content to keep experiments moving forward based on previous results.
PepArray pro is a proteomics tool to provide PepArray Layout file that contains information about peptides, peptide IDs, and the array-location of the peptides to be synthesized on chip. The Layout file is required by the synthesis of an addressable peptide microarray. Peptide microarrays (PepArrays) provide powerful proteomics technology platform for a broad range of applications in studying the interactions between protein-protein, protein-nucleic acid, and many other intermolecular interactions as signatures to cellular signaling pathways, and regulatory network activities. Such studies can be applied to not only basic research but also clinical biomedical tool development such as biomarker detection, diagnostic reagent discovery, drug development, and many more.

SVM-PEPARRAY is a Web-based program that constructs qualitative (SVM classification) and quantitative (SVM regression, or SVR) models with user-provided peptide microarray data. The dataset provided should be a list of peptide sequence: binding result pairs, where the binding result should be binary values (1 representing a binder and 0 representing a non-binder) for constructing an SVM classification model, and real-valued numbers (representing binding intensities obtained from an on-chip binding experiment) for constructing an SVR model.

Selecting or Uploading a Microarray Dataset

the user should select the option Construct a model. A list of all peptide microarray datasets previously uploaded by the user is displayed. The user can select a dataset from the list. Alternatively, the user can choose to provide a new dataset. After the user clicks the Submit button, the dataset is checked for errors and, if no errors are found, the dataset is accepted and a statistics summary of the dataset is displayed.

Constructing a Qualitative SVM Model

To establish a qualitative SVM model (or classification model), the user should click the link Construct a SVM classification model. In the Choose SVM classification model parameters page, the user chooses the non-kernel and kernel parameters for the model construction. After specifying the model parameter values, the user clicks the Start constructing model button to initiate the model construction process.

Constructing a Quantitative SVM Model

To construct a quantitative SVM model, a quantitative dataset must be selected. After the dataset is selected, the Configure SVR model construction page is displayed, where the user specifies the kernel selection, cross-validation option and peptide encoding scheme. After the model construction is completed and the best model is determined, a notification e-mail is automatically generated and sent to the user.

Examining a Newly Constructed Qualitative or Quantitative Model

A comprehensive summary of the model is displayed, which includes the model construction configurations, non-kernel and kernel parameters chosen, the performance assessment of the model, the original dataset used in the training of the model and the predictions made for each peptide in the original dataset under cross-validation.

Making Predictions Using an Established Qualitative or Quantitative Model

Click the Make predictions button, the predicted binding results will be displayed to the user. If the model is a SVM classification model, qualitative predictions would be made. Otherwise, if it is a SVR model, then quantitative predictions would be made.
Phospho-PepArray analysis of signaling interactome from breast cancer cells.

Steps in phospho-motif binding assay of endogenous cellular protein complexes in cells: (a) cells are cultured on plates. (b) Total protein is isolated from cultured cells after cell lysis and cell lysate is applied to the phosphopeptides synthesized on (c) PepArray chip through microfluidics by circulation at 4°C overnight. (d) Antibody based detection is used to identify the protein of interest in these complexes. A general detection method is to stain the binding surface using anti-GRB2 antibody and a fluorescence dye conjugated secondary antibody such as Alexa. Based on \textit{in vivo} substrate affinity of a specific phosphoprotein motif with binding domains on other cellular proteins, \textit{in vivo} protein complexes, from the pool of non-denatured total proteins, are bound to respective phospho-peptides (pY) on the chip.

Cell Signaling Network Customer Publications
