

## Poster H-17

### Construction of dephosphorylation site prediction system



#### Authors:

Seong-Jin Park (*Hanyang university*)

Soo-Young Cho (*Hanyang university*)

Young-Seek Lee (*Hanyang university*)

**Short Abstract:** Predictions of possible sites of phosphorylation have been studied by many researchers. However, prediction research of dephosphorylation site contains little. We construct the dephosphorylation site prediction system and predict signal transduction network. The prediction system information will allow biologists to easily retrieve extensive information about dephosphorylation signal transduction network.

#### Long Abstract:

A phosphorylation-dephosphorylation mechanism is the most important signal transduction events. It depends on the ability of each kinase and phosphatase to precisely phosphorylate and dephosphorylate particular sites on substrate. The identification of kinase substrates and the exact location of acceptor residues progress in prediction model and biological research. Predictions of possible sites of phosphorylation have been studied by many researchers. However, prediction research of dephosphorylation site contains little. To construct the dephosphorylation site prediction system, we obtained substrate information for phosphatase from Protein Lounge database and phosphatase information for annotation substrate from Swiss-prot database. The predictive models for dephosphorylation sites were made and evaluated using validating experiment for phosphatases and substrates information. The prediction system information will allow biologists to easily retrieve extensive information about dephosphorylation signal transduction network.