



**L.H. BAKER CENTER FOR BIOINFORMATICS AND  
BIOLOGICAL STATISTICS AND PLANT SCIENCES INSTITUTE  
SEMINAR SERIES**

# **RUTH NUSSINOV, Ph.D.**

**Nanobiology Program,  
National Cancer Institute, NIH**

**Department of Human Genetics,  
Tel Aviv University**

## **Proteome Scale Prediction of Protein-Protein Interactions Using Interfaces**

Nature is restricted to a limited number of protein interactions; hence, the number of binding architectures is also limited. In addition to similar binding preferences of homologous protein pairs, different protein pairs can also use the same binding architectures. Thus, extrapolation of known template architectures to whole target proteins should permit the modeling of the interactions of the proteome; and piecing these together can provide a detailed view of protein pathways. Here, for the first time, we introduce a knowledge-based combinatorial strategy to predict global functional associations of proteins which integrates a spatial alignment phase with flexible refinement and energy calculations. The spatial alignment phase considers known binding architectures and then seeks these on the target protein surfaces; flexible refinement applies efficient docking strategies with energy evaluation which makes this method more physical. This method is applicable to any pathway, as long as the respective protein structures are available.

**Date: Wednesday, April 11**

**Time: 4:00-5:00 PM**

**Room: 1414 Molecular Biology**