

## ORAL PRESENTATION O2

### Modeling the 3D structures of protein complexes

M.S. Madhusudhan

*Bioinformatics Institute, Singapore*

3D structures of biological complexes help in designing experiments to intervene and probe the mechanisms of its function in the cell. The method MODTIE builds 3D models of protein complexes using suitable structural templates. The targets are protein sequences whose 3D structural models are deposited in the model database MODBASE. The templates are experimentally determined 3D structures of protein complexes whose individual proteins are structurally similar to the target proteins. All MODTIE generated models are assessed using a statistical potential of residue contacts across protein interfaces. MODTIE has been applied on a large scale to predict the 3D structures of protein complexes in the Yeast proteome. Over 3,000 structural models of Yeast complexes are built and deposited in the database MODBASE. Some of the individual complexes predicted by MODTIE have been experimentally validated.