**Course: Advance Bio Informatics**

**Module Title: Prediction of Important Regions**

**Module No: 163**

**Prediction of Important Regions**

Identify relevant target to cause disease & progression. HG has 3000 Drug targets. It is the limitation of resources.

**Homology Modeling**

***Fold recognition***: families, sub & super-families.

It is modeling 3-D structure for designing inhibitors of HIV protease.

**Homology Modeling Tools**

**Modeller:** Alignment of sequences, high level of homology, 100 AAs

**Threading:** Fold recognition.

**Ab initio:** Structure with no prior knowledge, libraries of short segments

**Predicting Functional Feature of Proteins**

Positions from sequence for structure/function site. Apolar conserved residues clustering. Conserved functional group analysis by FSP. It has Sequence profile & neighboring residues.

**Structurally Related Proteins**

* Look for matches
* Fuzzy functional form
* PROCAT database
* Automated prediction