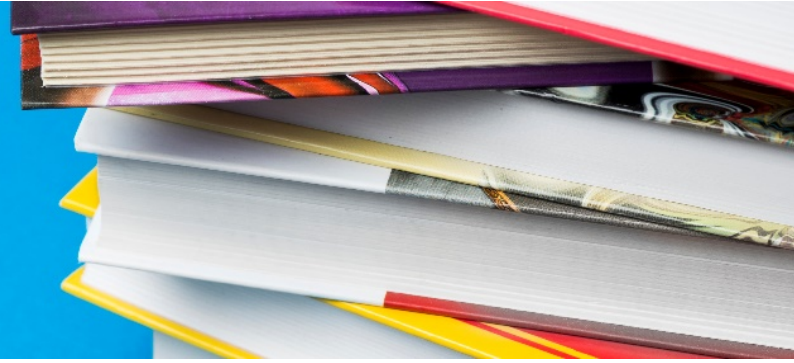




# Full Syllabus



## Course Title

Structure and function prediction in proteins

## Lecturer

Nir Ben-Tal

## Semester

B

## Course requirements

Biochemistry, introduction to bioinformatics

## Final grade components

Submitting 70% of exercises (without grades) is mandatory. Grade is based on project (70%) and exam (30%)

## Course schedule

Class no. / Date	Subject and Requirements (assignments, reading materials, tasks, etc.)
February 23	Introduction to protein structure; Forces and interactions.
March 2	Introduction to protein structure (continue); Overview of structure prediction
March 9	Biological sequence alignment, Dynamic programming, FASTA; BLAST, PSI-BLAST, CS-BLAST
March 16	Multiple sequence alignment, CLUSTALW, T-COFFEE, Muscle, MAFFT; Protein structural alignment, RMSD, GDT-TS, etc
March 23	
March 30	Threading; ITASSER; Prediction of secondary structure and unstructured regions, Homology modeling.
April 6	
April 10	Rosetta and RoseTTAFold
April 27	Contact prediction and coevolution
May 11	AlphaFold
May 18	Docking
May 25	Deep learning techniques in protein folding methods, Lectures (via YouTube) of John Jumper (AlphaFold), Jinbo Xu (RaptorX), Mohammed AlQuraishi.
June 1	Modeling of membrane proteins: Membrane topology prediction, and CPA
June 8	How proteins emerged and continue to evolve?

## Required course reading

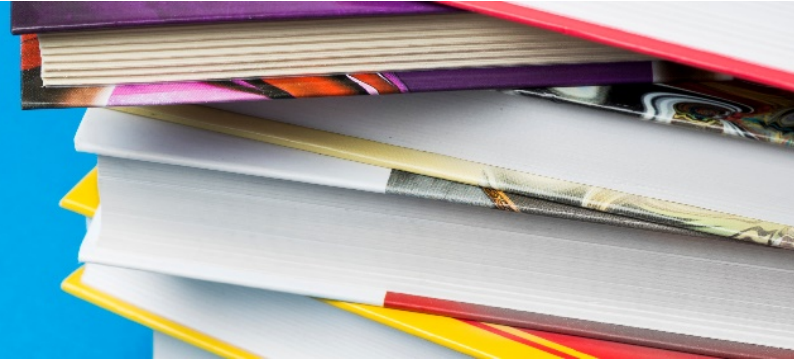
Will be included in presentations

## Optional course reading



TEL AVIV אוניברסיטת תל אביב  
UNIVERSITY תל אביב

# Full Syllabus



Comments