

Docking Predictions *of* Protein-Protein Interactions

14 - 17 October | 2008

Barcelona Supercomputing Center
SPAIN



The prediction and analysis in silico of protein-protein interaction plays an increasing role in functional genomics.

The course will present methods based on docking that predict how two proteins interact when their three-dimensional structure is known.

Applicants should be registered in a Master's or Ph. D. program of a European University in structural biology, molecular biology, biochemistry, biophysics, bioinformatics, computational biology or computational chemistry.

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Application Deadline

Deadline for applications: 25th April, 2008

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