



15,00

I seminari del Master in

TECNOLOGIE BIOINFORMATICHE APPLICATE ALLA MEDICINA PERSONALIZZATA

14 luglio 2006 – ore 15,00

Polaris – edificio 2 – sala conferenze

Loc. Piscinamanna - Pula (CA)

Programma dei lavori

Automated comparative protein structure modeling: principles and practical applications

Torsten Schwede – Bioinformatics Division Biozentrum, University of Basel

Chairman of the Biozentrum Research Core Program: Genome Scale Biology and Bioinformatics;

Member of the Executive Board of Directors of the Swiss Institute of Bioinformatics;

Chairman of the Division of Bioinformatics, Biozentrum Basel;

Group leader at the Swiss Institute of Bioinformatics;

Assistant Professor (tenure track) for Structural Bioinformatics, Biozentrum Basel; Bioinformatics Staff Scientist at Glaxo Wellcome Experimental Research, Geneva, Switzerland.

Expanding fold space by likelihood-based molecular replacement

Randy Read - Cambridge Institute for Medical Research

Professor of Protein Crystallography, Department of Haematology, University of Cambridge:

Protein crystallographer, with interests in both the methods for determining crystal structures and in the application of the results to the understanding of biology and disease.

In methods, his group has been applying ideas of maximum likelihood to develop improved methods to solve and refine crystal structures.

In structural biology, his group has studied the mechanism of action of bacterial toxins, such as pertussis toxin and the Shiga-like toxins of E. coli, as well as the mechanism by which serpins inhibit their target proteases.

Dibattito

Conclusione lavori

Per ulteriori informazioni e per iscriversi al seminario:

<http://www.consorzioventuno.it>