

CASPITA @ CASP5 - (session: Structural Genomics)

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We describe our participation at the CASP-5 experiment (2002) under the group name "CaspIta". The international CASP (Critical Assessment of techniques for protein Structure Prediction) experiments aim at establishing the current state of the art in protein structure prediction, identifying what progress has been made, and highlighting where future effort may be most productively focused [1].

We have developed our own suite of programs ranging from secondary structure prediction [2] to fold-recognition [3] and modelling [4].

We have submitted both secondary structure predictions and 3D models for all 65 target proteins. Our main interest was focused in targets with biological background information going beyond the simple target to template alignment, e.g. active-site residues known from the literature.

The results for our approach are as follows. For secondary structure prediction we ranked second (SOV) respective first (Q3). For comparative modelling we ranked among the top 20% (CM-only targets), whereas for fold-recognition targets we ranked among top 50%. Over 200 groups participated in both categories.

We present some of our better predictions.

[1] CASP5 web site: <http://predictioncenter.llnl.gov/casp5/>

[2] Albrecht M. et al. , Protein Engineering, in press. (2003)

[3] Bindewald E. et al. , Protein Engineering, in press. (2003)

[4] Tosatto S.C.E. et al. , Protein Engineering, 15(4):279-286.(2002)