

Guido Tiana



Protein folding: from simplified models to the design of folding inhibitors.

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Brief Curriculum

Guido Tiana was born in 1972, graduated in Physics at the University of Milano (Italy) and obtained his Ph.D. at the Niels Bohr Institute of Copenhagen (Denmark) in 2000. He also worked at the Centre for Biological Sequence Analysis (Lyngby, Denmark) and at the Department of Chemistry and Biological Chemistry of Harvard University. He is currently Researcher at the Department of Physics of the University of Milano and co-founder of a company aimed at developing folding inhibitors for viral proteins. He is also author of 51 articles in peer-reviewed journals, of 2 patents and organizer of 4 international conferences in biophysics.

Research interests

- 1) Statistical physics of protein folding, using simplified models to understand how such a complex system as a protein can display a low-entropy equilibrium state and reach it very fast.
- 2) Development of computational algorithms to study the conformational space of proteins with realistic models (at atomic detail, with explicit solvent).
- 3) Design of molecules to inhibit the folding of viral proteins (in particular, HIV protease) and experimental activity to test the efficiency of such molecules.
- 4) Computational and experimental study of protein aggregation.
- 5) Computational study of the molecular evolution of proteins.
- 6) Modelling of cellular regulatory networks.