

A Gauge/String Theory Approach to Protein Folding

Antti Niemi

Tour

Lundi 12 Octobre 2009 à 15:30

LPTENS – CONF-4

Résumé

The way how proteins fold into their native three-dimensional shape, is one of the great mysteries in biology. An understanding of the laws of protein folding enables us to predict the phenotypes of living organisms, and develop cures for illnesses that are caused by misfolded proteins including Alzheimer's and Parkinson's diseases and various forms of cancer. In this talk we describe how concepts of fundamental physics can be employed to develop a theoretical model that folds proteins into their native states in seconds with an ordinary PC. Our model provides a simple explanation for homochirality, describes all major secondary protein structures, predicts the emergence of a molten globule, and correctly computes the radius of gyration of biologically active proteins.

LABORATOIRE DE PHYSIQUE THEORIQUE DE L'ECOLE NORMALE SUPERIEURE
24, RUE LHOMOND
75231 PARIS, CEDEX 05

Tel. : +33-(0)1-44.32.30.00 ou (0)1-44.32.34.83