Abstract Submitted
for the MAR06 Meeting of
The American Physical Society

Analyzing knots in protein structures PETER VIRNAU, MEHRAN KARDAR, Department of Physics, MIT, LEONID MIRNY, Harvard-MIT Division of Health Sciences & Technology — Although globular homopolymers display an abundance of knots (Virnau et al, J. Am. Chem. Soc. 127, 15102 (2005)), only about one in a thousand protein structures are knotted. Can this absence of entanglement be explained in terms of statistical mechanics or is there an evolutionary bias? Do knots in proteins serve a purpose and how do they actually fold? To elaborate on this, we will present an overview of knotted proteins from the current version of the Protein Data Bank. We will also discuss some particularly intriguing examples of this set.

Peter Virnau
MIT

Date submitted: 06 Dec 2005 Electronic form version 1.4