

Abstract Submitted
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Equilibrium Stability of Transmembrane Proteins : A Hard-Core Gas Problem. KARIM WAHBA, DAVID SCHWAB, ROBIJN BRUINSMA, UCLA — Hydropathy plots, a moving average of amino acid hydrophobicity over a sequence, can be used to predict potential protein structure, in particular transmembrane proteins. Traditionally transmembrane regions are identified by peaks above an empirical cutoff. We treat the transmembrane segments as a one-dimensional gas of hard rods in a correlated random energy landscape. At zero temperature, where the entropic contribution due to the loops is negligible, we calculate the density profile as a function of the chemical potential in the case of the original as well as randomly generated landscapes. The density profile exhibits plateaus indicating regions where a transmembrane segment has been established. For designed versus random sequences we explore the distribution of the sizes of these plateaus and attempt to infer characteristic features that may be interpreted in terms of the stability of the protein in its inserted state.

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