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Three-Dimensional Molecular Modeling of Bovine Caseins: A Refined, Energy-Minimized κ-Casein Structure

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A refined three-dimensional molecular model of κ -case in has been produced using energy minimization techniques and a Kollman force field on a previously reported predicted three-dimensional structure. This initial model was constructed via molecular modeling techniques from sequence-based secondary structural prediction algorithms. Both the initial and refined structures agreed with global secondary structure analysis from vibration spectroscopy. The refined structure contained many of the features of the initial model, including two sets of antiparallel Bsheet structures containing predominantly hydrophobic side chains, which could form interaction sites with $\alpha_{\rm s1}$ casein. Two types of energy-minimized dimer and tetramer models are presented: 1) using Cys as potential intermolecular disulfide binding

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sites and 2) using the two sheets as possible hydrophobic self-association sites, without Cys interactions. All structures yielded good stabilization energies and are in agreement with chemical, biochemical, and physical chemical results obtained for κ -casein.

Key Words: casein structure • protein functionality • milk proteins

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