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The denaturation behaviour of calmodulin in sodium *n*-dodecyl sulphate, dodecyl trimethyl ammonium bromide, guanidine hydrochloride and urea

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Abstract

The denaturation behaviour of calmodulin (CaM) in sodium *n*-dodecyl sulphate (SDS), dodecyl trimethyl ammonium bromide (DTAB), guanidine hydrochloride (GuHCl) and urea was studied by fluorescence spectrophotometry at 25 and 37°C in Tris-HCl buffer, pH 7.4.

The sigmoidal denaturation curve was plotted in order to estimate the thermodynamic parameters, assuming a two-state mechanism in terms of the Pace model.

SDS and DTAB, anionic and cationic surfactants, affect CaM on a millimolar level as a result of direct interaction between CaM and surfactant as an amphipatic molecule. GuHCl and urea affect CaM on a molar level as a result of indirect interaction with the surroundings of CaM (a change in the water structure).

The thermodynamic data indicate a slight interaction in the case of SDS which induced incomplete unfolding of CaM. With DTAB, GuHCl and urea, unfolding of CaM took place to a much greater extent.

INTRODUCTION

Calmodulin (CaM), the ubiquitous intracellular Ca^{2+}-binding protein, is a multifunctional intracellular protein, which mediates in many biochemical processes [1, 2]. CaM undergoes conformational changes which produce specific interaction site(s) recognized by many different proteins. The unique ability of CaM to bind to and stimulate the activity of a large number of enzymes allows CaM to play a pivotal role in regulating cellular function [3].

The CaM molecule consists of four homologous calcium-binding domains, I, II, III and IV. Each domain contains a helix loop, a helical calcium-binding structure [4]. In the first step, calcium binds to the two

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