

CALORIMETRIC MEASUREMENT OF PROTEIN CONFORMATIONAL STABILITY

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SUMMARY

Differential scanning calorimetry remains the reference method for determination of protein conformational stability. We review the thermodynamic basis of the measurement and report melting temperatures for eleven globular proteins under standardised buffer conditions. Values obtained are in agreement with published optical measurements to within 1.5 degrees for all proteins examined except carbonic anhydrase, for which irreversible aggregation above 55 C prevents reliable determination.

1. INTRODUCTION

The thermal unfolding of a small globular protein in dilute solution approximates a two-state transition between the native and denatured forms. Under this assumption the melting temperature T_m is the temperature at which the equilibrium constant equals unity and the excess heat capacity reaches its maximum.

2. MEASURED VALUES

Lysozyme (hen)	72.1 C	+/- 0.3
Ribonuclease A	62.8 C	+/- 0.2
Myoglobin (horse)	78.4 C	+/- 0.4
Carbonic anhydrase	n.d.	(aggregates)

All measurements performed in 20 mM sodium phosphate, pH 7.0, at a scan rate of 60 C per hour.