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Data Article

Data on the role of accessible surface area on osmolytes-induced protein stabilization

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ABSTRACT

This paper describes data related to the research article "Testing the dependence of stabilizing effect of osmolytes on the fractional increase in the accessible surface area on thermal and chemical denaturations of proteins" [1]. Heat- and guanidinium chloride (GdmCl)-induced denaturation of three disulfide free proteins (bovine cytochrome *c* (b-cyt-*c*), myoglobin (Mb) and barstar) in the presence of different concentrations of methylamines (sarcosine, glycine-betaine (GB) and trimethylamine-N-oxide (TMAO)) was monitored by $[\Theta]_{222}$, the mean residue ellipticity at 222 nm at pH 7.0. Methylamines belong to a class of osmolytes known to protect proteins from deleterious effect of urea. This paper includes comprehensive thermodynamic data obtained from the heat- and GdmCl-induced denaturations of barstar, b-cyt-*c* and Mb.

Specifications Table

Subject area	Chemistry
More specific subject area	Protein chemistry
Type of data	Tables, figures

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How data were acquired	Experiments were performed using Jasco spectropolarimeter, Model J-1500-150 (JASCO Corporation, Japan), equipped with Peltier-type temperature controller
Data format	Raw, Plotted, analyzed
Experimental factors	All samples and buffers were filtered with 0.22 μm Millipore filters and degassed.
Experimental features	All CD spectra were recorded at 1 nm band width, temperature scan rate 1 °C/min and data was collected at every 0.1 °C
Data source location	Jamia Millia Islamia, New Delhi, India
Data accessibility	Data are accessible in this article

Value of the data

- Methylamines are stabilizing osmolytes. That is, they shift midpoint of denaturation curves to higher C_m (midpoint of the GdmCl-induced unfolding transition) and T_m (midpoint of the heat-induced unfolding transition). C_m and T_m increase with increase in concentrations of methylamines.
- Stabilization effect of methylamines in terms of ΔG^o_D (Gibbs free energy change) obtained from GdmCl-induced denaturation studies are found to be more than that from thermal transitions in cases of Mb and barstar.
- The stabilizing effect of methylamine against heat- and GdmCl-induced denaturation is same in the case of b-cyt-*c*.

1. Data

Heat- and GdmCl-induced transition curves of proteins were monitored by $[\Theta]_{222}$ measurements. These transition curves were analyzed for thermodynamic parameters according to Eqs.(1)–(4).

We have carried out GdmCl- and heat-induced denaturation experiments of barstar, b-cyt-*c* and Mb in the absence and presence of different concentrations of different methylamine by following the change in $[\Theta]_{222}$ (probe for measuring change in secondary structure). Fig. 1 shows GdmCl-induced denaturation curves of Mb, barstar and b-cyt-*c* in the absence and presence of 0.25 and 0.75 M of each of sarcosine, glycine-betaine and TMAO at pH 7.0 and 25 °C. Denaturation of each of protein was found to be reversible in entire range of methylamine concentrations. Each transition curve was measured at least three times, and analyzed for thermodynamic parameters using the Eq. (1). Values of ΔG^o_D, m_g and C_m thus obtained are given elsewhere [1].

Fig. 2 shows heat-induced denaturation curves of Mb, barstar and b-cyt-*c* in the presence of 0, 0.25 and 0.75 M sarcosine, glycine-betaine and TMAO at pH 7.0. Furthermore, Figs. 3–5 show heat-induced denaturation curves of these proteins in the presence of 0.25, 0.5, 0.75 and 1.0 M of each methylamine (sarcosine, glycine-betaine and TMAO) at pH values other than 7.0. All these denaturation curves (Figs. 2–5) were monitored by change in $[\Theta]_{222}$ and were measured at least in triplicate. Thermal denaturation of each protein in the entire range of each [methylamine], the molar concentration of methylamine, was reversible at all pH values. It was observed that the temperature-dependence of y_N, the optical property of the native (N) state of the protein depends on neither [methylamine] nor pH. However, y_D, the optical property of the denatured (D) state of the protein depends on pH (Figs. 2–5). Each denaturation curve of the protein at given (methylamine) was analyzed for thermodynamic parameters, namely ΔH_m, T_m, ΔC_p and ΔG^o_D using Eqs. (2)–(4), and the values are given in Tables 1–3 (values for pH 7.0 are given elsewhere [1]). Fig. 6 shows far-UV CD spectra of Mb and b-cyt-*c* in the absence and presence of different concentrations of GdmCl at 85 °C. It is seen in this figure that $[\theta]_{222}$ of Mb depends significantly on the (GdmCl). However, this dependence is insignificant in the case of b-cyt-*c*.