Table 10.3 Thermodynamic parameters for unfolding of various proteins.

Protein	Molecular weight	ΔH^o (25°C) [kJ•mol^{-1} per residue]	ΔS^o (110°C) [J•mol^{-1} per residue]	ΔC_P [J•K^{-1}•mol^{-1} per residue]
Protein G-B1	7200	1.4	16.1	53
Parvalbumin	11,500	1.4	16.8	46
Cytochrome *c*	12,400	0.64	17.8	67
Ribonuclease A	13,600	2.4	17.8	44
Hen lysozyme	14,300	2.0	17.6	52
Staph. nuclease	16,800	0.85	17.5	61
Myoglobin	17,900	0.04	17.9	75
Papain	23,400	0.93	17.0	60
β-Papain	23,800	1.3	17.9	58
α-Chymotrypsin	25,200	1.1	18.0	58
Average		1.2 ± 0.7	17.4 ± 0.6	57 ± 9

This table presents values of ΔH^o, ΔS^o, and ΔC_P for several proteins. The temperatures for which ΔH^o and ΔS^o are calculated were chosen to reflect the enthalpy and entropy of the protein chain itself, without the hydrophobic interaction (see Baldwin, 1986, in Further Reading). The values scale with the size of the protein; in order to make comparison easier, the values have been divided by the number of residues in the protein to give a "per residue" value. (Adapted from P. Alexander et al., and P. Bryan, *Biochemistry* 31: 3597–3603, 1992. With permission from the American Chemical Society.)