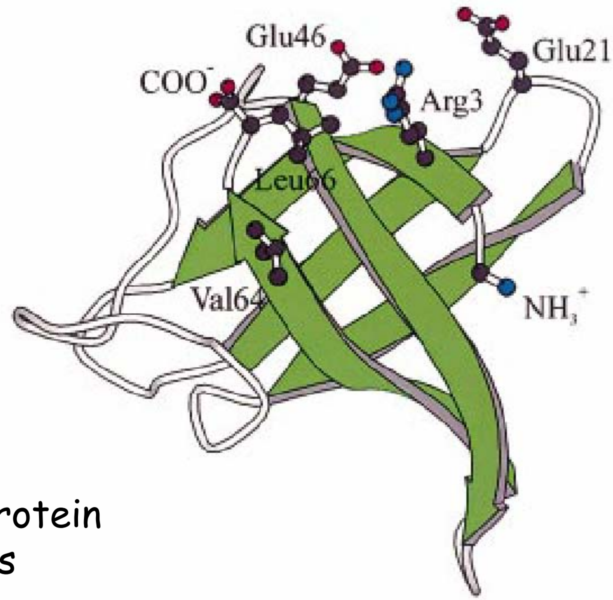
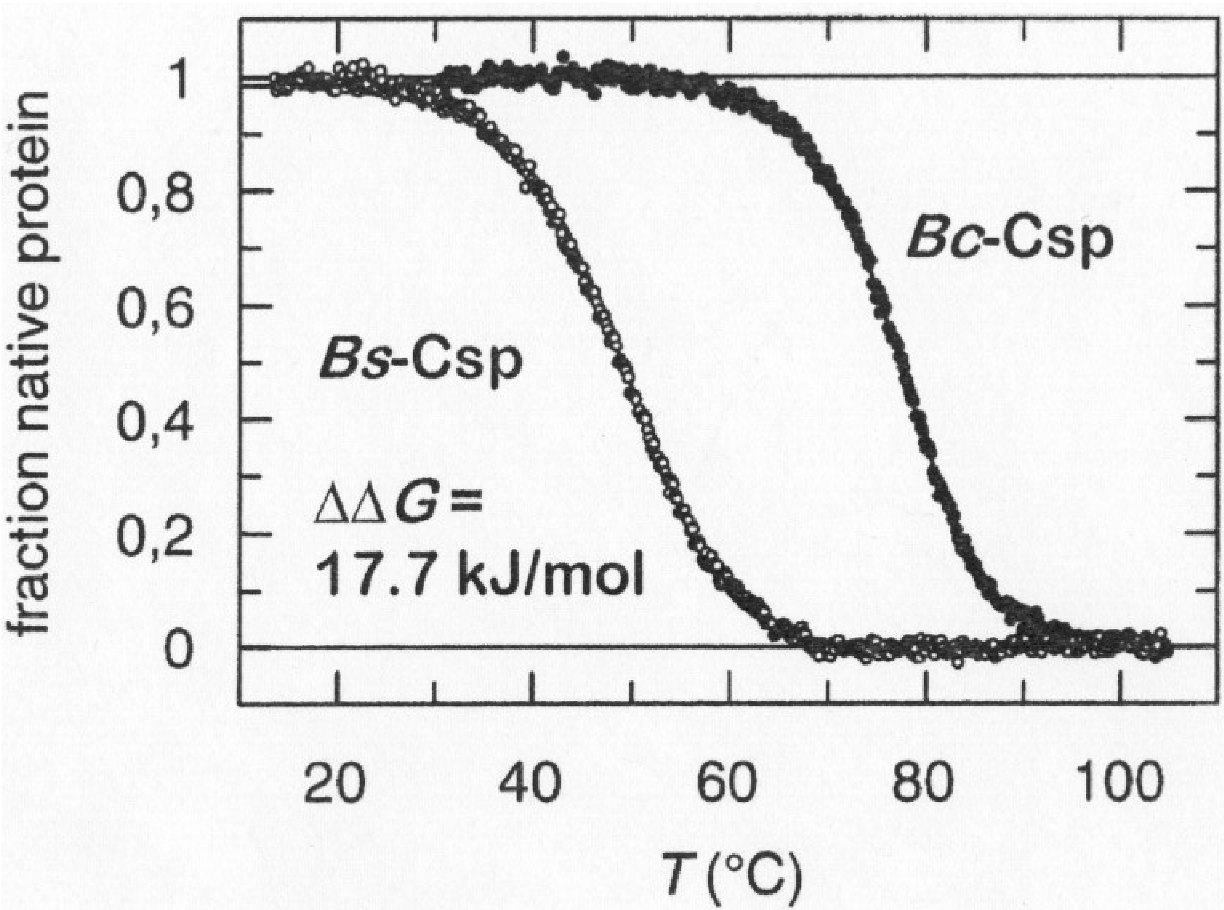


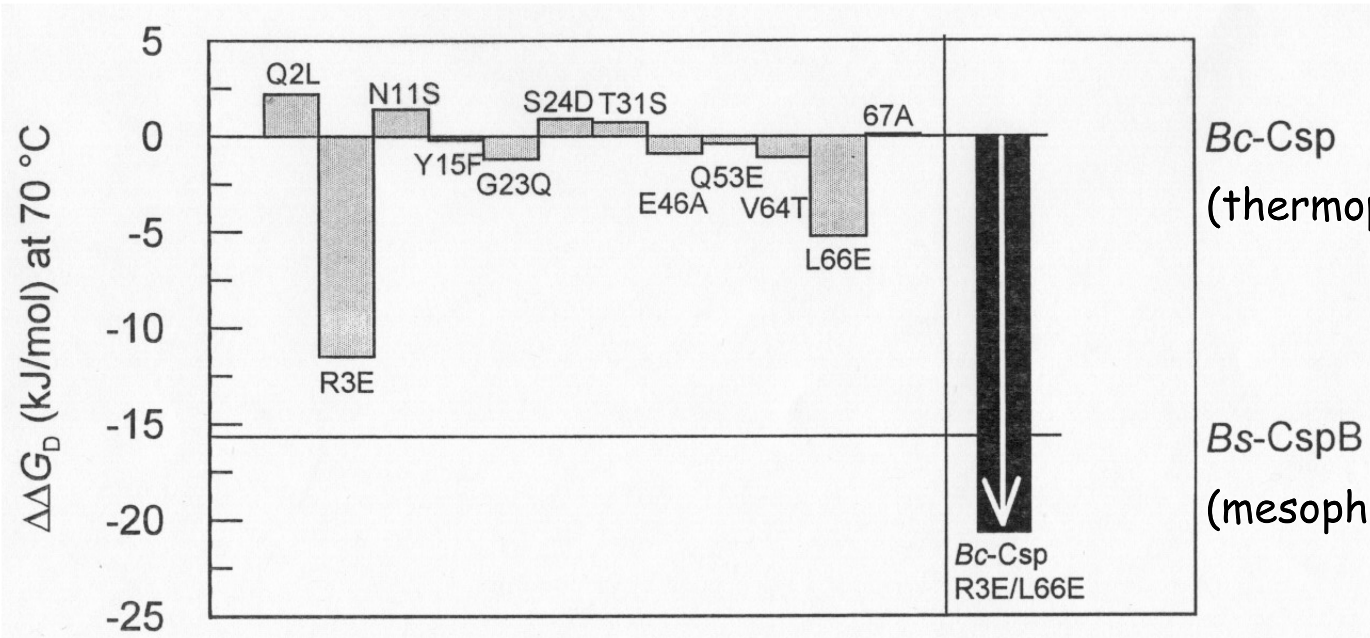
Thermophiles Kälteschockprotein
Csp aus Bacillus caldolyticus

[Mueller et al. (2000), J. Mol. Biol. 297, 975-988]

	1 5 10	15 20	25 30	35
Bc-Csp	MQRGKVKWFN	NEKGYGFIEV	EGGSDVFVHF	TAIQG
Bs-CspB	MLEGKVKWFN	SEKGFGFIEV	EGQDDVFVHF	SAIQG
	40	45 50	55 60	65
Bc-Csp	EGFKT	LEEGQEVSFE	IVQGNRGPQA	ANVVKL-
Bs-CspB	EGFKT	LEEGQAVSFE	IVEGNRGPQA	ANVTKEA

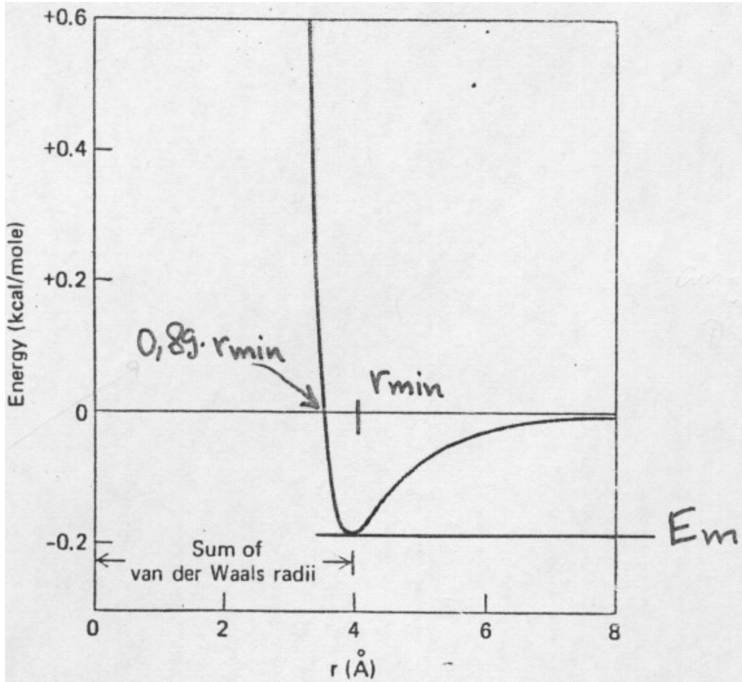

fraction native protein
1
0,8
0,6
0,4
0,2
0
Bc-Csp
Bs-Csp
ΔΔG =
17.7 kJ/mol
20
40
60
80
100
T (°C)

Rest für Rest Analyse der Stabilität von Bc-Csp relativ zu Bs-CspB



(thermophil)

(mesophil)



Representative profile of the energy of Van der Waals interaction as a function of the distance, r, between the centers of two atoms. The energy was calculated using the empirical equation

$$E = \frac{B}{r^{12}} - \frac{A}{r^{6}}$$

(Values for the parameters $B = 2.75 \times 10^6$ kcal Å^{12}/mole and $A = 1425$ kcal Å^6/mole, for the interaction between two carbon atoms, from M. Levitt, J. Mol. Biol. 82:393–420, 1974.)

Table 3-2. Parameters of Lennard–Jones 6–12 Potential for Electron Shell Repulsion and Dispersion Forces at a Nonbonded Contact[a]

	Momany *et al.* (69)		Lifson and Warshel (70, 71)	
	E_m (kcal/mol)	R_m (Å)	E_m (kcal/mol)	R_m (Å)
Aliphatic H . . . aliphatic H	−0.04	2.92	−0.01	2.94
Aliphatic C . . . aliphatic C	−0.04	4.12	−0.19	4.23
Carbonyl O . . . carbonyl O	−0.20	3.12	−0.23	3.00
Amide N . . . amide N	−0.11	3.51	−0.19	3.60

[a]Only contacts between identical types of atoms are considered. For a contact between nonidentical types i and j use $(E_m^{(ij)} = E_m^{(ii)} + E_m^{(jj)})^{12}$ and $R_m^{(ij)} = \frac{1}{2}(R_m^{(ii)} + R_m^{(jj)})$

Modell für die Lösung hydrophober Moleküle in Wasser

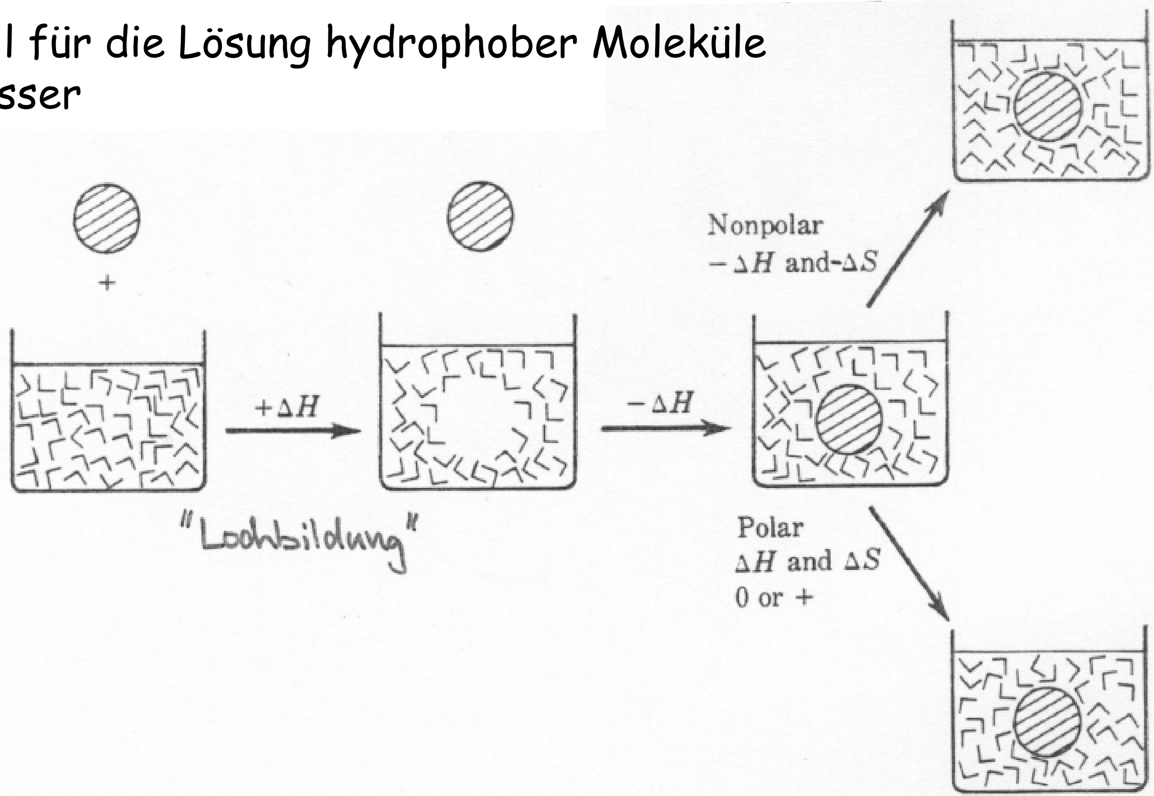
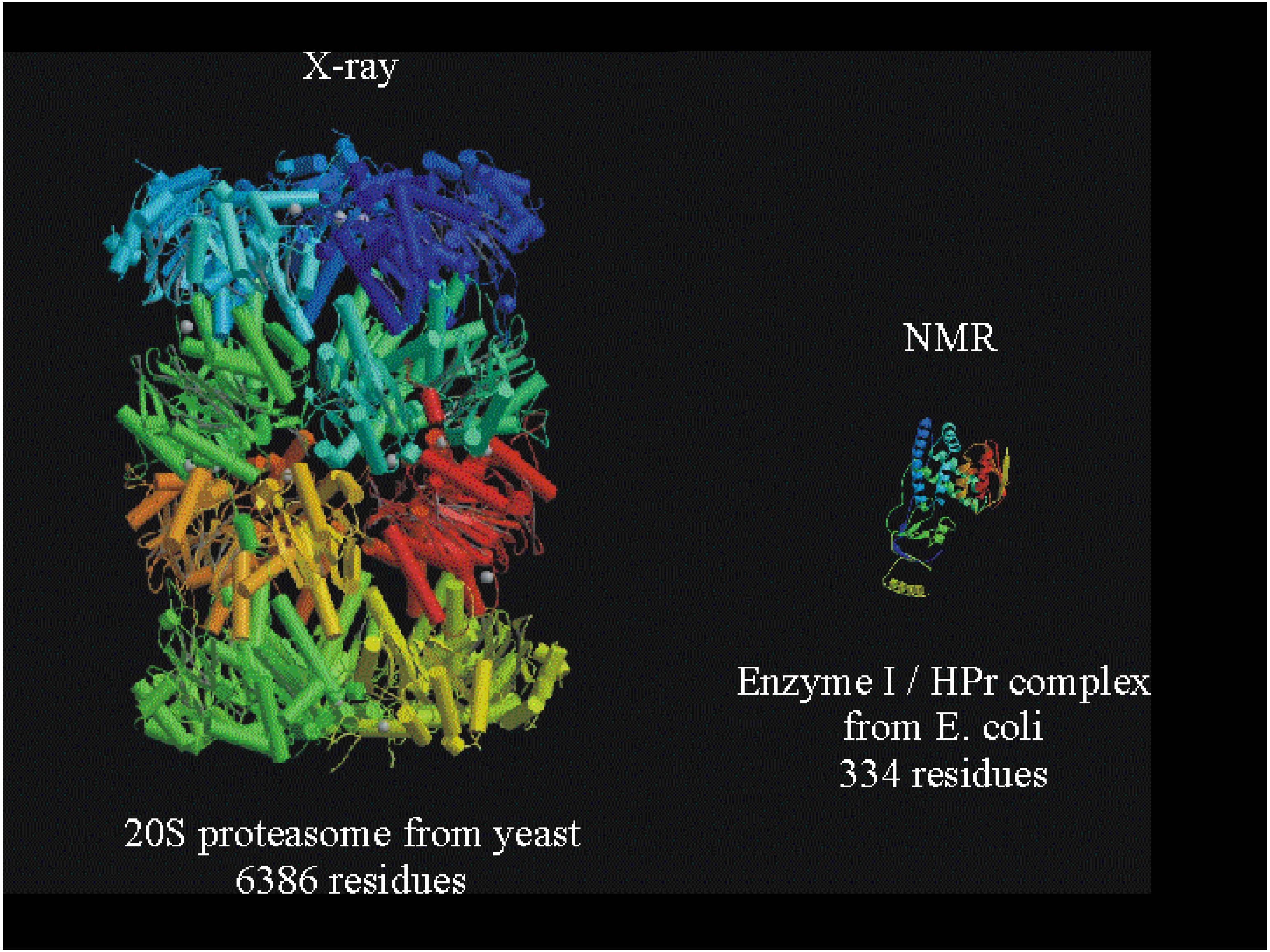
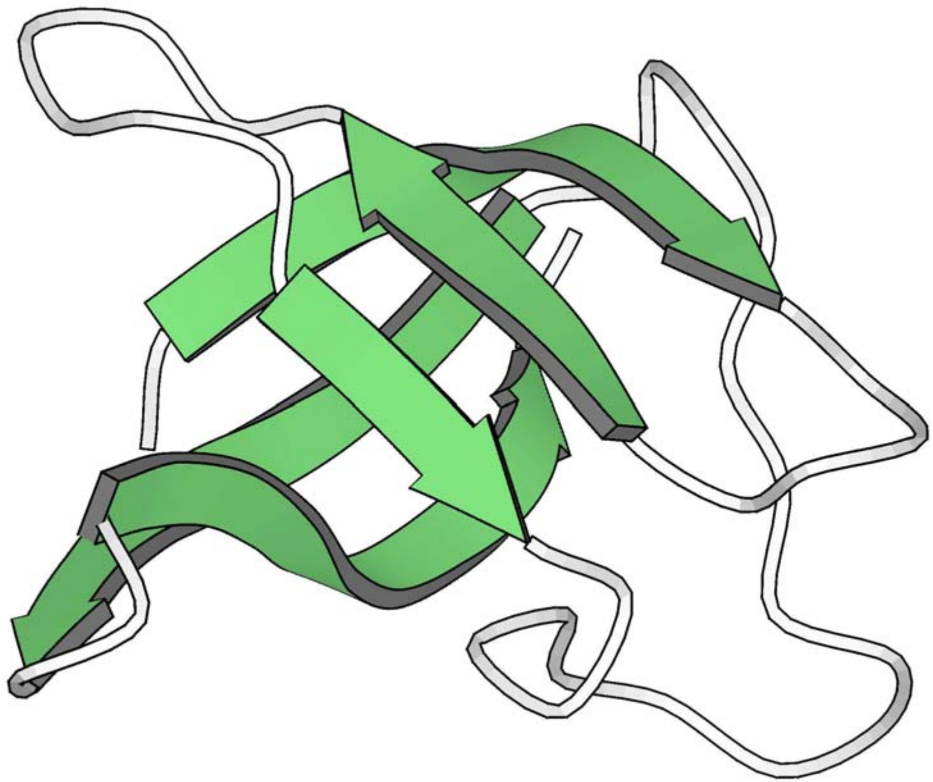
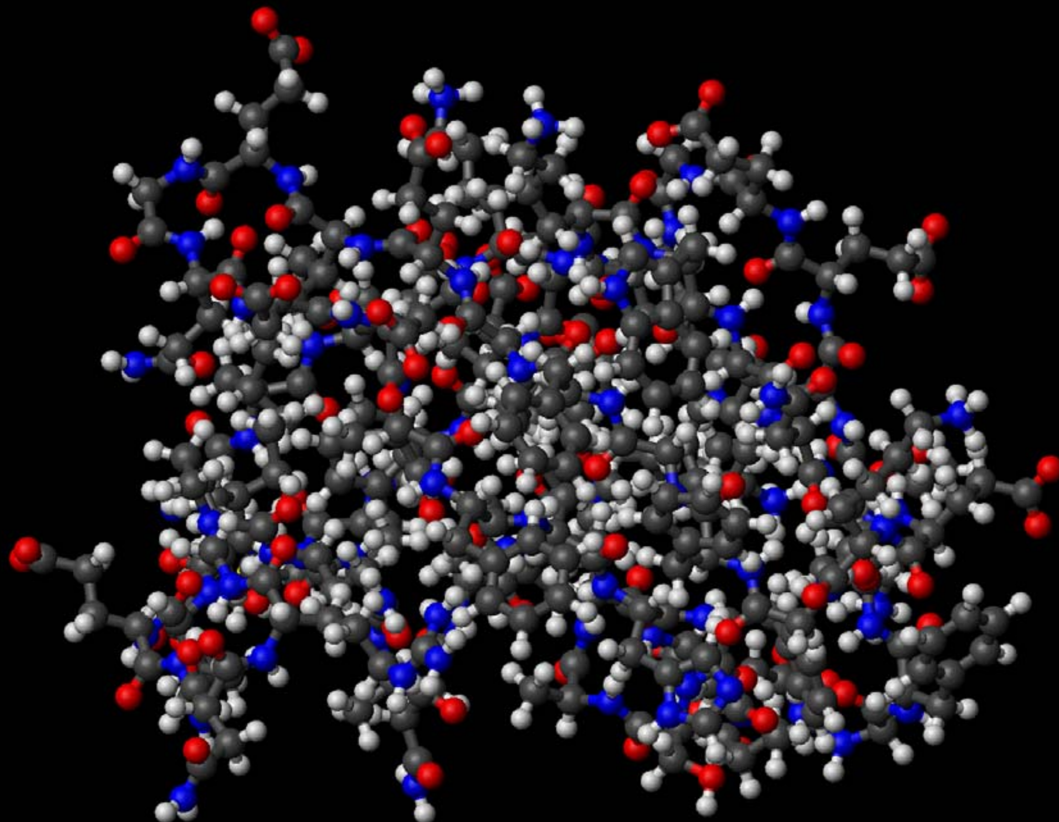


Fig 6. The solution of a nonpolar or polar molecule in water with the intermediate formation of a cavity. After the solute is placed in the cavity the solvent may rearrange to a greater degree of structure and hydrogen bonding (nonpolar solute), may undergo no change, or may decrease in structure and hydrogen bonding (polar, structure-breaking solute).


X-ray
20S proteasome from yeast
6386 residues
NMR
Enzyme I / HPr complex
from E. coli
334 residues

Kälteschockprotein CspB aus *Bacillus subtilis*





1020 Atome ($C_{331}H_{499}N_{85}O_{104}S_{1}$)
Molekulargewicht: 7365 Aminosäuren: 67

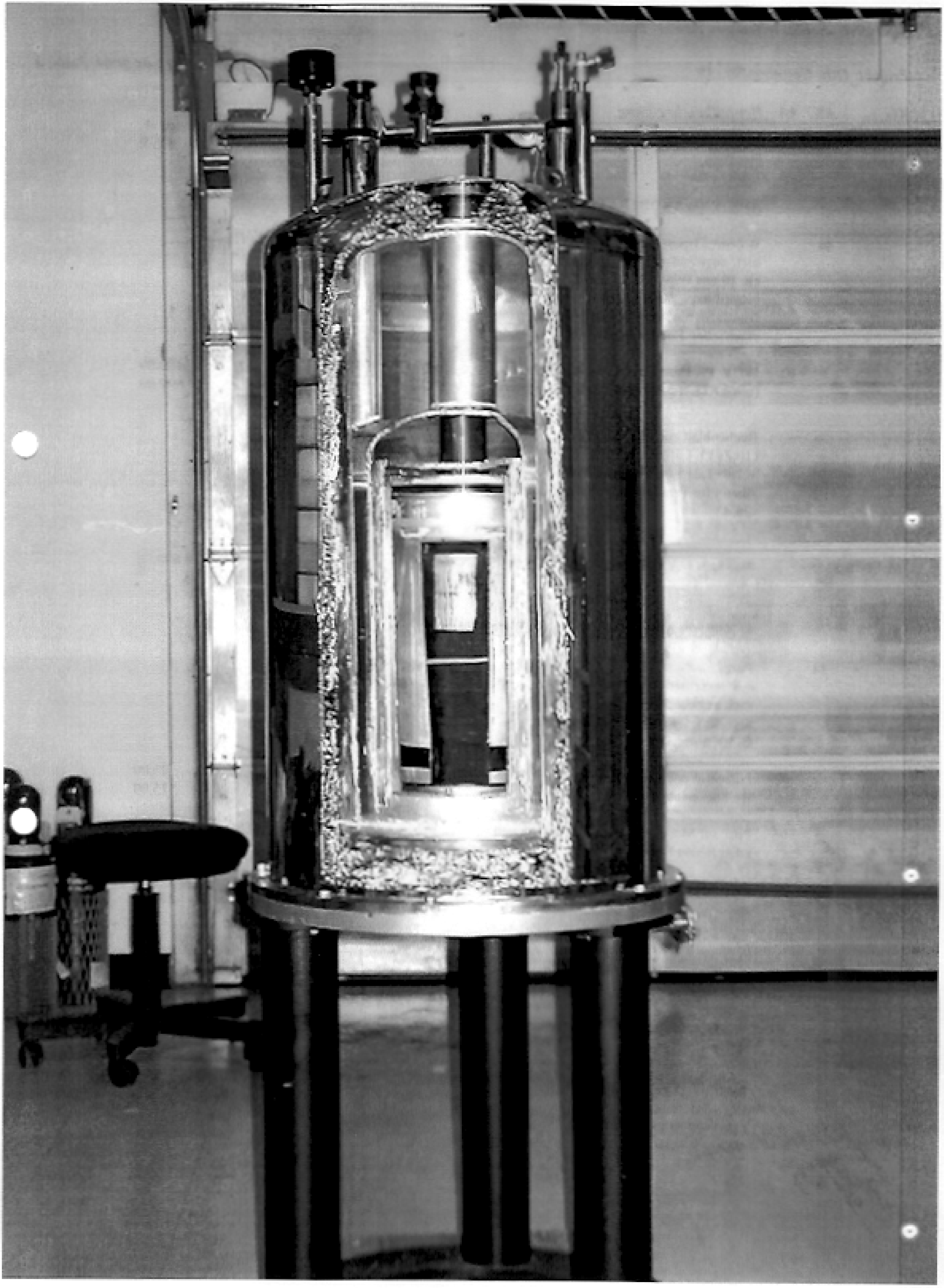


TABLE 1.1

Properties of Selected Nuclei[a]

Nucleus	I	γ $(T \cdot s)^{-1}$	Natural abundance (%)
^{1}H	$\frac{1}{2}$	2.6752×10^{8}	99.98
^{2}H	1	4.107×10^{7}	0.02
^{13}C	$\frac{1}{2}$	6.728×10^{7}	1.11
^{14}N	1	1.934×10^{7}	99.64
^{15}N	$\frac{1}{2}$	-2.712×10^{7}	0.36
^{17}O	$\frac{5}{2}$	-3.628×10^{7}	0.04
^{19}F	$\frac{1}{2}$	2.5181×10^{8}	100.00
^{23}Na	$\frac{3}{2}$	7.080×10^{7}	100.00
^{31}P	$\frac{1}{2}$	1.0841×10^{8}	100.00
^{113}Cd	$\frac{1}{2}$	5.934×10^{7}	12.26

[a] The angular momentum quantum number, I, and the gyromagnetic ratio, γ, and natural isotopic abundance for nuclei of particular importance in biological NMR spectroscopy are shown.

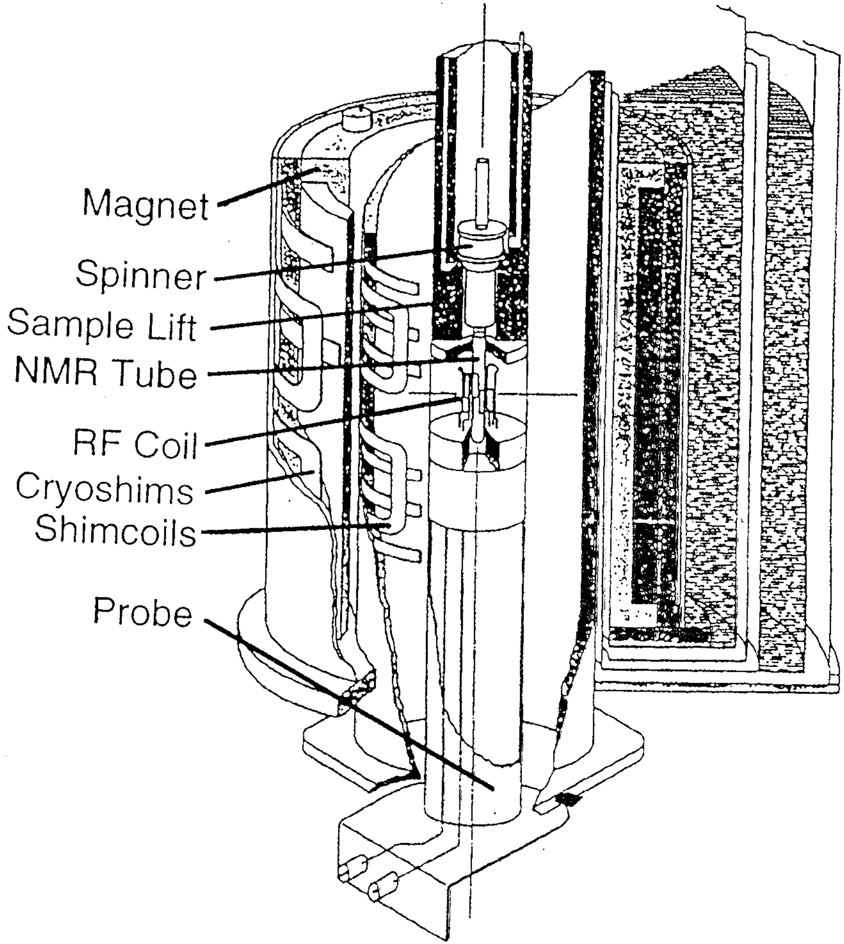


FIGURE 3.2 Cutaway diagram of a superconducting magnet. The probe, sample spinner, and room-temperature shim coils are positioned coaxially in the room-temperature bore of the magnet. The solenoid and cryoshim coils are immersed in liquid helium. The helium dewar is surrounded by a radiation shield and a liquid nitrogen dewar. Diagram courtesy of Bruker Instruments, Inc.