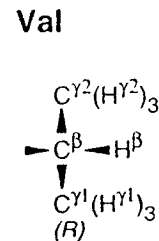
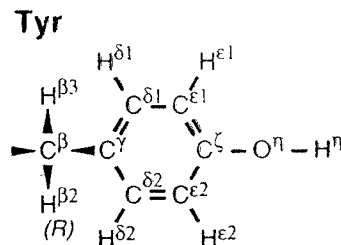
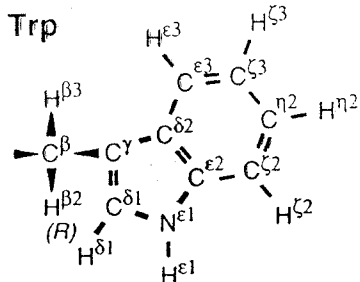
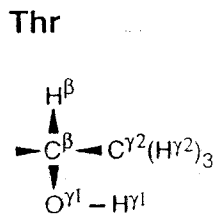
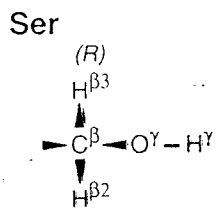
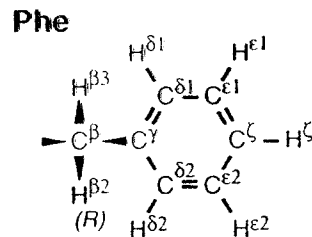
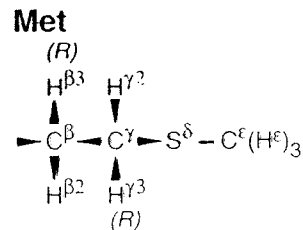
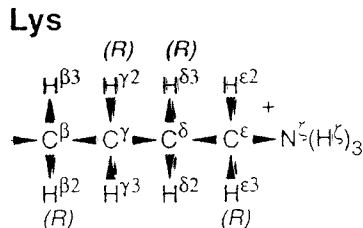
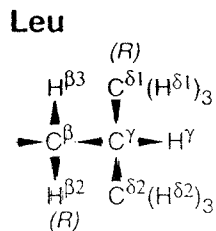
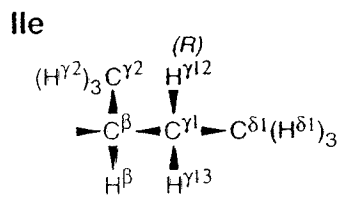
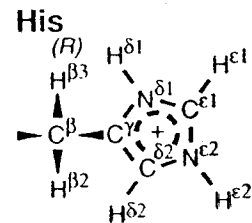
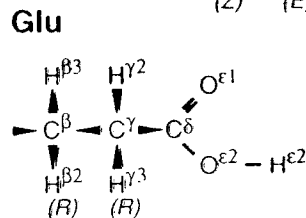
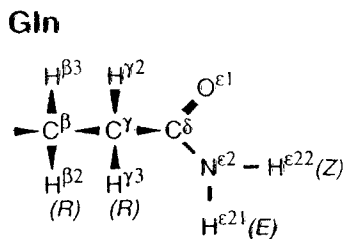
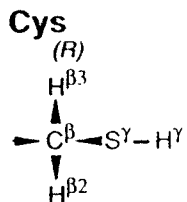
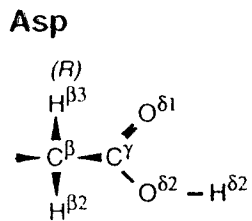
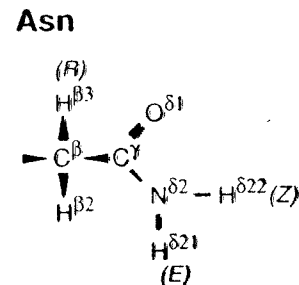
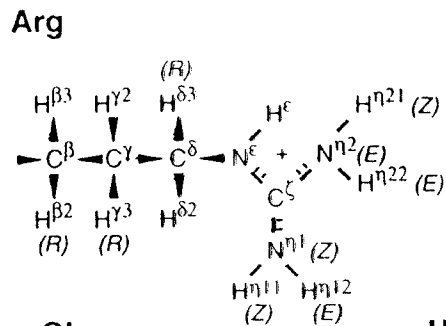
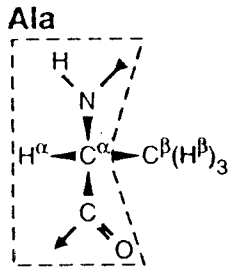
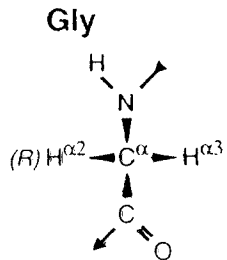
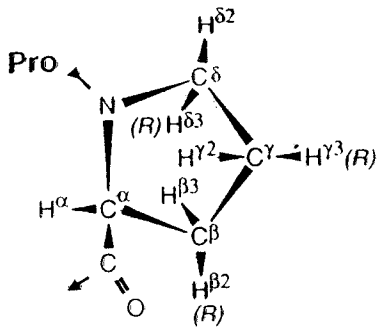


TABLE 2.3. Random Coil  $^1\text{H}$  Chemical Shifts for the 20 Common Amino Acid Residues<sup>a</sup>

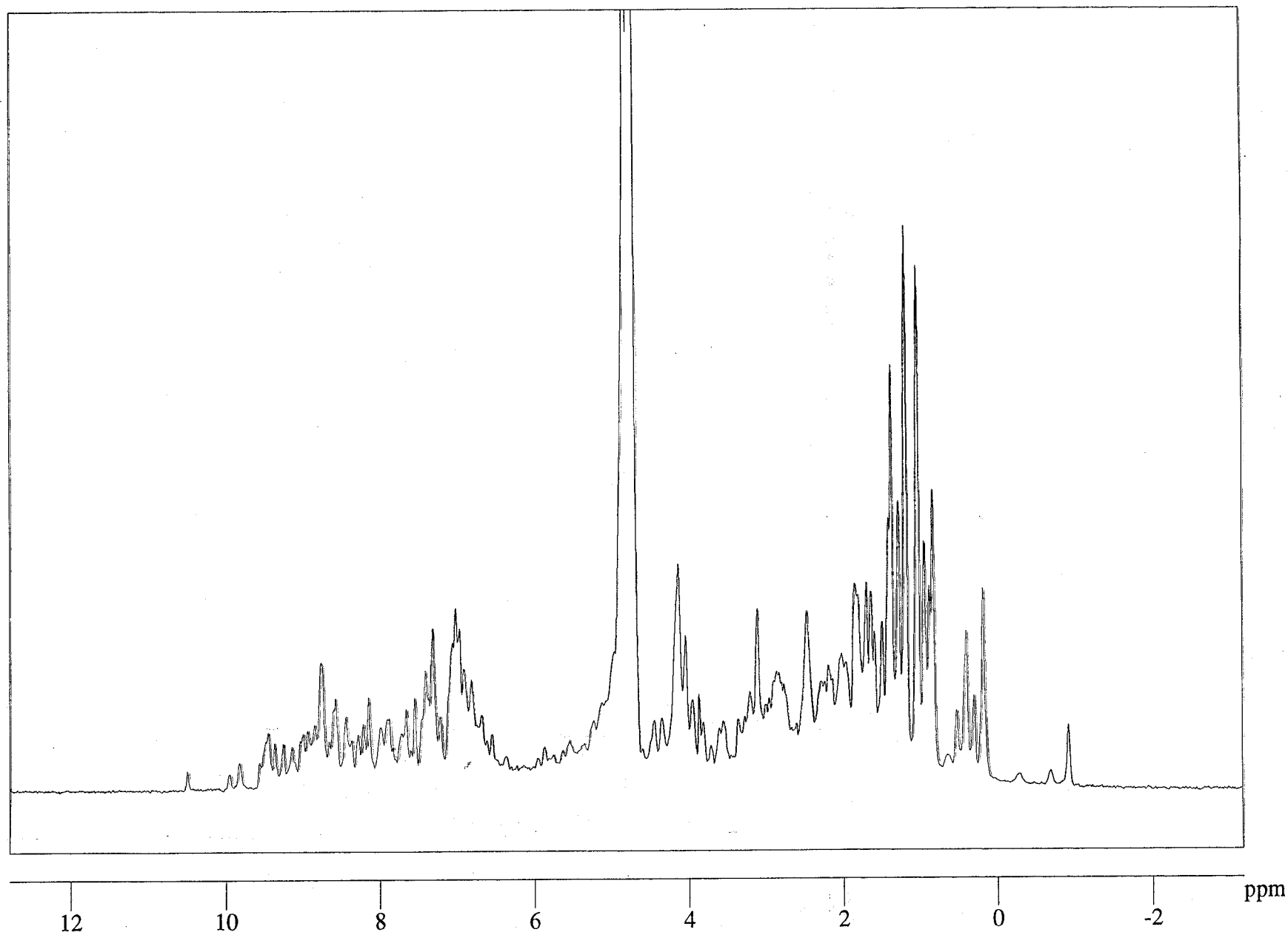
Residue	NH	$\alpha\text{H}$	$\beta\text{H}$	Others
Gly	8.39	3.97		
Ala	8.25	4.35	1.39	
Val	8.44	4.18	2.13	$\gamma\text{CH}_3$ 0.97, 0.94
Ile	8.19	4.23	1.90	$\gamma\text{CH}_2$ 1.48, 1.19 $\gamma\text{CH}_3$ 0.95 $\delta\text{CH}_3$ 0.89
Leu	8.42	4.38	1.65, 1.65	$\gamma\text{H}$ 1.64 $\delta\text{CH}_3$ 0.94, 0.90
Pro <sup>b</sup>		4.44	2.28, 2.02	$\gamma\text{CH}_2$ 2.03, 2.03 $\delta\text{CH}_2$ 3.68, 3.65
Ser	8.38	4.50	3.88, 3.88	
Thr	8.24	4.35	4.22	$\gamma\text{CH}_3$ 1.23
Asp	8.41	4.76	2.84, 2.75	
Glu	8.37	4.29	2.09, 1.97	$\gamma\text{CH}_2$ 2.31, 2.28
Lys	8.41	4.36	1.85, 1.76	$\gamma\text{CH}_2$ 1.45, 1.45 $\delta\text{CH}_2$ 1.70, 1.70 $\epsilon\text{CH}_2$ 3.02, 3.02 $\epsilon\text{NH}_3^+$ 7.52
Arg	8.27	4.38	1.89, 1.79	$\gamma\text{CH}_2$ 1.70, 1.70 $\delta\text{CH}_2$ 3.32, 3.32 NH 7.17, 6.62
Asn	8.75	4.75	2.83, 2.75	$\gamma\text{NH}_2$ 7.59, 6.91
Gln	8.41	4.37	2.13, 2.01	$\gamma\text{CH}_2$ 2.38, 2.38 $\delta\text{NH}_2$ 6.87, 7.59
Met	8.42	4.52	2.15, 2.01	$\gamma\text{CH}_2$ 2.64, 2.64 $\epsilon\text{CH}_3$ 2.13
Cys	8.31	4.69	3.28, 2.96	
Trp	8.09	4.70	3.32, 3.19	2H 7.24 4H 7.65 5H 7.17 6H 7.24 7H 7.50 NH 10.22
Phe	8.23	4.66	3.22, 2.99	2,6H 7.30 3,5H 7.39 4H 7.34
Tyr	8.18	4.60	3.13, 2.92	2,6H 7.15 3,5H 6.86
His	8.41	4.63	3.26, 3.20	2H 8.12 4H 7.14

<sup>a</sup> Data for the nonterminal residues X in tetrapeptides GGXA, pH 7.0, 35°C [from Bundi and Wüthrich (1979a), except that more precise data were obtained for Leu, Pro, Lys, Arg, Met, and Phe using new measurements at 500 MHz].

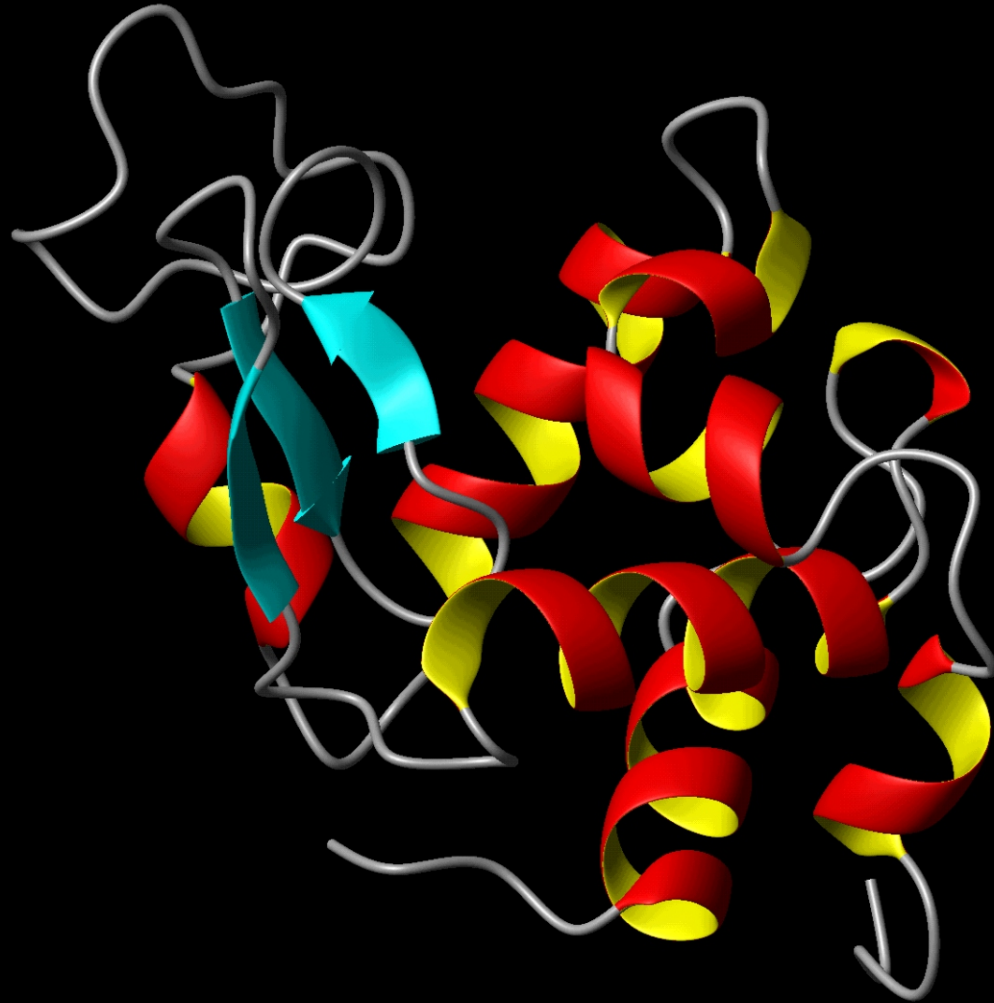
<sup>b</sup> Data for *trans*-Pro.

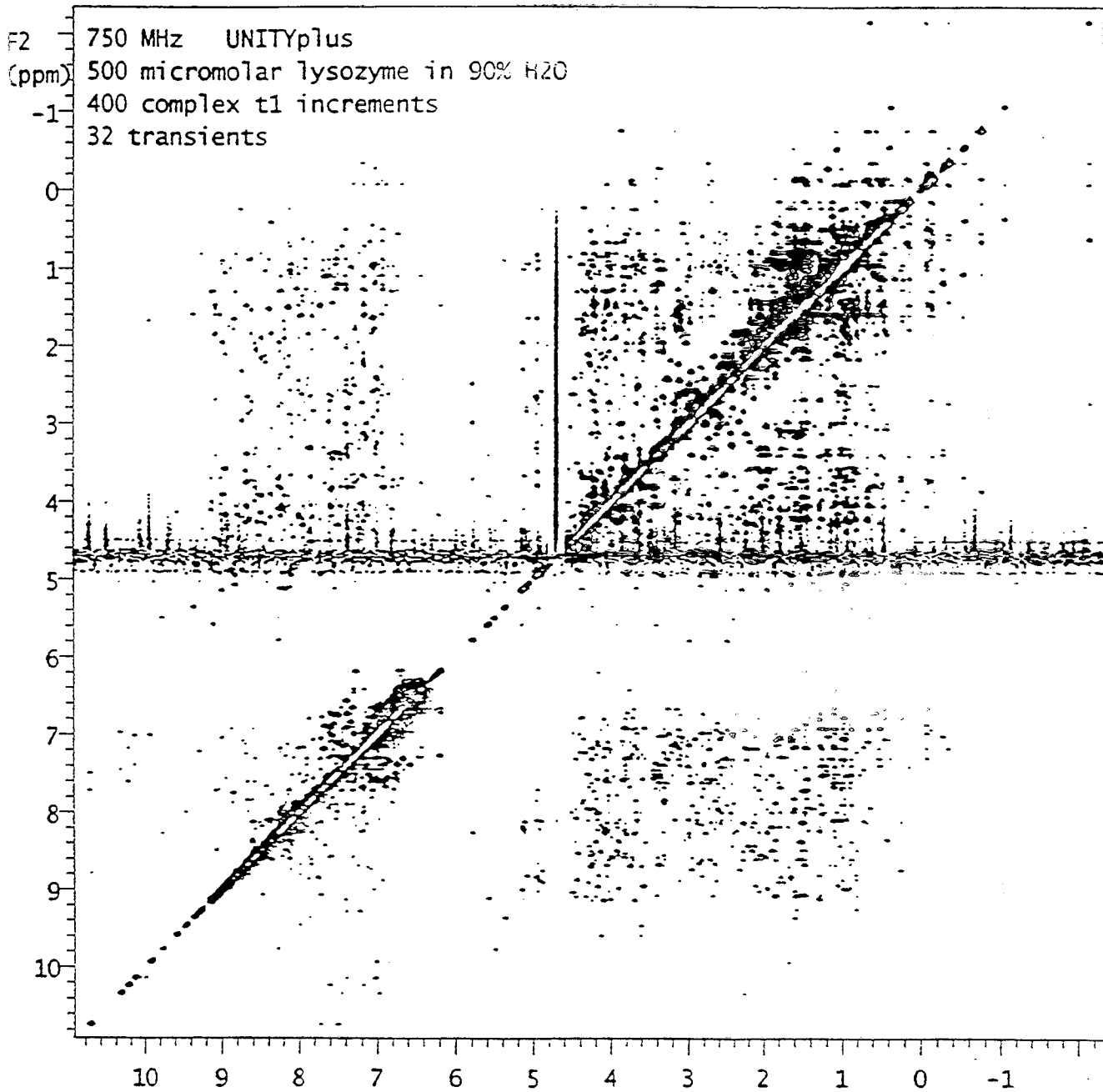


[S54GP55N] RNase T<sub>1</sub>; 40°C; 90%/10% H<sub>2</sub>O/D<sub>2</sub>O; <sup>15</sup>N-dec.; 32 scans



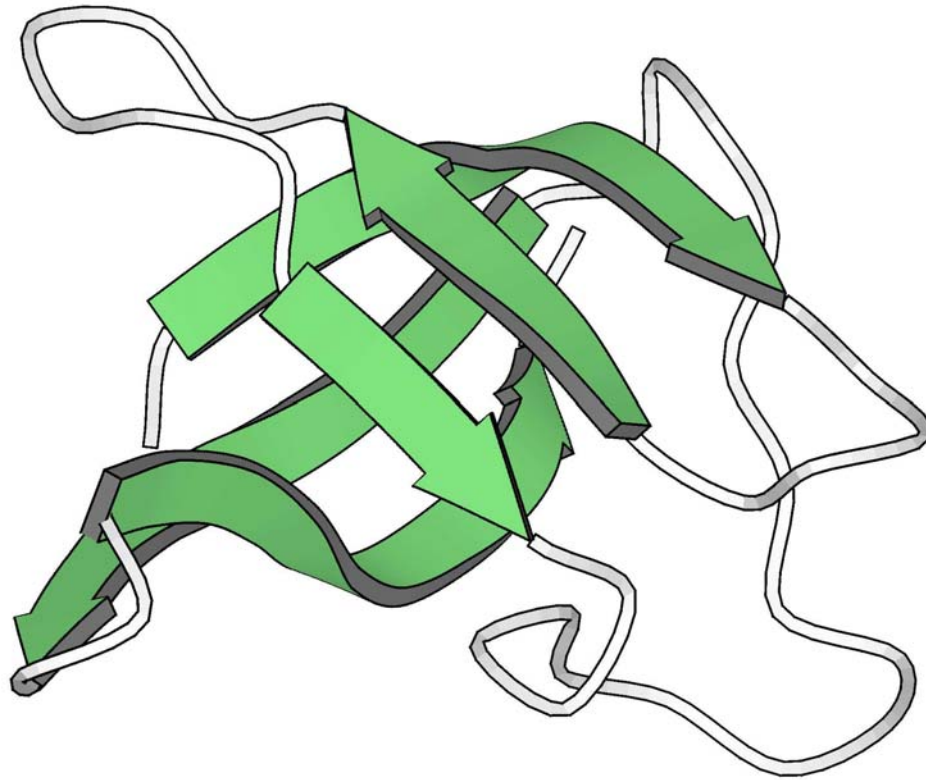
# hen egg white lysozyme



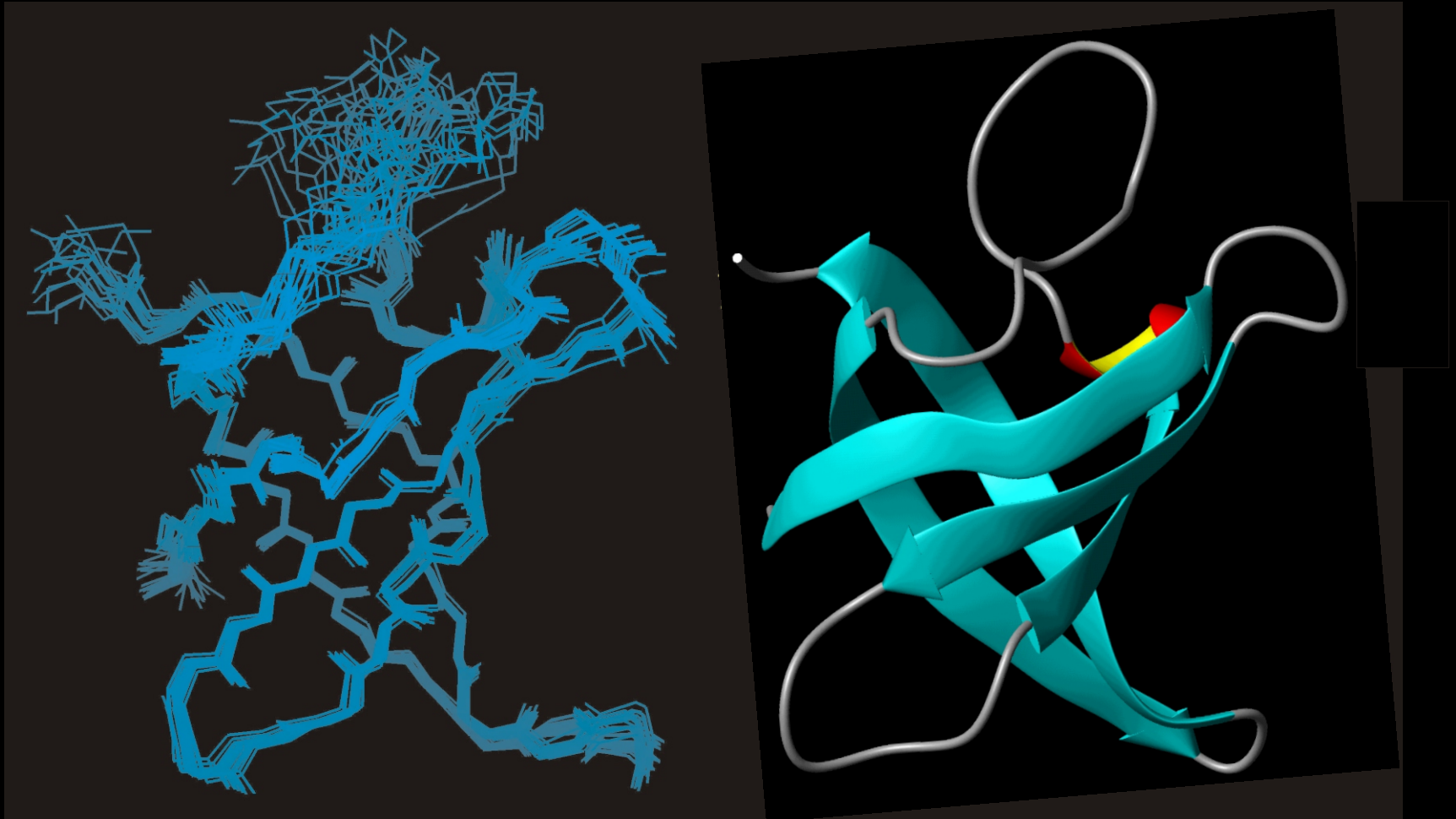


500 micromolar lysozyme in 90% H<sub>2</sub>O 10% D<sub>2</sub>O

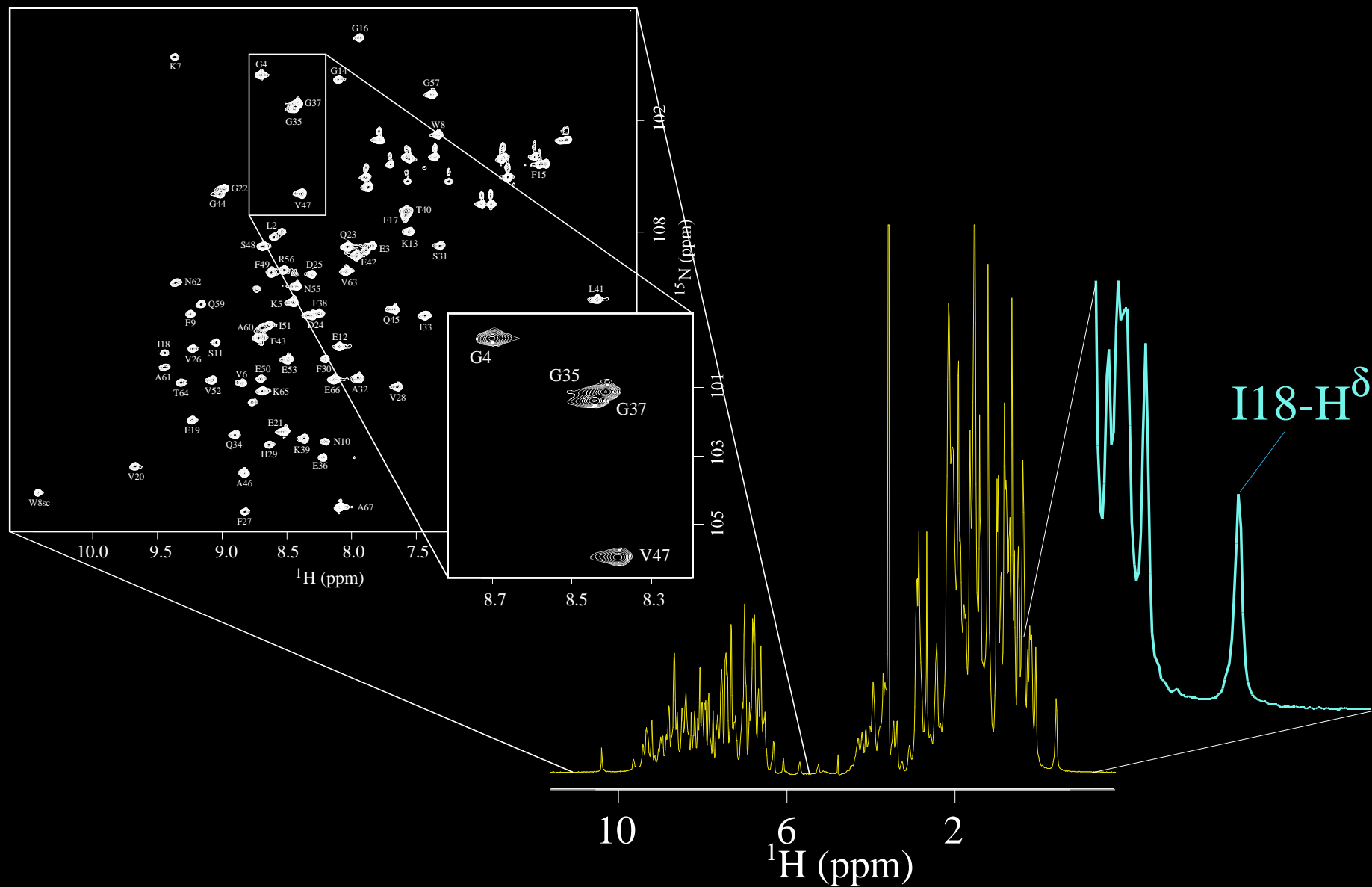
Kälteschockprotein CspB aus  
*Bacillus subtilis*



# NMR structure of the cold shock protein CspB

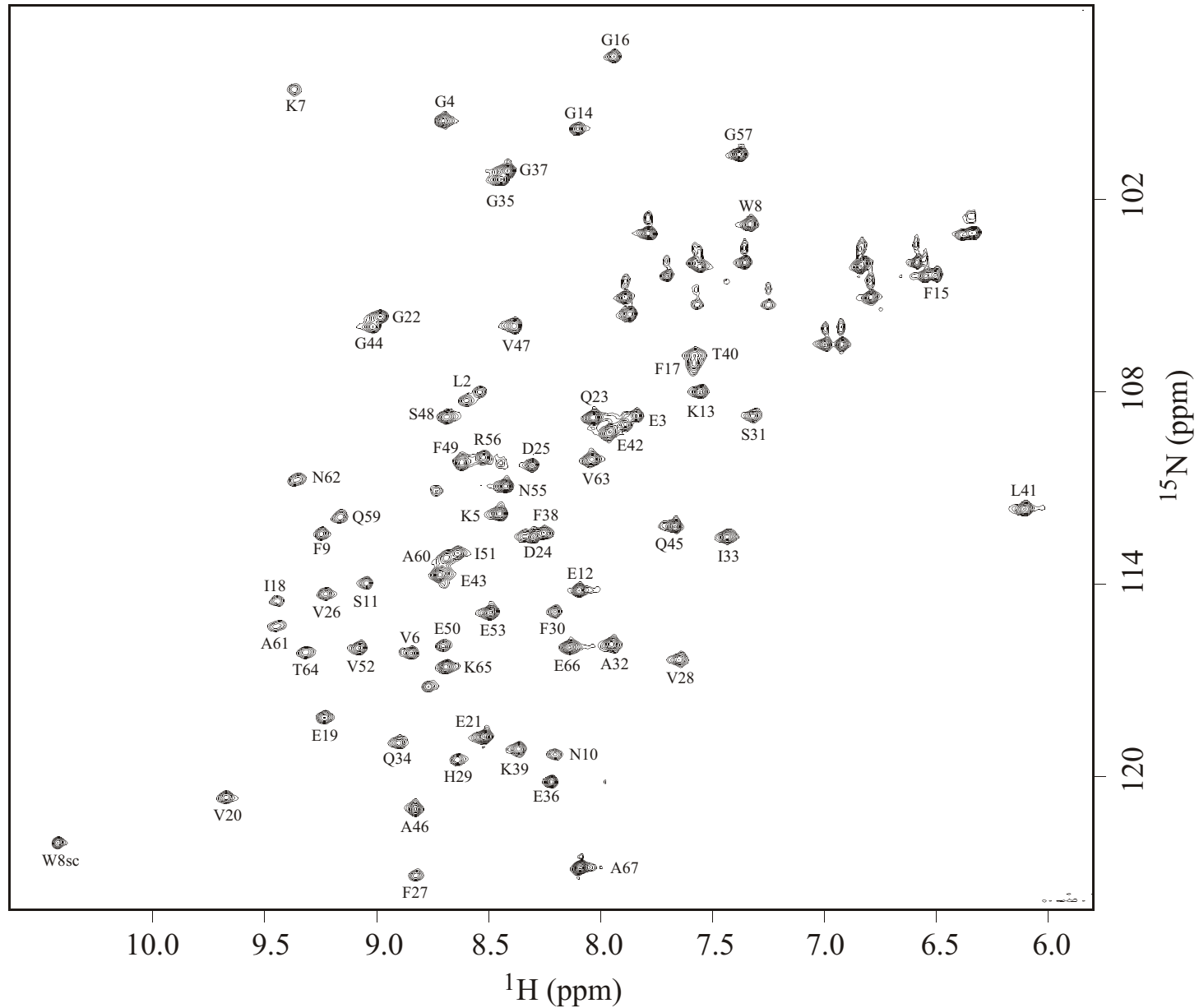


# NMR spectra of cold shock protein CspB

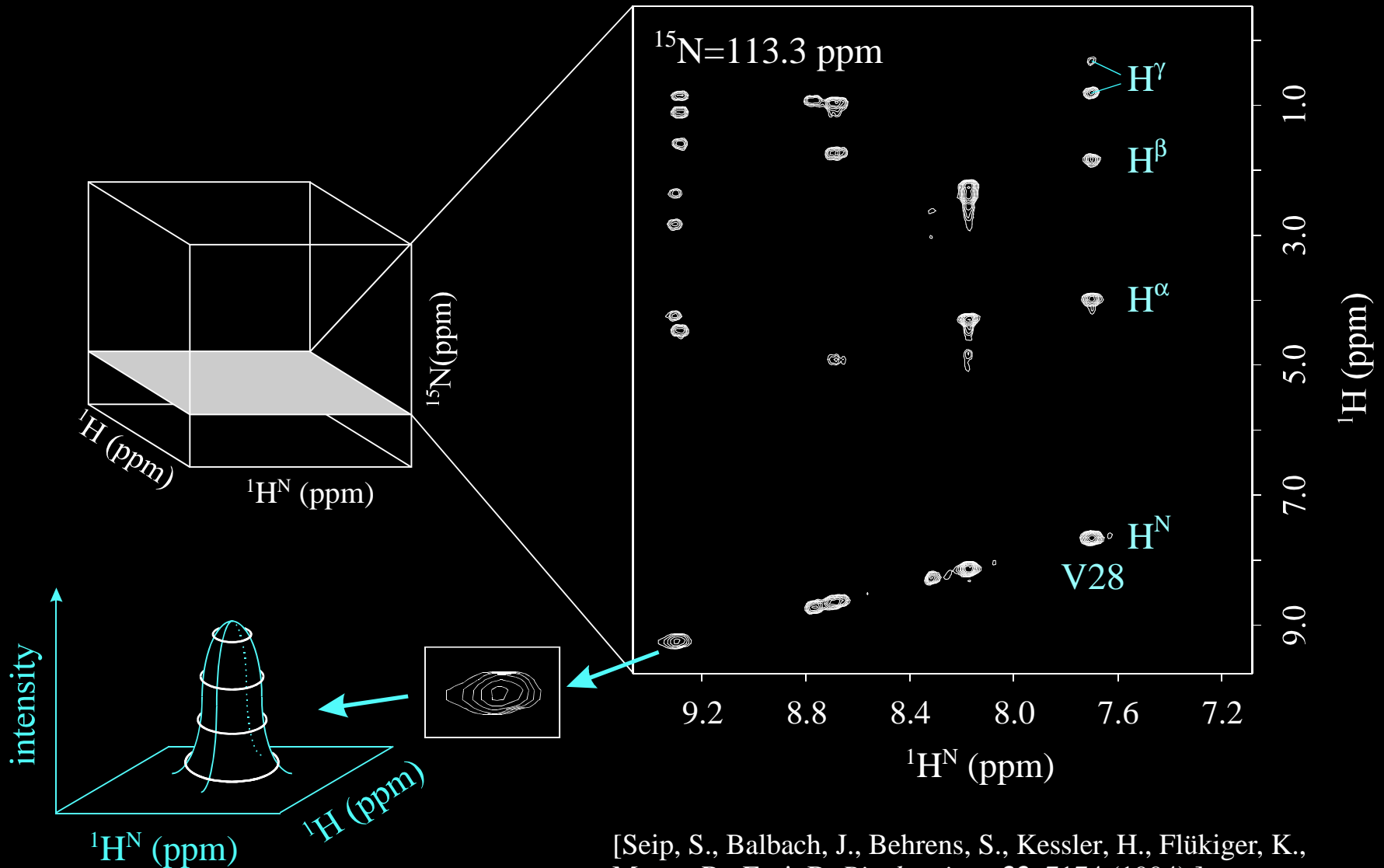




# 2D $^1\text{H}$ - $^{15}\text{N}$ Correlation (HSQC) of CspB



# 3D $^{15}\text{N}$ -TOCSY-HSQC



[Seip, S., Balbach, J., Behrens, S., Kessler, H., Flükiger, K., Meyer, R., Erni, B. *Biochemistry* **33**, 7174 (1994).]

## Single stranded DNA fragments

5'-ATC CTA CTG **ATT GGC** C CAA GGT G-3'

'Y-Box25'

5'-TTT TTT T-3'

'dT7'



# DNA binding interface of CspB



[Zeeb, M., Balbach, J. (2003), *Protein Science*, **12**, 112-123]

