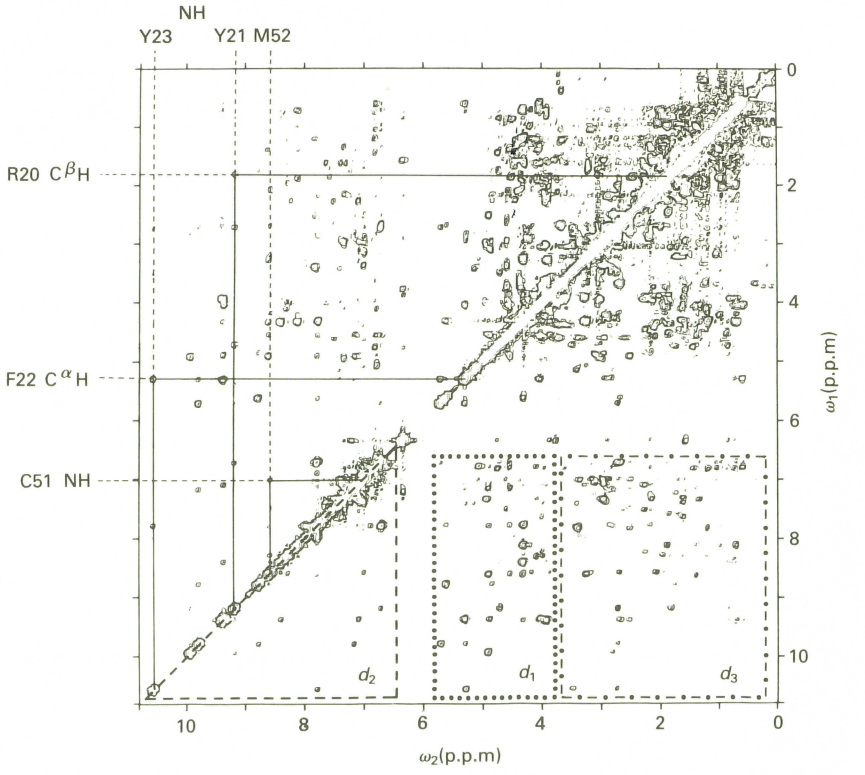

FIG. 9.7.4. Contour plot of a symmetrized, absolute-value 500-MHz ^{1}H NOESY spectrum of a 0.02 M solution of basic pancreatic trypsin inhibitor (BPTI) in D_2O, p^{2}H 4.6, $T = 36°C$. The spectrum was recorded in ~6 h, immediately after dissolving the protein in D_2O, so that, in addition to the non-labile protons, the resonances of ~30 backbone amide protons are seen between 7 and 10.6 p.p.m. In the lower right triangle, three spectral regions of interest for sequential resonance assignments are outlined, i.e. the regions where NOE connectivities between different amide protons (- - -), between amide protons and C^α protons (. . . .) and between amide protons and C^β protons (- · - · -) are usually observed. In the upper left triangle, the assignment of one of each of these types of connectivity is shown (C = cysteine, F = phenylalanine, M = methionine, R = arginine, Y = tyrosine). (From Ref. 9.30.)

eqn (9.4.8)

$$I_{AB}(\tau_m) \propto \frac{\tau_c}{r_{AB}^6}\tau_m. \qquad (9.7.21)$$

The correlation time τ_c refers to the reorientation of the internuclear vector $\mathbf{r}_{AB}$. In systems with isotropic reorientation, such as globular proteins, τ_c is usually assumed to be common to all AB pairs, although this assumption certainly breaks down for mobile side-chains (which, incidentally, may not fulfil the slow-motion approximation).