Biochemistry

 Volume 34, Number 41 October 17, 1995

Accelerated Publications

Measuring the Strength of Side-Chain Hydrogen Bonds in Peptide Helices: The Gln•Asp (i, $i + 4$) Interaction†

Beatrice M. P. Huyghues-Despointes, Tod M. Klingler, and Robert L. Baldwin*

Department of Biochemistry, Beckman Center, Stanford Medical Center, Stanford, California 94305-5307

Received July 7, 1995; Revised Manuscript Received August 29, 1995®

ABSTRACT: Whether hydrogen bonds between side chains are energetically significant in proteins and peptides has been controversial. A method is given here for measuring these interactions in peptide helices by comparing the helix contents of peptides with 1, 2, or 3 interactions. Results are given for the glutamine−aspartate (i, $i + 4$) hydrogen-bond interaction. The Gibbs energy of the interaction is −1.0 kcal/mol when aspartate is charged and -0.4_4 kcal/mol when it is protonated. Magnetic resonance experiments show that the aspartate carboxylate group interacts specifically with the *trans* amide proton (H_E) of glutamine. The interaction is observed only when the glutamine residue is N-terminal to the aspartate and when the spacing is (i, $i + 4$). The same stereochemistry is found in protein structures, where the (i, $i + 4$) glutamine−aspartate interaction occurs much more frequently than other possible arrangements.

Hydrogen-bond (H-bond) interactions between side chains are found frequently in protein structures. In a study of 42 proteins (Stickle et al., 1992), an average of 18 side-chain H-bonds per 160 residues was found. Thus, if each side-chain H-bond contributes −1 kcal/mol to $\Delta G°$ for folding, the overall contribution would be −18 kcal/mol for a 160-residue protein. This free energy would tip the balance between stable and unstable folding, given that values of $\Delta G°$ for typical protein-folding reactions are between −5 and −15 kcal/mol (Pace, 1990). Information about the energetics of side-chain H-bond interactions is quite limited and comes chiefly from directed mutagenesis experiments on proteins, including T4 lysozyme (Alber et al., 1987), barnase (Chen et al., 1993), ribonuclease T1 (Shirley et al., 1992), and staphylococcal nuclease (Thorson et al., 1995): see below.

Analyzing side-chain interactions in peptide helices has several desirable properties. Fairly weak interactions produce significant changes in the fraction helix. Both natural and non-natural amino acids can be studied. The necessary peptides can be made readily. The helix−coil transition theory of Lifson and Roig (1961) is well-suited to analyze helix formation by peptides with known sequences (Chakrabartty et al., 1991), and it is readily extended to include side-chain interactions (Scholtz et al., 1993). The theory has been modified to include N-cap and C-cap interactions (Doig et al., 1994). The parameters needed to use the theory, including the helix nucleation parameter (Scholtz et al., 1991a; Rohl et al., 1992), the helix propensities in alanine-based peptides (Chakrabartty et al., 1994), and the N-cap and C-cap propensities (Doig & Baldwin, 1995), have all been determined.

† This work was supported by National Institutes of Health Grant GM 31475 to R.L.B. and by the CAMIS grant to D. L. Brutlag from the National Library of Medicine LM 05305.

* To whom correspondence should be addressed.

® Abstract published in *Advance ACS Abstracts,* October 1, 1995.

[1] Abbreviations. CD, circular dichroism; NMR, nuclear magnetic resonance; Gln, glutamine; Asp, aspartate; Glu, glutamate; HOBT, 1-hydroxybenzotriazole; TSP, 3-(trimethylsilyl)propionic acid; PDB, protein data bank; Thr, threonine; Asn, asparagine.

0006-2960/95/0434-13267$09.00/0

The H-bond interaction studied here, Gln•Asp (i, $i + 4$), was first observed unexpectedly in a study of how the interaction between charged aspartate and the helix dipole depends on the aspartate position (Huyghues-Despointes et al., 1993a), and a parallel observation of a Gln•Glu (i, $i + 4$) interaction (Scholtz et al., 1993) was also made. We set out to find methods of detecting and measuring the interaction that would leave no doubt about its reality. We describe here one method of detecting the Gln•Asp interaction, which also gives information about its stereochemistry, and a separate method of measuring the strength of the interaction.

EXPERIMENTAL PROCEDURES

Peptide Synthesis and Purification. Peptides were synthesized by the solid-phase method using an active ester-coupling procedure, employing pentafluorophenyl esters of 9-fluorenylmethyloxycarbonyl (Fmoc)-labeled amino acids (Atherton & Sheppard, 1985) purchased from Milligen/Millipore. The Fmoc−amino acid derivative of L-Gln labeled at the amide nitrogen with ^{15}N (99%) (Cambridge Isotope Laboratory) was made (Stewart & Young, 1984) and then coupled to the growing peptide chain by using BOP (Castro's reagent), diisopropylethylamine, and the HOBT activating method, in 1:1 dichloromethane:dimethylformamide solution (Atherton & Sheppard, 1989). Peptides were cleaved and purified as described by Huyghues-Despointes et al. (1993b). Peptide purity was assessed by C18 reverse-phase chromatography using the Pharmacia FPLC system; purity was greater than 95% for each peptide. The primary-ion molecular weight of each peptide was confirmed by fast atom bombardment or electronspray mass spectrometry. The conditions for storing and handling the peptides were described elsewhere (Huyghues-Despointes et al., 1993a).

Circular Dichroism Spectroscopy. CD was measured with an AVIV 60 DS spectropolarimeter. The ellipticity was calibrated with (+)-10-camphorsulfonic acid. Cuvettes with either a 1-mm or a 1-cm path length were used. Samples for CD measurements were prepared as described by Huyghues-Despointes et al. (1993a,b). Concentrations of the peptide stock solutions were determined by measuring tyrosine absorbance in water ($\epsilon_{275} = 1390\ M^{-1}\ cm^{-1}$) and in 6 M guanidine hydrochloride with 20 mM phosphate buffer ($\epsilon_{275} = 1450\ M^{-1}\ cm^{-1}$) (Brandts & Kaplan, 1973). The purpose of the glycine preceding the C-terminal tyrosine is to eliminate the aromatic contribution to the CD signal (Chakrabartty et al., 1993a). Some peptides were made and studied before the discovery of this effect. The fraction helix was computed as described previously (Scholtz et al., 1991a). All peptides in this study show typical α-helical characteristics exhibited by other alanine-based peptides (Scholtz & Baldwin, 1992). The helix content is not dependent on peptide concentration, suggesting that helix formation does not occur from peptide association and is probably monomeric (Padmanabhan et al., 1990).

NMR Spectroscopy. All NMR spectra were recorded at 2 °C on a 500-MHz General Electric GN-Omega spectrometer, using a 6000-Hz spectral width for one-dimensional data collection. Spectra were processed on Silicon Graphics Personal Iris and Indigo computers using FELIX (Hare Research, Inc.). Samples for pH titration were prepared by making a 1−2 mM peptide solution containing 10 mM NaCl, 7% D_2O, and 3 mM sodium phosphate. The free induction decay was the sum of 16−64 scans consisting of 4096 complex points. The pH dependence of chemical shifts was measured against the TSP standard, after taking account of the pH dependence of chemical shift of TSP (De Marco, 1977). The assignments of the glutamine *cis* and *trans* amide protons are based on the reported chemical shifts of several primary amide compounds (Redfield & Waelder, 1979).

Table 1. The Gibbs Energy of the Gln•Asp (i, $i + 4$) H-Bond in Helical Peptides[a]

Peptide[b]	f_H[c]	f_H(ref)[c]	p[d]	$\Delta G°$(cal/mol)[e]
pH 2				
1QD	0.35	0.26	2.7	−540
2QD	0.42	0.20	2.1	−390
3QD	0.53	0.26	1.9	−350
pH 7				
1QD	0.48	0.29	5.0	−870
2QD	0.61	0.11	7.1	−1060
3QD	0.75	0.15	6.2	−990

[a] Conditions: 10 mM NaCl, 0 °C; similar results were obtained in 1 M NaCl. [b] The peptides contain either 1, 2, or 3 interacting pairs of Gln, Asp, residues, as indicated: see Figure 2a for their sequences and those of the reference peptides. [c] The fraction helix (f_H) is measured by circular dichroism; f_H(ref) is the fraction helix of the reference peptide. [d] The apparent equilibrium constant for the interaction: $\Delta G° = -RT \ln p$. [e] The standard Gibbs energy of the Gln•Asp (i, $i + 4$) interaction, given per interaction.

Data Analysis. The standard Gibbs energy, $\Delta G°$, of the interaction was computed from the fraction helix by an algorithm (Stapley et al., 1995) that incorporates the interaction into the Lifson and Roig theory (1961) [see also Scholtz et al. (1993)]. The "homopolymer approximation" was used: the reference peptide was treated as a homopolymer, except for the Asp residues and an equal number of corresponding Gln residues, and an average helix propensity $\langle w \rangle$ was computed. This value of $\langle w \rangle$ was assigned to all residues in the test peptide except for the Asp residues and the interacting Gln residues. The values used for the helix propensities (Chakrabartty et al., 1994) and nucleation parameter (Rohl et al., 1992) were $w_Q = 0.56$, $w_D = 0.35$, and $v = 0.048$. The interaction is included by assigning an additional statistical weight p to conformations in which residues i through $i + 4$ are helical, as defined by the backbone ϕ and φ angles. The interaction parameter (see Table 1) is defined as the equilibrium constant for the interaction in a completely helical peptide. This equilibrium constant is related to the standard Gibbs energy by the relation $\Delta G° = -RT \ln p$. In peptides with two or more interacting residue pairs, the interactions are treated as being independent of each other.

Protein Structure Searches. The protein sequences were extracted from a nonhomologous set of chains from the Brookhaven Protein Data Bank (Berstein et al., 1977). A detailed description of the procedures is given by Klinger and Brutlag (1994). The set includes 212 high-resolution (>2.5 Å), nonhomologous, nonmutant, nonmodel structures. We use the Iditis program from Oxford Molecular (Thornton & Gardner, 1989), a program for querying the PDB in relational form to extract sequences of specific secondary structure assigned by the extended DSSP method (Kabsch & Sander, 1983) and implemented in Iditis. The helices are identified by hydrogen bonding, and the program includes one residue at each end of the helix, usually at the capping positions. The expected number of (i, $i + 4$) XY pairs is

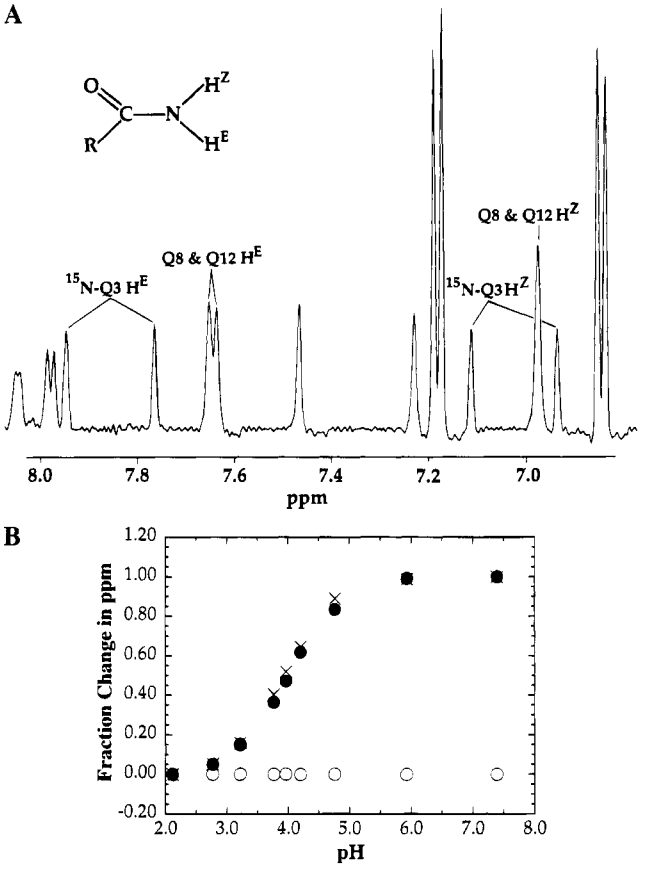

FIGURE 1: Detection of the Gln•Asp (i, i + 4) interaction and identification of the interacting Gln amide proton by pH titration of chemical shifts. A. ^{1}H-NMR spectrum of peptide Q3D7 in 10 mM NaCl pH 7.4, 2 °C. The amide group of Q3 is labeled with ^{15}N; the wide splitting of each ^{15}NH resonance is used to identify the amide protons of Q3. H_E is the *trans* proton, and H_Z is the *cis* amide proton (see inset). The sequence of Q3D7 is Ac-AAQ-AAADQAAAAQAAY-NH_2. B. Titration curves of the H_E (●) and H_Z (○) resonances of Q3 and of the β-CH_2 (×) resonance of D7.

calculated from the product of the frequency of residue X at position i and the frequency of residue Y at position i + 4; the expected number of (i, i + 4) YX pairs is calculated from the product of the frequency of residue Y at position i and the frequency of residue X at position i + 4. Since these frequencies may be different, the expected number of XY (i, i + 4) pairs may not be similar to the expected number of YX (i, i + 4) pairs. In the distance-based identification of H-bonds in the structure set, the maximum allowed distance between the donor and acceptor atoms is 3.9 Å.

RESULTS

pH Titration of Chemical Shifts. To identify the two interacting groups, the amide nitrogen of the glutamine residue in the Gln•Asp (i, i + 4) residue pair was labeled with ^{15}N (see Experimental Procedures). The label causes a characteristic splitting of each amide proton resonance, shown in Figure 1A. Generally, the H_E (*trans*) proton is found downfield of the H_Z (*cis*) proton in primary amides (Redfield & Waelder, 1979). Measurement of the pH titration curves of these resonances (Figure 1B) shows that only the H_E proton changes its chemical shift as the aspartate carboxylate group titrates. There is a substantial change between pH 6 and pH 2 in the chemical shift of the *trans* resonance (0.22 ppm) but no measurable change in the *cis* resonance. No change in the chemical shift of any Gln amide

A

Peptide	Sequence
1QD	Ac-AAQAAADQAAAAQAAY-NH_2
1QDref	Ac-AAQAADAQAAAAQAAY-NH_2
2QD	Ac-AAQAAADQAAADAAAGY-NH_2
2QDref	Ac-AAAQAADAQAADAAAGY-NH_2
3QD	Ac-AAQAAADQAAADQAAADAAAGY-NH_2
3QDref	Ac-AAAQAADAQAADAQAADAAAGY-NH_2

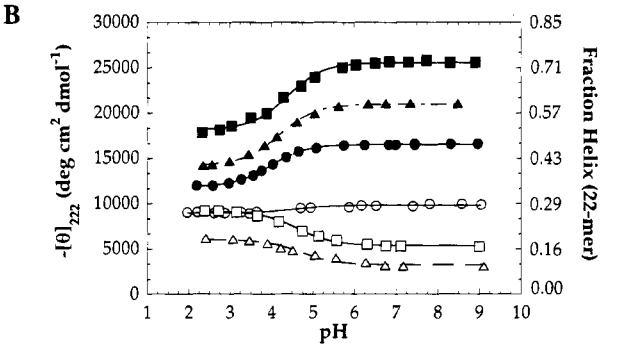

FIGURE 2: Measurement by circular dichroism of the increase in helix content caused by the Gln•Asp (i, i + 4) interaction in peptides with 1, 2, or 3 interacting pairs of Gln, Asp residues. A. Sequences of the peptides studied and of the corresponding reference peptides. B. pH titration curves of helix content measured by circular dichroism. Filled symbols show the test peptides, open symbols show the corresponding reference peptides: (●) 1QD, (▲) 2QD, (■) 3QD. $[\Theta]_{222}$ is the mean residue ellipticity measured at 222 nm.

resonances is found in peptides with either the Asp•Gln (i, i + 4) or the Gln•Asp (i, i + 3) sequences (data not shown). Thus, the amide group of Gln i interacts specifically with the carboxylate group of Asp i + 4, and only the *trans* amide proton participates in the interaction.

Helix Contents of Peptides with 1, 2, and 3 Gln•Asp (i, i + 4) Pairs. To measure the standard Gibbs energy of the Gln•Asp (i, i + 4) interaction, peptides were made that contain either 1, 2, or 3 Gln•Asp (i, i + 4) pairs and their helix contents were measured by circular dichroism. The change in helix content with pH was also measured to determine the effect of protonating the aspartate residues. Matching reference peptides were made, and their helix contents and pH titration curves were measured. The peptide sequences are given in Figure 2A, and the titration curves of helix content are given in Figure 2B.

It is essential to design a reference peptide that matches as closely as possible the test peptide and lacks the Gln•Asp (i, i + 4) interaction. In each reference peptide used here, the length is the same as in the test peptide, the amino acid compositions of both peptides are the same, and the positions of the aspartate residues are the same, or nearly the same, as in the test peptide. These are the main variables, other than specific side-chain interactions and electrostatic interactions, that affect the helix content. The position of a charged aspartate residue affects the helix content via both its low helix propensity and the charge−helix dipole interaction (Huyghues-Despointes et al., 1993a). These effects can be seen in the reference peptides. The fact that the helix contents of the reference peptides do not change in a regular manner as the number of aspartate residues is varied emphasizes that the length of the peptide and the position of the charged aspartate residues are also variables that

Table 2. Frequencies of (i, $i + 4$) Side-Chain H-Bond Interactions in Protein Helices

sequence	no.[a]	H-bond[b]	*i trans*[c]	$i + 4$ *gauche+*[d]
QD	35 (18.5)	19	29 (14.4)	32 (27.6)
QE	52 (31.7)	18	32 (21.4)	25 (31.8)
EQ	29 (31.8)	2	11 (11.4)	18 (18.0)
DQ	22 (21.3)	1	5 (3.9)	13 (13.6)

[a] The number of sequences with (i, $i + 4$) spacing in protein helices; the expected number, based on single-residue frequencies, is given in parentheses. [b] The average Gln·Asp H-bond distance is 3.1 ± 0.2 Å; the average Gln·Glu H-bond distance is 3.1 ± 0.5 Å. None of the Gln·Asp H-bond interactions is at the N- or C-cap position. [c] The number of instances that residue i has a *trans* χ_1 rotamer; the expected number is given in parentheses. [d] The number of instances that residue $i + 4$ has a *gauche* + χ_1 rotamer; the expected number is given in parentheses.

significantly affect the helix content. An increase in helix content with decreasing pH is observed for 2QDref and 3QDref. An unfavorable interaction between aspartate near the C-terminus and the helix dipole is removed upon protonation of aspartate. This effect is not observed for 1QDref because the single aspartate is near the center of the peptide. The glutamine residues in all three reference peptides are spaced either (i, $i + 2$) or (i, $i + 3$) from the nearest aspartate. Previous data show that glutamine and aspartate do not interact in these spacings (Huyghues-Despointes et al., 1993a).

Figure 2 shows that the helix content of each test peptide is greater than that of its reference peptide, both at pH 2 and at pH 7, that the difference in helix content between the test and reference peptide increases with the number of Gln·Asp pairs, and that the difference in helix content follows the pH titration curve of aspartate, and is greater at pH 7 than at pH 2. The helix content does not scale linearly with the interaction strength (just as an equilibrium constant does not scale linearly with the amount of product in a reaction), and there is a larger difference in helix content between 1QD and 2QD than between 2QD and 3QD, at both pH 2 and pH 7. These results show that the Gln·Asp (i, $i + 4$) interaction is effective in stabilizing peptide helices and that the interaction persists at pH 2, where aspartate is protonated, although the interaction is stronger at pH 7 than at pH 2.

Table 1 shows that, within error, the value for the ΔG° of the interaction is the same, per interaction, in peptides with 1, 2, or 3 interactions. At pH 2, where an uncharged Gln·Asp H-bond is made, $\Delta G^\circ = -0.4_4$ kcal/mol, while at pH 7, where a charged H-bond is made, $\Delta G^\circ = -1.0$ kcal/mol^{-1}. The measurements of helix content and of ΔG° were repeated in 1 M NaCl to find out if screening of electrostatic interactions between aspartate residues is important. Similar values of ΔG° were obtained in 1 M NaCl as at 10 mM NaCl, both at pH 7 and pH 2 (data not shown).

Data on Gln·Asp Interactions from the Protein Structure Data Base. Table 2 gives the number of Gln·Asp (i, $i + 4$) sequences found in helices in 212 protein structures taken from the Brookhaven Protein Data Bank. The observed number of Gln·Asp (i, $i + 4$) pairs is large compared to the number expected for random occurrence, and 19 pairs are observed to be H-bonded on the basis of the N···O distance. In all of these H-bonded pairs, glutamine has the *trans* χ_1 rotamer, aspartate has the *gauche+* rotamer, and the *trans* (H_E) amide proton of the Gln−NH_2 group interacts with the Asp−COO^- group (see Figure 3). The number of Asp·Gln (i, $i + 4$) sequences matches the number expected for random occurrence, and only one H-bonded sequence is found. Aspartate strongly prefers the *gauche+* over the *trans* χ_1 rotamer (McGregor et al., 1987) because there is a close contact between the peptide CO group and the side-chain COO^- group in the *trans* conformation. This rotamer preference can help to explain why H-bonded Asp·Gln (i, $i + 4$) pairs occur rarely. No Gln·Asp or Asp·Gln (i, $i + 3$) H-bonded pairs are found (data not shown). Data for Gln·Glu and Glu·Gln sequences are also given in Table 2; they follow a similar pattern as for Gln·Asp or Asp·Gln sequences.

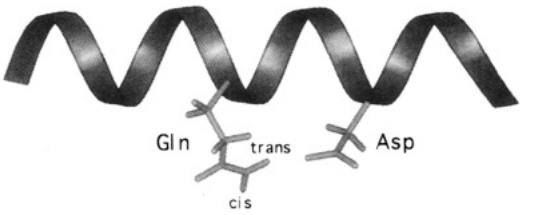

FIGURE 3: Model of the Gln·Asp (i, $i + 4$) interaction in a peptide helix.

DISCUSSION

H-Bonds in Peptide Helices Compared to Proteins. These results show clearly that the Gln·Asp (i, $i + 4$) H-bond interaction stabilizes peptide helices and that the same interaction occurs commonly in protein helices. The charged H-bond interaction at pH 7 is stronger than the H-bond made between glutamine and protonated aspartate at pH 2, but the uncharged H-bond is also helix-stabilizing.

The value of ΔG° found here for a side-chain H-bond is substantially smaller than the values reported from mutagenesis experiments in proteins (Fersht et al., 1985; Alber et al., 1987; Shirley et al., 1992; Chen et al., 1993; Thorson et al., 1995). At least two main factors are involved. First, side chains are more constrained in proteins than in alanine-based peptide helices, so there is a greater loss of side-chain conformational entropy when the interaction is formed in a peptide helix. Second, a polar side chain that is buried in a protein without another H-bonding group nearby is often unable to H-bond to water, whereas in a peptide helix it would be able to H-bond to water. Consequently, the penalty for breaking the H-bond by directed mutagenesis is larger in the protein than in the peptide. Because structural rearrangements are likely to occur in proteins, it is important to determine the X-ray structures of the mutants. Data for mutants in which the H-bond is broken and no major structural rearrangement occurs were reported for three cases (Leu, Ala, Phe) in T4 lysozyme, with $\Delta\Delta G^\circ$ values of 1.3, 1.4, and 2.4 kcal/mol (Alber et al., 1987), respectively, and for two mutants of barnase with $\Delta\Delta G^\circ$ values of 1.4 and 1.9 kcal/mol (Chen et al., 1993), respectively. A new approach to the problem has just been reported (Thorson et al., 1995) in which a non-natural amino acid can be introduced at a specific location via protein synthesis *in vitro*, so that the H-bond can be left intact but the strength of the H-bond can be varied over wide limits. Values of −1.5 to −2.0 kcal/mol were found for the Tyr·Glu H-bond interaction at two sites in staphylococcal nuclease. An NMR study of the effects of specific side-chain interactions in a histidine-containing protein has just appeared (Hammen et al., 1995).

The results reported here add to the evidence that H-bonds are important in stabilizing α-helices in water. The favorable

enthalpy of forming the helix backbone (−1 kcal per mole of residues) is the major factor driving formation of alanine-based peptide helices in water (Scholtz et al., 1991a,b), and formation of the peptide H-bond is an important factor in determining this enthalpy change. Note, however, that this favorable enthalpy of stabilizing an isolated helix may change when the helix is buried in a protein and the backbone is desolvated (Ben-Naim, 1991; Yang et al., 1992). The N-cap interaction made between a polar side chain such as Asn or Thr at N-cap and an unsatisfied main-chain NH group was first detected in protein helices (Presta & Rose, 1988; Richardson & Richardson, 1988) and was later studied in peptide helices, where there is now general agreement that this side-chain−main-chain H-bond makes an important contribution to helix stability (Bruch et al., 1991; Forood et al., 1993; Lyu et al., 1993; Chakrabartty et al., 1993b). Side-chain−side-chain H-bonds can now be added to this list.

ACKNOWLEDGMENT

We thank Dr. Peter Schultz for a preprint of his manuscript. We thank the Mass Spectrometry Facility, University of San Francisco (supported by NIH Grant RR 01614), for mass spectra. B.H.D. is a predoctoral fellow of the NIH Biophysics Training Program, and T.K. is a predoctoral fellow of the National Library of Medicine.

REFERENCES

Alber, T., Dao-pin, S., Wilson, K., Wozniak, J. A., Cook, S. P., & Matthews, B. W. (1987) *Nature 330*, 41−46.
Atherton, E., & Sheppard, R. C. (1985) *J. Chem. Soc., Chem. Commun. 3*, 165−166.
Atherton, E., & Sheppard, R. C. (1989) in *Solid Phase Peptide Synthesis: A Practical Approach* p 84, IRL Press, New York.
Ben-Naim, A. (1991) *J. Phys. Chem. 95*, 1437−1444.
Brandts, J. R., & Kaplan, K. J. (1973) *Biochemistry 12*, 2011−2024.
Bruch, M. D., Dhingra, M. M., & Gierasch, L. M. (1991) *Proteins 10*, 130−139.
Chakrabartty, A., Schellman, J. A., & Baldwin, R. L (1991) *Nature 351*, 586−588.
Chakrabartty, A., Kortemme, T., Padmanabhan, S., & Baldwin, R. L. (1993a) *Biochemistry 32*, 5560−5565.
Chakrabartty, A., Doig, A. J., & Baldwin, R. L. (1993b) *Proc. Natl. Acad. Sci. U.S.A. 90*, 11332−11336.
Chakrabartty, A., Kortemme, T., & Baldwin, R. L. (1994) *Protein Sci. 3*, 843−852.
Chen, Y. W., Fersht, A. R., & Henrick, K. (1993) *J. Mol. Biol. 234*, 1158−1170.
De Marco, A. (1977) *J. Magn. Reson. 26*, 527−528.
Doig, A. J., Chakrabartty, A., Klingler, T. M., & Baldwin, R. L. (1994) *Biochemistry 33*, 3396−3403.
Doig, A. J., & Baldwin, R. L. (1995). *Protein Science 4*, 1325−1336.
Fersht, A. R., Shi, J., Knill-Jones, J., Lowe, D. M., Wilkinson, A. J., Blow, D. M., Brick, P., Carter, P., Waye, M. M., & Winter, G. (1985) *Nature 314*, 235−238.
Forood, B., Feliciano, E. J., & Nambiar, K. P. (1993) *Proc. Natl. Acad. Sci. U.S.A. 90*, 838−842.
Hammen, P. K., Scholtz, J. M., Anderson, J. W., Waygood, E. B., & Klevit, R. E. (1995) *Protein Sci. 4*, 936−944.
Huyghues-Despointes, B. M. P., Scholtz, J. M., & Baldwin, R. L. (1993a) *Protein Sci. 2*, 1604−1611.
Huyghues-Despointes, B. M. P., Scholtz, J. M., & Baldwin, R. L. (1993b) *Protein Sci. 2*, 80−85.
Kabsch, W., & Sanders, C. (1983) *Biopolymers 22*, 2577−2637.
Klingler, T. M., & Brutlag, D. L. (1994) *Protein Sci. 3*, 1847−1857.
Lifson S., & Roig, A. (1961) *J. Chem. Phys. 34*, 1963−1974.
Lyu, P. C., Wemmer, D. E., Zhou, H. X., Pinker, R. J., & Kallenbach, N. R. (1993) *Biochemistry 32*, 421−425.
McGregor, M. J., Islam, S. A., & Sternberg, M. J. (1987) *J. Mol. Biol. 198*, 295−310.
Pace, C. N. (1990) *Trends Biochem. Sci. 15*, 14−17.
Padmanabhan, S., Marqusee, S., Ridgeway, T., Laue, T. M., & Baldwin, R. L. (1990) *Nature 344*, 268−270.
Presta, L. G., & Rose, G. D. (1988) *Science 240*, 1632−1641.
Redfield, A. G., & Waelder, S. (1979) *J. Am. Chem. Soc. 101*, 6151−6162.
Richardson, J. S., & Richardson, D. C. (1988) *Science 240*, 1648−1652.
Rohl, C. A., Scholtz, J. M., York, E. J., Stewart, J. M., & Baldwin, R. L. (1992) *Biochemistry 31*, 1263−1269.
Scholtz, J. M., Qian, H., York, E. J., Stewart, J. M., & Baldwin, R. L. (1991a) *Biopolymers 31*, 1463−1470.
Scholtz, J. M., Marqusee, S., Baldwin, R. L., York, E. J., Stewart, J. M., Santoro, M., & Bolen, D. W. (1991b) *Proc. Natl. Acad. Sci. U.S.A. 88*, 2854−2858.
Scholtz, J. M., & Baldwin, R. L. (1992) *Annu. Rev. Biophys. Biomol. Struct. 21*, 95−118.
Scholtz, J. M., Qian, H., Robbins, V. H., & Baldwin, R. L. (1993) *Biochemistry 32*, 9668−9676.
Shirley, B. A., Stanssens, P., Hahn, U., & Pace, C. N. (1992) *Biochemistry 31*, 725−732.
Stapley, B. J., Rohl, C. A., & Doig, A. J. (1995) *Protein Sci.* (in press).
Stewart, J. M., & Young, J. D. (1984) in *Solid Phase Peptide Synthesis* pp 67−68, Pierce Chemical Co., Rockland, IL.
Stickle, D. F., Presta, L. G., Dill, K. A., & Rose, G. D. (1992) *J. Mol. Biol. 226*, 1143−1159.
Thornton, J. M., & Gardner, S. P. (1989) *Trends Biochem. Sci. 14*, 300−304.
Thorson, J. S., Chapman, E., & Schultz, P. G. *J. Am. Chem. Soc.*, in press.
Yang, A., Sharp, K. A., & Honig, B. (1992) *J. Mol. Biol. 227*, 889−900.

BI951542+