

References

- Andersen, N. H., Brodsky, Y., Neidigh, J. W., and Prickett, K. S. (2002). Medium-dependence of the secondary structure of exendin-4 and glucagon-like-peptide-1. *Bioorg Med Chem*, 10(1):79.
- Bai, Y., Karimi, A., Dyson, H. J., and Wright, P. E. (1997). Absence of a stable intermediate on the folding pathway of protein A. *Protein Science*, 6(7):1449–1457.
- Blanco, F. J., Jimenez, A., Rico, M., Santoro, J., Herranz, J., and Nieto, J. L. (1992). The homologous angiogenin and ribonuclease N-terminal fragments fold into very similar helices when isolated. *Biochem Biophys Res Commun*, 182:1491–1498.
- Bruch, M. D., Dhingra, M. M., and Gierasch, L. M. (1991). Side chain-backbone hydrogen bonding contributes to helix stability in peptides derived from an α -helical region of carboxypeptidase A. *Proteins: Structure, Function, and Genetics*, 10(2):130–139.
- Burke, C., Mayo, K. H., Skubitz, A. P., and Furcht, L. T. (1991). ^1H NMR and CD secondary structure analysis of cell adhesion promoting peptide F-9 from laminin. *Journal of Biological Chemistry*, 266:19407–19412.
- Callihan, D. and Logan, T. (1999). Conformations of peptide fragments from the FK506 binding protein: comparison with the native and urea-unfolded states. *Journal of Molecular Biology*, 285(5):2161–2175.
- Chakrabartty, A., Kortemme, T., and Baldwin, R. L. (1994). Helix propensities of the amino acids measured in alanine-based peptides without helix-stabilizing side-chain interactions. *Protein Science*, 3:843–852.
- Demarest, S. J., Fairman, R., and Raleigh, D. P. (1998). Peptide models of local and long-range interactions in the molten globule state of human α -lactalbumin. *Journal of Molecular Biology*, 283:279–291.
- Demarest, S. J., Zhou, S. Q., Robblee, J., Fairman, R., Chu, B., and Raleigh, D. P. (2001). A comparative study of peptide models of the α -domain of α -lactalbumin, lysozyme, and α -lactalbumin/lysozyme chimeras allows the elucidation of critical factors that contribute to the ability to form stable partially folded states. *Biochemistry*, 40(7):2138–2147.
- Dyson, H. J., Merutka, G., Waltho, J. P., Lerner, R. A., and Wright, P. E. (1992a). Folding of peptide fragments comprising the complete sequence of proteins. models for initiation of protein folding. I. Myohemerythrin. *Journal of Molecular Biology*, 226(3):795–817.
- Dyson, H. J., Sayre, J. R., Merutka, G., Shin, H. C., Lerner, R. A., and Wright, P. E. (1992b). Folding of peptide fragments comprising the complete sequence of proteins. models for initiation of protein folding. II. Plastocyanin. *Journal of Molecular Biology*, 226(3):819–835.
- Esteve, V., Blondelle, S., Celda, B., and Perez-Paya, E. (2001). Stabilization of an α -helical conformation in an isolated hexapeptide inhibitor of calmodulin. *Biopolymers*, 59:467–476.

- Fairman, R., Armstrong, K. M., Shoemaker, K. R., York, E. J., Stewart, J. M., and Baldwin, R. L. (1991). Position effect on apparent helical propensities in the C-peptide helix. *Journal of Molecular Biology*, 221:1395–1401.
- Fiori, W. R., Lundberg, K. M., and Millhauser, G. L. (1994). A single carboxy-terminal arginine determines the amino-terminal helix conformation of an alanine-based peptide. *Nature Structural Biology*, 1(6):374–377.
- Forood, B., Feliciano, E. J., and Nambiar, K. P. (1993). Stabilization of α -helical structures in short peptides via end capping. *Proceedings of the National Academy of Sciences USA*, 90(3):838–842.
- Goodman, E. M. and Kim, P. S. (1989). Folding of a peptide corresponding to the α -helix in bovine pancreatic trypsin inhibitor. *Biochemistry*, 28:4343.
- Guang, S., Wu, J., Tao, L., Xia, Y., and Shi, Y. (1998). Solution structure of a fragment of the dimerization domain of E2F-1 determined by circular dichroism, ^1H nuclear magnetic resonance and distance geometry. *Biochimica et Biophysica Acta*, 1388(1):111.
- Hamada, D., Kuroda, Y., Tanaka, T., and Goto, Y. (1995). High helical propensity of the peptide fragments derived from β -lactoglobulin, a predominantly β -sheet protein. *Journal of Molecular Biology*, 254(4):737.
- Hua, Y. and Raleigh, D. P. (1998a). Conformational analysis of the interdomain linker of the central homology region of chloroplast initiation factor IF3 supports a structural model of two compact domains connected by a flexible tether. *FEBS Lett*, 433:153–156.
- Hua, Y. and Raleigh, D. P. (1998b). On the global architecture of initiation factor IF3: a comparative study of the linker regions from the Escherichia coli protein and the Bacillus stearothermophilus protein. *Journal of Molecular Biology*, 278:871–878.
- Jimenez, M. A., Bruix, M., Gonzalez, C., Blanco, F. J., Nieto, J. L., Herranz, J., and Rico, M. (1993). CD and ^1H -NMR studies on the conformational properties of peptide fragments from the C-terminal domain of thermolysin. *Eur J Biochem*, 211(3):569.
- Kemmink, J. and Creighton, T. E. (1993). Local conformations of peptides representing the entire sequence of bovine pancreatic trypsin inhibitor and their roles in folding. *Journal of Molecular Biology*, 234(3):861.
- Kim, Y., Welch, J. T., Lindstrom, K. M., and Franklin, S. J. (2001). Chimeric HTH motifs based on EF-hands. *J Biol Inorg Chem*, 6(2):173–181.
- Kuhlman (1997). Calcium binding peptides from α -lactalbumin: Implications for protein folding and stability. *Biochemistry*, 36:4607–4615.
- Kuhlman, B., Yang, H. Y., Boice, J. A., Fariman, R., and P., R. D. (1997). An exceptionally stable helix from the ribosomal protein L9: Implications for protein folding and stability. *Journal of Molecular Biology*, 270:640.
- Kuroda, Y. (1993). Residual helical structure in the C-terminal fragment of cytochrome c. *Biochemistry*, 32:1219.

- Li (1993). Peptide environment specifies conformation. helicity of hydrophobic segments compared in aqueous, organic, and membrane environments. *Journal of Biological Chemistry*, 268:22975.
- Liu, L. and Deber, C. M. (1998). Uncoupling hydrophobicity and helicity in transmembrane segments. α -helical propensities of the amino acids in non-polar environments. *Journal of Biological Chemistry*, 273:23645.
- Luisi, D. L., Wu, W., and Raleigh, D. P. (1999a). Conformational analysis of a set of peptides corresponding to the entire primary sequence of the N-terminal domain of the ribosomal protein L9: evidence for stable native-like secondary structure in the unfolded state. *Journal of Molecular Biology*, 289:167.
- Luisi, D. L., Wu, W., and Raleigh, D. P. (1999b). Conformational analysis of a set of peptides corresponding to the entire primary sequence of the N-terminal domain of the ribosomal protein L9: evidence for stable native-like secondary structure in the unfolded state. *Journal of Molecular Biology*, 287:395–407.
- Lyu, P. C., Liff, M. I., Marky, L. A., and Kallenbach, N. R. (1990). Side chain contributions to the stability of alpha-helical structure in peptides. *Science*, 250:669.
- Manhart, S., Hinke, S. A., McIntosh, C. H. S., Pederson, R. A., and Demuth, H. (2003). Structure-function analysis of a series of novel GIP analogues containing different helical length linkers. *Biochemistry*, 42:3081.
- McLeish, M. J., Nielsen, K. J., Najbar, L. V., Wade, J. D., Lin, F., Doughty, M. B., and Craik, D. J. (1994). Conformation of a peptide corresponding to T4 lysozyme residues 59-81 by NMR and CD spectroscopy. *Biochemistry*, 33:11174.
- Moriarty, D. F., Demarest, S. J., Robblee, J., Fairman, R., and Raleigh, D. P. (2000). Local interactions and the role of the 6-120 disulfide bond in α -lactalbumin: implications for formation of the molten globule state. *Biochimica et Biophysica Acta*, 1476:9.
- Munier, H., Blanco, F. J., Precheur, B., Diesis, E., Nieto, J. L., Craescu, C. T., and Barzu, O. (1993). Characterization of a synthetic calmodulin-binding peptide derived from Bacillus anthracis adenylate cyclase. *Journal of Biological Chemistry*, 268(3):1695–1701.
- Munoz, V. and Serrand, L. (1994). Elucidating the folding problem of helical peptides using empirical parameters. *Nature Structural Biology*, 1:399.
- Najbar, L. V., Craik, D. J., Wade, J. D., and McLeish, M. J. (2000). Identification of initiation sites for T4 lysozyme folding using CD and NMR spectroscopy of peptide fragments. *Biochemistry*, 39:5911–5920.
- Padmanabhan, S., Jimenez, M. A., and Rico, M. (1999). Folding propensities of synthetic peptide fragments covering the entire sequence of phage 434 Cro protein. *Protein Science*, 8:1675–1688.
- Park, S. H., Shalongo, W., and Stellwagen, E. (1993a). Modulation of the helical stability of a model peptide by ionic residues. *Biochemistry*, 33:12901–12905.

- Park, S. H., Shalongo, W., and Stellwagen, E. (1993b). Residue helix parameters obtained from dichroic analysis of peptides of defined sequence. *Biochemistry*, 32:7048–7053.
- Petukhov, M., Yumoto, N., Murase, S., Onmura, R., and Yoshikawa, S. (1996). Factors that affect the stabilization of α -helices in short peptides by a capping box. *Biochemistry*, 35:387–397.
- Pintar, A., Chollet, A., Bradshaw, C., Chaffotte, A., Cadieux, C., Rومان, M., Hallenga, K., Knowles, J., Goldberg, M., and Wodak, S. (1994). Conformational properties of four peptides corresponding to α -helical regions of Rhodospirillum cytochrome c_2 and bovine calcium binding protein. *Biochemistry*, 33:11158–11173.
- Precheur, B., Siffert, O., Barzu, O., and Craescu, C. T. (1991). NMR and circular dichroic studies on the solution conformation of a synthetic peptide derived from the calmodulin-binding domain of Bordetella pertussis adenylate cyclase. *Eur J Biochem*, 196:67–72.
- Reed, J., Hull, W. E., Ponstingl, H., and Himes, R. H. (1992). Conformational properties of the β (400-436) and β (400-445) C-terminal peptides of porcine brain tubulin. *Biochemistry*, 31:11888–11895.
- Reymond, M. T., Merutka, G., Dyson, H. J., and Wright, P. E. (1997). Folding propensities of peptide fragments of myoglobin. *Protein Science*, 6:706–716.
- Sancho, J., Niera, J. L., and Fersht, A. R. (1992). An N-terminal fragment of barnase has residual helical structure similar to that in a refolding intermediate. *Journal of Molecular Biology*, 224:749–758.
- Scholtz, J. M., Marqusee, S., Baldwin, R. L., York, E. J., Stewart, J. M., Santoro, M., and Bolen, D. W. (1991). Calorimetric determination of the enthalpy change for the α -helix to coil transition of an alanine peptide in water. *Proceedings of the National Academy of Sciences USA*, 88:2854–2858.
- Scholtz, J. M., Robbins, V. H., and Baldwin, R. L. (1993). The energetics of ion-pair and hydrogen-bonding interactions in a helical peptide. *Biochemistry*, 32:9668–9676.
- Shin, H., Merutka, G., Waltho, J., Wright, P. E., and Dyson, H. J. (1993). Peptide models of protein folding initiation sites. 2. The G-H turn region of myoglobin acts as a helix stop signal. *Biochemistry*, 32:6348–6355.
- Spector, S., Rosconi, M., and Raleigh, D. P. (1999). Conformational analysis of peptide fragments derived from the peripheral subunit-binding domain from the pyruvate dehydrogenase multienzyme complex of Bacillus stearothermophilus: Evidence for nonrandom structure in the unfolded state. *Biopolymers*, 40:29–40.
- Strehlow, K. G. and Baldwin, R. L. (1989). Effect of the substitution Ala \rightarrow Gly at each of five residue positions in the C-peptide helix. *Biochemistry*, 28:2130–2133.
- Waltho, J. P., Feher, V. A., Merutka, G., Dyson, H. J., and Wright, P. E. (1993). Peptide models of protein folding initiation sites. 1. Secondary structure formation by peptides corresponding to the G- and H-helices of myoglobin. *Biochemistry*, 32:6337–6347.

- Williams, L., Kather, K., and Kemp, D. S. (1998). High helicities of Lys-containing, Ala-rich peptides are primarily attributable to a large, context-dependent Lys stabilization. *Journal of the American Chemical Society*, 120:11033–11043.
- Yumoto, N., Murase, S., Hattori, T., Yamamoto, H., Tatsu, Y., and Yoshikawa, S. (1993). Stabilization of α -helix in C-terminal fragments of neuropeptide Y. *Biochem Biophys Res Commun*, 196(3):1490–1503.
- Zhou, N. E., Kay, C. M., Sykes, B. D., and Hodges, R. S. (1993). A single-stranded amphipathic α -helix in aqueous solution: design, structural characterization, and its application for determining α -helical propensities of amino acids. *Biochemistry*, 32:6190–6197.