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This Week's Citation Classic

Fasman G D, ed. *Protein models for conformational studies.*
New York: Marcel Dekker, 1967. 764 p.
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This book was an effort to bring together significant research on the properties of model proteins, by authors whose work helped revolutionize the field. The variety of systems involving poly-ct-amino acids is a testament to the importance of the field covered in this work. [The *SCI*® indicates that this book has been cited in more than 500 publications.]

Poly-α-Amino Acids

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After apprenticing in the laboratories of Ephraim Katzir, Weizmann Institute, Rehovoth, Israel (1953-1954) and Elkan Blout, Harvard Medical School (1955-1961), in the arts and science of poly-α-amino acids, I became a faculty member at Brandeis University and continued using poly-α-amino acids as models for studies of protein conformation and conformational transitions. The X-ray diffraction-determined structures of proteins was yielding new insights on protein conformation in the 1960s, and the research on poly-α-amino acids was at its height.

This *Citation Classic* compendium covers various physical-chemical and biological areas in which poly-α-amino acids served as models par excellence. Included in this volume are X-ray diffraction (A. Elliot), infrared spectroscopy (T. Miyazawa), scattering and hydrodynamics (H. Benoit, L. Freund, and G. Spach), X-ray diffraction of polypeptide solvent systems (P. Saludjian and V. Luzzati), ultraviolet absorption spectra of polypeptides (W.B. Gratzer), optical rotatory dispersion (J.T. Yang), circulardichroism (S. Beychok), hydrogen exchange (S.W. Englander), dielectric properties (A. Wada), theory of noncovalent structure (D. Poland and H. Scheraga), factors responsible for conformational stability (G. Fasman), biological properties (H.I. Silman and M. Sela) and poly-L-proline (L. Mandelkern). In providing some of the seminal information, these international experts demonstrated the multiple applications of poly-a-amino acids to problems relevant to understanding the properties of proteins.

The a-helix was first demonstrated experimentally (X-ray diffraction) on poly-y-methyl glutamate.[1] The helix<=>β-sheet<=>random coil transitions were clearly demonstrated with these models. The use of poly-α-amino acids played, and still plays, a vital role in unraveling the mechanisms of the immune system.[2,3]

I was introduced to these facile models as a Weizmann fellow in the laboratory of Katzir, one of the founders of this discipline, and my studies continued in the laboratory of Blout. Having been seduced by the lectures of Linus Pauling on protein conformation, as a graduate student at Cat tech, the entrapment into the web of poly-α-amino acid fibers was all too natural. By using the circular dichroism (CD) spectra of poly-L-lysine in the a-helical, (5-sheet, and random conformations, the first method was published to deconvolute the CD spectra of proteins into their secondary structural elements.[4]

The sheer number of papers published utilizing poly-α-amino acids, and the immense variety of systems in which they have been perceptively used (cell biology, unraveling the genetic code, immunology, etc.), probably account for this publication becoming a *Citation Classic.* New uses are described daily. Perhaps, it is time for a revision of this classic.

1. **Perutz M.** The 1.5-A reflection from proteins and polypeptides. *Nature* 168:653-4, 1951. (Cited 450 times.)
2. **Benacerraf B.** Role of MHC gene products in immune regulation. Science 212:1229-38, 1981. (Cited 440 times.)
3. **Sela M & Katchaiski E**. *Biological properties of poly-α-amino acids.* San Diego. CA: Academic Press, 1959. Vol. 14. p. 392-478.
4. **Greenfield N & Fasman G D.** Computed circular dichroism spectra for the evaluation of protein conformation. *Biochemistry* 8:4108-16, 1969. (Cited 1,550 times.) [See also: **Greenfield N**. Citation Classic. *Current Contents/Life Sciences* 25(26):28, 28 June 1982.]
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