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The advance that realized the potential of protein Fourier-transform infrared spectroscopy

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ABSTRACT

In 1987, Susi & Byler published a groundbreaking paper for the determination of the secondary structure of proteins. Notably, they determined the characteristic signature of the β -strand in the infrared spectrum. As a result, Fourier-transform infrared spectroscopy became a general method to determine protein structure.

The bonds that keep atoms together in molecules are fidgety connections that are in constant movement. Bond vibrations absorb energy in the infrared range, and as a result, they can be studied by infrared spectroscopy. This technique has yielded fundamental insights into the inner workings of biomolecules such as nucleic acids, lipids, and proteins. These advances were made possible by first determining in what region of the infrared spectrum the bonds characteristic of a particular molecule absorb radiation. Proteins have several characteristic absorption modes, the most important of them being the amide I region, which comprises between 1600 and 1700 cm^{-1} . Several groundbreaking investigations, including the contribution of Heino Susi, one of the authors of the manuscript introduced here, had previously established that the α -helix was characterized by a well-defined absorption value at $\sim 1650 \text{ cm}^{-1}$. This advance opened the door for using Fourier-transform infrared (FTIR) spectroscopy to dissipate the shadows that still clouded our view of basic protein structure. If we only understood that the FTIR bands arising from β -strands, turns, and disordered regions, this technique could provide a quantitative understanding of the secondary structure components that make up proteins. This would represent a groundbreaking advance in the mid-1980s, when obtaining high-resolution structural information on a model protein was a feat only achieved by a few scientific artisans, like Max Perutz, John C. Kendrew or Fred Richards.

At the time, hopes to achieve this vision were dim, as theoretical studies predicted a disastrous overlap between absorption in the amide I of α -helices and parallel β -strands, which would preclude secondary structure quantification for the many proteins that contained both types of structure. Susi and Byler came to the rescue! They collected high-quality FTIR spectra of flavodoxin and triosephosphate isomerase, and compared the results with their crystal structures [1]. Their work shows

that parallel and antiparallel β -strands similarly absorb infrared light in the form of two peaks that surround, but are separate from, that of the α -helix. While discriminating between the two types of β -strand orientation would be, and will remain, challenging, their groundbreaking insight had made possible to quantify the two fundamental types of protein secondary structure, β -strands and α -helices. This scientific advance had a lasting impact on the FTIR technique. Decades later, as a graduate student, I would use Susi and Byler's discovery as part of the peak deconvolution routine to perform assignment of protein secondary structure [2–4], as it became standard in the field [5,6].

The fact that this advance in biophysical chemistry was carried out by scientists working at a research center of the US Department of Agriculture might surprise in today's scientific culture. However, it represents just one between a myriad of examples of how investments in basic science pay off in the long term.

This manuscript was written in a crisp and matter-of-fact prose. However, there is a sentence that seems to transpire the emotion felt by the authors: "The general agreement between band areas and X-ray results is quite satisfactory". One can only guess that Susi and Byler were then aware of the long-term relevance of their discovery, which forever transformed protein FTIR.

Data availability

No data was used for the research described in the article.

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References

- [1] H. Susi, D.M. Byler, Fourier transform infrared study of proteins with parallel beta-chains, *Arch. Biochem. Biophys.* 258 (2) (1987) 465–469.
- [2] M.C. Lidon-Moya, F.N. Barrera, M. Bueno, R. Perez-Jimenez, J. Sancho, M.G. Mateu, J.L. Neira, An extensive thermodynamic characterization of the dimerization domain of the HIV-1 capsid protein, *Protein Sci.* 14 (2005) 2387–2404.
- [3] J.A. Encinar, M.L. Molina, J.A. Poveda, F.N. Barrera, M.L. Renart, A.M. Fernandez, J.M. Gonzalez-Ros, The influence of a membrane environment on the structure and stability of a prokaryotic potassium channel, KcsA, *FEBS Lett.* 579 (2005) 5199–5204.
- [4] M.L. Renart, F.N. Barrera, M.L. Molina, J.A. Encinar, J.A. Poveda, A.M. Fernandez, J. Gomez, J.M. Gonzalez-Ros, Effects of conducting and blocking ions on the structure and stability of the potassium channel KcsA, *J. Biol. Chem.* 281 (2006) 29905–29915.
- [5] J. De Meutter, E. Goormaghtigh, Evaluation of protein secondary structure from FTIR spectra improved after partial deuteration, *Eur. Biophys. J.* 50 (3–4) (2021) 613–628.
- [6] O. Rathore, D.Y. Sogah, Self-assembly of beta-sheets into nanostructures by poly (alanine) segments incorporated in multiblock copolymers inspired by spider silk, *J. Am. Chem. Soc.* 123 (22) (2001) 5231–5239.