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TRACKING TRENDS & PERFORMANCE IN BASIC RESEARCH



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2008 : June 2008 : Peter Güntert

EMERGING RESEARCH FRONTS - 2008

June 2008



Peter Güntert talks with *ScienceWatch.com* and answers a few questions about this month's Emerging Research Front Paper in the field of Engineering.



Article: Protein NMR structure determination with automated NOE assignment using the new software CANDID and the torsion angle dynamics algorithm DYANA

Authors: Herrmann, T;Güntert, P;Wuthrich, K

Journal: J MOL BIOL, 319 (1): 209-227 MAY 24 2002

Addresses: RIKEN, Genom Sci Ctr, 1-7-22 Suehiro, Yokohama, Kanagawa 2300045, Japan.

ETH Zurich, Inst Mol Biol & Biophys, CH-8093 Zurich, Switzerland.

SW: Why do you think your paper is highly cited?

The computational tools presented in this paper have become a quasi-standard for protein structure analysis by NMR (nuclear magnetic resonance) spectroscopy, which is widely used in structural biology and structural genomics/proteomics.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

This paper introduced a method that greatly improves the efficiency of protein structure determination by NMR.

SW: Would you summarize the significance of your paper in layman's terms?

Thanks to the research described in this paper and other innovations it has become possible to determine the spatial structure of thousands of proteins with unprecedented speed, thus extending our knowledge about life at the molecular level.

SW: How did you become involved in this research and were any particular problems encountered along the way?

I became involved in biomolecular NMR in the research group of Nobel Laureate Kurt Wüthrich at the Swiss Federal Institute of Technology (ETH) in Zurich, Switzerland, where I worked on applying computational methods in conjunction with NMR measurements to questions in structural biology. This paper marks a break-through in automating the analysis of NMR spectra that was preceded by a series of trials, failed attempts, and small incremental improvements until two new ideas, described in the paper, opened the way to success.

"This paper marks a break-through in automating the analysis of NMR spectra..."

SW: Where do you see your research leading in the future?

We hope to extend protein structure analysis by NMR to larger proteins, protein complexes, membrane-bound proteins, and proteins measured directly in living cells, as well as to achieve the complete automation of NMR protein structure determination.

SW: Do you foresee any social or political implications for your research?

Understanding proteins and their role in living organisms contributes to our basic knowledge of life and helps in the development of drugs that can improve the quality of human life.

Prof. Dr. Peter Güntert

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Keywords: NMR protein structure analysis, NMR spectra, protein complexes, membrane-bound proteins, NMR measurements, structural biology, CANDID software, DYANA, Kurt Wüthrich.

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