

## (2) Protein Structure Determination on Demand

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### **Abstract**

Protein structure prediction by computers at best may serve as a screening method, and the current high-throughput protein structure determination methods are costly and will never exhaust all proteins. A complementary approach is "protein structure determination on demand", say in a week. We will discuss two approaches that would realize this goal: automatic protein structure determination using NMR data and mass spectrometry data.

### **Biography**

Ming Li is a Canada Research Chair in Bioinformatics and a University Professor at the University of Waterloo. He is a fellow of the Royal Society of Canada, ACM, and IEEE. He is a recipient of E.W.R. Steacie Fellowship Award in 1996, the 2001 Killam Fellowship, and the 2010 Killam Prize. Together with Paul Vitanyi they have co-authored the book "An Introduction to Kolmogorov Complexity and Its Applications". He is a co-managing editor of Journal of Bioinformatics and Computational Biology.