

motions of TM2 may accompany the transducer structural change at the cytoplasmic surface.

A structure of the missing TM2 segment, which seems within reach given the success of Gordeliy *et al.*¹, and light-induced structures of the SRII-HtrII complex will add more exciting chapters to this fascinating, rapidly developing story.

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picture story

And the Nobel goes to...

Swiss scientist Kurt Wüthrich is one of three scientists awarded the 2002 Nobel Prize in Chemistry on October 9, 2002.

The honorees are recognized jointly “for the development of methods for identification and structure analyses of biological macromolecules”. Professor Wüthrich (ETH and The Scripps Research Institute) is awarded half the prize “for his development of nuclear magnetic resonance spectroscopy for determining the three-dimensional structure of biological macromolecules in solution”, while the other half is shared by John B. Fenn (USA) and Koichi Tanaka (Japan) “for their development of soft desorption ionisation methods for mass spectrometric analyses of biological macromolecules” (www.nobel.se/chemistry/laureates/2002/).

Professor Wüthrich has been using NMR to study proteins and nucleic acids since 1967 (for a personal view of the history of using NMR to study biological macromolecules, see *Nature Struct. Biol.* **8**, 923–925; 2001). In the 1970's, he worked with Richard Ernst (Nobel Prize in Chemistry, 1991) to develop two-dimensional NMR approaches for studying proteins and nucleic acids. These methods, such as COSY and NOESY, have become the foundation upon which modern NMR

techniques for acquiring structural information of biomolecules are built.

Throughout his distinguished career, he has been instrumental in the development of new methodologies to push the limits of NMR spectroscopy in protein structure studies. His latest achievements have challenged the common perception that NMR structure determination is limited to biomolecules below a certain size (~40–50 kDa). In a recent paper in *Nature*, Wüthrich and collaborators (Fiaux *et al.* **418**, 207–211; 2002) used CRIPT-TROSY to study the >900 kDa chaperonin

GroEL–GroES complex (spectrum of GroES in complex with a single-ring mutant of GroEL, right).

In recognizing Kurt Wüthrich, the Nobel committee has honored a scientist still at the forefront of his field. The results of Fiaux *et al.* begin a new chapter on the utility of NMR in structural biology. Methods such as CRIPT-TROSY coupled with improvements in instrumentation, should make detailed analysis of other large protein complexes possible over the next several years.

Elizabeth H. Cox



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