

# NMR Approach for Investigation of Large Molecule Systems

## Ultra High Field MRI for Molecular Brain Imaging

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The size limit is a serious problem for solution NMR. The size limit is caused by the signal broadening due to rapid transverse relaxation in a slowly tumbling molecule and by the signal overlapping due to the huge number of resonating nuclear spins in a protein. The former has been improved by means of deuteration of the protein and innovative pulse techniques. Development of TROSY spectroscopy has contributed to a revolutionary improvement of the resolution of  $^1\text{H}$ - $^{15}\text{N}$  and  $^1\text{H}$ - $^{13}\text{C}$ (aromatic) correlation spectra. The combination of deuteration and TROSY raised the molecular mass limit to more than 50 kDa.

$\text{F}_0\text{F}_1$ -ATP synthase is a multisubunit enzyme that catalyzes ATP synthesis in oxidative phosphorylation and photophosphorylation. This enzyme consists of two components,  $\text{F}_0$  and  $\text{F}_1$ . The simplest  $\text{F}_1$  ( $\text{F}_1$ -ATPase) comprises five kinds of subunits with a stoichiometry of *ab<sub>3</sub>gde*. The molecular mass is about 360 kDa. In the crystal structure of  $\text{F}_1$  from bovine heart mitochondria ( $\text{MF}_1$ ), the three catalytic sites are not equivalent. The *b* subunit in  $\text{F}_1$  takes on the closed form in the presence of a bound nucleotide, while it takes on the open form in its absence. We have applied segmental isotope-labeling by intein splicing reaction to the *b* subunit of  $\text{F}_0\text{F}_1$ -ATP synthase in this work, and have succeeded in obtaining the detailed information on the conformational change of the *b* subunit monomer (1).

Solid-state NMR is a promising method for investigations of membrane proteins and supramolecular systems because there is no size limit. We have been developing multidimensional solid-state NMR under MASS for the structural analysis of uniformly and specifically isotope-labeled samples (2-4). Newly developed methods were applied to  $\text{H}^+$ -ATP synthase *g* subunit and Mastoparan X bound to the lipid membrane. Mastoparan X is a wasp venom and known to activate a G-protein. Uniformly and specifically labeled Mastoparans X were bound to DPPC-DPPG bilayer membranes under a hydrated condition. Its structure was successfully determined.

It can be concluded that the combination of solution and solid-state NMR is a powerful approach to investigate a large molecule systems.

**References:** 1. H. Yagi, T. Tsujimoto, T. Yamazaki, M. Yoshida, and H. Akutsu, *J. Am. Chem. Soc.*, 126, 16632-16638 (2004). 2. T. Fujiwara, K. Sugase, M. Kainosho, A. Ono, A(M) Ono, and H. Akutsu, *J. Am. Chem. Soc.*, 117, 11351-11352 (1995). 3. T. Fujiwara, T. Shimomura, Y. Ohigashi, and H. Akutsu, *J. Chem. Phys.*, 109, 2380-2393 (1998). 4. T. Fujiwara, Y. Todokoro, H. Yanagisita, M. Tawarayama, T. Kohno, K. Wakamatsu and H. Akutsu, *J. Biomol. NMR*, 28, 311-325 (2004).