

Structural Studies on the Carboxyl-Terminal Domain of *S. coelicolor* A3(2) RNA Polymerase Alpha Subunit by NMR

KIM Jong-Wan¹, BAE Jae-Bum², ROE Jung-Hye² and LEE Bong-Jin^{1*}

¹*Dept. of Pharmacy, Seoul National University, Seoul 151-742*

²*Dept. of Microbiology, Seoul National University, Seoul 151-742*

**Corresponding Author: lbj@nmr.snu.ac.kr*

The C-terminal domain of *S. coelicolor* A3(2) RNA polymerase α subunit (S α CTD) is a protein composed of 117 amino acids, with molecular weight 12,279Da, and plays an essential role in the formation of α dimer in RNA polymerase and a contact site for transcription regulation proteins in the process of transcription. We performed the prediction of the secondary structure of S α CTD by computational methods, followed by spectroscopic measurements (CD, NMR) for the determination of the three-dimensional structure of S α CTD. As a result of computational methods to predict the secondary structure of whole α subunit, the structure of CTD was supposed to be different from that of *E. coli*. From the analysis of CD data, we knew that S α CTD had mainly α helices in its structure, but also has loose structure partially. To determine the three-dimensional structure of S α CTD by NMR, spectra of conventional pulses and triple resonance pulses (HNCO, HNCACO, HNCA, HNCOCA, CBCANH, CBCACONH, HCCH-TOCSY, etc.) were measured and analyzed. The assignment for resonances was performed considerably, and the work is in progress.