# CDB SEMINAR

**Speaker:** **Mariko Ariyoshi**

＜MRC-Laboratory of Molecular Biology ＞

**Title:** **"Structure and function of Spen proteins: A conserved repressive function in developmental signalling pathways"**

**Date:** **Thursday, October 23**

**Time:** **16:00 P.M.～17:00 P.M.**

**Place:** **7th floor Conference Room, CDB**

## Summary

Spen proteins, which have been identified in worms, flies and vertebrates, play a crucial role in the regulation of diverse developmental signalling pathways. They are large proteins characterised by amino-terminal RNA-binding motifs and a highly conserved carboxy-terminal SPOC domain. The biological role of the SPOC domain, and hence the common function of Spen proteins, has been unclear to date. The human Spen protein, SHARP, was identified as a component of transcriptional repression complexes in both nuclear receptor and Notch/RBP-Jk signalling pathways. We have determined the crystal structure of the SPOC domain from SHARP. This structure shows that essentially all the conserved surface residues map to a positively charged region. Structure-based mutational analysis indicates that this conserved region is responsible for the interaction between SHARP and the universal transcriptional co-repressor SMRT/NCoR. We demonstrate that this interaction involves a highly conserved acidic motif at the carboxy-terminus of SMRT/NCoR. These findings suggest that the conserved function of the SPOC domain is to mediate interaction with SMRT/NCoR corepressors and that Spen proteins play an essential role in the repression complex.

**Host** **Masatoshi Takeichi** **Cell Adhesion/Tissue Patterning, CDB**

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