

for biological products.]

[PC1-49] [10/17/2002 (Thr) 13:30 - 16:30 / Hall C]

Methylation by Protein Arginine Methyltransferase

Woo Yunna[○], Cho Eun-Jung, Hong Sungyoul, Lee Hoi Young, Han Jeung-Whan, . Lee Hyang Woo

Lab. of Biochemistry, College of Pharmacy, Sungkyunkwan university Department of Genetic Engineering, College of Life Science and Natural Resources, Sungkyunkwan University, College of Medicine, Konyang University

Arginine methylation is a common post-translation protein modification in eukaryotic cells. Protein-arginine N-methyltransferase transfer methyl groups from S-adenosyl-L-methionine to the guanidino group of arginine residues. However, The significant of this modification has been questionable, because it occurs rarely and is present at very low abundance. Recently, the discovery of two protein arginine methyltransferase, PRMT1 and CARM1, as cofactors required for responses to nuclear hormone receptors provided an indication that arginine methylation have an important role in transcriptional regulation. Substrate for protein-arginine methyltransferase include many RNA-binding protein, RNA-transporting protein, transcription factor, nuclear matrix protein, and cytokines. To expand our knowledge on the regulation and role of PRMT1 and CARM1 in cells, we used the yeast two-hybrid system to identify proteins that interact with PRMT1 and CARM1. Bait plasmid pGBKT7-PRMT1 and pGBKT7-CARM1 were used to screen the pACT cDNA library from the human fetal brain poly(A+) mRNA. Vectors encoding pGBKT7-PRMT1 and pGBKT7-CARM1 were constructed by inserting an EcoRI-BamHI fragment of pM-PRMT1 and an EcoRI-BglII fragment of pSG5 • HA-CARM1 into the EcoRI-BamHI site of pGBKT7. We will identify proteins that interact with protein-arginine methyltransferase, and elucidate the biological role of these proteins and protein-arginine methyltransferase in vivo.

[PC1-50] [10/17/2002 (Thr) 13:30 - 16:30 / Hall C]

Conformational Study of Cyclic Ac-Cys-Pro-Xaa-Cys-NHMe Peptides: a Model for Chain Reversal and Active Site of Disulfide Oxidoreductase

Park Hae Sook[○], Kim choonmi, Kang Young Kee

Cheju Halla College; Ewha Womans University; Chugbuk University

The conformational study on cyclic Ac-Cys-Pro-Xaa-Cys-NHMe (Ac-CPXC-NHMe; X = Ala, Val, Leu, Aib, Gly, His, Phe, Tyr, Asn, and Ser) peptides has been carried out using the ECEPP/3 force field and the hydration shell model in the unhydrated and hydrated states. This work has been undertaken to investigate structural implications of the CPXC sequence as the chain reversal for the initiation of protein folding and as the motif for active site of disulfide oxidoreductases. The backbone conformation DAAA is in common the most feasible for cyclic CPXC peptides in the hydrated state, which has a type I β -turn at the Pro-Xaa sequence. The proline residue and the hydrogen bond between backbones of two cystines appear to play a role in stabilizing this preferred conformation of cyclic CPXC peptides. However, the distributions of backbone conformations and β -turns may indicate that the cyclic CPXC peptide seems to exist as an ensemble of β -turns and coiled conformations. The intrinsic stability of the cyclic CPXC motif itself for the active conformation appears to play a role in determining electrochemical properties of disulfide oxidoreductases.

Poster Presentations - Field C2. Microbiology

[PC2-1] [10/17/2002 (Thr) 13:30 - 16:30 / Hall C]