[Jpn. J. Cancer Res., **87**, 549-554 (1996)] [Lab. of Biochemistry]

Suppressing Effects of 6-(2,5-Dichlorophenyl)-2,4-diamino-1,3,5-triazine and Related Synthetic Compounds on Azoxymethane-induced Aberrant Crypt Foci in Rat Colon.

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The modifying effects of dietary administration of 6-(2,5-dichloro-phenyl)-2,4-diamino-1,3,5-triazine and 5 related compounds on the occurrence of azoxymethane-induced colonic aberrant crypt foci (ACF) were investigated in rats. At the termination of experiment, all of the compounds caused a siginificant reduction in ACF freqency, which might be associated with suppression of the expression of proliferation biomarkers (The number of AgNORs, BrdU-labeling index, polyamine levels).

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Involvement of Two Basic Residues (Lys-17 and Arg-39) of Mouse Lung Carbonyl Reductase in NADP(H)-Binding and Fatty Acid Activation: Site-Directed Mutagenesis and Kinetic Analyses.

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Mouse lung carbonyl reductase shows a strong coenzyme preference for NADP(H) over NAD(H), and is activated by fatty acids. The present study shows that mutations of Lys-17 to His (K17H) or Ser (K17S) and of Arg-39 to Ala (R39A) bring about decrease of the affinities for NADP(H). The activation by fatty acids was completely attenuated by the mutation of K17H and K17S but not by R39A. These results indicate that the 2'-phosphate group of NADP(H) is recognized by Lys-17 and Arg-39, of which Lys-17 is a component of the binding site for the activator.

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Molecular Cloning of a Gene Encoding Acid α-Glucosidase from *Tetrahymena pyriformis*.

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Lysosomal acid α-glucosidase is essential for the degradation of glycogen to glucose in lysosomes. We have earlier reported the purification and characterization of acid α-glucosidase from *T. pyriformis*. In the present study we have isolated a full length cDNA clone encoding acid α-glucosidase. The isolated clone (3019 bp) contained an open reading frames encoding 923 amino acid. Northern blot analysis revealed that the isolated cDNA hybridized to a 2.8-kb mRNA transcript. The deduced amino acid sequence was found to have 34% identity and 45% similarity with that of the human lysosomal enzyme, with 75% identity in the 16 amino acids at its proposed active site.