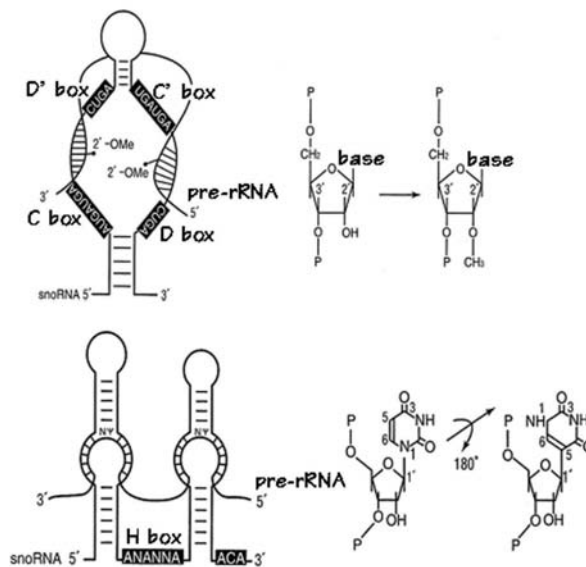


Prediction of snoRNAs in Human Genome

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Small nucleolar RNAs (snoRNAs) are taken part in processing and base modification (2'-O-ribose methylation and pseudouridylation) in precursor ribosomal RNA (pre-rRNA). In this research, we predict snoRNAs in human genome using computational sequence analysis methods which is named "SOKOS" using stochastic context free grammars (SCFGs). We also develop a Predicted Human Intron database produced from exons predicted by Gene Decoder which is a gene finding technology based on Hidden markov models (HMMs).



Secondary structure of snoRNAs

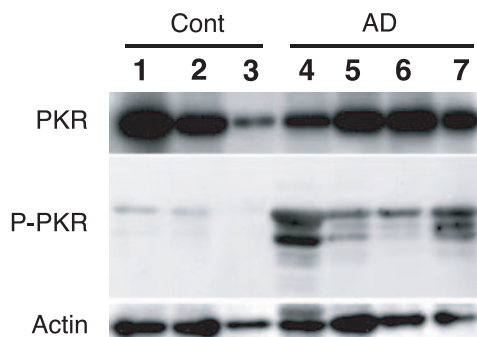
Identification of Pro-apoptotic Factors Related to Alzheimer's Disease using a Randomized Ribozyme Library

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Long-term accumulation of unfolded protein depends on several stresses, so called ER-stress, which leads to apoptosis. Recent studies have shown that ER-stress is associated with neurodegenerative disorders, such as Alzheimer's disease (AD). In this study, we employed a randomized ribozyme (Rz) library to identify the pro-apoptotic factors. One of the isolated Rzs effectively suppressed Tunicamycin (Tm)-induced apoptosis, and it recognized the mRNA of a double-stranded RNA-dependent protein kinase (PKR). Nuclear PKR was phosphorylated in an ER stress-dependent manner, and the level of this protein was increased in Tm-mediated SK-N-SH cells. The level of phosphorylated PKR was only

increased in nucleus autopsy samples from the brains of AD patients. These results indicate that phosphorylated PKR plays an important role both in ER-stress and AD.



The level of PKR and phosphorylated PKR in nucleus autopsy samples from the brains of AD patients