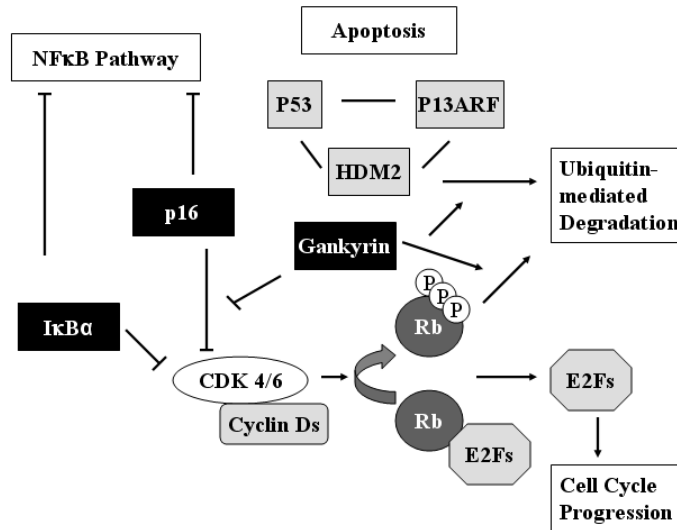


Tumor Suppressors and Cancer Proteins (1996-present). We have been working on the structure-function relationship of the INK4 tumor suppressor proteins, and a number of related proteins related to cancer.



The tumor suppressor p16, discovered in 1995, was found to be mutated more frequently than the best known tumor suppressor p53 in various cancer cells. Its main function is to serve as a negative regulator of the cell cycle by binding to and inhibiting cyclin-dependent kinase 4 (CDK4). Our lab was the first to solve the tertiary structure of free p16 and identified key binding residues (*Molecular Cell*, 1998). Several more papers have been published subsequently to address the structural and functional properties of p16 and its homologous proteins p15, p18, and p19. Nikola Pavletich's group has later solved the structure of p16-CDK6 complex by X-ray.

Gankyrin. Our studies with the INK4 family, which are ankyrin-repeat proteins, led us to study another newly discovered ankyrin-repeat oncogenic protein called gankyrin, which contains six ankyrin repeats. It has been reported to be involved in the phosphorylation and degradation of the retinoblastoma gene product, Rb. Using *in vitro* systems, we have identified a peptide fragment of gankyrin responsible for binding of gankyrin to Rb. We further demonstrated a different mechanism for gankyrin to facilitate the phosphorylation of Rb – by binding with CDK4. This binding does not inhibit the Rb-phosphorylating kinase activity of CDK4, but it competes with p16 binding to CDK4 and counteracts the inhibitory function of p16. We then showed that the two mechanisms involve different structural regions of gankyrin: the Rb-binding motif is located at the fifth ankyrin repeat, whereas the CDK4-binding region is located in the first three or four ankyrin repeats. Subsequently we solved the structure of gankyrin by NMR.

Other Ankyrin-repeat Proteins: In another study, we showed that the Tax oncoprotein encoded by human T-cell leukemia virus 1 (HTLV-1) binds to and activates CDK4 *in vitro*, and that such binding counteracts against the inhibition of p16 and p18, and acts as the major path to regulate Tax-mediated activation of CDK4. We have identified the binding region lies in the first 40 residues. These results of *in vitro* studies demonstrate a potentially novel, p16-independent route to regulate CDK4 activity by the Tax oncoprotein in HTLV-1 infected cells. Likewise, we

investigated the biochemical and functional properties of the ankyrin-repeat fragment of I κ B α and the oncogenic protein p34^{SEI-1}.

Future Directions: In collaboration with Dr. Junan Li of the Ohio State University, we are proceeding in the following directions: (a) comparison of structural and biophysical properties of various ankyrin repeat proteins involved in cell cycles; (b) structure-based protein engineering to change the CDK4-binding and modulating of gankyrin; (c) examine the biological effects of the mutants with interesting properties by cell culture studies; and (d) apply the structural and functional information obtained to drug discovery. Furthermore, in collaboration with Dr. Wen-Hwa Lee of UC Irvine, we are tackling the structure-function relationship of a number of other cancer-related proteins.

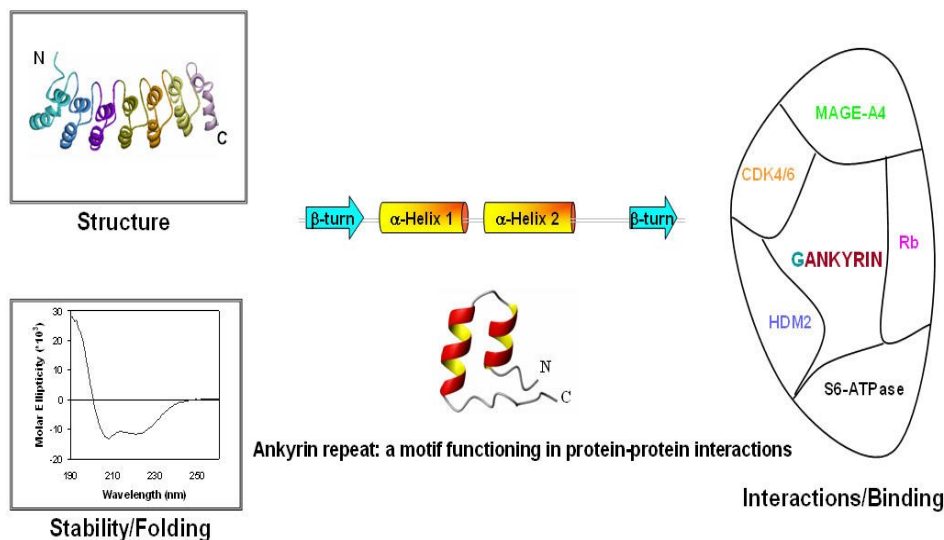


Figure. Illustration of our current approaches to elucidate the relationship between structure, folding, and biological functions of ankyrin-repeat proteins in cancer-related signaling pathways.

Publications:

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