

Experimental and Computational Modeling of Kinesin Light Chain Tetratricopeptide Repeats

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Kinesin is a motor protein that actively transports intracellular cargo by walking along microtubules. It consists of a head and a tail connected by a stalk-like region. The tail serves as the cargo-binding site and is composed of two light chains. These light chains are made up of six tetratricopeptide repeats, each of which contains 34 amino acids that form a helix-loop-helix domain. The aim of this project is to determine and study the structure of these repeats using a combined experimental and computational approach. By expressing and isolating the *Drosophila* kinesin light chain, X-ray crystallography, circular dichroism, and nuclear magnetic resonance can be used to study the structure. Computationally, the 3D structure of these light chains can be predicted by studying the *Drosophila* TPR structure along with various homology models using molecular dynamics.