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Understanding the Dynamics of Linker Histone Using Mathematical Modeling and FRAP Experiments

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Abstract : Linker histones or histones H1 are highly mobile nuclear proteins that regulate the organization of chromatin and limit DNA accessibility by binding to the chromatin structure (DNA and associated proteins). It is known that this binding process is driven by both slow (strong binding) and rapid (weak binding) interactions. However, the exact binding mechanism has not been fully described. Moreover, the existing models only account for one type of bound population that does not distinguish explicitly between the weakly and strongly bound proteins. Thus, we propose different systems of reaction-diffusion equations to describe explicitly the rapid and slow interactions during a FRAP (Fluorescence Recovery After Photobleaching) experiment. We perform a model comparison analysis to characterize the binding mechanism of histone H1 and provide new meaningful biophysical information on the kinetics of histone H1.

Keywords : FRAP (Fluorescence Recovery After Photobleaching), histone H1, histone H1 binding kinetics, linker histone, reaction-diffusion equation
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