

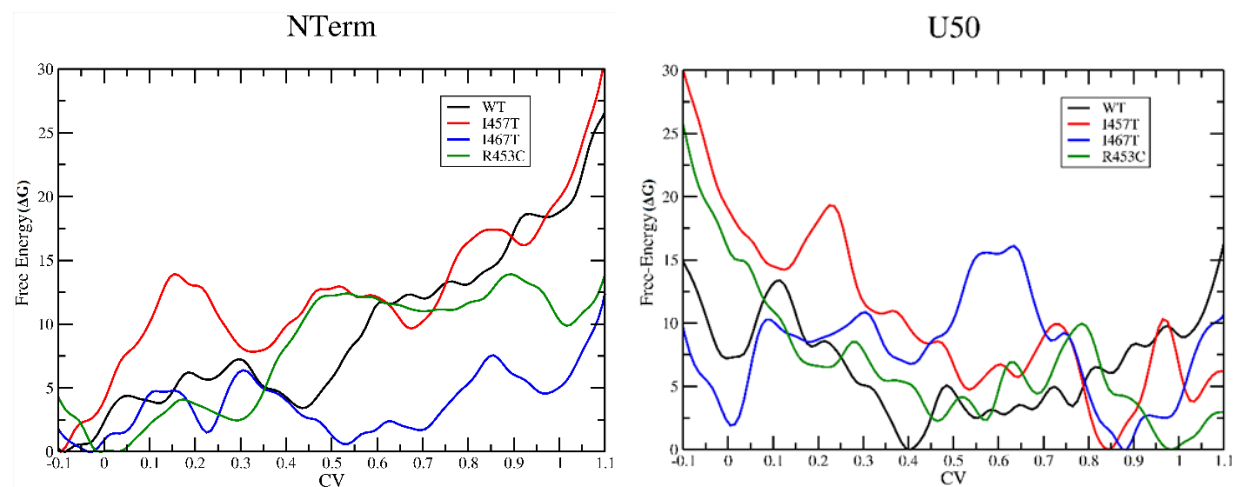
# Investigation of the Recovery Stroke and ATP Hydrolysis and Changes Caused Due to the Cardiomyopathic Point Mutations in Human Cardiac Beta Myosin

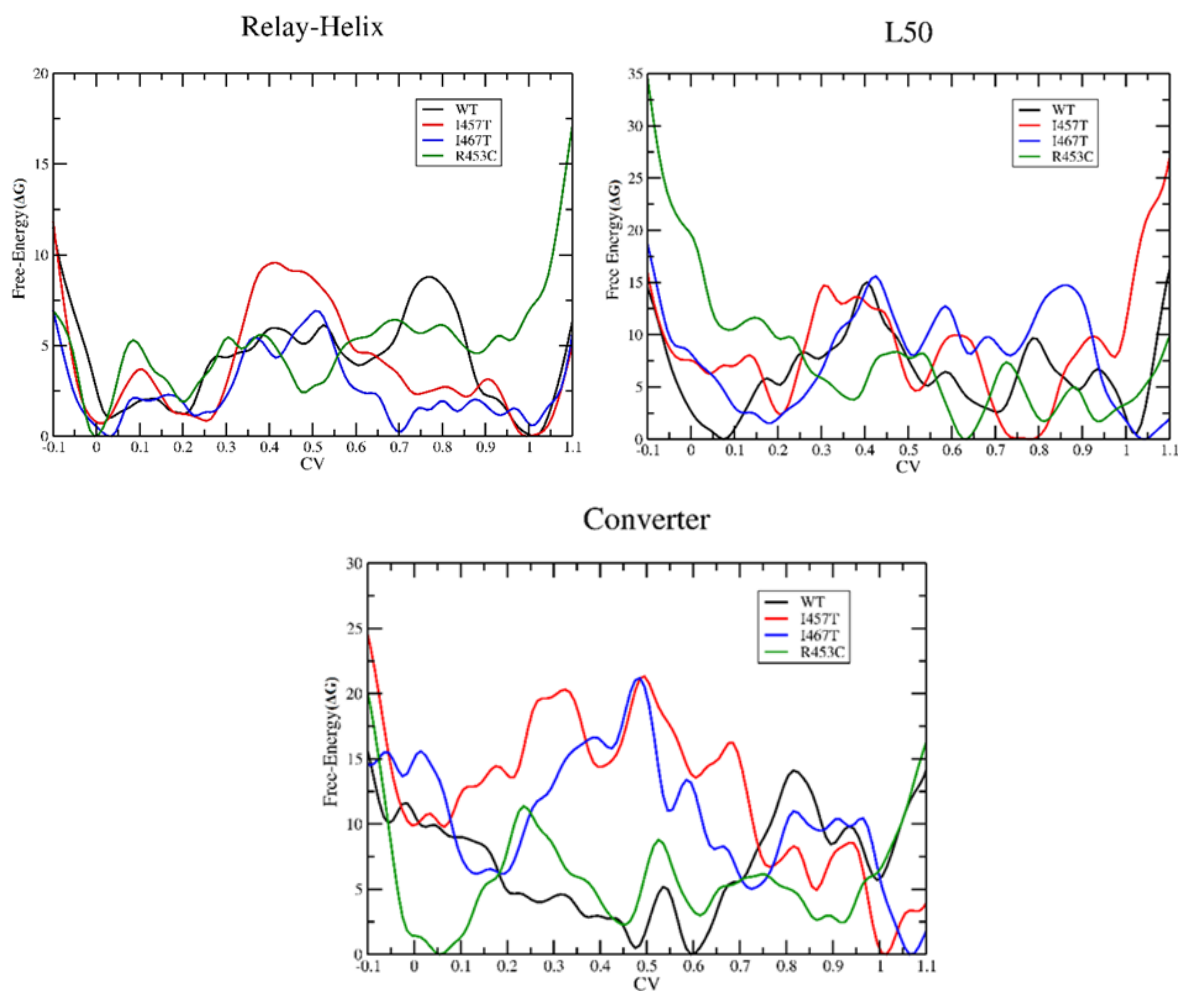
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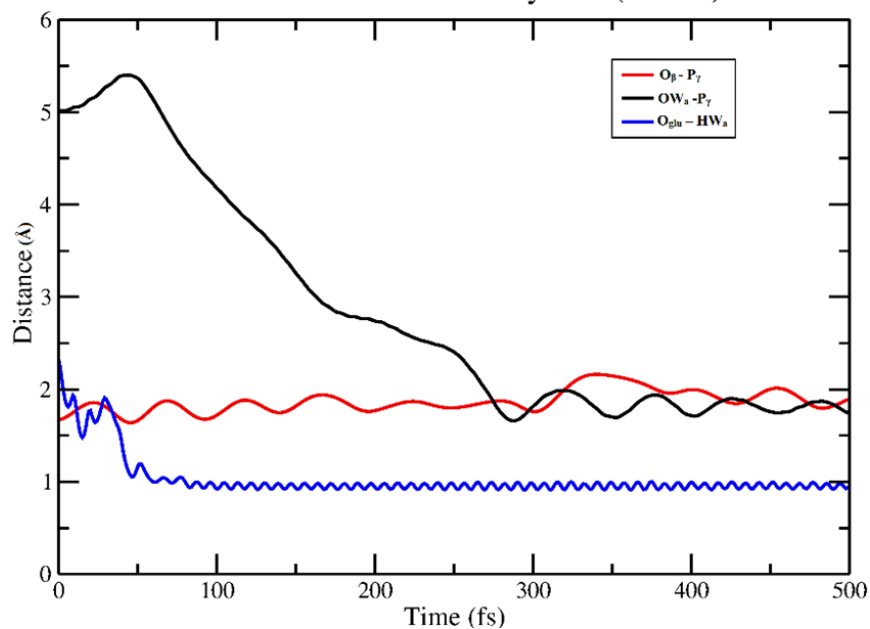
## Supplemental Information:





**Figure S1:** Converged FES profiles (in kcal/mol) for the (Top Left) Nterminal (residues 1 to 129), (Top Right) U50 (residues 130 to 460), (Middle Left) Relay-Helix (residues 461 to 505), (Middle Right) L50 (residues 506 to 710) and (Bottom) Converter (residues 711 to 782) domains for the recovery stroke.

## Bond Breaking-Bond Forming Human Cardiac-Beta Myosin (I467T)



**Figure S2.** Plot of atomic distances for the gamma phosphate ( $P_{\gamma}$ ), beta oxygen ( $O_{\beta}$ ) bond of ATP along with the deprotonation of the attacking water ( $HW_a$ ) by GLU466 ( $O_{glu}$ ) and subsequent attack of the newly formed hydroxide ( $OW_a$ ) to the gamma phosphate from a representative trajectory for the mutated myosin (I467T).