Poster Presentation

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Structural Characterization of BRCA2 functional domain

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BRCA2, also known as breast cancer type 2 susceptibility protein, is an important protein involved in DNA double strand breaks repair mechanism through homologous recombination pathway [1]. Germ-line mutations identified in BRCA2 increases risk of hereditary breast and ovarian cancer [2]. The hotspot mutations have been identified in the DNA region which encodes carboxy terminal domain of BRCA2. The C-terminal domain of BRCA2 comprising 2350-2545 amino acids is known to interact with FANCD2 which is an important protein of Fanconi Anemia pathway [3]. This interaction provides further evidence of hereditary nature of C-terminal domain of BRCA2. The C-terminal domain of BRCA2 was cloned, expressed and purified in bacterial system to characterize the secondary structure and folding pattern. Site-directed mutagenesis approach was used to clone the mutation and confirmed by DNA sequencing. Both wild type and mutant BRCA2 proteins were then expressed and purified. To examine the difference between secondary and tertiary structures of wild type and mutant proteins, purified proteins were subjected to Circular dichroism and Fluorescence spectroscopy.

[1] Xia, B. et al. (2006). Molecular Cell, Vol. 22, 719-729
[2] Venkitaraman, A.R. (2002). Cell, Vol. 108, 171–182
[3] Hussain S, et al. (2003). Human Molecular Genetics, Vol. 12, No. 19, 2503-2510

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