

Abstract No. huan250

High Throughput Screening (HTS) of Cancer Proteins

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Beamline(s): X9A

ABSTRACT: Candidate genes from the *C. elegans* genome were selected based on their sequence homology to the known DNA mismatch repair and cell cycle control genes in yeast. These genes were used as baits in the two-yeast hybrid screening to search for other potential interactors. Both the bait genes as well as their interactors were subcloned into His-tagged and MBP fusion vectors to enter the high throughput pipeline for expression, purification, and structure determination. Upon completion of the project, we are hoping to elucidate the mechanistic basis for the physical interactions among the key players in cancer related pathways. To date, we have screened through more than 259 candidate genes and found 126 clones that showed expression in *E. coli*. Twenty-four of the expressed proteins are soluble. Eleven of the soluble proteins have less than 30% homology to known structures, and thus are ideal targets for structural genomics.