

## **“The Sarcoma Genome Project Phase II: A Comprehensive Molecular Characterization of Soft Tissue Sarcoma to Identify Subtype Specific Therapies”**

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**Abstract:** The overall goal of this proposal is to perform a comprehensive, integrated genomic and functional analysis of liposarcoma and synovial sarcoma, so as to elucidate the mutational programs and candidate pathways involved in sarcomagenesis and then use this knowledge to identify novel therapeutic targets in liposarcoma and synovial sarcoma. The specific goals are to perform: (1) a comprehensive cancer genome characterization of liposarcoma and synovial sarcoma to include microRNA expression profiling, genome-wide copy number changes, detection of activating mutations and gene rearrangements (2) functional screens for genes and microRNAs involved in sarcoma survival, proliferation, and differentiation, guided by the integrated genomics datasets generated by Aim 1. To achieve these goals we have marshaled an integrated, multidisciplinary group of investigators all armed with a unique resource, a clinical-pathological and outcomes database prospectively collected over a 24 year period containing over 7000 patients treated for soft tissue sarcoma at MSKCC linked to comprehensive sarcoma tissue bank with over 1800 sarcoma samples and 47 primary sarcoma cell lines. This highly interactive and synergistic collaboration between MSKCC, Broad and Rockefeller will ensure maximum productivity and will enhance molecular target identification through multi-platform genome-wide gene discovery, pathway and functional analysis. This information will then be used to develop new subtype specific targeted molecular therapeutics for liposarcoma and synovial sarcoma.