Section: Contact Information

First Name : **Harry**
Last Name : **Ostrer**
Institution : **Albert Einstein College of Medicine**
Address 1 : **1300 Morris Park Avenue**
Address 2 :
City : **Bronx**
State/Province/Region : **NY**
Country : **US**
Zip/Postal Code : **10461**
Phone Number : **7184308605**
Alternate Phone Number :
Email Address : **harry.ostrer@einsteinmed.org**

Section: Project Requirements and Description

Group: Requirements to submit AOI

A comprehensive review of previously published data has been completed. : **Yes**
The specific aims are clear and focused. : **Yes**
The investigator has appropriate experience and expertise to develop the concept proposal; if not, has identified a mentor or senior co-investigator. : **Yes**
The investigator agrees to develop an initial draft of the concept proposal within 6 weeks of approval of the AOI and to finalize the concept proposal within 6 months. : **Yes**
Project Title : **Robust Genetic Predictors of Secondary Cancer Risks**
Planned research population (eligibility criteria) :
1. All CCSS subjects for whom lymphoblastoid cell lines are available
Proposed specific aims :
1. To identify the prevalence of germline defects in the double strand break repair and mismatch repair pathways in survivors of childhood cancer by primary cancer type using flow variant assays (FVAs).

2. To identify the prevalence of DNA repair defects in SN and adjacent normal tissues in survivors of childhood cancer by cancer type and radiotherapy exposure using whole genome sequencing (WGS).
Will the project require non-CCSS funding to complete? : **Yes**
If yes, what would be the anticipated source(s) and timeline(s) for securing funding? :
NIH R01 support with proposal submission June, 2020.

Group: Does this project require contact of CCSS study subjects for:

Additional self-reported information : **No**
Biological samples : **Yes**
Medical record data : **Yes**
If yes to any of the above, please briefly describe. :
All lymphoblastoid cell lines for FVA testing. Additional frozen PBMCs for LCL transformation and FVA testing. Tumor blocks for dissection, DNA extraction and whole genome sequencing

Prior genetic testing results

Secondary malignancies

Group: What CCSS Working Group(s) would likely be involved? (Check all that apply)

Second Malignancy : **Secondary**
Chronic Disease :
Psychology / Neuropsychology :
Genetics : **Primary**
Cancer Control :
Epidemiology / Biostatistics :

Section: Outcomes or Correlative Factors

Late mortality : **Secondary**
Second Malignancy : **Primary, Correlative Factors**

Group: Health Behaviors

Tobacco :
Alcohol :
Physical activity :
Medical screening :
Other :
If other, please specify :

Group: Psychosocial

Insurance :
Marriage :
Education :
Employment :
Other :
If other, please specify :

Group: Medical Conditions

Hearing/Vision/Speech :
Hormonal systems :
Heart and vascular :
Respiratory :
Digestive :
Surgical procedures :
Brain and nervous system :
Other :
If other, please specify :

Group: Medications

Describe medications :

Group: Psychologic/Quality of Life

BSI-18 :

SF-36 :
CCSS-NCQ :
PTS :
PTG :
Other :
If other, please specify :

Group: Other

Pregnancy and offspring :
Family history : **Primary**
Chronic conditions (CTCAE v3) :
Health status :

Group: Demographic

Age : **Primary**
Race : **Primary**
Sex : **Primary**
Other :
If other, please specify :

Group: Cancer treatment

Chemotherapy :
Radiation therapy :
Surgery :

Section: Anticipated Sources of Statistical Support

CCSS Statistical Center :
Local institutional statistician : **Yes**
If local, please provide the name(s) and contact information of the statistician(s) to be involved. :
Yongzhao Shao, Ph.D. - yongzhao.shao@nyulmc.org

Lindsay Mortin, Ph.D. - mortonli@mail.nih.govindsay
Will this project utilize CCSS biologic samples? : **Yes**
If yes, which of the following? : **Lymphoblastoid cell lines, PBMCs, tissue blocks**
If other, please explain :

Section: Other General Comments

Other General Comments :
Flow variant assays were developed in my laboratory to identify germline defects in genetic pathways. We have developed assays for the DSB repair and MMR pathways and are applying these for predicting adult cancer risks. Sequencing of tumors and radiation exposed normal tissue represents an alternative method for identifying defects in DNA repair pathways.

We will develop a bidirectional workflow with Lindsay Morton to share data and analyses.
I agree to share this information with St. Jude : **Yes**