SUMMARY STATEMENT

PROGRAM CONTACT:
Jerry Li
240-276-6210
jerry.li@nih.gov

(Privileged Communication)

Release Date: **04/27/2017**
Revised Date:

Application Number: **1 R01 CA209781-01A1**

Principal Investigator

GERSTEIN, MARK BENDER

Applicant Organization: YALE UNIVERSITY

Review Group: **ZRG1 OBT-B (55)**
Center for Scientific Review Special Emphasis Panel
PAR Panel: Basic Research in Cancer Health Disparities/Diversity

Meeting Date: **03/30/2017**
Council: **MAY 2017**
Requested Start: **07/01/2017**

RFA/PA: **PAR15-093**
PCC: **J3SB**

Project Title: **The Genomic Basis of Racial Disparities in Kidney Cancer**

SRG Action: **++**
Next Steps: **Visit https://grants.nih.gov/grants/next_steps.htm**
Human Subjects: **44-Human subjects involved - SRG concerns**
Animal Subjects: **10-No live vertebrate animals involved for competing appl.**

Project Year	Direct Costs Requested
1	250,000
2	250,000
3	250,000
4	250,000
5	250,000
TOTAL	1,250,000

++NOTE TO APPLICANT: Members of the Scientific Review Group (SRG) were asked to identify those applications with the highest scientific merit, generally the top half. Written comments, criterion scores, and preliminary impact scores were submitted by the assigned reviewers prior to the SRG meeting. At the meeting, the more meritorious applications were discussed and given final impact scores; by concurrence of the full SRG, the remaining applications, including this application, were not discussed or scored. The reviewers' comments (largely unedited by NIH staff) and criterion scores for this application are provided below. Because applications deemed by the SRG to have the highest scientific merit generally are considered for funding first, it is highly unlikely that an application with an ND recommendation will be funded. Each applicant should read the written critiques carefully and, if there are questions about the review or future options for the project, discuss them with the Program Contact listed above.

1R01CA209781-01A1 Gerstein, Mark

SCIENTIFIC REVIEW OFFICER'S NOTES

DESCRIPTION (provided by applicant): Recent studies have shown significant racial disparities in kidney cancer including early disease onset for African-Americans, different histologic distribution, and worst disease outcome, even when controlling for treatment. No study has evaluated a biologic or cause of racial disparities in kidney cancer. In our study, we intend to investigate whether these disparities are due to recurrent coding or non-coding germline and somatic alterations and whether these alterations are more common in African-American or Caucasian individuals with clear cell and papillary kidney cancer. For this purpose, we have developed four specific aims. In our first aim, we intend to perform whole genome sequencing of 15 African-Americans in order to increase the number of African- Americans currently existing in TCGA with kidney cancer. For these individuals, we intend to perform high-quality mutation calls for structural and genomic variation including SNPs, indels, inversions and copy number variations for both coding and non- coding regions. Our second aim is to assemble a comprehensive list of somatic & germline mutations associated with cancer and prioritize regions with greatest impact. To complete our aim, we will use our novel and already developed tools including i) FunSeq, a sophisticated algorithm that prioritizes high impact variants, ii) LARVA, a burden test algorithm that identifies significant mutation enrichment in non coding elements, iii) an extension of FunSeq to construct connected genetic modules based on molecular and protein interactions and iv) an extension of LARVA to include additional covariates such as mutation rate, replication time etc. In our third aim, we will test a list of prioritized regions and modules obtained from aim 2 to identify racial genomic differences. More specifically, we intend to test for disparities across i) germline mutations in coding regions using WES data, ii) genomic regions with higher mutational burdens, iii) germline mutations in non-coding prioritized regions using WGS data and iv) somatic mutations in prioritized regions. Finally, in our fourth objective, we intend to validate racial disparities from a list of 550 prioritized regions using a Yale Validation Cohort, a cohort consisting of total 384 individuals; an equal number of 96 Caucasian and African-American clear cell and papillary tumors. To validate for racial disparity, we will use the MassArray system, a highly accurate technology for rapid detection of known or suspected somatic or germline alterations.

PUBLIC HEALTH RELEVANCE: Narrative We investigate the genomic cause of racial disparities in renal cell carcinoma. We will evaluate clear cell and papillary renal tumors from African American and Caucasians to identify and prioritize both common and rare, germline and somatic variants, in coding and non-coding regions. Utilizing a range of cancer genome data and novel bioinformatics tools, our goal is to prioritize variants contributing to racial disparity.

CRITIQUES: The written critiques of individual reviewers are provided in essentially unedited form below. These critiques were prepared prior to the meeting and may not have been revised afterwards.

CRITIQUE 1

Significance: 3
Investigator(s): 2
Innovation: 3
Approach: 5
Environment: 1

Overall Impact: Renal cell carcinoma (RCC) is the urological malignancy with the highest mortality. RCC incidence has been increasing in most populations, with the highest increase reported in African Americans (AA). The reasons for such incidence rate increase remain unknown. This application proposes to investigate whether genomic differences between AA and non-Hispanic Whites (NHW) can account for existing racial disparities in incidence. Specifically, these investigators propose to carry out

whole genome sequencing (WGS) of RCCs from AA (Aim 1), to identify germline and somatic RCC associated variants (Aim 2), to identify risk variants that differ between AA and NHW RCCs (Aim 3) and to perform a validation of variants likely associated with racial disparities in an independent cohort. The score driving elements include the focus on the genomic study of a malignancy that was not well characterized by the TCGA study and the tremendous expertise on cancer genomics of the PI. The study however has a number of weaknesses. It lacks a well-defined guiding hypothesis and its Aims are inter-dependent. The germline analyses could have been more rigorous: they have limited power to detect risk variants and the use of publicly available controls may not be fully appropriate. The lack of studies on the mechanistic/functional aspects of RCC in AA is also another limitation of the study. Overall, the weaknesses of the study outweigh its strengths and the proposal, as presented, is likely to have a low to moderate impact.

1. Significance:
Strengths

- RCC incidence has been rising during the last four decades and genomic analyses can provide some clues associated with such increase.
- The study will fill an existing gap on the genomics of RCC in AAs.
- The study has a moderate scientific premise.

Weaknesses

- The racial disparity in RCC has changed over time (starting in the 90's, based on Figure 1), which suggests a role of a changing environment rather than biology in the observed disparity.
- A higher incidence of pRCC in AA is not well supported by the data. Extreme care should be exercised when using subtype prevalence information from TCGA, as such study was not designed as either a clinic-based or a population-based epidemiological study.

2. Investigator(s):
Strengths

- Dr. Gerstein is a world leading expert in cancer genomics and has expertise in cancer genome characterization projects such as the one proposed here.
- Dr. Adeniran will provide expertise in RCC clinical and translational research.

Weaknesses

- Limited experience of these researches in disparities research

3. Innovation:
Strengths

- The use of a new population in a genome sequencing study is mildly innovative.

Weaknesses

- None noted

4. Approach:
Strengths

- The proposal will be carried out by a highly-qualified team.
- The focus on genomics of an understudied cancer in an understudied minority population is a strength.
- Most analyses, particularly those involving somatic mutation analyses, are rigorously described and consider relevant biological variables.

Weaknesses

- There seems to be a lack of guiding hypothesis and the proposal reads more like a large sequencing study with little mechanistic insights.
- The aims are interdependent.
- The germline analyses have limited power and potential issues with stratification.

5. Environment:
Strengths

- The scientific environment and resources at Yale are excellent for the proposed studies.

Weaknesses

- None noted

Protections for Human Subjects:
Unacceptable Risks and/or Inadequate Protections

- This section is missing in the application.

Inclusion of Women, Minorities and Children:

- Sex/Gender: Distribution not justified scientifically
- Race/Ethnicity: Distribution not justified scientifically
- For NIH-Defined Phase III trials, Plans for valid design and analysis: Not applicable
- Inclusion/Exclusion of Children under 18: Excluding ages <18; not justified scientifically
- Sections on inclusion of women, minorities and children are missing in the application

Vertebrate Animals:
Not Applicable (No Vertebrate Animals)

Biohazards:
Not Applicable (No Biohazards)

Resubmission:

- The application addresses some of the concerns raised in the previous review.

Resource Sharing Plans:
Acceptable

Authentication of Key Biological and/or Chemical Resources:
Not Applicable (No Relevant Resources)

Budget and Period of Support:
Recommend as Requested

CRITIQUE 2

Significance: 3
Investigator(s): 1
Innovation: 3
Approach: 5
Environment: 1

Overall Impact: This is a revised R01 grant application from an outstanding PI to study the genomic cause of racial disparity in kidney cancer. There are racial disparities in kidney cancer among African American versus Caucasian Americans. The proposed work will evaluate clear cell and papillary renal tumors from African American and Caucasians to identify germline and somatic variants in coding and non-coding regions. The proposal is supported by some preliminary data; and it can partly address the genetic causes of cancer health disparities in kidney cancer. The investigators are highly qualified to conduct the proposed study. The research environment and the facilities at the Yale University is

excellent. In this revised application, some concerns brought by previous reviewers are nicely addressed. Some new preliminary data have been included to demonstrate that genes required for the development and progression of kidney cancer are racially burdened with deleterious mutations. Some of the missing controls have been added. However, it is still not clear how the variants will be segregated. How the genetic difference between clear cell versus papillary RCC will be addressed? The feasibility of Aim-3 is totally dependent on the success of Aim-2. Although the proposal is based on a strong scientific premise, there are remaining concerns in the experimental approach section. Together, the overall impact of the proposal is considered to be moderately high.

1. Significance:
Strengths

- The proposed study can address the genetic causes of cancer health disparities in kidney cancer.

Weaknesses

- It would have been important to dissect the genetic difference between clear cell versus papillary RCC (instead of only racial disparities).

2. Investigator(s):
Strengths

- The investigators (PI and co-investigators) are highly qualified to conduct the proposed study as evident by the publications.

Weaknesses

- None noted

3. Innovation:
Strengths

- There are limited data for the genetic basis (Met, VHL etc) of renal cancer growth. The whole genome analysis can improve our understanding of the genetic causes of kidney cancer, with importance to health disparities.

Weaknesses

- The innovative information expected to be generated from this study are limited.

4. Approach:
Strengths

- The proposed study is based on some important preliminary data.

Weaknesses

- The feasibility of Aim-3 is totally dependent on the success of Aim-2.
- How the genetic difference between clear cell versus papillary RCC will be addressed.
- It is still not clear how the variants will be segregated, and there are weaknesses in the scientific rigor.

5. Environment:
Strengths

- The research environment at the Yale University is outstanding.

Weaknesses

- None noted

Protections for Human Subjects:

Not Applicable (No Human Subjects)

Vertebrate Animals:

Not Applicable (No Vertebrate Animals)

Biohazards:
Not Applicable

Resource Sharing Plans:
Acceptable

Authentication of Key Biological and/or Chemical Resources:
Not Applicable (No Relevant Resources)

Budget and Period of Support:
Recommend as Requested

Additional Comments to Applicant:

- Some of the concerns raised during the previous review have been addressed. However, there are still remaining concerns.

CRITIQUE 3

Significance: 3
Investigator(s): 1
Innovation: 4
Approach: 7
Environment: 1

Overall Impact: Renal cell carcinoma is a lethal GU malignancy, with African Americans (AA) exhibiting higher incidence and mortality rates than Caucasians. In addition, ethnicity-associated differences are also observed in the distribution of RCC histologic subtypes, with the frequency of pRCC being more frequent in AAs when compared to Caucasian. Several risk factors for RCC have been identified including obesity, male gender, smoking, kidney disease, yet they do not fully account for the observed disparate RCC burdens in the AA population. This proposal accordingly attempts to determine whether there are molecular/genetic differences between AA versus Caucasian RCCs that could inform on additional molecular etiologic factors potentially contributing to RCC disparities. The strengths of the proposal include the stellar investigative team, adequate physical and computational resources available to conduct the studies, feasibility of the proposed informatics pipelines. However, there are several key weaknesses in the proposal including: Aims are highly descriptive in nature and overtly ambitious in scope; prior studies on molecular differences between ccRCC and pRCC are not discussed in this context and whether any effort to follow on these prior studies to initially test for specific molecular differences in AA versus Caucasian CRCs is missing; lack of solid preliminary data informing on the likelihood of genetic differences existing between AA versus Caucasian RCC cases. In response to the comments on pilot data from the initial submission, the investigators have included some preliminary results showing a heavier inherited mutational burden in AAs affecting 14 kidney cancer associated genes using the 1000 genomes and the ExAC databases. However, a proper null/background control is missing in these analyses. For example, how do the burden test results compare to assessments of random sets of 14 genes that are not associated with kidney cancer, permuted multiple times? no approach was provided on how ethnicity-associated differences in germline/somatic variants will be assessed in the context of clinical outcomes; the investigators propose to validate the germline differences in a fresh FFPE cohort in Aim 4. Given the possibility of ascertainment bias in hospital-based case cohorts with co-morbidities, it is important to include at-risk non-RCC AA and Caucasian controls derived locally for the germline studies; given the migratory patterns of AA's within United States, it is possible that any distinct RCC mutational signature/panel in

AAs might be influenced by differences in geographical location of AAs (in other words, local environment), and the proposal does not address this significant pitfall; confirmation of representative genomics signals using orthogonal platforms are not provided especially given that Aim 4 will be using FFPE samples; plans for wet-lab assessments on informatics-predicted deleterious events missing; the proposal lacks any mechanistic studies; aims appear inter-dependent and are based on the success of identifying molecular differences in AA versus Caucasian RCC cases. Overall, the weaknesses markedly outweigh the strengths of the proposal, significantly diminishing the impact of the proposal.

Protections for Human Subjects:
Unacceptable Risks and/or Inadequate Protections

- The proposal utilizes blood/discarded tissues from human subjects with demographic and co-morbid information, and will perform genome-scale profiling including genotyping. As such, details should be provided on how all this information will be secured, deidentified, and plans for IRBs specifically to disseminate the genetic information in accordance with NIH GDS policies.

Vertebrate Animals:
Not Applicable (No Vertebrate Animals)

Biohazards:
Not Applicable (No Biohazards)

Resubmission:

- While this A1 proposal attempted to address some of the concerns raised in the initial submission, the key weaknesses have not been satisfactorily resolved.

Resource Sharing Plans:
Acceptable

Authentication of Key Biological and/or Chemical Resources:
Not Applicable (No Relevant Resources)

Budget and Period of Support:
Recommend as Requested

SCIENTIFIC REVIEW OFFICER'S NOTES:
The applicant proposes to use tumor tissues and blood from patients undergoing kidney cancer surgery in the planned research, but claims the project as a No Human Subjects study. Based on the NIH SF424 application guideline, “If the answer is “No” to the question (**Are Human Subjects Involved)** but your proposed research involves human specimens and/or data from subjects you must provide a justification in this section for your claim that no human subjects are involved”. The applicant does not include a justification for why the project using human biospecimens are not human subjects research. If the human bio-specimens are considered as human subjects, a plan for protection of human subjects should be submitted.

Footnotes for 1 R01 CA209781-01A1; PI Name: Gerstein, Mark Bender

NIH has modified its policy regarding the receipt of resubmissions (amended applications). See Guide Notice NOT-OD-14-074 at http://grants.nih.gov/grants/guide/notice-files/NOT-OD-14-074.html. The impact/priority score is calculated after discussion of an application by averaging the overall scores (1-9) given by all voting reviewers on the committee and

multiplying by 10. The criterion scores are submitted prior to the meeting by the individual reviewers assigned to an application, and are not discussed specifically at the review meeting or calculated into the overall impact score. Some applications also receive a percentile ranking. For details on the review process, see http://grants.nih.gov/grants/peer_review_process.htm#scoring.

MEETING ROSTER
Center for Scientific Review Special Emphasis Panel

CENTER FOR SCIENTIFIC REVIEW
PAR Panel: Basic Research in Cancer Health Disparities/Diversity
ZRG1 OBT-B (55)
03/30/2017 - 03/31/2017

Notice of NIH Policy to All Applicants: Meeting rosters are provided for information purposes only. Applicant investigators and institutional officials must not communicate directly with study section members about an application before or after the review. Failure to observe this policy will create a serious breach of integrity in the peer review process, and may lead to actions outlined in NOT-OD-14-073 at https://grants.nih.gov/grants/guide/notice-files/NOT-OD-14-073.html and NOT-OD-15-106 at https://grants.nih.gov/grants/guide/notice-files/NOT-OD-15-106.html, including removal of the application from immediate review.

CHAIRPERSON(S)

BARTON, MICHELLE ANN, PHD
PROFESSOR
DEPARTMENT OF EPIGENETICS AND MOLECULAR CARCINOGENESIS
GRADUATE SCHOOL OF BIOMEDICAL SCIENCES
THE UNIVERSITY OF TEXAS MD ANDERSON CANCER CENTER
HOUSTON, TX 77030

MEMBERS

ALEXANDER, CAROLINE MARGARET, PHD
PROFESSOR
MCARDLE LABORATORY FOR CANCER RESEARCH
UNIVERSITY OF WISCONSIN-MADISON
MADISON, WI 53705

APLIN, ANDREW E, PHD
PROFESSOR
DEPARTMENT OF CANCER BIOLOGY
ASSOCIATE DIRECTOR, BASIC SCIENCES
SIDNEY KIMMEL CANCER CENTER
THOMAS JEFFERSON UNIVERSITY
PHILADELPHIA, PA 19107

BANERJEE, SUSHANTA K, PHD
PROFESSOR
DIVISION OF HEMATOLOGY AND ONCOLOGY
DEPARTMENT OF MEDICINE
UNIVERSITY OF KANSAS MEDICAL CENTER
KANSAS CITY, KS 66160

CARVAJAL CARMONA, LUIS GUILLERMO, PHD
ASSOCIATE PROFESSOR
GENOME CENTER & DEPARTMENT OF BIOCHEMISTRY AND MOLECULAR MEDICINE
SCHOOL OF MEDICINE
UNIVERSITY OF CALIFORNA, DAVIS
DAVIS, CA 95616

CHENG, IONA C, PHD
RESEARCH SCIENTIST III
DEPARTMENT OF EPIDEMIOLOGY
CANCER PREVENTION INSTITUTE OF CALIFORNIA
FREMONT, CA 94538

CLAUS, ELIZABETH B, PHD, MD
PROFESSOR AND DIRECTOR OF MEDICAL RESEARCH
DEPARTMENT OF BIOSTATISTICS
SCHOOL OF PUBLIC HEALTH
YALE UNIVERSITY
NEW HAVEN, CT 06510

CLEVENGER, CHARLES V, MD, PHD
PROFESSOR AND CAROLYN WINGATE HYDE CHAIR IN CANCER RESEARCH
CHAIR, DEPARTMENT OF PATHOLOGY
VIRGINIA COMMONWEALTH UNIVERSITY
RICHMOND, VA 23284

COOPERWOOD, JOHN S, PHD
PROFESSOR OF MEDICINAL CHEMISTRY
DIVISION OF BASIC SCIENCES
COLLEGE OF PHARMACY AND PHARMACEUTICAL SCIENCES
FLORIDA AGRICULTURAL AND MECHANICAL UNIVERSITY
TALLAHASSEE, FL 32307

DEMISSIE, KITAW, MD, PHD
PROFESSOR AND CHAIR
DEPARTMENT OF EPIDEMIOLOGY
DIRECTOR, INSTITUTE FOR THE ELIMINATION OF HEALTH DISPARITIES RUTGERS BIOMEDICAL AND HEALTH SCIENCES
RUTGERS SCHOOL OF PUBLIC HEALTH
PISCATAWAY, NJ 08854

DIERGAARDE, BRENDA B, PHD
ASSOCIATE PROFESSOR
DEPARTMENTS OF EPIDEMIOLOGY AND HUMAN GENETICS
UNIVERSITY OF PITTSBURGH CANCER INSTITUTE
PITTSBURGH, PA 15213

EUBANK, TIMOTHY D, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF MICROBIOLOGY, IMMUNOLOGY AND CELL BIOLOGY
WEST VIRGINIA UNIVERSITY
MORGANTOWN, WV 26506-9177

FARUQUE, MEZBAH U, PHD, MD
ASSISTANT PROFESSOR
DEPARTMENT OF COMMUNITY AND FAMILY MEDICINE
PRINCIPAL INVESTIGATOR
NATIONAL HUMAN GENOME CENTER
HOWARD UNIVERSITY COLLEGE OF MEDICINE
WASHINGTON, DC 20060

GARCIA-MATA, RAFAEL, PHD
ASSISTANT PROFESSOR
DEPARTMENT OF BIOLOGICAL SCIENCES
UNIVERSITY OF TOLEDO
TOLEDO, OH 43606

GASKINS, H REX, PHD
PROFESSOR
CARL R. WOESE INSTITUTE OF GENOMIC BIOLOGY
UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN
URBANA, IL 61801

GUDA, KISHORE, PHD, DVM
ASSISTANT PROFESSOR
GENERAL MEDICAL SCIENCES (ONCOLOGY)
CASE COMPREHENSIVE CANCER CENTER
SCHOOL OF MEDICINE
CASE WESTERN RESERVE UNIVERSITY
CLEVELAND, OH 44106

GUERRERO-CAZARES, HUGO, MD, PHD
ASSOCIATE CONSULTANT
DEPARTMENT OF NEUROSURGERY
MAYO CLINIC
JACKSONVILLE, FL 32082

HEDIN, KAREN E, PHD
PROFESSOR
IMMUNOLOGY GRADUATE PROGRAM DIRECTOR
DEPARTMENT OF IMMUNOLOGY
MAYO CLINIC COLLEGE OF MEDICINE
ROCHESTER, MN 55905

HU, YANFEN, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF MOLECULAR MEDICINE
UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER
SAN ANTONIO, TX 78229

LIANG, CHENGYU, PHD, MD
ASSOCIATE PROFESSOR
DEPARTMENT OF MOLECULAR MICROBIOLOGY
AND IMMUNOLOGY
KECK SCHOOL OF MEDICINE
UNIVERSITY OF SOUTHERN CALIFORNIA
LOS ANGELES, CA 9033

LIPKIN, STEVEN M, MD, PHD
PROFESSOR
DIRECTOR, ADULT AND CANCER GENETICS CLINIC
VICE CHAIR FOR BASIC AND TRANSLATIONAL RESERACH
SANFORD AND JOAN WEILL DEPARTMENT OF MEDICINE
WEILL CORNELL COLLEGE OF MEDICINE
NEW YORK, NY 10021

LOCKER, JOSEPH D, PHD, MD
PROFESSOR
DEPARTMENT OF PATHOLOGY
UNIVERSITY OF PITTSBURGH
PITTSBURGH, PA 15261

LOESCHE, MATHIAS, PHD
PROFESSOR
DEPARTMENT OF PHYSICS
CARNEGIE MELLON UNIVERSITY
PITTSBURGH, PA 15213

LOUIE, MAGGIE C, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF NATURAL SCIENCES
AND MATHEMATICS
DOMINICAN UNIVERSITY OF CALIFORNIA
SAN RAFAEL, CA 94901

MAHESWARAN, SHYAMALA, PHD
ASSOCIATE PROFESSOR OF SURGERY
MASSACHUSETTS GENERAL HOSPITAL CANCER CENTER
HARVARD UNIVERSITY
CHARLESTOWN, MA 02129

MIRANDA, KATRINA M, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF CHEMISTRY AND BIOCHEMISTRY
UNIVERSITY OF ARIZONA
TUCSON, AZ 85721

MOHAMMED, SULMA IBRAHIM, PHD, DVM
ASSOCIATE PROFESSOR
DEPARTMENT OF COMPARATIVE PATHOBIOLOGY
PURDUE UNIVERSITY CENTER FOR CANCER RESEARCH
WEST LAFAYETTE, IN 47907

OUELLETTE, MICHEL M, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF INTERNAL MEDICINE
UNIVERSITY OF NEBRASKA MEDICAL CENTER
OMAHA, NE 68198

PAL, SOUMITRO, PHD
ASSOCIATE PROFESSOR
DIVISION OF NEPHROLOGY
BOSTON CHILDREN'S HOSPITAL
HARVARD MEDICAL SCHOOL
BOSTON, MA 02115

PAYNE, KIMBERLY J, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF BASIC SCIENCES
DIVISION OF ANATOMY
SCHOOL OF MEDICINE
LOMA LINDA UNIVERSITY
LOMA LINDA, CA 92350

RAY, RATNA B., PHD
PROFESSOR
DEPARTMENT OF PATHOLOGY
SAINT LOUIS UNIVERSITY
ST. LOUIS, MO 63104

SHANKER, ANIL, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF BIOCHEMISTRY AND CANCER BIOLOGY
MEHARRY MEDICAL COLLEGE
MEMBER, VANDERBILT-INGRAM CANCER CENTER
NASHVILLE, TN 37208

SINGH, KESHAV K, PHD
PROFESSOR AND JOY AND BILL HARBERT ENDOWED CHAIR
DEPARTMENTS OF GENETICS, PATHOLOGY
AND ENVIRONMENTAL HEALTH
THE UNIVERSITY OF ALABAMA AT BIRMINGHAM
BIRMINGHAM, AL 35294

SINGH, POMILA, PHD
PROFESSOR
DEPARTMENT OF NEUROSCIENCE
AND CELL BIOLOGY
UNIVERSITY OF TEXAS MEDICAL BRANCH
GALVESTON, TX 77555

SMITH, JEFFREY W, PHD
PROFESSOR
CANCER METABOLISM AND SIGNALING NETWORKS PROGRAM
SANFORD BURNHAM PREBYS MEDICAL DISCOVERY INSTITUTE
LA JOLLA, CA 92037

TORRES-RUIZ, JOSE A, PHD
PROFESSOR OF BIOCHEMISTRY
PROVOST AND VICE PRESIDENT ACADEMIC AFFAIRS
PONCE HEALTH SCIENCES UNIVERSITY
PONCE, PR 00716

WU, ZHAOHUI, PHD, MD
ASSOCIATE PROFESSOR
DEPARTMENT OF PATHOLOGY
UNIVERSITY OF TENNESSEE HEALTH SCIENCE CENTER
MEMPHIS, TN 38103

YEE, AMY S, PHD
PROFESSOR
DEPARTMENTS OF DEVELOPMENTAL, MOLECULAR AND CHEMICAL BIOLOGY
SCHOOL OF MEDICINE
TUFTS UNIVERSITY
BOSTON, MA 02111

MAIL REVIEWER(S)

GHOSH, DEBASHIS, PHD
PROFESSOR
DEPARTMENT OF PHARMACOLOGY
UPSTATE CANCER RESEARCH INSTITUTE
SUNY UPSTATE MEDICAL UNIVERSITY
SYRACUSE, NY 13210

KRIDEL, STEVEN J, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF CANCER BIOLOGY
WAKE FOREST UNIVERSITY HEALTH SCIENCES
WINSTON-SALEM, NC 27157

YU, JIANHUA, PHD
ASSOCIATE PROFESSOR
DEPARTMENT OF INTERNAL MEDICINE
DIVISION OF HEMATOLOGY
COLLEGE OF MEDICINE
OHIO STATE UNIVERSITY
COLUMBUS, OH 43210

SCIENTIFIC REVIEW OFFICER

HOWARD, OLA MAE ZACK, PHD
SCIENTIFIC REVIEW OFFICER
CENTER FOR SCIENTIFIC REVIEW
NATIONAL INSTITUTES OF HEALTH
BETHESDA, MD 20892

NG, ANGELA Y, PHD, MBA
SCIENTIFIC REVIEW OFFICER
CENTER FOR SCIENTIFIC REVIEW
NATIONAL INSTITUTES OF HEALTH
BETHESDA, MD 20892

EXTRAMURAL SUPPORT ASSISTANT

ROGERS, YVETTE
EXTRAMURAL SUPPORT ASSISTANT
CENTER FOR SCIENTIFIC REVIEW
NATIONAL INSTITUTES OF HEALTH
BETHESDA, MD 20892

Consultants are required to absent themselves from the room during the review of any application if their presence would constitute or appear to constitute a conflict of interest.