

10th ANNUAL DEPARTMENT OF PATHOLOGY YOUNG INVESTIGATORS' DAY
POSTER SESSION

POSTER #

4

(for Admin. use)

Thursday, April 17th, 2008
TURNER CONCOURSE
REGISTRATION FORM

Applicant's Name: Kathleen H. Burns Degree: M.D., Ph.D.

Applicant's Division: Hematopathology

Faculty Preceptor: Michael J. Borowitz
(Must hold a primary appointment in Pathology)

Appointment Category: House Staff Clin Fellow Research Fellow
 Medical Student Graduate Student (Program: _____)

Register for: Clinical Research Translational Research Basic Research

Full Poster Title * Comprehensive transposon mapping in the human genome.

Where has the work been presented?

Meeting Name Structural, Functional & Evolutionary Genomics Gordon Conference

Meeting Date July 29-August 3, 2007

Not Previously Presented _____

Where is this work being published? Not yet published or submitted.

Journal Name, Volume, Page, Date _____

In Preparation (Y/N) - Where? _____

Author(s) (First & Last) _____

In-House Address: Carnegie 400, Pathology, 600 North Wolfe Street Baltimore, MD
(Room # and Building Name, Lab, etc.)

Telephone: (410) 955-3980 Beeper: (410) 283-6213

Fax: (410) 502-1493 E-mail: kburns@jhmi.edu

***INCLUDE A ONE-PAGE ABSTRACT (including title and all authors) OF THE WORK YOU WILL BE PRESENTING**

**E-mail COMPLETED Registration form and abstract to:
Stacey Morgan (smorgan9@jhmi.edu) on or before
Friday, March 14th, 2008**

If you have questions or problems regarding your submission, please contact Stacey Morgan via e-mail (smorgan9@jhmi.edu)

Comprehensive transposon mapping in the human genome.

Kathleen H. Burns, Cheng Ran Huang, Sarah J. Wheelan, David Valle, Ralph H. Hruban, Michael J. Borowitz, Curt I. Civin, Jef D. Boeke

Transposons are mobile genetic elements which have shaped eukaryotic genomes over evolutionary time. Subsets remain animated in our modern human genomes, contributing to genetic diversity, heritable disease, and oncogenesis to degrees not well understood. Some of the most dynamic transposons are LINES, which multiply in the genome by “copy-and-paste” through an RNA intermediate. They have been difficult to study because: *(i.)* LINE prevalence in the genome precludes accurate copy number quantification, *(ii.)* LINE transcription cannot be accurately assessed by RT-PCR, Northern blots, or expression microarrays, *(iii.)* there are no robust, widely-available antibodies against LINE-encoded proteins, *(iv.)* many genome projects rely on sequencing strategies that fail to detect full-length, 6 kb LINE insertions and non-exonic insertions, and *(v.)* until now, no method for finding new insertions in the vastness of the genome was feasible. The Boeke laboratory previously reported a method to map Ty transposons in yeast by coupling a transposon insertion profiling (TIP) PCR with microarray amplicon analysis (TIP-chip). We now demonstrate that this approach can be applied to the human genome to identify positions of active T(a)LINE retrotransposons. The PCR strategy amplifies genomic DNA flanking T(a)LINE integration sites, and shows excellent discrimination between T(a)LINEs and older inactive LINEs. In addition to allowing genotyping for known T(a)LINE insertions, limited application of the technique has demonstrated numerous novel polymorphic insertions, as well as candidate disease-causing insertions in patients with heritable diseases whose specific sequence defects have been elusive. The technique is being scaled for comprehensive genome coverage for the evaluation of transposon instability in the development of solid tumors and leukemias. We expect this will add a new dimension to our understanding of structural variation in the human genome and provide new insights into human disease.