

**9th ANNUAL DEPARTMENT OF PATHOLOGY YOUNG INVESTIGATORS' DAY
POSTER SESSION**

**Thursday, April 5th, 2007
TURNER CONCOURSE
REGISTRATION FORM**

**E-mail COMPLETED Registration form and abstract to:
Stacey Morgan (smorgan9@jhmi.edu) on or before
Friday, March 16th, 2007**

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

Applicant's Name: Yu Li Degree: BA

Applicant's Division: _____

Faculty Preceptor: Dr. Jonathan Schneck
(Must hold a primary appointment in Pathology)

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

Register for: Clinical Research Translational Research Basic Research

Full Poster Title * Profiling the Mammalian Cell Surface Glycome

Where has the work been presented?

Meeting Name _____

Meeting Date _____

Not Previously Presented _____

Where is this work being published? _____

Journal Name, Volume, Page, Date _____

In Preparation _____

Author(s) (First & Last) Yu Li, Sheng-Ce Tao (Co-author), Jonathan Schneck, Heng Zhu

In-House Address: Ross Research Building, Room 664G
(Room # and Building Name, Lab, etc.)

Telephone: x4-0642 Beeper: _____

Fax: _____ E-mail: yxli@jhmi.edu

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

Glycosylation is one of the most complex posttranslational modifications with an extremely high level of diversity that has made it refractory to detailed analysis. To facilitate studies in glycosylation, we have developed a comprehensive lectin microarray for use as a high-throughput analysis of investigating cell surface glycosylation in mammalian cells. Using this approach, we have established a "GlycoCode" and hierarchical organization of 23 mammalian cell lines based on the profile of their surface glycan structures. We also show the potential use of this approach as a sensitive analysis of cell development and differentiation by probing immune system cells. Lectin microarrays represent a novel approach to high-throughput analysis of cell heterogeneity; the results of which can be used to studying diverse cell processes including cell development and differentiation, cell-cell communication, pathogen-host recognition, cell surface biomarker identification, and to aid in development of novel therapeutics.