### Technology Brief: Proteomics Signature Discriminating Common Adenocarcinomas

**Docket Number:** 05A014

#### Summary
- Cancer management stems from initial classification of the patient’s tumor.
- It is often difficult to identify the tissue site-of-origin of a metastatic cancer when no primary tumor has been identified, and few markers have been identified that allow such classification.
- Scientists at Moffitt Cancer Center have developed a protein-based classification system that discriminates six common types of adenocarcinoma.

#### Features and Benefits
- The classifier is based on global protein approach using two-dimensional gels for fractionation, enabling a thorough identification of reliable markers by mass spectrometry.
- Tumor samples were 77 human tumors from primary sites, improving the accuracy of the signature.
- Six common tumors were studied: ovary, breast, colon, kidney, lung and stomach.
- 173 proteins in the signature were found unique to individual tumor types, representing candidate tumor biomarkers for each type.
- The proteomics signature can be applied using other protein fractionation and detection methods.

#### Stage of Development
Proof of concept in six human tumor types. The signature is ready to be validated with a larger number of samples.

#### Inventor
Drs. G. Bloom, S. Eschrich, T. Yeatman and J. Zhou

#### Publication and Patent

#### Contact Information:

**Haskell Adler PhD MBA**  
Senior Licensing Manager  
Email: haskell.adler@moffitt.org  
Telephone: 813-745-6596

**H. Lee Moffitt Cancer Center and Research Institute, Inc.**  
Office of Technology Management and Commercialization  
12902 Magnolia Drive MRC-TTO  
Tampa, FL 33612  
Website: [http://www.moffitt.org/OTMC](http://www.moffitt.org/OTMC)