**Technology Brief:** Proteomics Signature Discriminating Common Adenocarcinomas

**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.

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**Publication and Patent**
- Patent application pending.

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