MOFFITT CANCER CENTER

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	G. Bloom et al. (2006) Int. J. Cancer 120:769-775. Patent application pending.

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