BROWN TECHNOLOGY INNOVATIONS

# Methylation Cytometry Diagnostic for Immuno-Oncology

## Overview

DNA methylation-based biomarkers have great potential to transform the diagnosis, monitoring, and treatment of cancer and other diseases. DNA methylation is an epigenetic mechanism used by cells to control gene expression. During DNA methylation, methyl groups are added to the DNA molecule, changing the DNA activity but not the sequence. Errors in methylation have been linked to a variety of diseases. Currently, clinicians use DNA methylation tests to screen for certain genetic changes that can affect processes such as methionine metabolism and hormone balance.

## Market Opportunity

Few DNA methylation-based biomarkers have been successfully translated into clinical practice. There is limited technology to assess epigenetic information cost effectively at a large scale. Leukocytes, or white blood cells, mount the immune response to pathogens and foreign antigens. Until now, the distribution of leukocytes has been determined by examination under a microscope or with a flow cytometer. Flow cytometry is limited by the availability of fluorescent antibody tags, the labor-intensive process of antibody tagging, and the need for large volumes of fresh cells.

## Innovation and Meaningful Advantages

With our cost-effective, versatile invention, DNA methylation analysis is not limited to tissue specimens and can be easily extended to most bodily fluids. Our invention quantifies alterations in the distribution of cells in blood or tissue, using both fresh and archival samples. Eventually, our invention may be modified not only to diagnose, prognose, and monitor cancer, but to treat it.

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## Collaboration Opportunity

We are interested in exploring 1) startup opportunities with investors in the diagnostic space; 2) research collaborations with leading immuno-oncology companies to develop this tool for patient identification and stratification; and 3) licensing opportunities with diagnostic companies.

## Principal Investigator

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## IP Information

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## Publications

Houseman EA, Accomando WP, KoestlerDC, Christensen BC, Marsit CJ, Nelson HH, Wiencke JK, Kelsey KT. DNA methylation arrays as surrogate measures of cell mixture distribution. *BMC Bioinformatics* 13, 86. 2012 May 08;13. Doi.org/10.1186/1471-2105-13-86.

Michaud DS, Mengyuan R, Koestler DC, Alonso L, Molina-Montes E, Pei D, Marsit CJ, De Vivo I, Malats N, Kelsey KT. DNA Methylation–Derived Immune Cell Profiles, CpG Markers of Inflammation, and Pancreatic Cancer Risk. *Cancer Epidemiology, Biomarkers & Prevention.* 2020 Aug;29(8). Doi: 10.1158/1055-9965.EPI-20-0378.

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