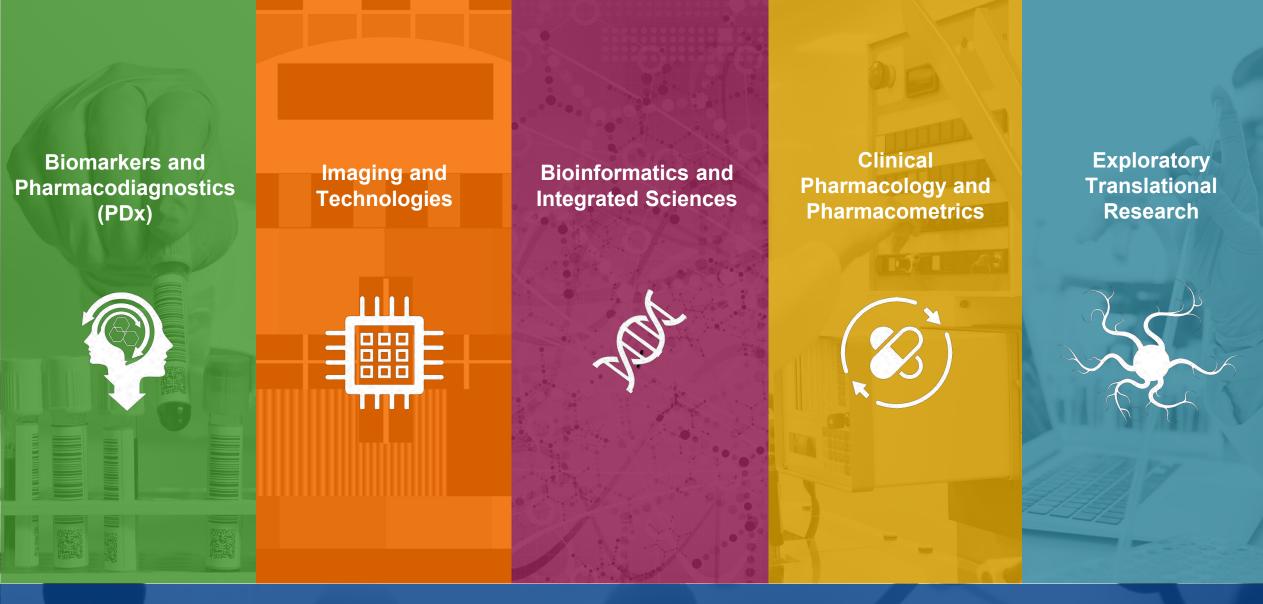
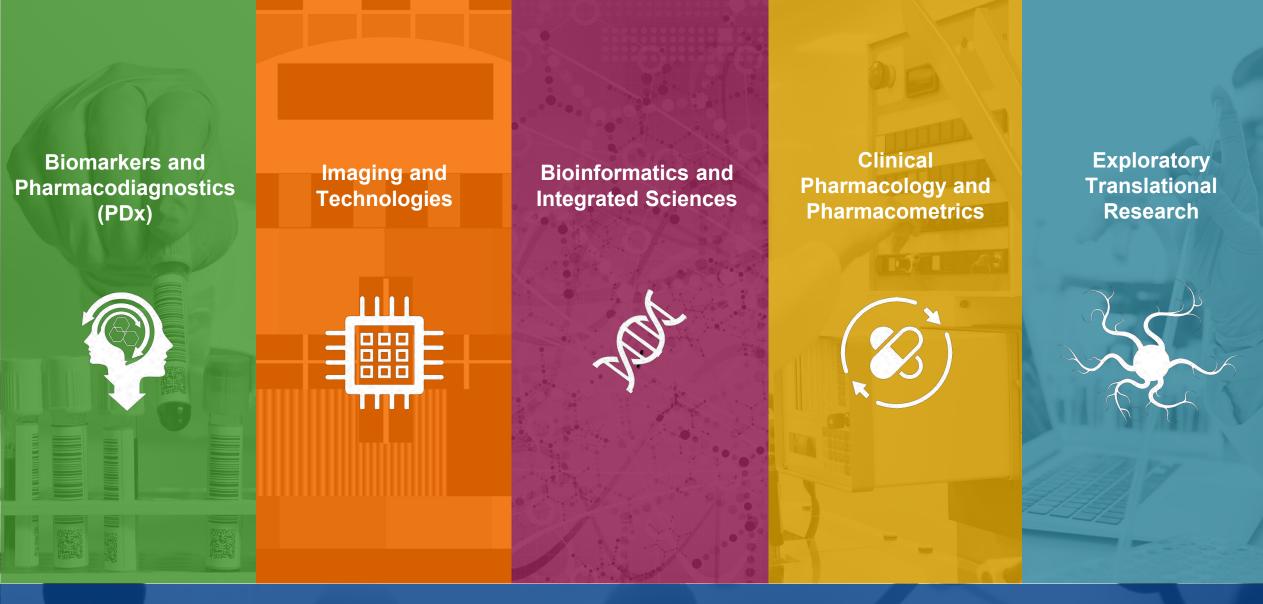
Bristol-Myers Squibb

Bristol-Myers Squibb is actively conducting translational medicine research to further our understanding of cancer biology and to identify which patient populations may be more likely to derive benefit from Immuno-Oncology (I-O) agents.



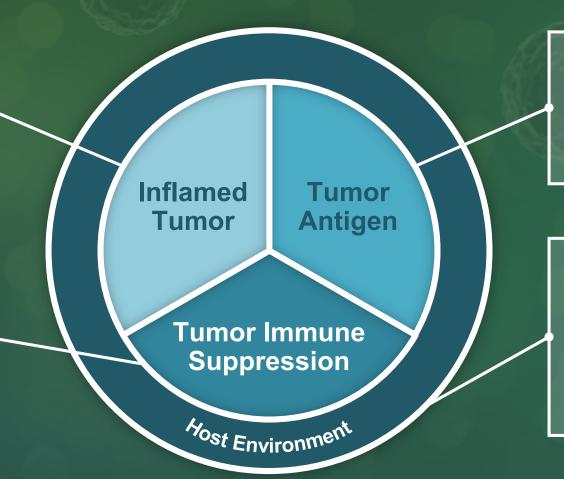






Inflamed Tumor Microenvironment: Biomarkers within the tumor, T cells or microenvironment that may predict response

Tumor Immune Suppression: Biomarkers related to mechanisms of resistance via specific immune pathways that may be addressed with I-O treatment



Tumor Antigens: Biomarkers to identify hypermutation and neoantigens that may predict response to I-O

Host Environment: Biomarkers to characterize the host environment, beyond the tumor microenvironment, which may reveal immune-related mechanisms predictive of response

Pharmacodiagnostics (PDx):

Inflamed Tumor Microenvironment: Biomarkers within the tumor, ⁻ cells or microenvironment tha may predict response

For example, PD-L1 is expressed in a variety of healthy cell types and tumor cells. PD-L1 binds to the PD-1 receptor on T cells, inhibiting T cell activation.¹⁻² PD-L1 may be expressed only on a portion of the tumor cell and expression levels may change over time.³

CLICK TO VIEW VIDEO >

Tumor Immune Suppression: Biomarkers related to mechanisms of resistance via specific immune pathways that may be addressed with I-O treatment

Tumor Immune Suppression

Tumor

Antigen

Most Environment

Tumor Antigens: Biomarkers to identify hypermutation and neoantigens that may predict response to I-O

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> Inactive T cell CSF1 CSFIR Inmunosuppressive factors Tumor-associated macrophage

For example, CSF1R is a receptor on the surface of macrophages and other cells of the myeloid lineage.¹ High levels of CSF1, the ligand for CSF1R, may indicate that tumors are using CSF1R pathway to drive immunosuppression.²⁻⁴

Inflamed Tumor Antigen Tumor Immune Suppression

R is a receptor nacrophages and nyeloid lineage.¹ 1, the ligand for the that tumors

rmacodiagnostics (PDx):

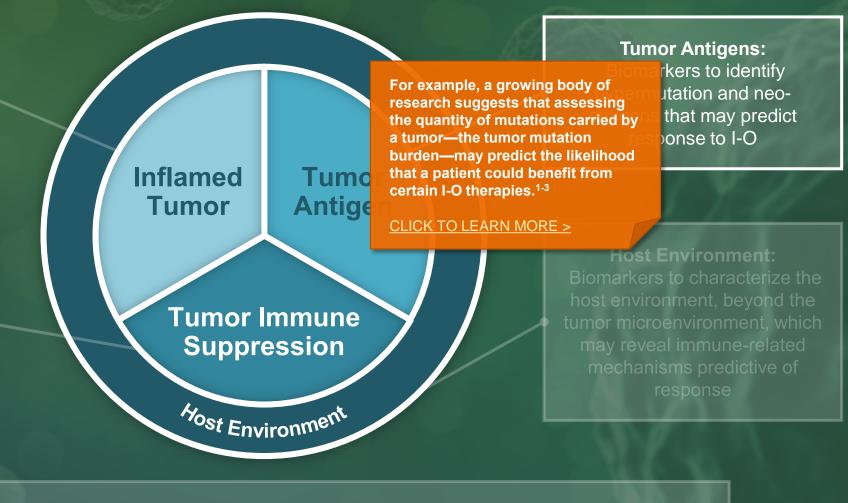
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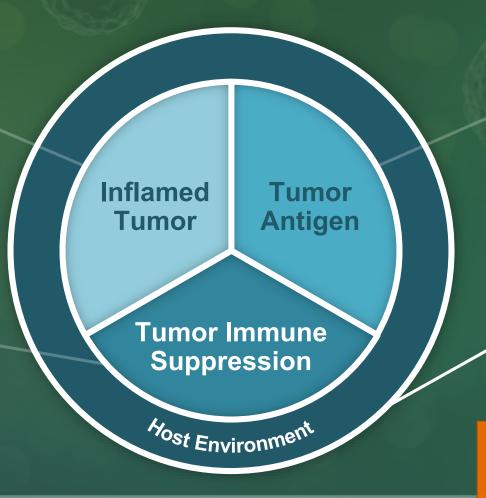
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For example, markers in microorganisms (i.e., microbiome) may play a role in developing resistance to I-O treatment¹

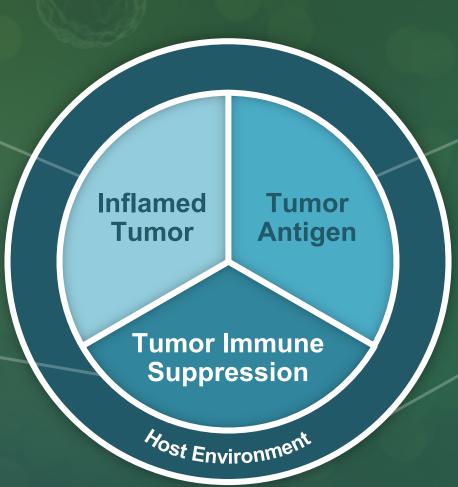


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Pharmacodiagnostics

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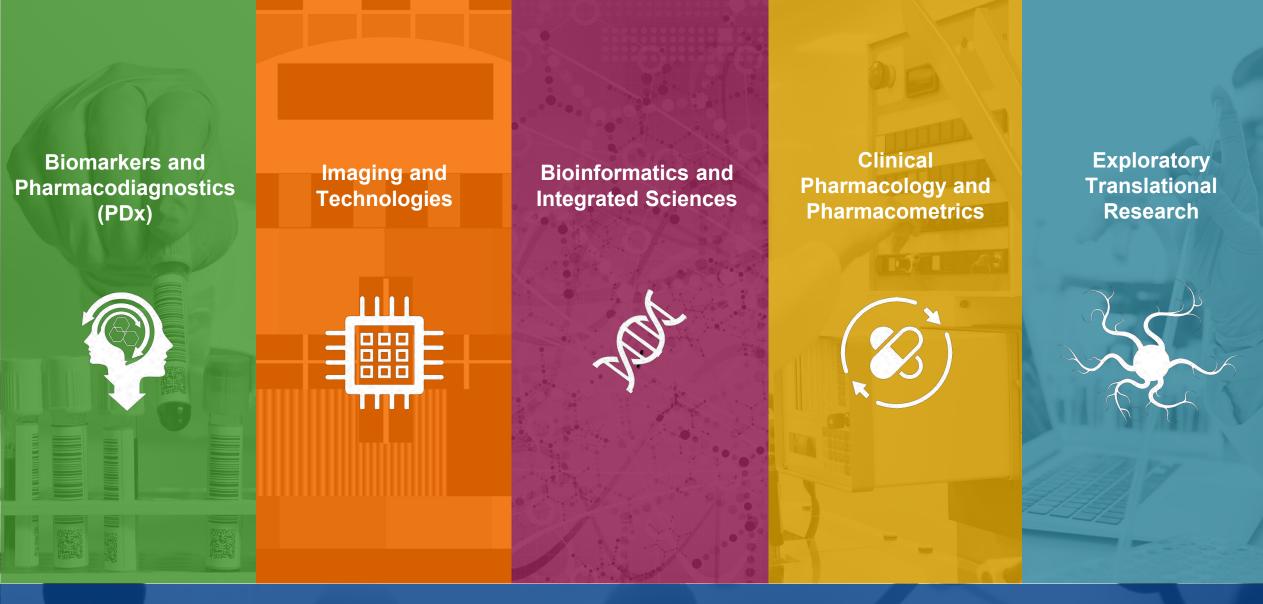
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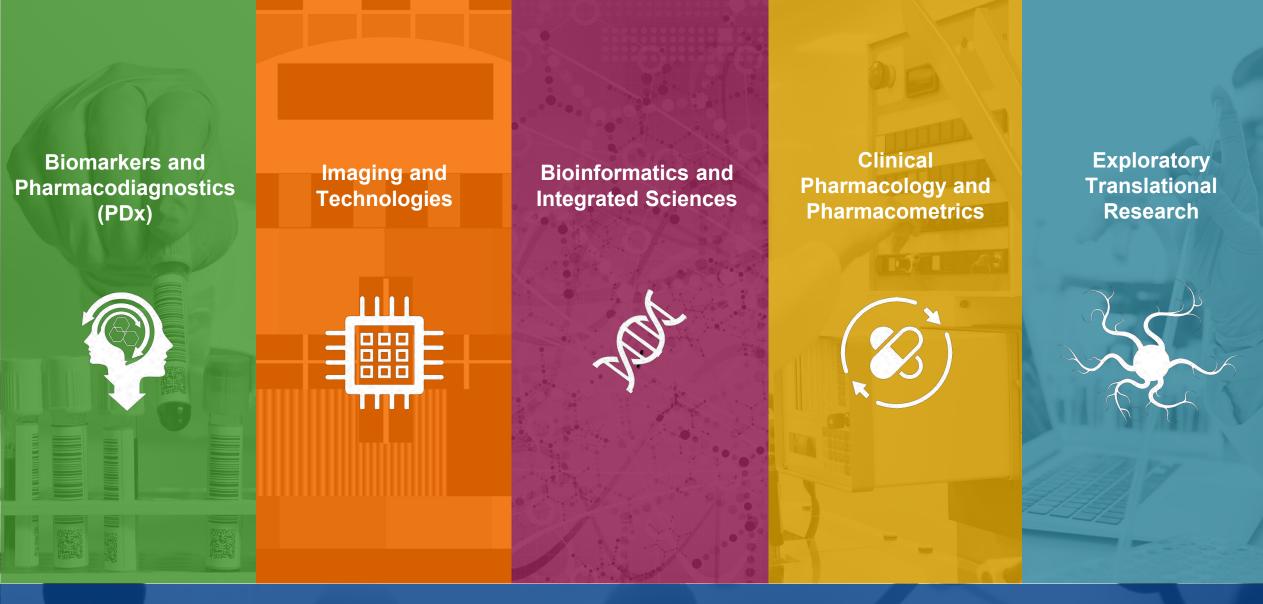


PD-L1 assays are in vitro diagnostic tests used to detect PD-L1 in certain types of cancer. This test can help determine appropriate treatment. ¹

Pharmacodiagnostics (PDx):











IMAGING

Molecular imaging allows researchers to study specific targets and guide treatment decisions without invasive procedures

GENOMICS & GENETICS

Mapping, characterizing and quantifying gene expression and mutations to allow for a deeper understanding of disease biology and mechanisms of drug response

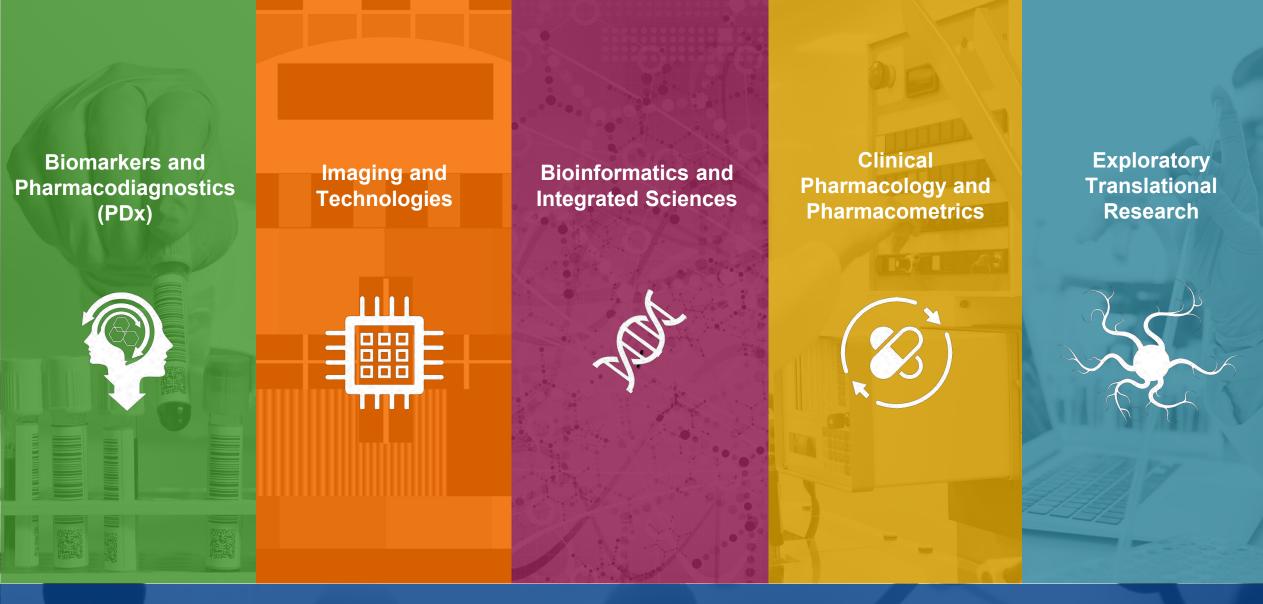
FLOW CYTOMETRY & FUNCTIONAL BIOLOGY

Method of single-cell analysis that allows for cell sorting, detection of disease biomarkers and a better understanding of cell biology

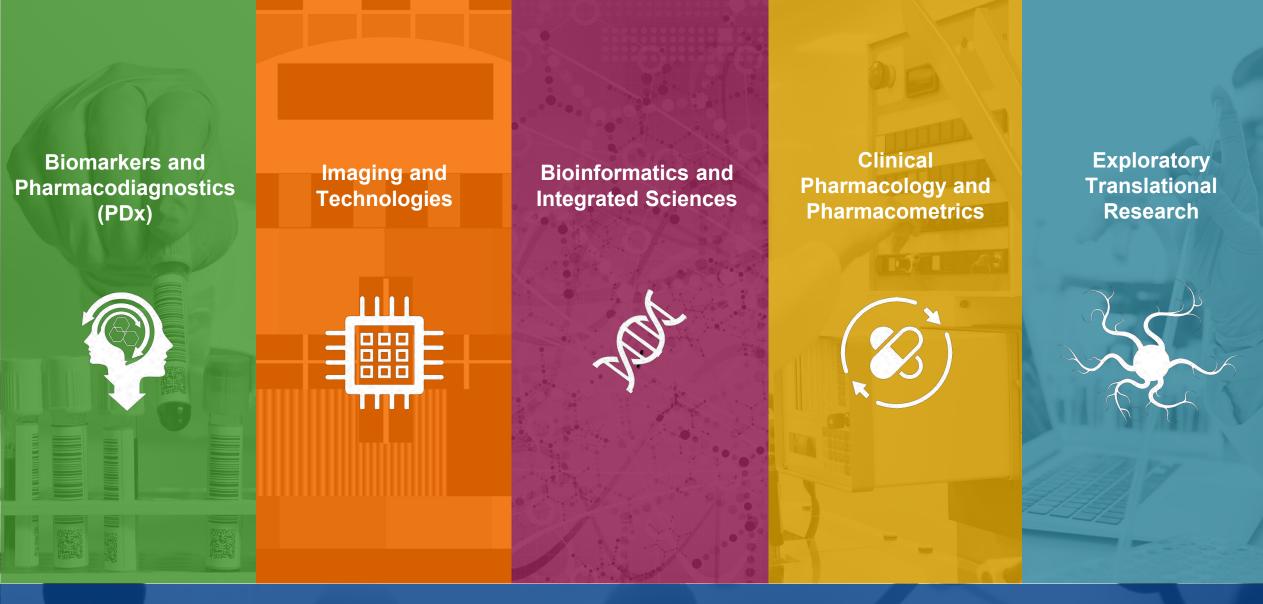


SAMPLE MANAGEMENT

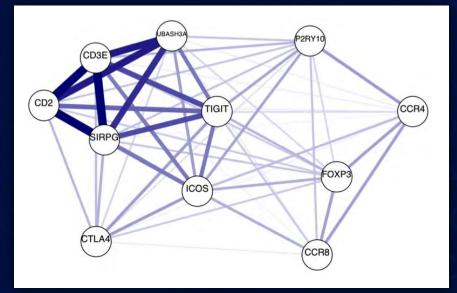
System for storing and organizing samples for efficient future use



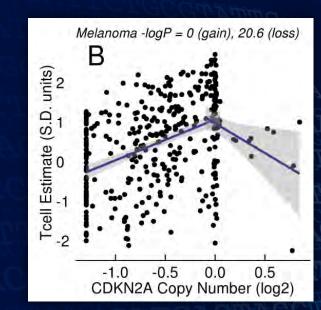








Gene expression network derived from analysis of TCGA RNA sequencing data



GGAAGCA

TDDDATS

AGUARGACAGA

NAGATEGAGEC?

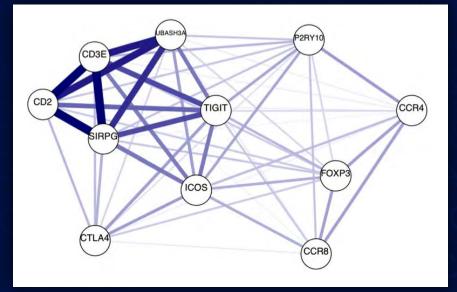
TCGGTCCTGCT

CAGGIGI

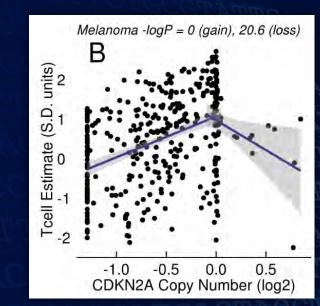
Loss of CDKN2A is associated with reduced estimates of T cells in the tumor microenvironment in some cancers

Our Translational Bioinformatics team uses cutting-edge methods to perform integrative data analysis. We study the interplay of tumor genomes, their regulation and the tumor microenvironment to further our understanding of response to I-O agents.

Our comprehensive analysis of The Cancer Genome Atlas (TCGA) identified networks of co-expressed genes that can be used to identify specific types of immune cells in the tumor microenvironment. In some tumors, certain genetic mutations correlate with the abundance of such cells.



Gene expression network derived from analysis of TCGA RNA sequencing data



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Our comprehensive analysis of The Cancer Genome Atlas (TCGA) identified networks of co-expressed genes that can be used to identify specific types of immune cells in the tumor microenvironment. In some tumors, certain genetic mutations correlate with the abundance of such cells. Our team analyzes tumor mutation burden, RNA sequencing, serum cytokine, and other large-scale biomarker data sets generated from clinical trials.

Partnerships with leading data bioinformatics companies enhance

our in-house capabilities.

TEDDDARK

GGAAGCP

MAGATEGAGGC

The mandate of integrated sciences is to integrate, analyze and synthesize data derived from both external and internal studies addressing fundamental translational questions in I-O to develop actionable insights and hypotheses that help drive discovery and clinical development

300

250

200

150

100

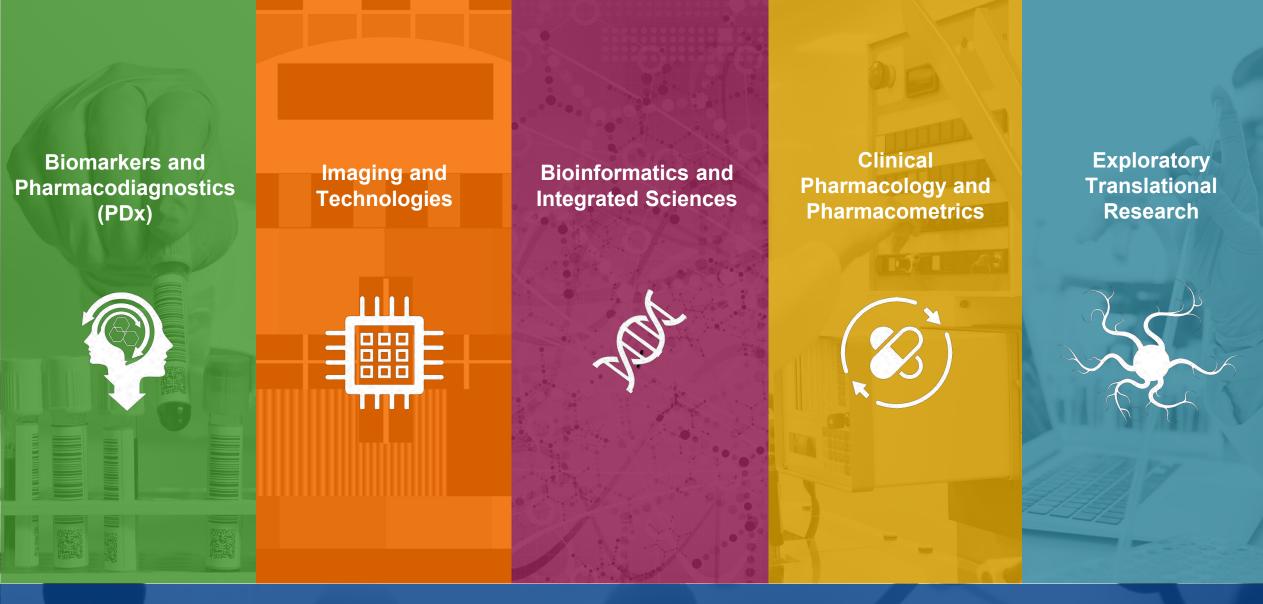
GG-17

100ml

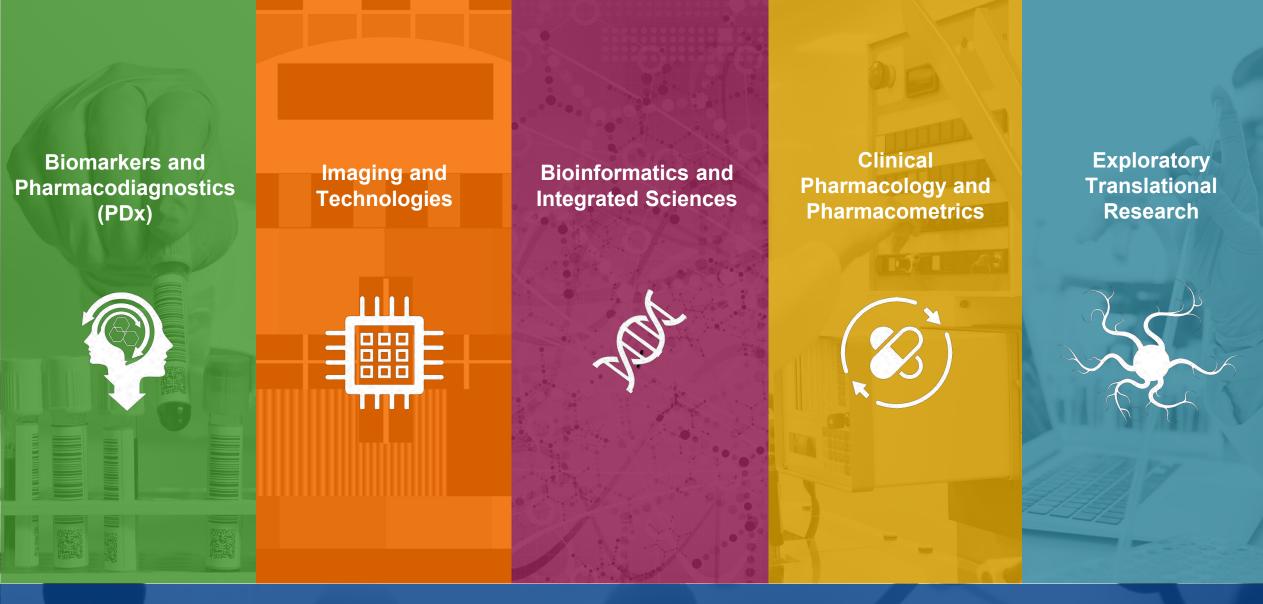
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100

APPROX

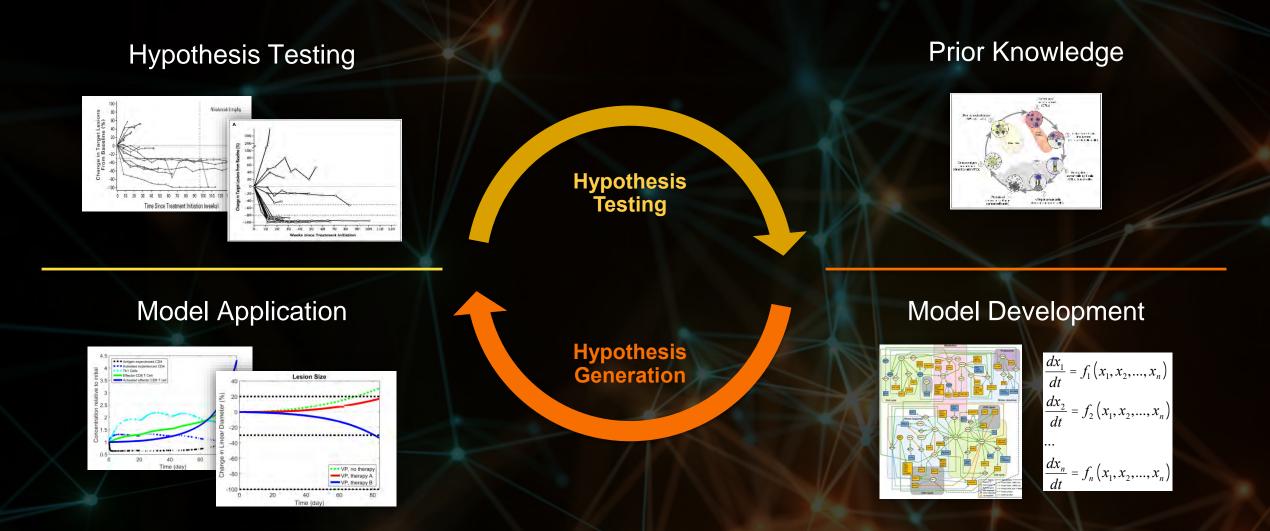




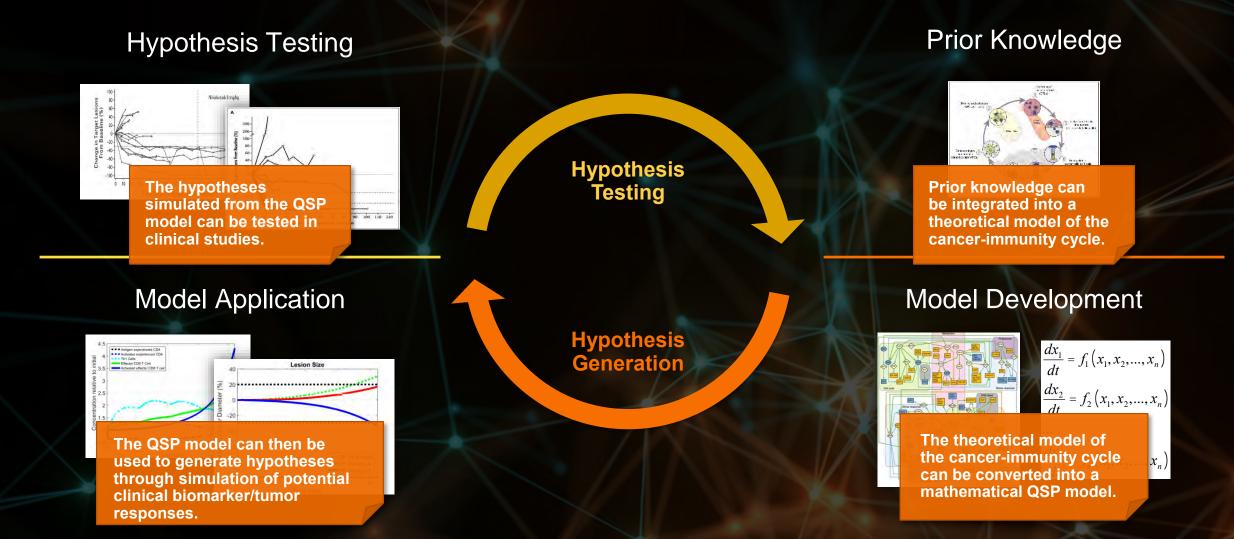


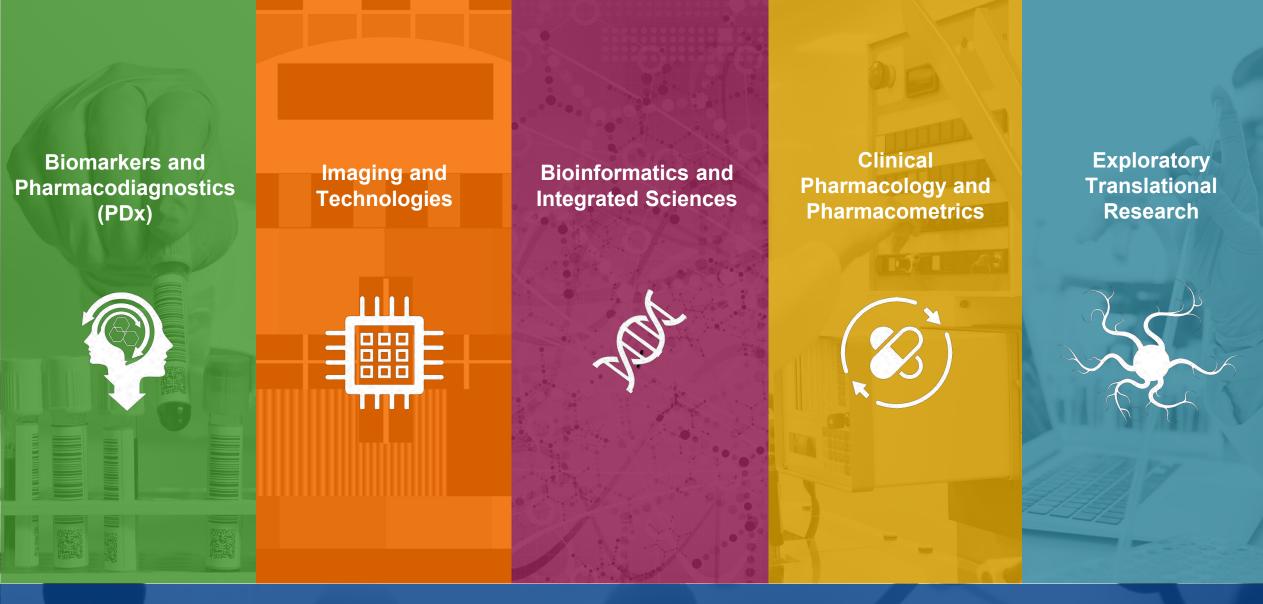


Mechanistic Modeling (QSP) Fuels New Questions and Continued Exploration in Immuno-Oncology

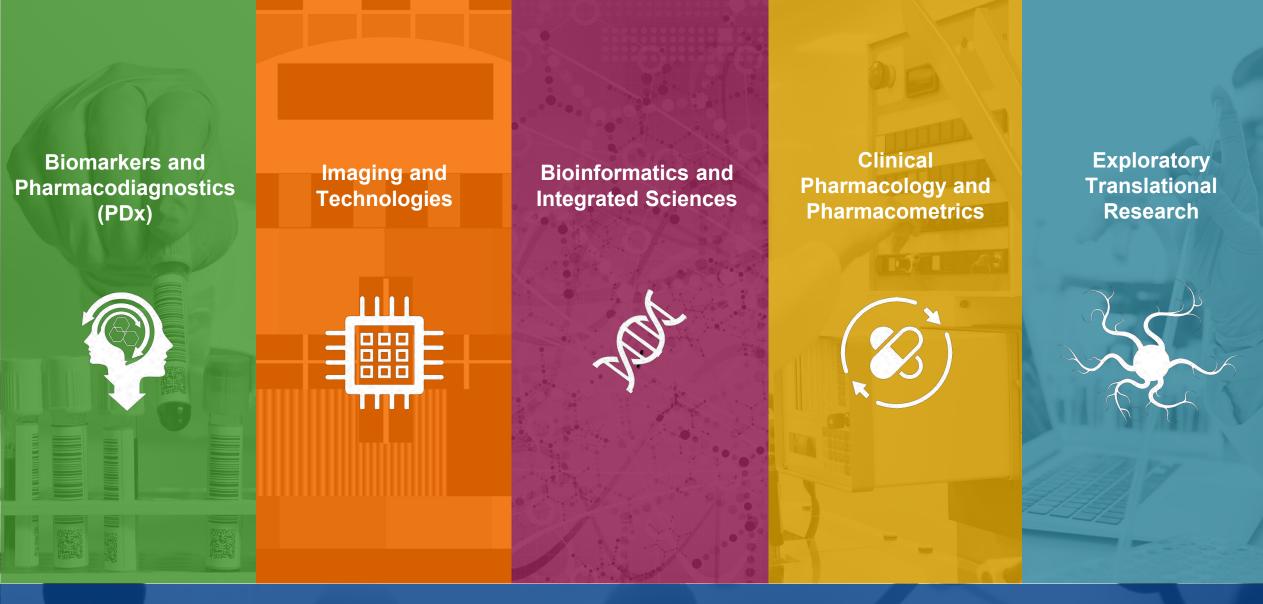


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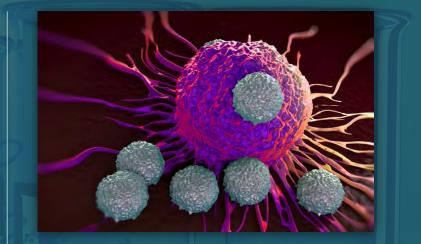




Experimentation provides the knowledge and data to form hypotheses that can be tested in the clinic



We leverage existing and advanced clinical assays to explore and test new hypotheses using biologic samples



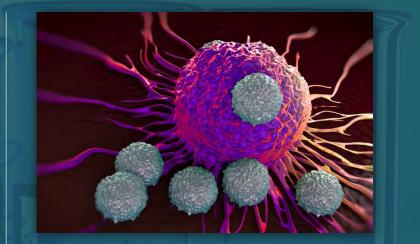
Insights gained from this research can quickly be implemented in prospective clinical trials to enhance and accelerate our pipeline



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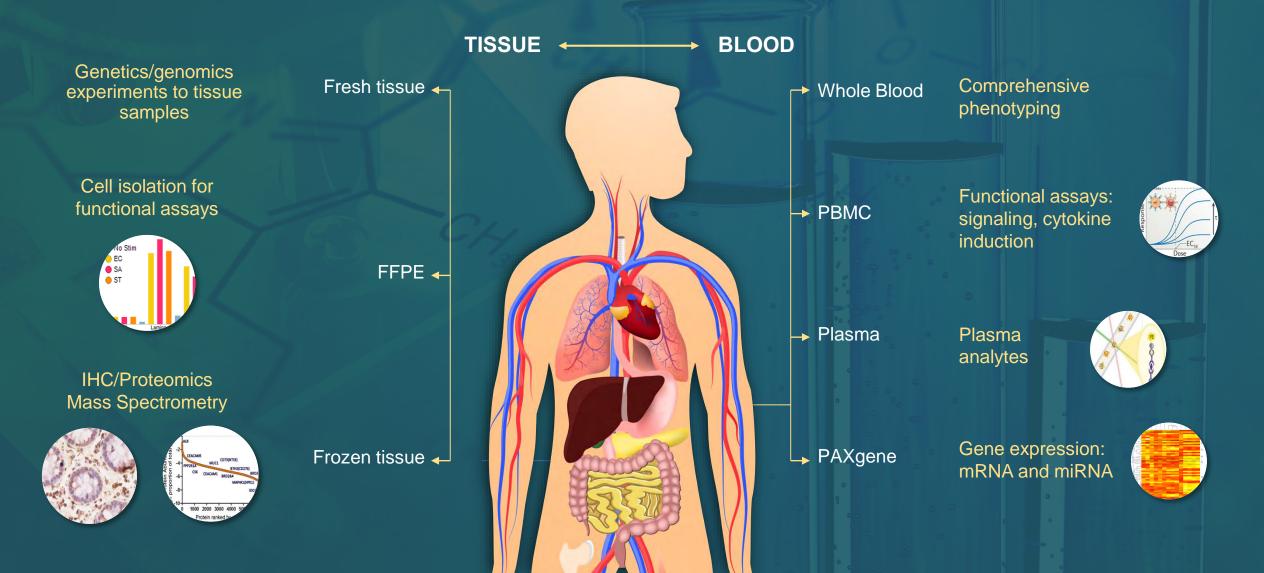


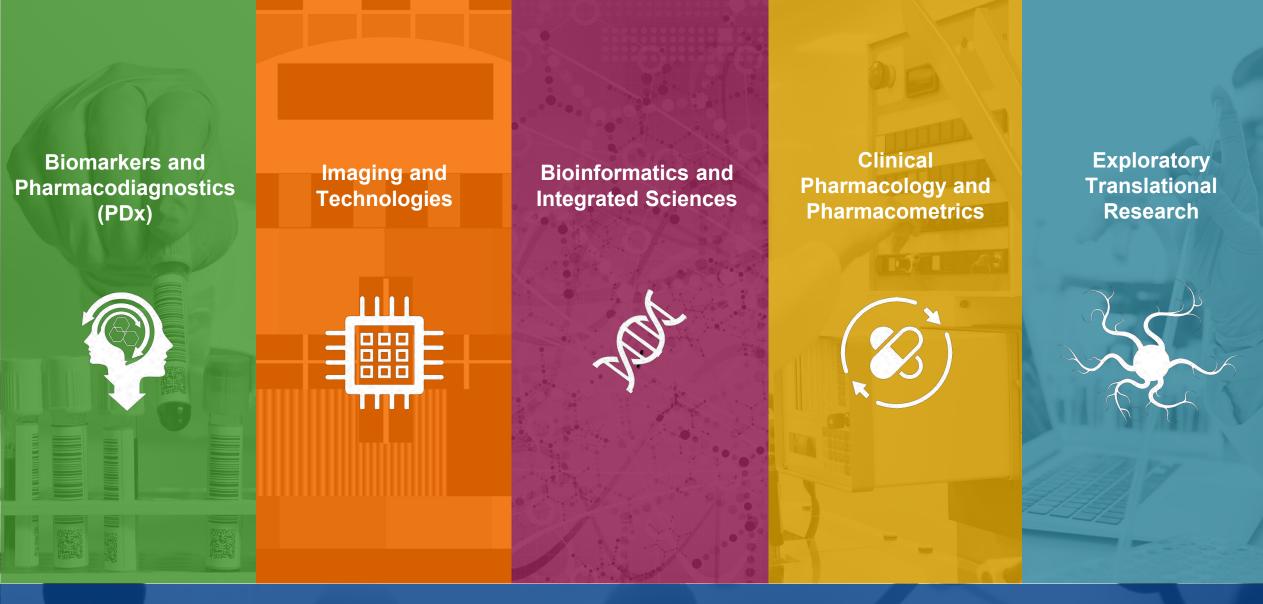
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SINGLE CELL GENOMICS:

Leveraging next generation technologies to examine sequence information from individual cells. PROTEOMICS: Study of proteins and how they interact within tumor microenvironment.

Conducting Research to Understand the Immune System in Patients with Cancer













Our scientific collaborations with academic centers around the globe expand our research capabilities and accelerate our collective ability to advance the science.



We seek to partner with other I-O experts to expand our translational medicine capabilities.



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A global peer-to-peer collaboration between Bristol-Myers Squibb and academia that aims to advance I-O science and translational medicine to benefit patients.

CLICK TO LEARN MORE>



Research collaborations with select European research institutions to appropriately accelerate, expand and more effectively advance I-O research.



We seek to partner with other I-O experts to expand our translational medicine capabilities. Working with partners like <u>Foundation Medicine</u> and <u>GRAIL</u> helps to drive the identification, validation and application of predictive biomarkers. Our robust translational medicine program informs key areas of research, including:



Disease targeting and responsive patient segmentation



Ideal treatment strategies, including combinations, for each patient



Optimal dosing, schedule and clear understanding of MOA

