



ProFACT
PROTEOMICS
MAKING A FUNCTIONAL DIFFERENCE

SeraFILE™

Proteomic connections to function, small molecule modulation, and gene expression

BIONJ BioPartnering 2010

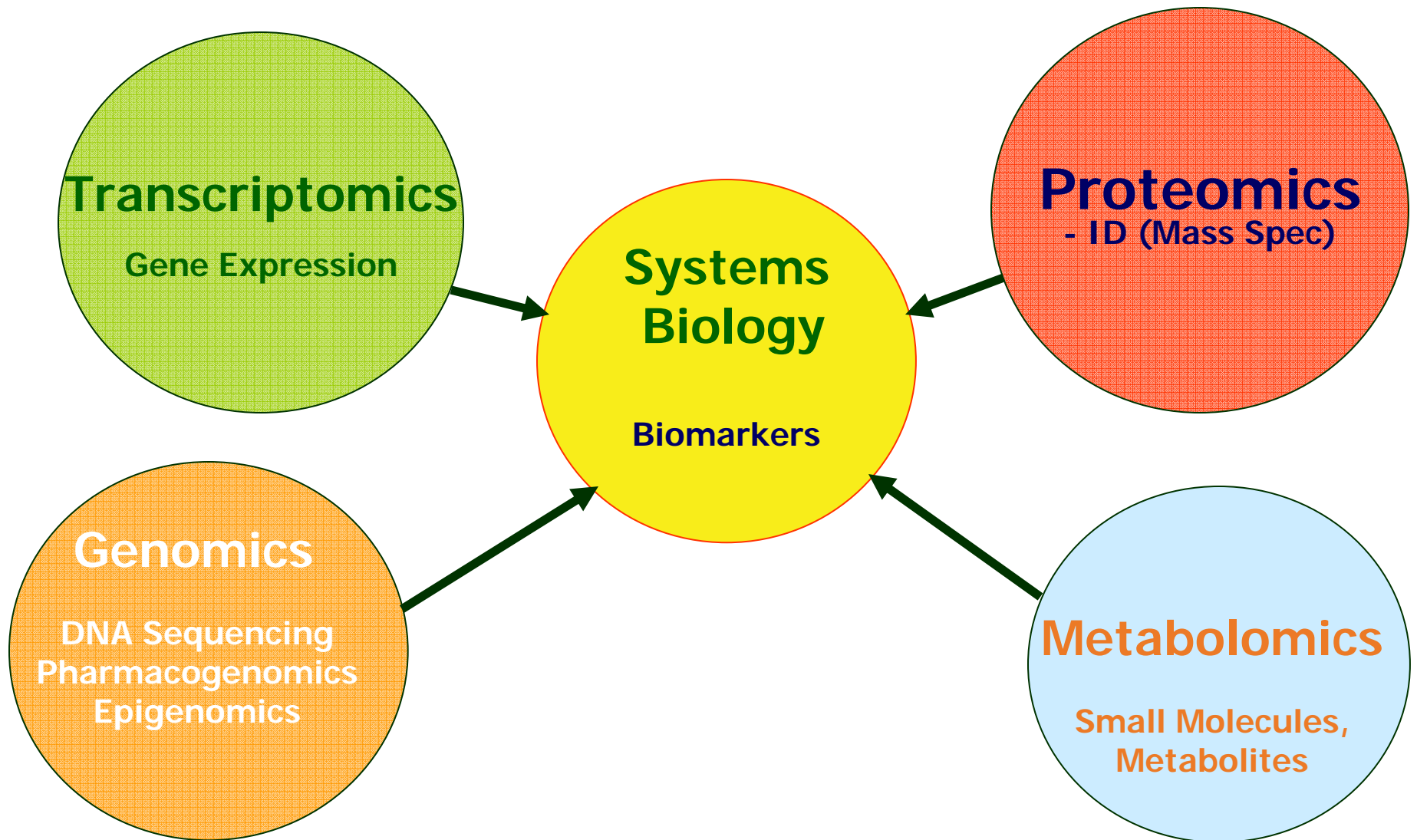
June 14, 2010

About ProFACT Proteomics, Inc.

- **Early stage**
- **3 Patents Pending surrounding SeraFILE™**
- **5 New Jersey CST Grants**
- **HT Functional Proteomics Infrastructure**
- **Molecular Profiling and Discovery Services,
Transferable Protocols & Consumable Reagents**
- **Partners and Collaborators sought in Industry and
Academia**

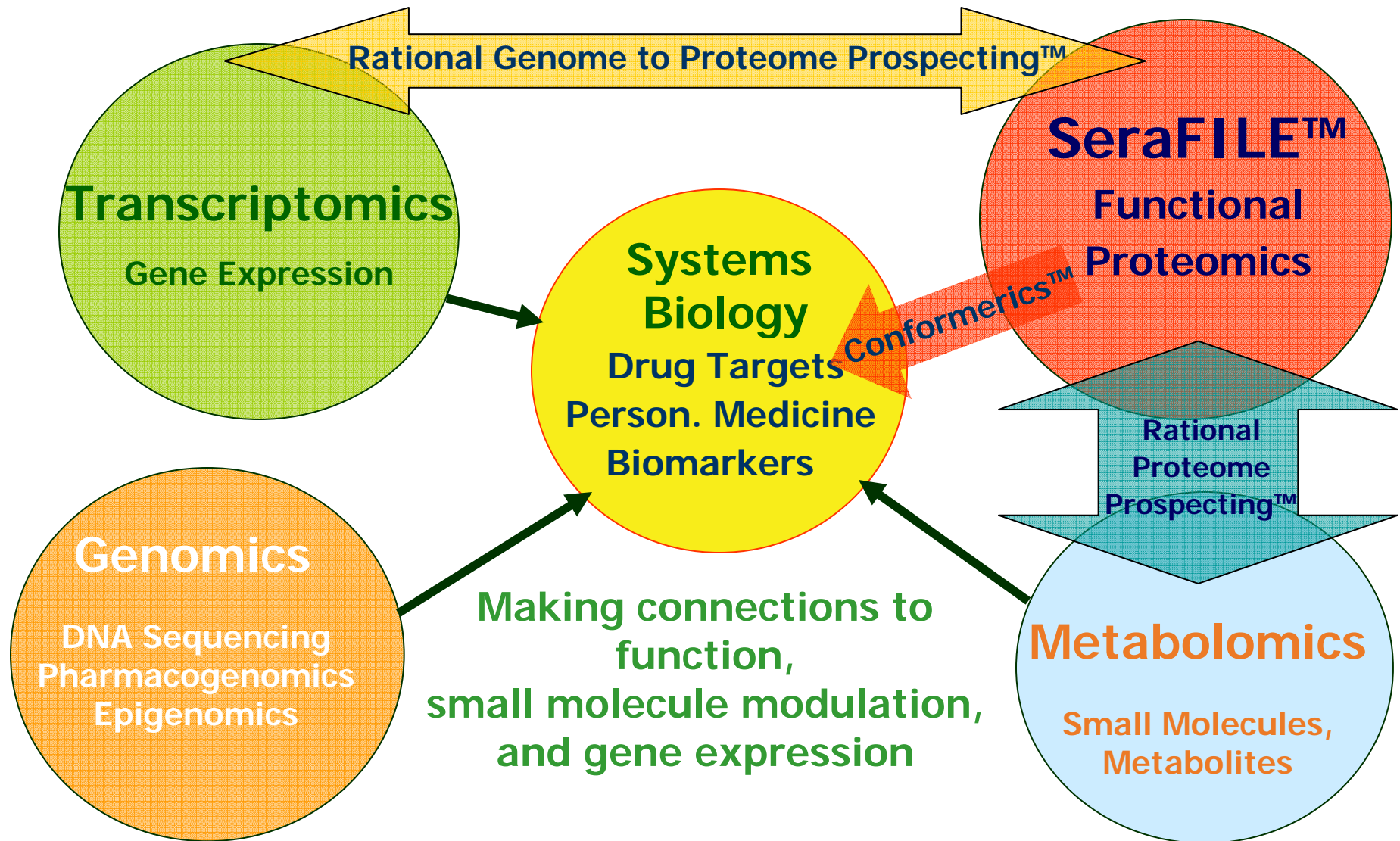
**1 Deer Park Drive, Suite P
Monmouth Junction, NJ 08852
www.profactproteomics.com**

The "Omics" Information Universe



The SeraFILE™ "Omics" Information Universe

Functional Profiling, not Mass Spec. Driven



SeraFILE™

A Biomarker and Drug Discovery Engine

**Efficiently Combines Protein Complexity Reduction
with Functional Preservation**

Purpose

**Overcomes the disconnect between Proteomics and
functional mechanisms.**

SeraFILE™

A Biomarker and Drug Discovery Engine

Efficiently Combines Protein Complexity Reduction
with Functional Preservation

Purpose

Overcomes the disconnect between Proteomics and functional mechanisms.

Utility

Simultaneously surveys the functional characteristics of a target protein set.

- Pure discovery - differentiating features through comparison of sample sets.
- Enrichment strategies for client target proteins.

SeraFILE™

A Biomarker and Drug Discovery Engine

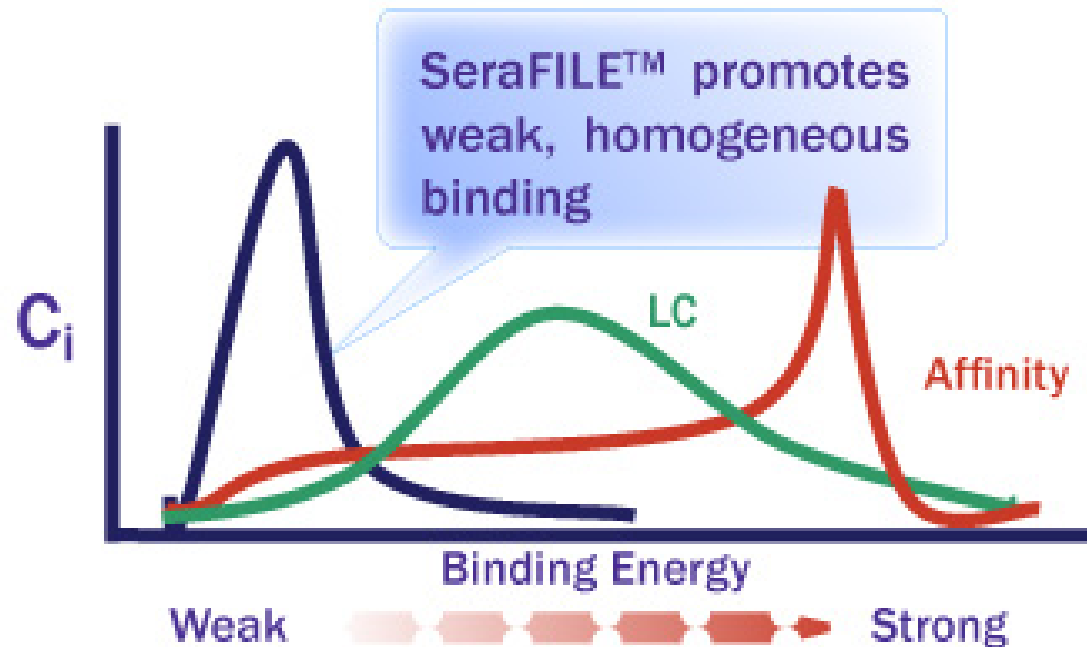
Efficiently Combines Protein Complexity Reduction
with Functional Preservation

Unique Enablement

- compartmentalizes conformational variants
- compares sub-proteome kinetics between samples

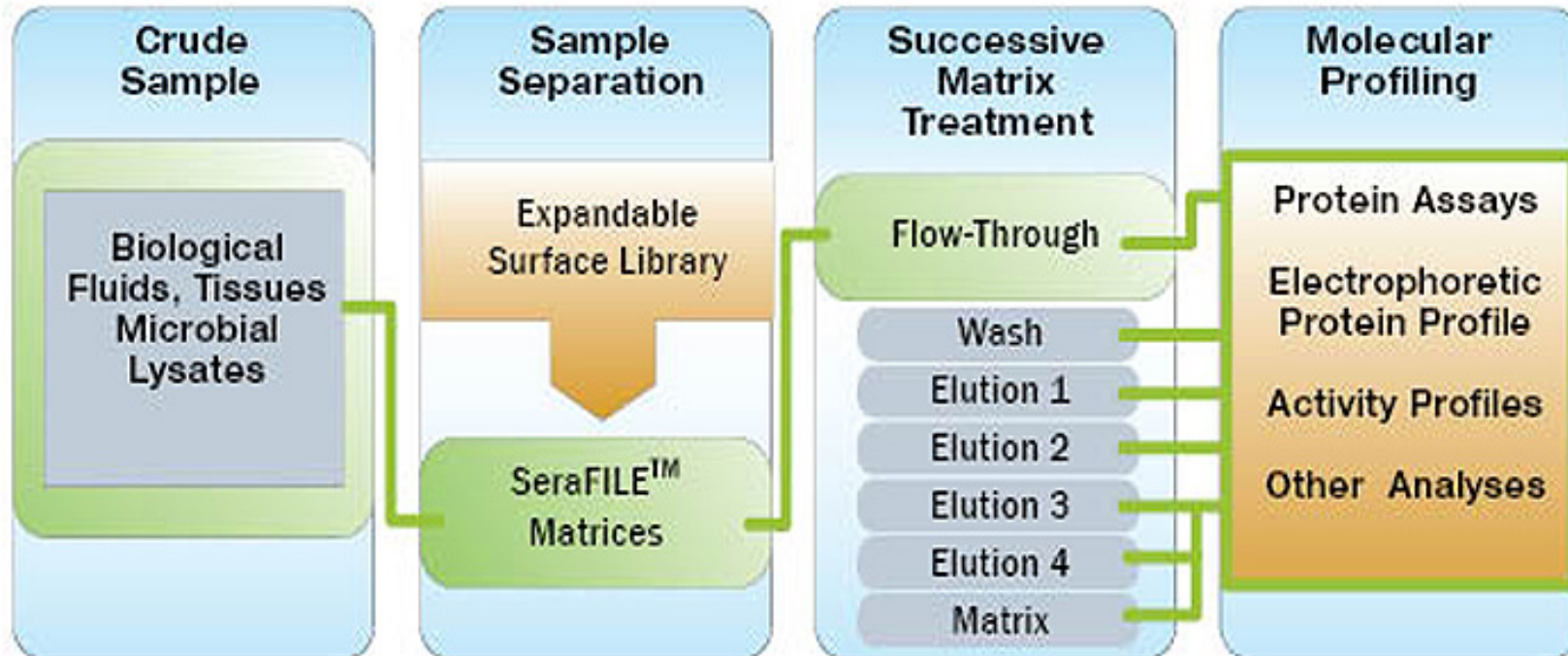
SeraFILE™ provides critical data for drug development

SeraFILE™ Surface Library



- **Surface Interactions** - mixed mode (ionic, aliphatic, aromatic, polymer) presentation/architecture modulates selectivity
- **Mild Elution, Retains function, Direct Hand-off, Universal**

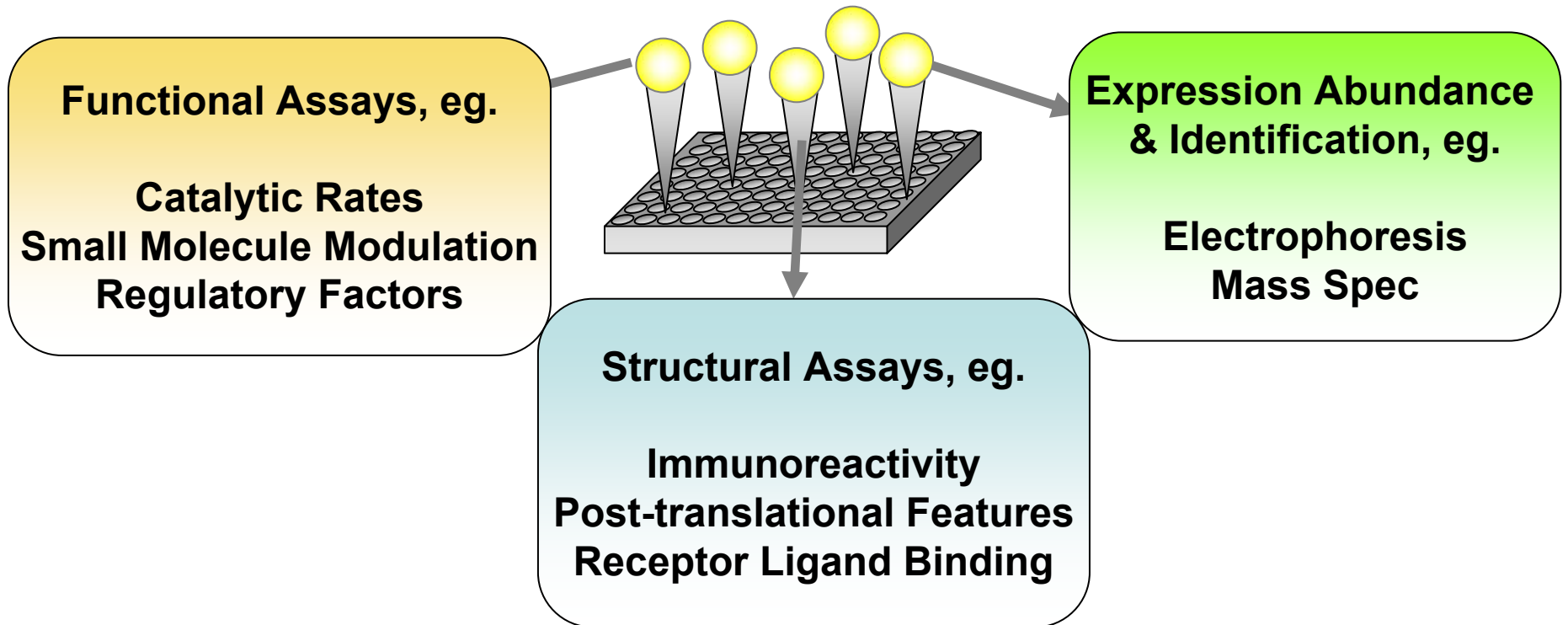
SeraFILE – Subfractionation Process



- Preserves and Observes the Entire Proteome
- Preserves functional characteristics of derivative sub-proteomes
- Differentiates “Close Cousins” and Conformational Variants
- Separations 1 hour, parallel protocols

Follow-on Interrogation Options

● SeraFILE™ Differential Sub-proteomes



Molecular profiles can correlate these measurements.

ProFACT extrapolates three prospecting strategies

SeraFILE™

Key Advantages Provide New Prospecting Strategies

I. Rational Proteome Prospecting™

for target discovery and enrichment

- iteratively scores direct and indirect measurements of function

II. Conformerics™

for differentiating, profiling and enriching conformational variants and close cousins

- compartmentalizes functional characteristics, kinetic activity and small molecule modulation
- new drug development paradigm – develop assays for functional variants at lower stoichiometry and higher specificity

III. Rational Genome to Proteome Prospecting™

- bridges the disconnect between gene and protein expression for biomarker discovery

SeraFILE™

Proteomic connections to function, small molecule modulation, and gene expression

Enrichment Strategies

Specific Activity

- Immunological
- Catalytic Rates
- Conformation Variants
- Cellular Response

Purification

Identification/Characterization

Discovery

Comparisons - Cell Models

- Environmental Stimuli
- Oxygen Stress
- Interfering RNA
- Drugs

Comparison of Normal/Disease

- Tissue
- Blood/Serum

ProFACT-MGL Biomarker Discovery

A Collaboration in Rational Genome to Proteome Prospecting

MGL Americas

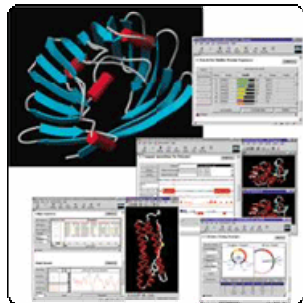
Diversified IT Solutions Provider

www.mgl.com

Query Results
(list of genes)

Gene Data
(complete info)

Genome



Information

The screenshot displays the OncoMaster software interface. The main window shows search results for BRCA1, including a table of query results and a detailed view of the BRCA1 gene. The detailed view includes fields for Gene ID/Alias, Gene Name, Gene Category, Protein Class, Subcellular Location, Domains, Cancer type, and Pathways. A separate window shows a pathway diagram for G2/M DNA Damage Checkpoint State, and another window shows a 3D X-ray diffraction structure of a protein.

No.	Gene Name	Chromosomal Location	Sub Cellular Location	Pathway	Cancer Type	E.C.
1	Tumor Protein p53 (Li-Fraumeni Syndrome)	17p13.1	Nucleus	SAPK/JNK Signaling Cascades Mitochondrial Control of Apoptosis ATM Signaling Pathway Cell Cycle G2M Checkpoint Cell Cycle G1/S Check Point G1/S Checkpoint state G2M DNA Damage Checkpoint State	Colorectal cancer	
2	Breast Cancer 1, early onset	17q21	Nucleus	ATM Signaling Pathway Cell Cycle G2M Checkpoint G2M DNA Damage Checkpoint State	Breast cancer 1 Ovarian cancer Breast-ovarian cancer	

BRCA1 Details:

- Gene ID/Alias: BRCA1/PSCP
- Gene Name: Breast Cancer 1, early onset
- Gene Category: Tumour Suppressor Genes
- Protein Class: Alpha and beta proteins (a/b)
- Subcellular Location: Nuclear
- Domains: Ring finger ; Zinc finger ; BRCA1 C Terminus (BRCT) domain ; breast cancer carboxy-terminal domain
- Cancer type: Breast cancer-1 ; Ovarian cancer ; Breast-ovarian cancer
- Pathways: G2-M DNA Damage Checkpoint State

Pathway images

2D-Gel images

3D structure visualization

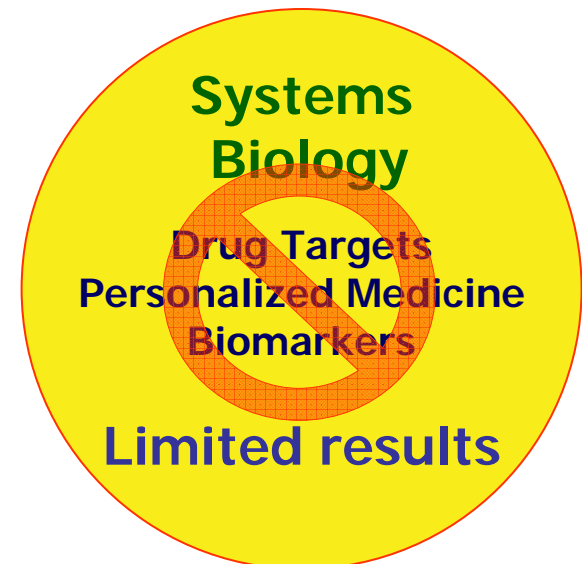
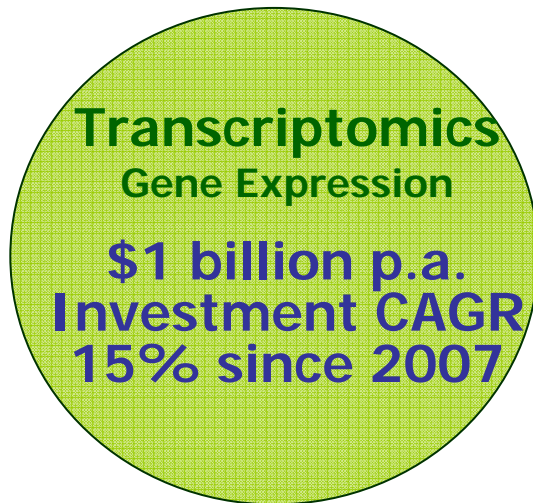
Individualized Healthcare



Molecular Medicine

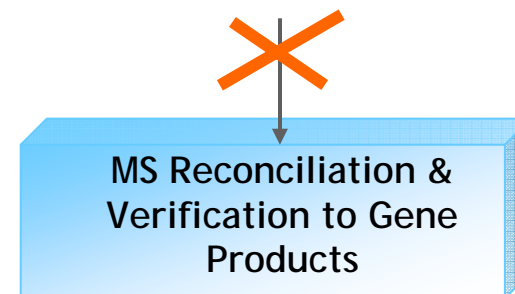
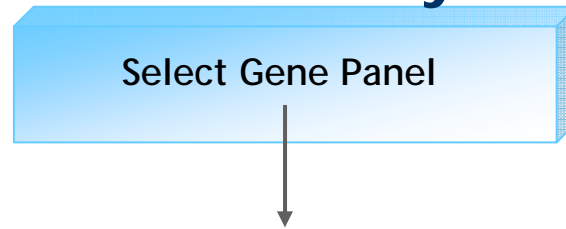
Industry Pain

-the disconnect between gene and protein expression for biomarker discovery



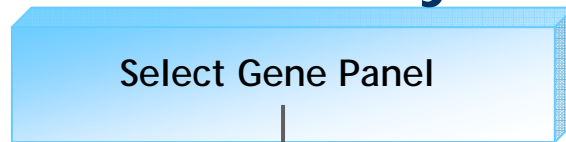
Industry Pain

-the disconnect between gene and protein expression for biomarker discovery



Industry Pain

-the disconnect between gene and protein expression for biomarker discovery



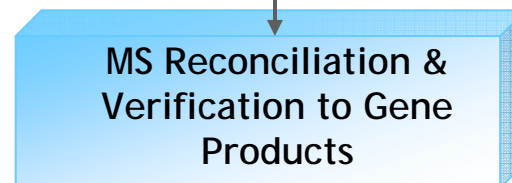
- mRNA expression poorly correlates with protein expression
- Both Biology & Detection components contribute:

Biology

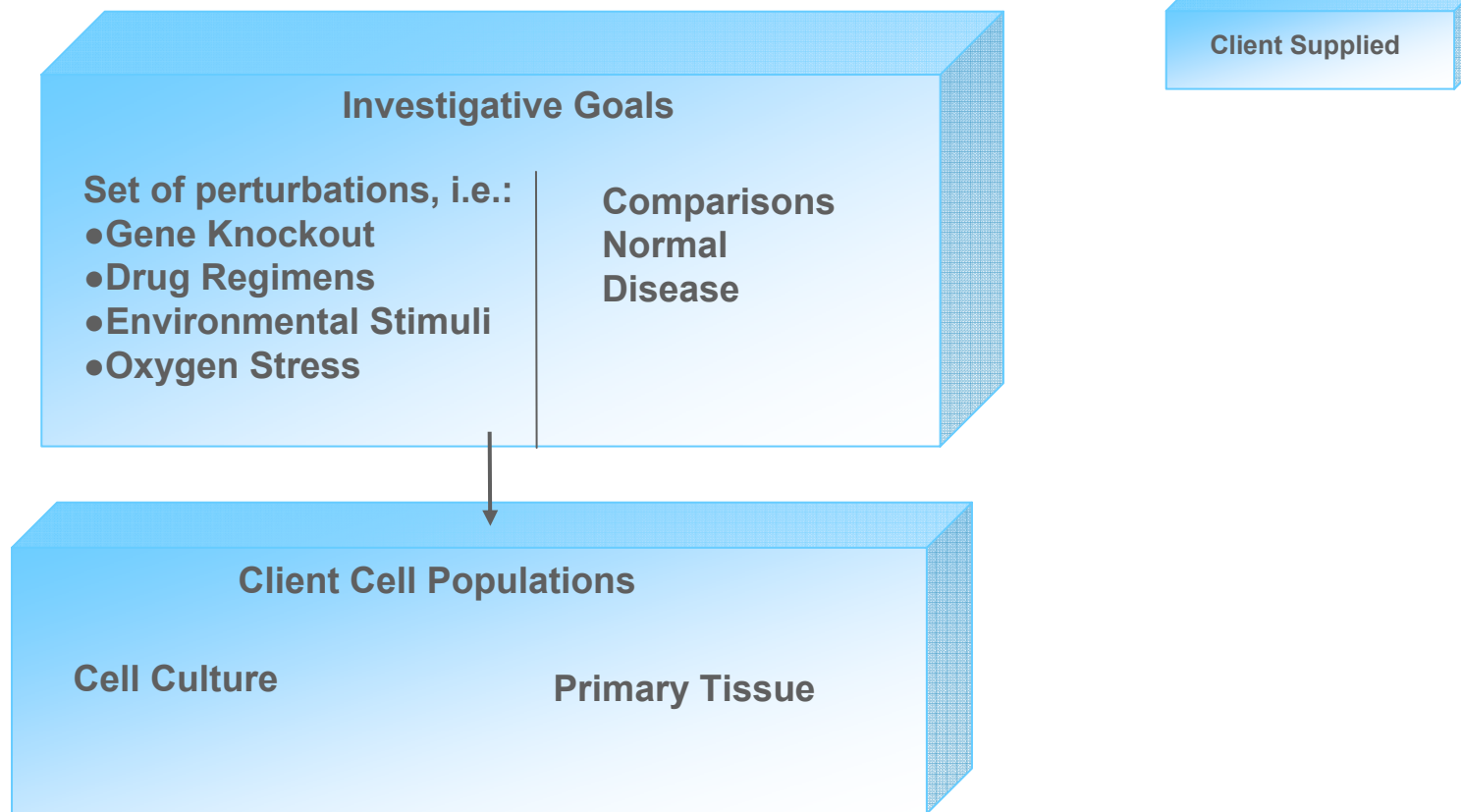
- Codon bias
- 5' secondary structure
- miRNA regulation
- Proteolysis
- Polypeptide length & folding

Detection MS-iness

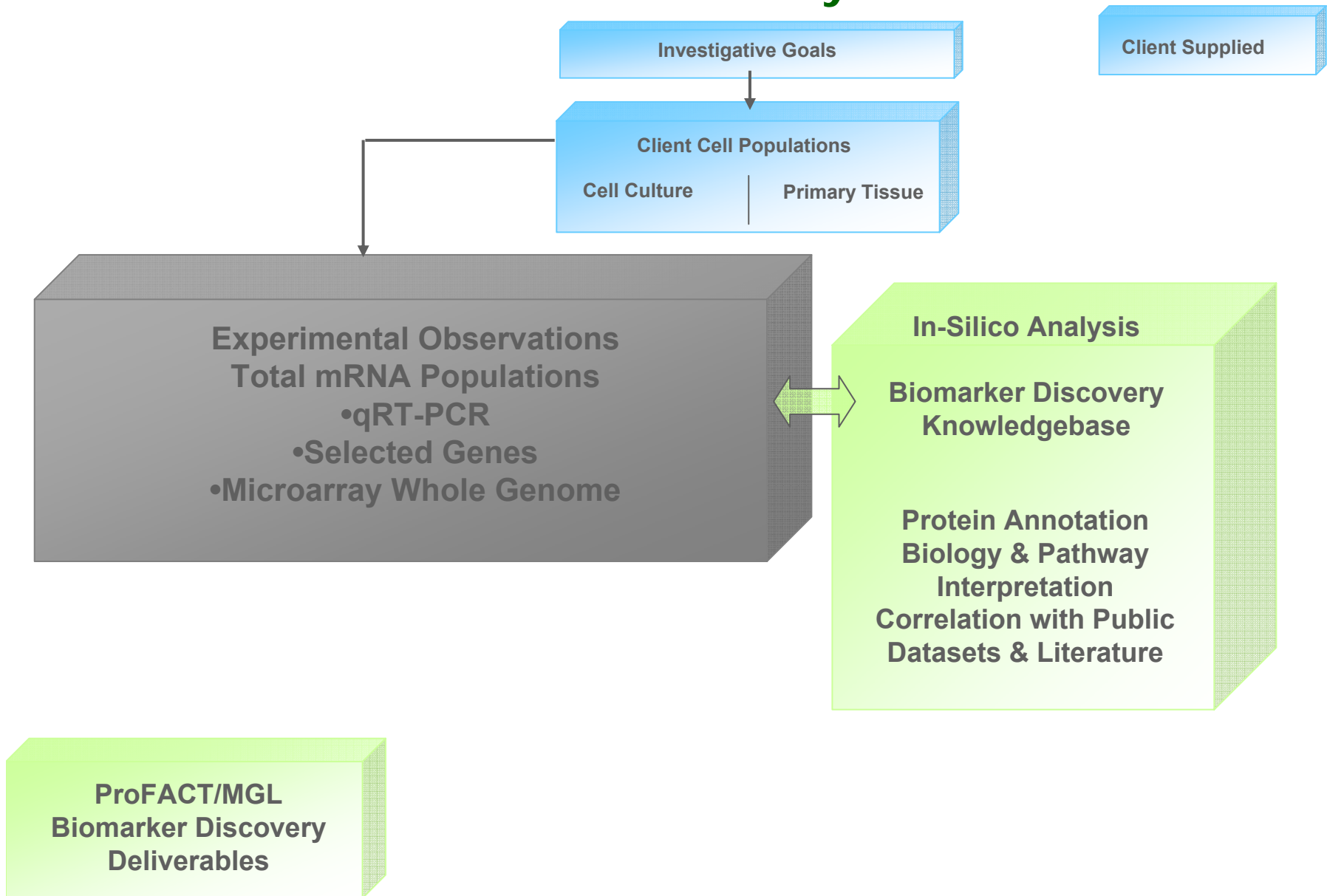
- High abundance masking
- Ion suppression
- Mass to gene data interpretation



Rational Genome to Proteome Prospecting™ Biomarker Discovery Workflow



Rational Genome to Proteome Prospecting™ Biomarker Discovery Workflow



BioInformatic Interpretation

Public Data, Predictive Algorithms and Priority Filters

Pathway Filter

- Disease Association
- Pathway Surrogates

Detection Filter

- Polyclonal Optimization
- Tryptic Peptides
- Functional (Enzyme Assays)

Mutation Filter

- Sequential variations

Biomarker Discovery Knowledgebase

Public Data

- Protein Annotation
- PTMs & Localization
 - Glycosylation
 - Phosphorylation
 - Sub-unit assembly
 - Nuclear
 - Extracellular
 - Membrane
 - Cytosolic

Class and Structure Filter

- Splice Variants
- Sub-unit assembly
- Known Ligands

Mechanism Filter

- Drug Targets

Tissue Filter

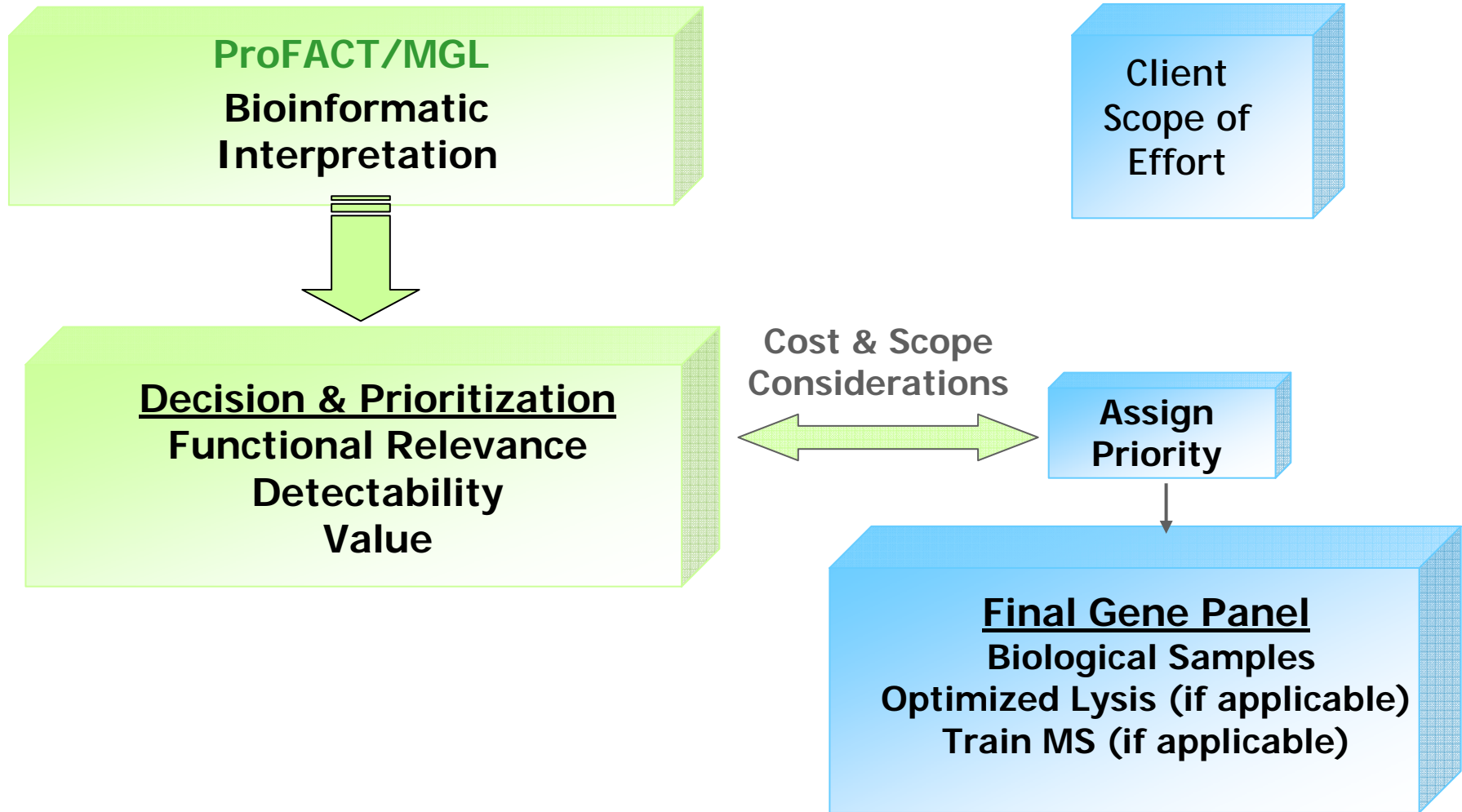
- Background Proteins
- 2DE

Comparative Genomics

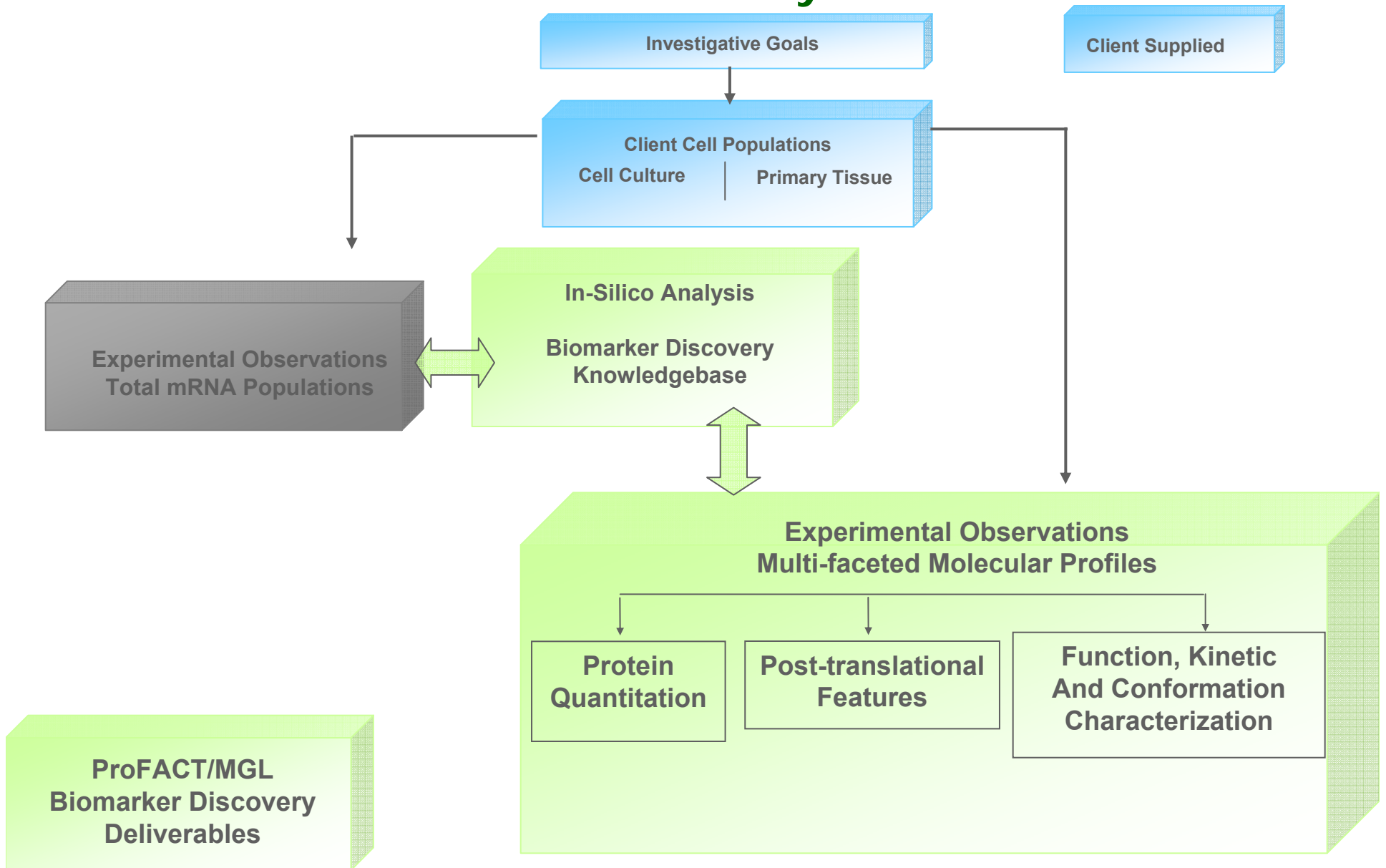
- Alternate Model Organisms

ProFACT/MGL
Biomarker Discovery
Deliverables

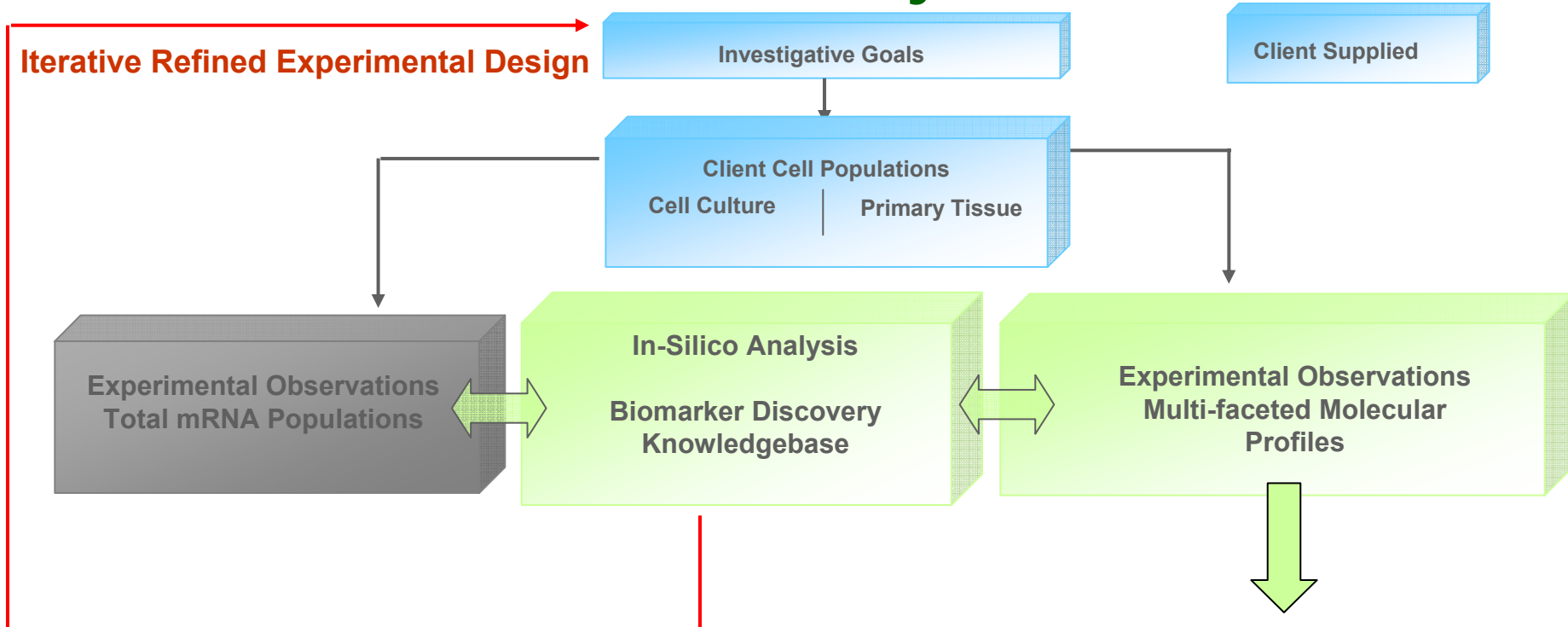
Rational Genome to Proteome Prospecting™ Biomarker Discovery Workflow



Rational Genome to Proteome Prospecting™ Biomarker Discovery Workflow



Rational Genome to Proteome Prospecting™ Biomarker Discovery Workflow



New Protein Biomarkers

New Drug Targets

Personalized Medicine

ProFACT/MGL Biomarker Discovery Deliverables

ProFACT Proteomics, Inc.

Seeking Partners and Collaborators

Biomarker Discovery

Gene Expression to Protein Reconciliation
Functional Protein Profiling
Targeted Enrichment
Pathway Cataloging

Drug Discovery

Enzyme classes in progress and of interest
Phosphodiesterases
Kinases/Phosphatases
Proteasome
Proteases
Others
Allosteric Regulation and Kinetics
Conformer Cataloging and Small Molecule Screening

Proprietary Biomarker Discovery Knowledgebase

Investors, advisors, contributors, other stakeholders



**1 Deer Park Drive, Suite P
Monmouth Junction, NJ 08852
www.profactproteomics.com**

**Contact:
Matthew Kuruc, President
732-230-3021
mkuruc@profactproteomics.com**