

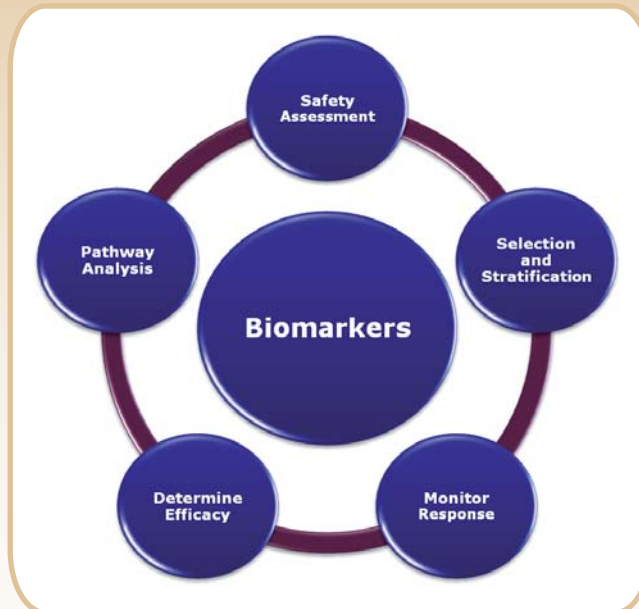
discoveryexpress™ ◇ Biomarker Discovery Service

For Research:

- Target discovery and validation
- Lead compound optimization
- Safety assessment
- Translational medicine

For Development

- Patient selection
- Monitoring compound efficacy
- Monitoring for adverse events
- Exploring alternative indications



NextGen Sciences offers a suite of proteomic techniques for biomarker discovery and will work with you to decide on the best technique for your biomarker needs.

Proteomic Platforms

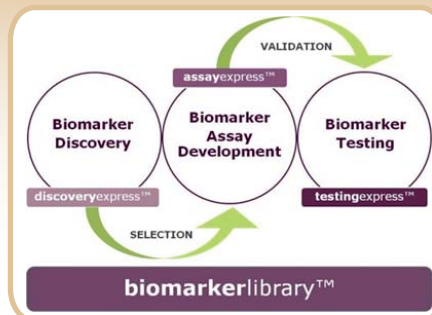
- GeLC-MS
- Differential mass spectrometry (dMS, label-free)
- Phosphoprotein analysis
- iTRAQ and SILAC
- 2D gel electrophoresis

Sample Type (any biological species)

- Biofluids
- Tissues
- Cells and conditioned media
- FFPE tissue
- Proximal fluids
- Plants

biomarkerexpress™ services

NextGen Sciences, Inc has developed a suite of biomarker services to significantly decrease timelines and increase the success rates traditionally associated with the various stages of biomarker development.



Gel LC-MS Platform ◇ **Differential and Quantitative Protein Profiling**

Features:

- High number of proteins detected
- Provides information-rich proteome maps
- Rapid transition to protein assay
- Low sample requirement
- Fast turn-around time
- Low cost

Process:

1. Run sample on SDS-PAGE
2. Segment each lane
3. Digest proteins
4. Mass spectrometry for protein identification and quantification
5. Data analysis – lists of potential biomarkers

iTRAQ

Feature:

- Comparison across 4 to 8 samples simultaneously

Process:

- Sample prep and protein digest
- Label peptides with iTRAQ reagents
- Fractionation and LC-MS/MS
- Data analysis

SILAC

Features:

- Pair wise comparison of samples
- High number of proteins detected and quantified

Process:

- Cells grown in special medium to label proteins
- Sample prep and fractionation
- Protein digestion and LC-MS/MS
- Data analysis

Phosphoprotein

Feature:

- Detection and quantification of phosphorylated proteins

Process:

- Sample prep
- Enrichment of phosphoproteins or phosphopeptides
- LC-MS/MS
- Data analysis

Differential Mass Spectrometry (dMS, label-free MS)

Features:

- High throughput
- Amenable to large number of samples
- Focused on differentially expressed proteins
- Fractionation provides higher numbers of proteins with a lower throughput

Process:

- Sample preparation & protein digestion
- LC-MS/MS
- Alignment of peptide chromatographic peaks
- Calculation of relative quantification
- Identification of differentially expressed proteins

Please visit our website for additional technical information:

www.nextgensciences.com

To request more information or to speak to one of our scientists contact:

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