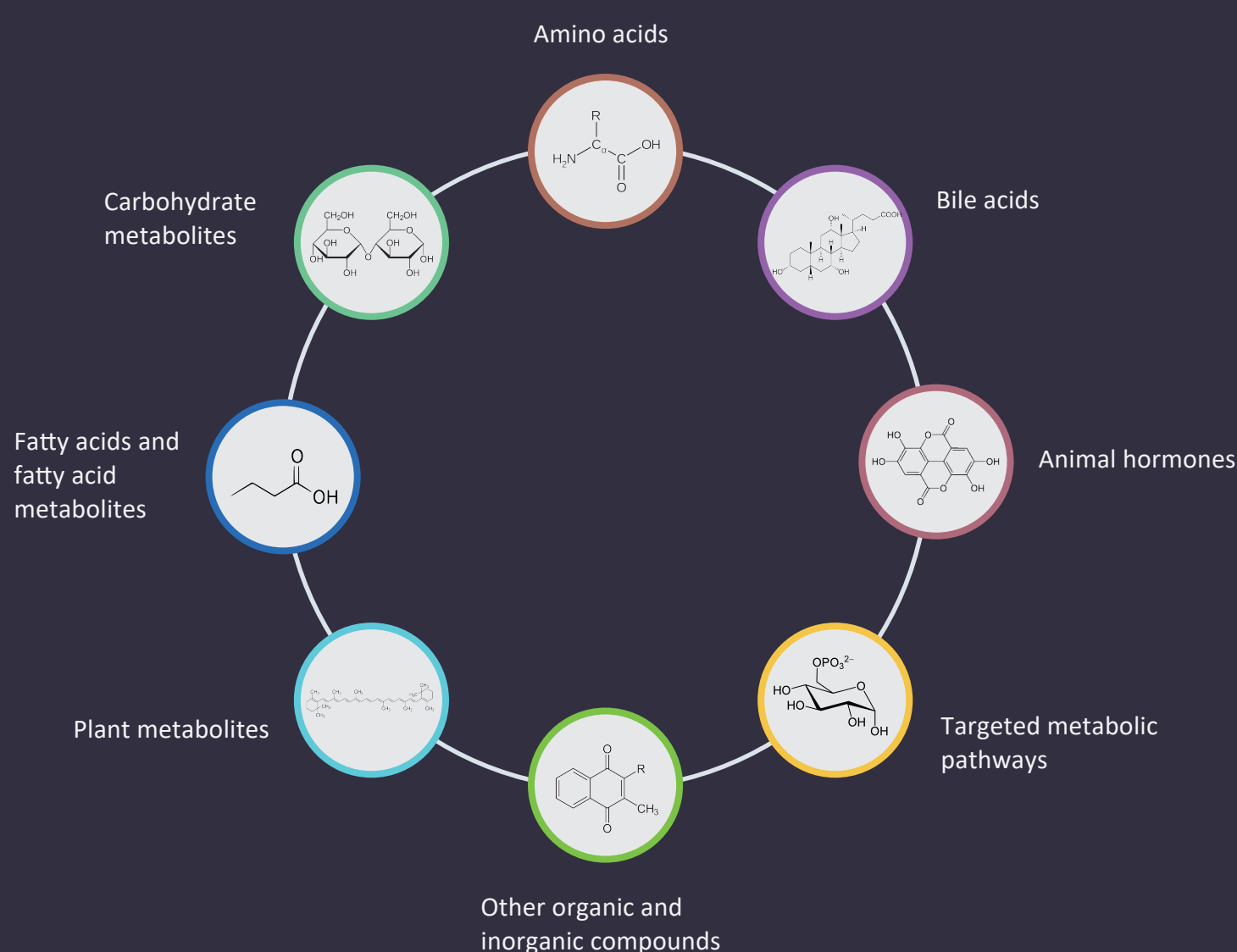


TARGETED METABOLOMICS

Targeted Metabolomics is an important part of metabolomics research, characterized by strong specificity, high detection sensitivity and accurate quantification.

Through the enrichment and accurate quantitative and qualitative analysis of a specific metabolite in blood, urine or other body fluids and tissues, targeted metabolomics can be combined with other experimental data to reveal the relevant molecular mechanism of action, and can also provide strong support for the further research, development and utilization of metabolic molecular markers. In addition, targeted metabolomics can be used to verify the hypotheses proposed by non-targeted metabolomics experiments, and to study metabolic models for specific metabolites.



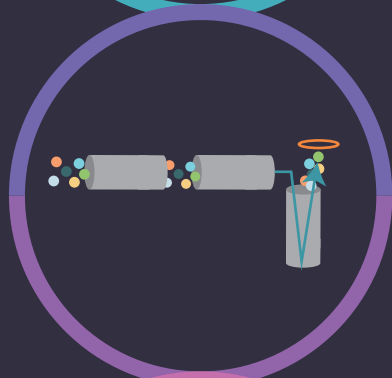
Why choose targeted metabolomics?

- Validation of biomarkers found in untargeted metabolomics
- Hypothesis driven
- Absolute quantification of specific features
- Validation of identified feature (but requires a commercially available chemical standard for validation)
- High sensitivity reaching pg level, achieving quantification of low-abundance metabolites



Sample preparation

- Extraction procedure for specific metabolites



Data acquisition

- Chromatographic separation
- MS ionization (negative and positive modes) (EI, ESI, APC, MALDI)
- Mass detection
- Multiple Reaction Monitoring (MRM)



Data processing

- Data preprocessing
- Statistical analysis
- Absolute quantitation of metabolite concentrations



Data interpretation

- Bioinformatics
- Integrative OMICS
- Enrichment analysis
- Pathway analysis
- Metabolic network

For our targeted metabolomics methodologies, Creative Proteomics uses a triple quadrupole mass spectrometer to detect through multiple reaction monitoring (MRM). A vast amount of mass spectrometry information can be generated to help you perform identification and quantification of metabolites with high sensitivity, precision and accuracy, allowing you to intuitively design targeted experiments and capture data related to important changes in the sample.