The Queensland Node of Metabolomics Australia

Metabolomics Australia offers services to all science researchers in academia and industry. We combine high-throughput analytical technologies for the detection and quantification of metabolites in biological systems with the application of bioinformatics tools for data analysis, mining and interpretation.

Services offered

Targeted/Quantitative:

LCMS Absolute quantitation of central carbon metabolites, vitamins, short-chain fatty acids, nucleotides/nucleosides.

UHPLC: Amino acids, organic acids, sugars, short chain fatty acids, terpenoids, aromatic compounds.

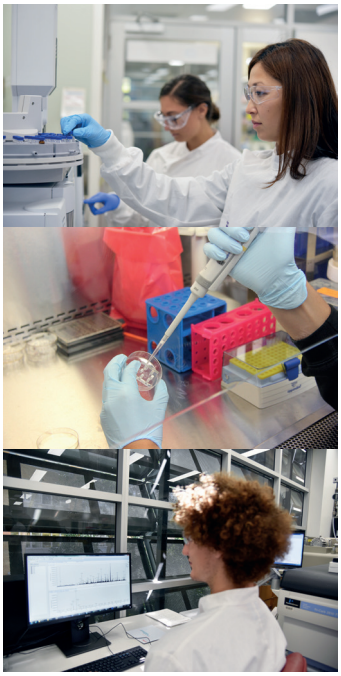
GC-MS: Target metabolites or metabolite classes are analysed quantitatively relative to authentic standards providing absolute concentration of each metabolite per fresh weight of material.

Untargeted

GC-MS (semi-quantitative): Identification of organic acids, fatty acids, sterols, amino acids, sugars, sugar phosphates/alcohols, hydrocarbons, terpenes.

Data analysis

Data processing workflows



We combine complementary analytical and informatics platforms to detect the response of metabolites to genetic and environmental stimuli.

Our node specialises in servicing the industrial biotechnology sector

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METABOLOMICS AUSTRALIA

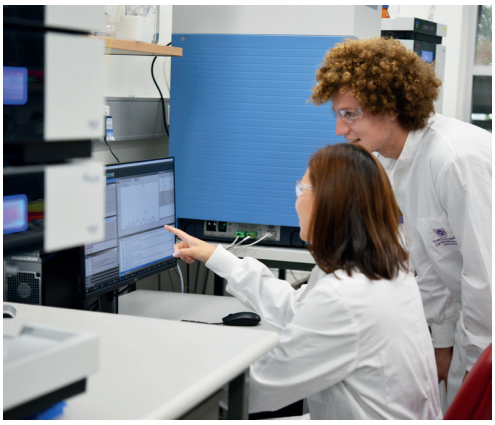
BIOPLATFORMS AUSTRALIA

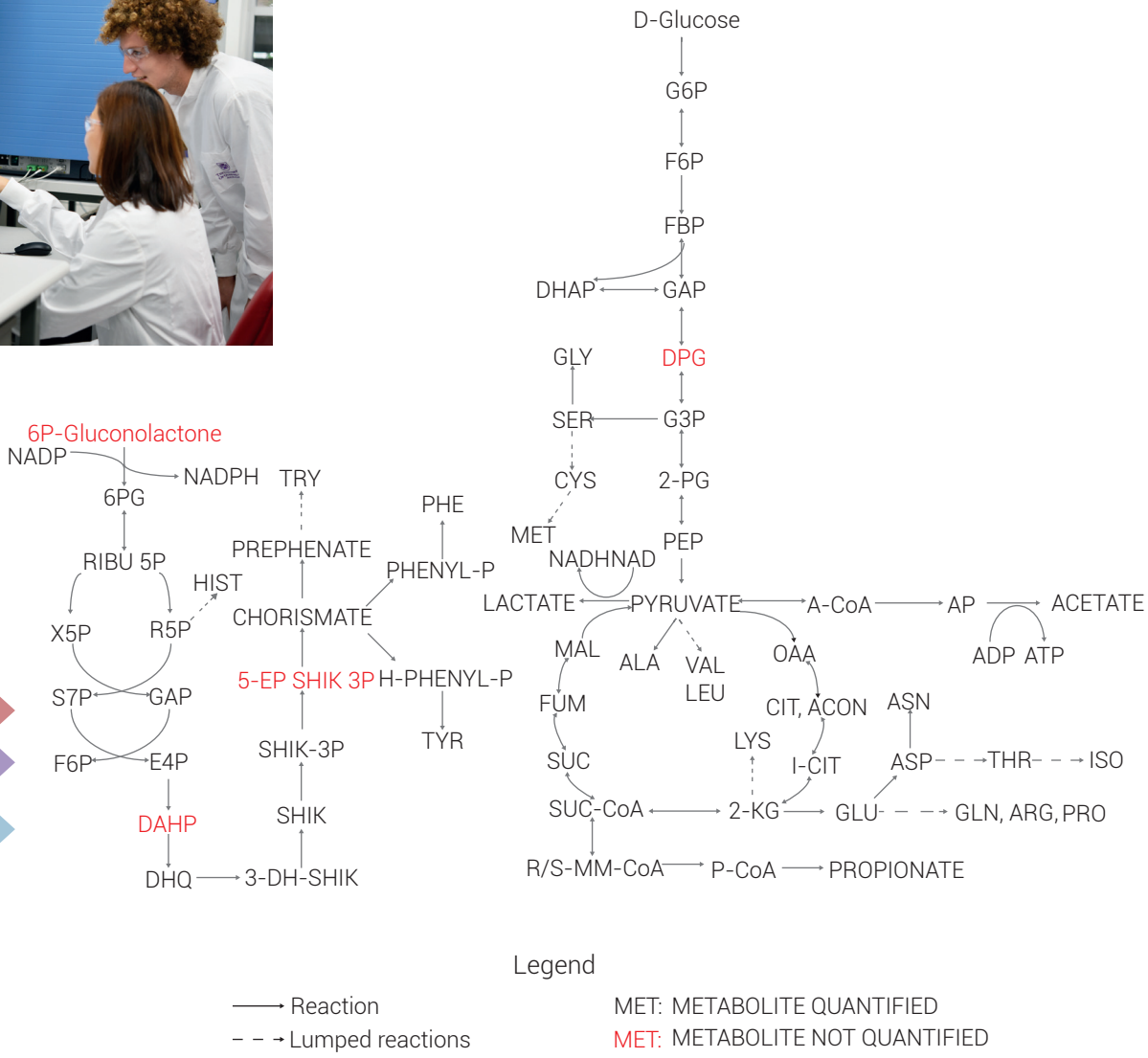
NCRIS National Research Infrastructure for Australia

An Australian Government Initiative

Quantitation of central carbon intermediates

The Queensland Node of Metabolomics Australia offers specialized expertise in metabolic engineering, where quantitating metabolites from the central carbon metabolism (glycolysis, the pentose phosphate pathway and the TCA cycle) is important. For example, the shikimate pathway provides carbon skeletons for the biosynthesis of aromatic amino acids from which many industrially relevant products are derived. The pathway below shows all the intermediates leading to the aromatic amino acids. Out of the 72 organic acids, amino acids and cofactors present in the figure, the node is able to quantify 68 metabolites using LCMS, UHPLC or GCMS. The information provided can be used to identify bottlenecks in the pathway and for strain optimization.





Legend

Reaction
Lumped reactions

MET: METABOLITE QUANTIFIED
MET: METABOLITE NOT QUANTIFIED

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