

## VTT's Research on Systems biology in nutrition and health

### Contacts:

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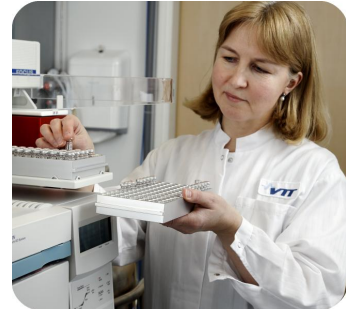
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### 1. Metabolomic analysis and bioinformatics of human intervention trials (effects of diet, lifestyle, food components etc.)

- ✚ Metabolomic analysis of trial samples (biofluids, tissue biopsies, cells)
  - Non-targeted global lipidomic and metabolomic analysis (UPLC/MS and GCxGC-TOF/MS)
  - Targeted quantitative methods (GC, UPLC, UPLC/MS/MS, GC/MS, GCxGC-TOF/MS) for specific classes of metabolites: bile acids, eicosanoids, endocannabinoids, amino acids and related metabolites, free and esterified fatty acids, metabolites of central carbon metabolism (i.e. glycolysis, pentose phosphate pathway, TCA cycle), branched chain amino acids and their keto-acids, nucleotides, ketone bodies
  - Development of customized platforms for specific customer needs
- ✚ Bioinformatics for metabolomics: Data processing including ability to deal with stable isotope tracer data, quantification, metabolite identification using extensive spectral libraries (incl. in house), metabolic pathway mapping, statistical analysis (univariate, multivariate)

### 2. Characterisation of metabolome in health and disease

- ✚ Analysis of samples (biofluids, tissue biopsies, cells) from healthy individuals and from those being at risk for or having different diseases/syndromes
  - e.g. metabolic syndrome, type 1 and 2 diabetes, fatty liver disease, cardiovascular disease, celiac disease, schizophrenia and related psychiatric disorders, Alzheimer's disease, breast cancer
  - analyses as above

### 3. Phenotype characterization of *in vivo* and *in vitro* models

- ✚ Metabolomic analysis of samples in nonclinical studies (animal models, tissue and cell cultures), with methods as above.
  - Combining metabolomic data with other levels, incl gene expression, proteomics
  - Statistical modelling of complete data (across tissues/cells/biofluids, different platforms), pathway mapping.

### 4. Integrative bioinformatics and modelling

- ✚ Combining data across multiple omics datasets (e.g. GWAS, gene expression, metabolomics) and clinical data
- ✚ Advanced methods for modelling of complex datasets in the biological context.