

Our ultra-high resolution Orbitraps offer the highest standard in sensitivity, performance and reproducibility to solve complex Metabolomics and Proteomics challenges.



Orbitrap Eclipse

- Protein identification and quantification at the nanogram level
- Single cell protein identification and quantification using TMT technology
- FAIMS ion source filter for increased sensitivity and extended protein sequence coverage
- Post-translational modification analysis
- Small molecule profiling and MS³

Orbitrap Exploris 480

- Protein identification and quantification at low microgram or sub-million cells level
- FAIMS ion source filter for increased sensitivity and extended protein sequence coverage
- Post-translational modification analysis





Orbitrap Q Exactive HF

- Protein identification and quantification at milligram or many millions of cells level
- Small molecule open profiling

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State of the art equipment



LC-MS/MS

- Two Shimadzu 8060
- Sciex QTRAP 4000
 - > Targeted quantitative analyses: e.g. central carbon metabolism, short chain fatty acids
 - ➤ Fluxomics: e.g. U¹³C central carbon metabolism
 - Targeted metabolites belonging to specific metabolic pathways: e.g. isoprenoids

GC-MS/MS

- Two Shimadzu TQ 8050 ultra-high sensitivity triple quadrupole GC-MS/MS
- Agilent 5975C GC-MS
 - > Open profiling of a library of hundreds of compounds : e.g. amino acids, organic acids, sugars, fatty acids
 - > Targeted quantitative analyses: e.g. alcohols
 - > Headspace: e.g. volatile organic, permanent & light gases





UHPLC

- Three Thermo Scientific Vanquish Duo UHPLC
- Two Agilent HPLC
- Detectors: FLD, DAD, RID, ELSD, CAD
- Targeted quantitative analyses: e.g. amino acids, organic acids, sugars, alcohols, aromatic compounds, crotonic acid, isoprenoids & more

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