

Summary

EpiQMAX offers a full service for the quantitative analysis of proteins and protein interactions (including PTM's) by means of mass spectrometry. Since 2018 we are a partner for the development of drugs and biomarker research with a focus in the epigenetic field. Headquartered nearby Munich, we operate state-of the-art mass spectrometers to ultimately facilitate proteomic screenings into clinical applications.

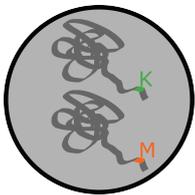
Contact

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Our service portfolio

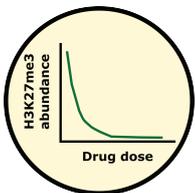
Epigenetic analyses



- Histone PTM analysis
- Histone mutation analysis
- Identification and quantification of new histone PTM's

- Bux, E., et. al., "Determining histone H4 acetylation patterns in human peripheral blood mononuclear cells using mass spectrometry", *Clinical Mass Spectrometry*, 2019.
 - Alabert, C., Loos, C., Voelker-Albert, M., et. al., "Domain model explains propagation dynamics and stability of histone H3 K27 and K36 methylation landscapes", *Cell reports*, 2020.

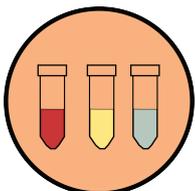
Drug efficacy studies



- Drug efficacy testing
- LOD and LOQ determination
- Small molecule analysis

Several studies with leading pharmaceutical companies in the context of drug efficacy testing. Further information upon request.

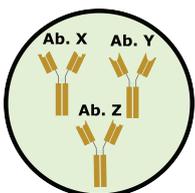
Proteomics



- Proteome wide screenings by LC-MS/MS
- Data-dependent and data-independent acquisition (DDA/SWATH/MRM)
- Data analysis and reporting tools

- Völker-Albert, M., et. al., "A quantitative proteomic analysis of in vitro assembled chromatin." *Molecular and Cellular Proteomics*, 2016.

Antibody/Biologics characterization



- Intact mass analysis
- Peptide mapping
- Multiple attribute monitoring (MAM)
- Antibody-Drug Conjugate (ADC) analysis
- Lot-to-Lot Comparability

Current studies with the LMU Munich, Leibniz Institute and BioTech & Research Institute Denmark

Customized solutions



- Crosslinking mass spectrometry
- Protein-protein interaction studies
- Software tools for data analysis and data integration

- Ivic, N., Potočnjak, M., Solis, M., et. al., "Fuzzy Interactions Form and Shape the Histone Transport Complex." *Molecular Cell*, 2019
 - Fischböck-Halwachs, J., Singh, S., Potočnjak, M., Hagemann, G., Solis, V. et. al., "The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore. *eLife*. 2019.

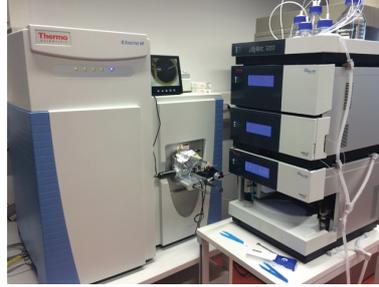
Machines:



**X500B
Q-TOF**

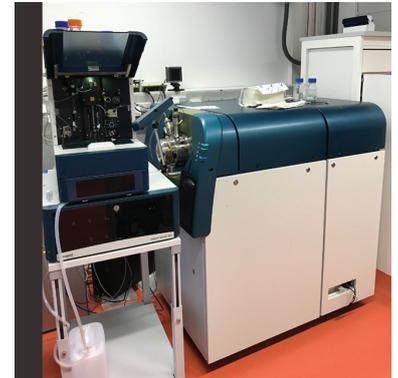
- Engineered for standard biotherapeutic characterization analyses and MAM workflows.
- Robust and reliable acquisition in combination with Exion UHPLC.
- Dedicated program for Antibody-Drug Conjugate studies.

Accessible Machines:



Q-Exactive HF

- High-performance platform for bottom-up and top-down proteomics studies.
- Biomarker verification and analysis via parallel reaction monitoring (PRM), with high-resolution data-independent acquisition (DIA).



**TTOF
6600**

- Very fast acquisition speed and SWATH measurements.
- More complete data-with high-resolution MS/MS data on every detectable analyte.
- Enhanced quantitation-with extended linear dynamic range.

Team



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CEO



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Head of technology



Prof. Dr. Axel
Imhof,
Advisor

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