Bioanalysis with Gubra

Bioanalysis of plasma samples using LC-MSMS

Determination of pharmacokinetic (PK) parameters, bioavailability, clearance or exposure of your drug candidate (f.e. a peptide or small molecule) are a valuable add-on to any in vivo study. Mass spectrometry (LC-MSMS and LC-HRMS) is the method of choice for highly sensitive and specific quantitative bioanalysis. Everything from sample collection to analysis are done in-house to ensure high data quality and fast turn-around times.

Designated laboratory and staff

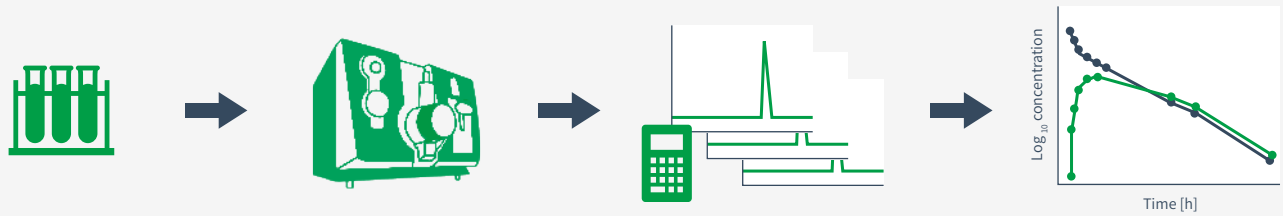
Plasma samples are processed by highly trained specialists to ensure reproducibility and robustness of the analysis. For removal of plasma proteins, an organic solvent is added to the plasma sample followed by centrifugation. The compound of interest is then analysed by LC-MSMS.

Our laboratory is equipped with state-of-the-art instrumentation allowing both metabolite identification and accurate quantification of analytes.

PK data analysis

Plasma concentrations are determined by preparation of calibration curves in an identical matrix, extensive quality control is performed for each analysis. Pharmacokinetic parameters are calculated by Non-compartmental analysis (NCA).

Sample flow
Illustration of the sample flow from sample collection and preparation to LC-MSMS analysis and data analysis.



1. Sample preparation: Plasma proteins are removed by addition of organic solvent and subsequent centrifugation.
2. LC-MSMS analysis: For every compound, a dedicated LC-MSMS method is developed to ensure high specificity and selectivity.
3. Compounds are quantified based on their EICs relative to a standard curve that is prepared in an identical matrix.
4. Non-compartmental PK analysis (NCA): Time-concentration curves are plotted and analysed using the NonCompart R package. Typical PK parameteres such as $t_{1/2}$, MRT, V_{AUC}, C_{max} and T_{max} are reported.

gubra
discovery@gubra.dk | +45 3152 2650