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## Introduction

Mid-infrared spectroscopy provides detailed information about proteins that cannot be obtained with conventional UV detectors. The most powerful IR bands for protein quantification and secondary structure analysis are the amide I (1700-1600  $\text{cm}^{-1}$ ) and amide II (1600-1500  $\text{cm}^{-1}$ ) bands.

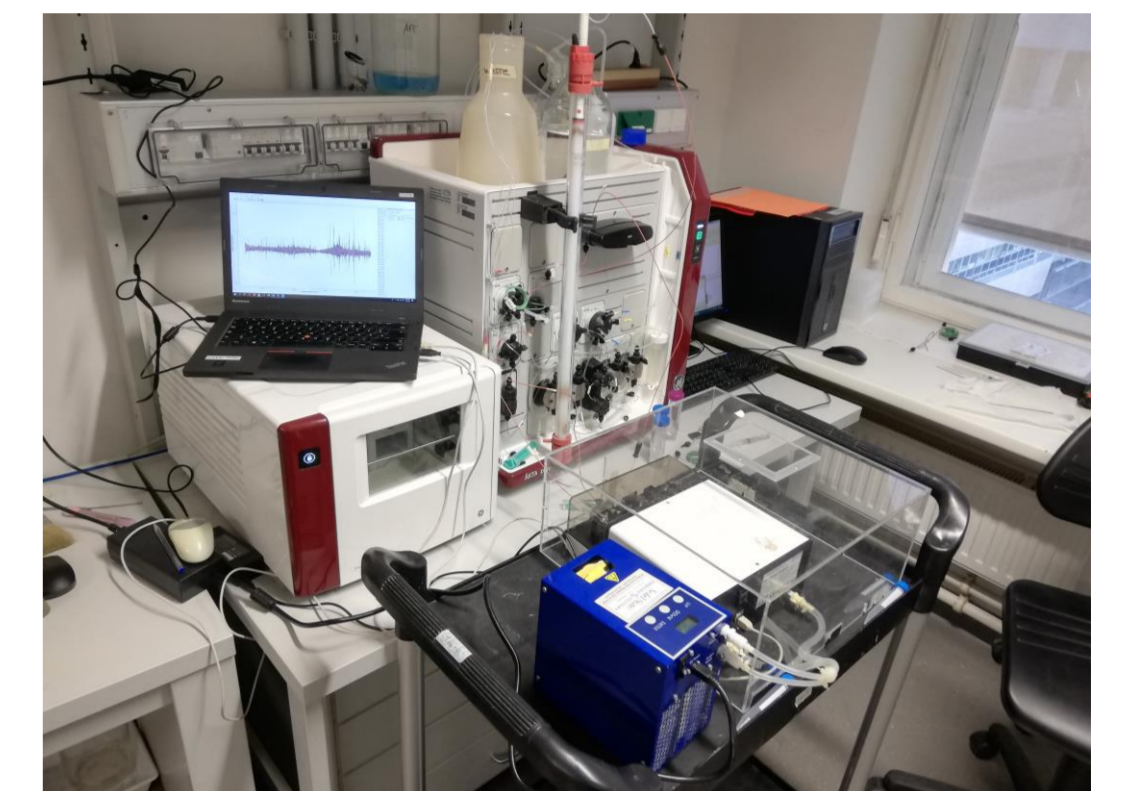
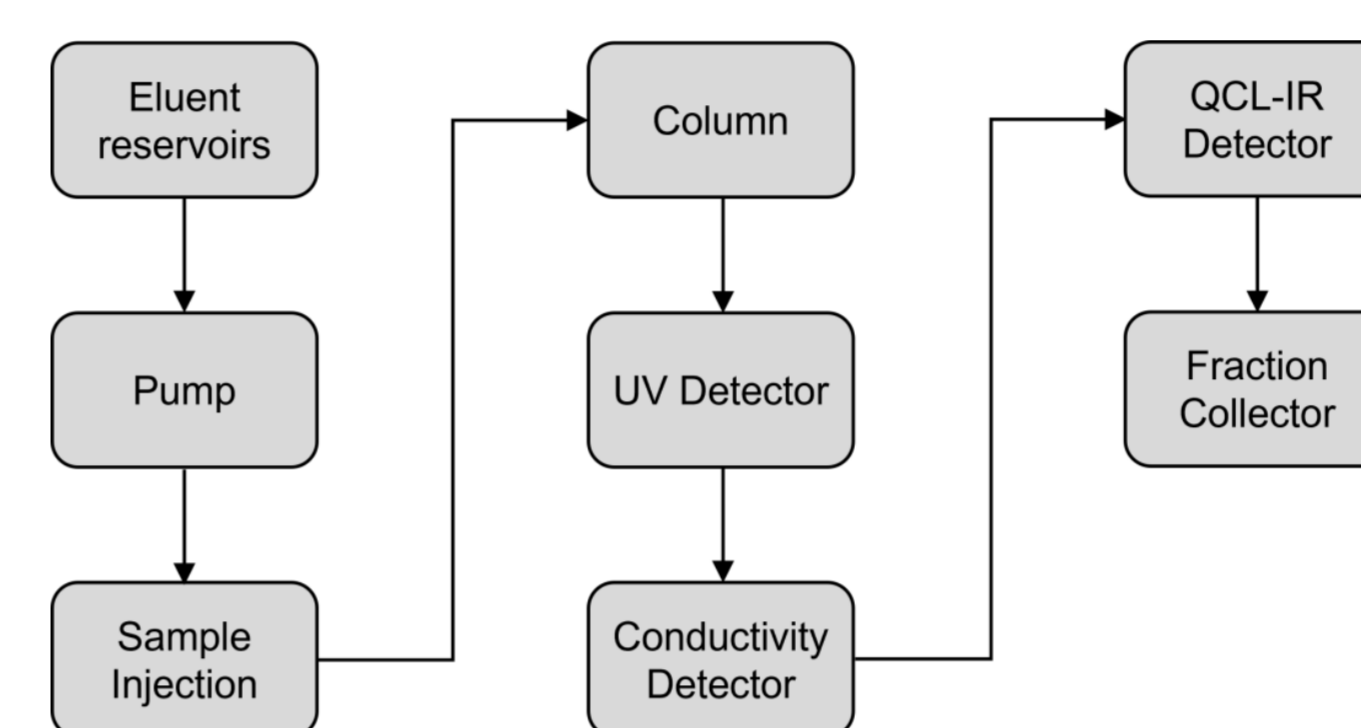
A pronounced challenge in measurements of aqueous protein solutions is the strong absorption of  $\text{H}_2\text{O}$  at approx. 1640  $\text{cm}^{-1}$  that overlaps with the amide I band. In conventional Fourier-transform infrared (FTIR) spectroscopy, the optical path-length is restricted to  $<10 \mu\text{m}$  to avoid total IR absorption. These small path lengths are unsuitable for flow-through operations due to low robustness.

External cavity-quantum cascade lasers (EC-QCLs) offer higher optical powers compared to the thermal sources used in FTIR spectroscopy, leading to increased sensitivity and larger applicable optical path lengths. These advantages open a wide range of possible applications, including near real-time protein monitoring from downstream operations.

Here, an EC-QCL based mid-IR spectrometer was coupled to a preparative liquid chromatography (LC) system. Two different model systems, based on ion-exchange chromatography (IEX) and size exclusion chromatography (SEC) were employed to demonstrate the high flexibility of LC-QCL-IR coupling.

## LC-QCL-IR Setup

- ÄKTA pure system (Cytiva Life Sciences, MA, USA) equipped with an U9-M UV monitor, a C9 conductivity monitor and a F9-C fraction collector
- ChemDetect Analyzer (Daylight Solutions Inc., San Diego, USA), equipped with an EC-QCL (1350-1750  $\text{cm}^{-1}$ ) and a 25  $\mu\text{m}$  transmission cell [1]
- The collected fractions were additionally analyzed by reference analysis with high-performance liquid chromatography (HPLC)



## Ion Exchange Chromatography (IEX)

- IEX runs were performed using a 1 mL HiTrap Canto Q column, flow rate of 0.5 mL/min, elution buffer A of 50 mM Tris/HCl (pH 8.5) and elution buffer B with additionally 1 M NaCl [2]

- A reference blank run (no proteins) and sample runs (2 proteins) with different gradients were performed:

**Blank run:** linear gradient within 60 min from 0 to 1 M NaCl

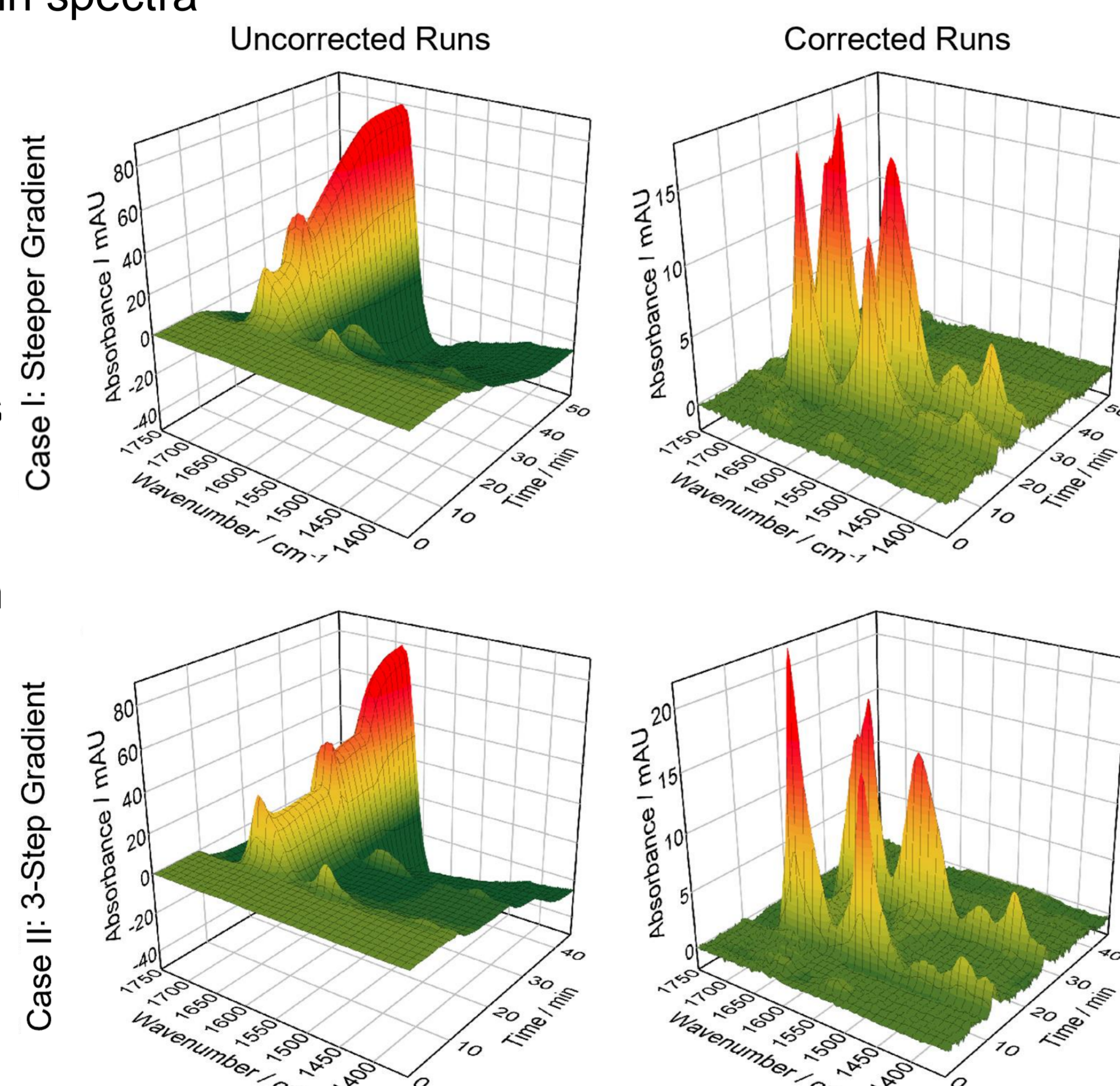
**Case I:** steeper linear gradient within 30 min from 0 to 1 M NaCl

**Case II:** 3-step gradient: 0.25 M, 0.5 M, 1 M NaCl

- A significant challenge was caused by overlapping IR absorbances of proteins and NaCl gradient. Even though amide I and II bands were visible in spectra of uncorrected runs, the effect of the NaCl gradient was clearly dominating
- A novel background correction approach was applied, where a single blank run is sufficient for correcting sample runs of highly different gradient profiles, showing excellent protein spectra

### Background compensation:

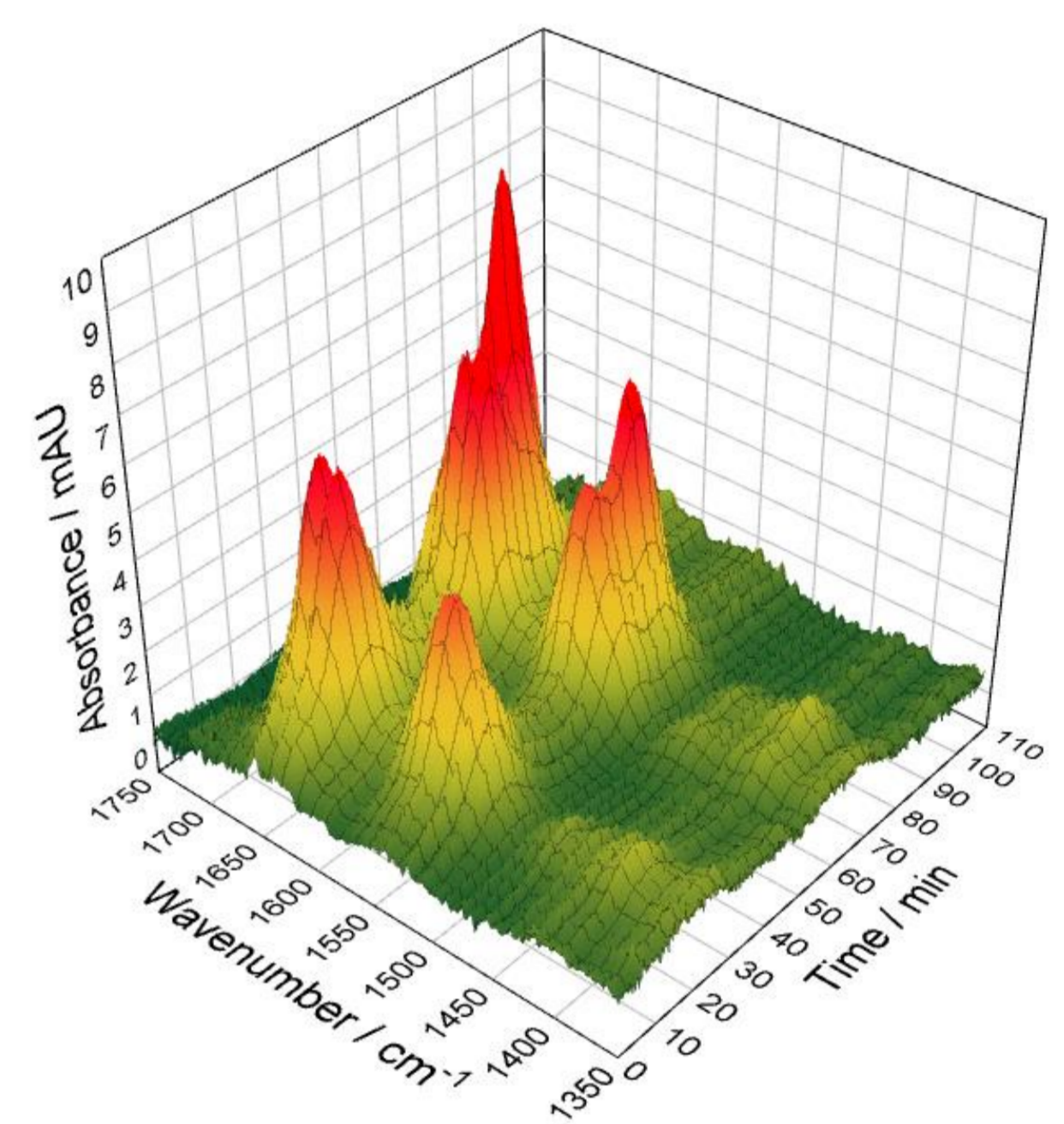
- 1) Relate conductivity detector signal to QCL-IR spectra of blank and sample runs
- 2) Take sample run spectrum and search for reference spectrum with closest conductivity value
- 3) Subtract selected reference spectrum from sample spectrum
- 4) Continue with next sample spectrum



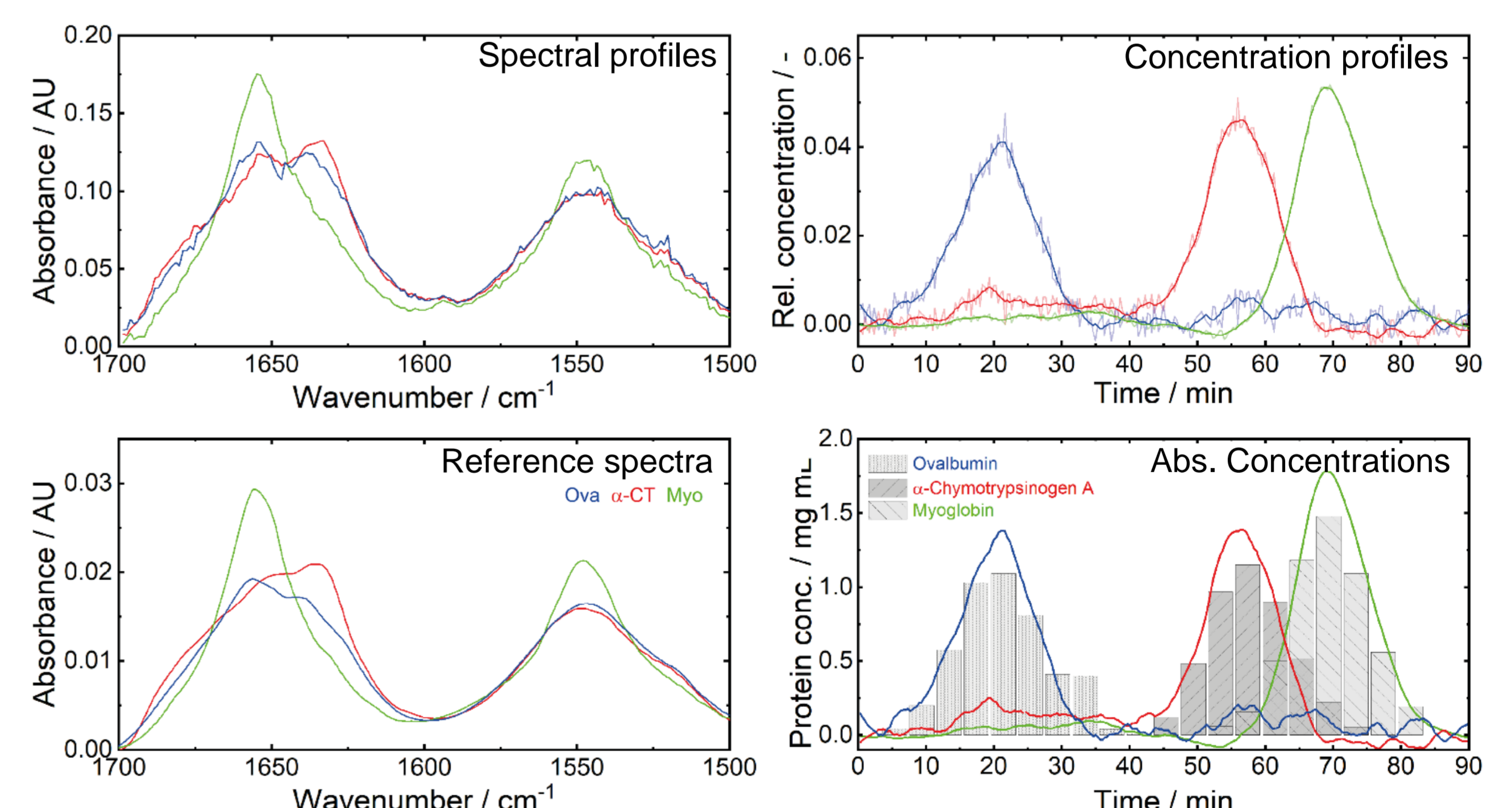
## Size Exclusion Chromatography (SEC)

- A SEC run was performed using a HiLoad 16/60 Superdex 200 pg column and isocratic elution with 50 mM phosphate buffer (pH=7.4) and 0.25 mL/min flow rate [3]

- Three model proteins with different secondary structures and molecular weights were injected into the system
- QCL-IR spectra showed a stable baseline across the chromatographic run and specific amide I and amide II bands for the three proteins



- Chemometric analysis based on Simple-to-use Interactive Self-modeling Mixture Analysis (SIMPLISMA) and Multivariate Curve Resolution (MCR) was applied
- Spectral and concentration profiles of the individual proteins were obtained without initial knowledge
- Chemometric spectral profiles showed excellent agreement in band shape & position to reference off-line IR spectra of pure protein solutions
- Absolute protein concentrations were calculated via Beer-Lambert law, showing excellent agreement to HPLC off-line measurements



## References

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- [2] C. K. Akhgar, J. Ebner, O. Spadiut, A. Schwaighofer, B. Lendl, "QCL-IR Spectroscopy for In-line Monitoring of Proteins from Preparative Ion-Exchange Chromatography" *Anal. Chem.*, 94, 5583-5590 (2022).
- [3] C. K. Akhgar, J. Ebner, O. Spadiut, A. Schwaighofer, B. Lendl, "Laser-based mid-infrared spectroscopy enables in-line detection of protein secondary structure from preparative liquid chromatography" *Proc. SPIE*, 11957 (2022).

## Conclusions & Outlook

- A QCL-IR spectrometer was successfully coupled to a preparative LC system for in-line monitoring of protein secondary structure
- For IEX, a novel gradient compensation approach was introduced. Here, a single reference blank run was sufficient for correcting various gradient profiles
- In SEC, qualitative and quantitative information about individual proteins from overlapping chromatographic peaks was obtained
- LC-QCL-IR coupling holds high potential for complementing laborious and time-consuming off-line methods

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