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Development of a high-throughput and high ion mobility resolution approach using automatic stitching of multiple ion mobility ranges on a TIMS-ToF instrument: application to chiral analysis

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INTRODUCTION

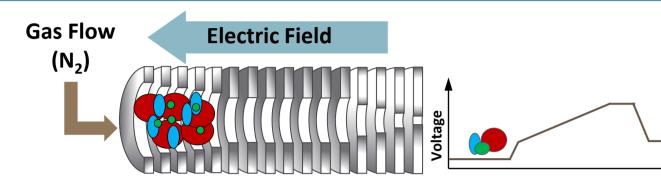
- The characterization and identification of metabolites of interest in biological matrices is often achieved using hyphenated methods such as liquid chromatography coupled with mass spectrometry (LC-MS) but it remains an analytical challenge.
- Ion mobility spectrometry is based on gas-phase mobility and its coupling with MS (IM-MS) offers an additional separation dimension and may allow CCS determination of analytes without lengthening the acquisition time. High resolution conditions are nevertheless essential to distinguish ions with very close ion mobilities such as chiral compounds.
- A high-throughput and high IM resolution approach was developed to allow exhaustive IM-MS measurements on a



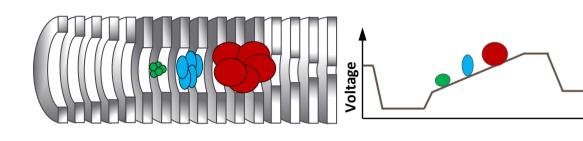
- Direct infusion of proteinogenic chiral L- and D-AAs (1 μM each) with the addition of **Cu^{II}** and ^L**Phe** & ^L**Pro** as chiral references (20) μ M each) in H₂O/MeOH. Analysis of each individual AA at 5 μ M.
- Study of all combinations between the analyte, references and Cu^{II} (dimers AA/Pro, AA/Phe and AA/AA; trimers AA/Pro/Pro, AA/Phe/Pro, AA/Phe/Phe, AA/AA/Pro, AA/AA/Phe and AA/AA/AA).

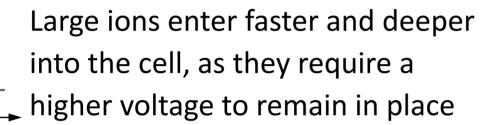
trapped ion mobility spectrometry time-of-flight (TIMS-ToF) instrument. Chiral amino acids (AAs) were chosen as model chiral compounds, and enantiomer couples were separated as non covalent complexes with Cu^{II}.

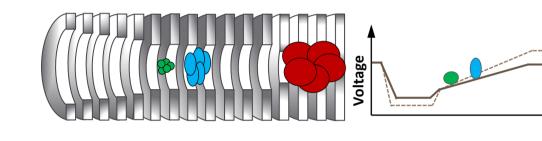
INSTRUMENTATION



Sequential steps of TIMS: Ions are pushed through the mobility cell by a gas and trapped by an electric gradient







Trapped ions are then eluted towards the MS by gradually lowering the voltage

TIMS separation

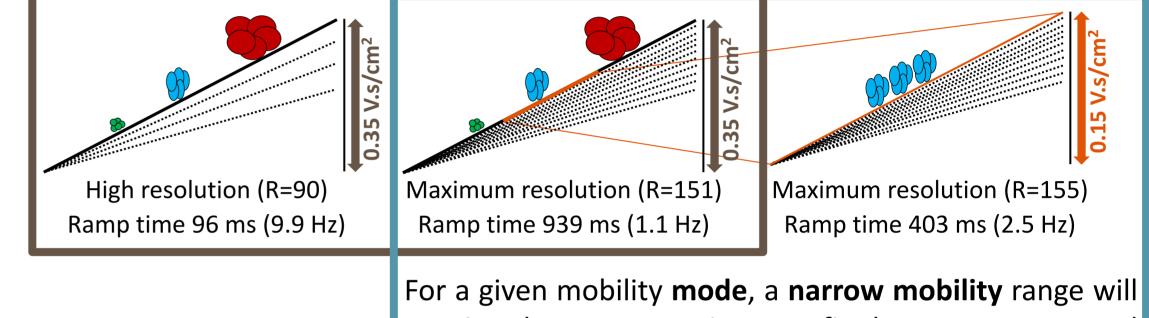
In practice

Three mobility modes are available (normal, high and maximum resolution), each corresponding to fixed spectra rate values (Hz).

The mobility range 1/K₀ (V.s/cm²) is fixed, and the ramp time (ms) is adjusted to fit the spectra rate.

High resolution => low spectra rate & long ramp time

For a given mobility range, a higher resolution mobility mode will require longer ramp times => more MS scans per elution step



require shorter ramp times to fit the spectra rate and keep the resolution constant, while increasing sensitivity => **SIM² mode** (Single ion mobility monitoring)[1]

RESULTS

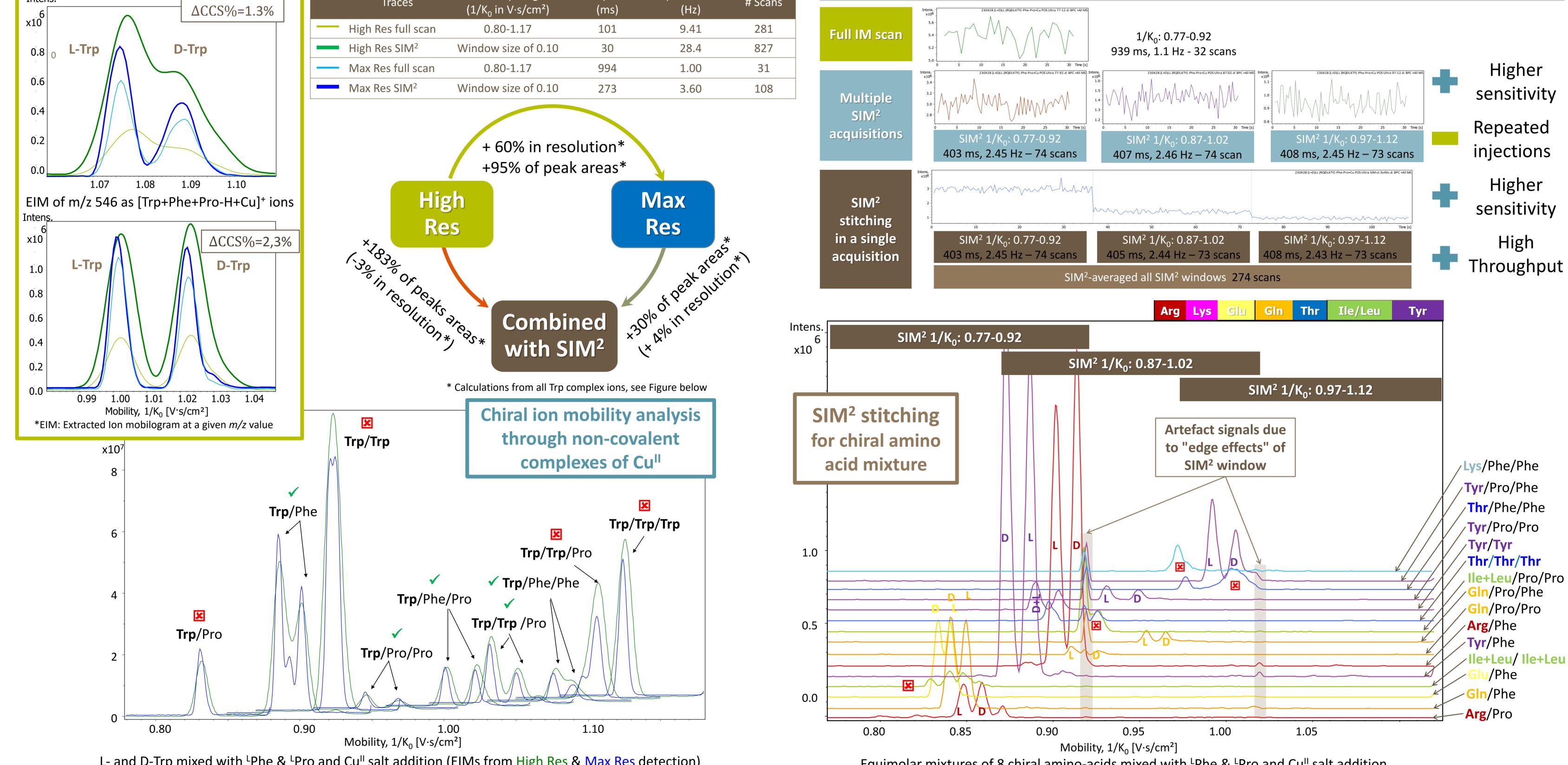
High resolution ion mobility for chiral analysis

EIM of m/z 596 as [Trp,Phe,Phe-H+Cu^{II}]⁺ ions Intens.

Optimization of TIMS conditions

Mobility range Spectra rate Ramp time

SIM² stitching for high throughput and high resolution analysis of complex mixture



L- and D-Trp mixed with ^LPhe & ^LPro and Cu^{II} salt addition (EIMs from High Res & Max Res detection)

Equimolar mixtures of 8 chiral amino-acids mixed with ^LPhe & ^LPro and Cu^{II} salt addition (EIMs using Max Res mode and SIM² stitching acquisition)

CONCLUSION

- Fast chiral IM analysis of AAs as non-covalent Cu^{II} complexes with Phe and Pro as chiral references
- 70% of all possible complexes are detected in a mix solution (92% in individual mix), and 19% are separated (vs 28%)
- SIM² stitching allows exhaustive ion mobility measurements while maintaining high resolution and sensitivity on large mobility range

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REFERENCES

[1] E. Rathahao-Paris, A. Delvaux, M. Li et al.; J Mass Spectrom, **57** (2022)





Single acquisition by collection of adjacent SIM² windows, high mobility resolution & sensitivity (possible edge effects)

Ultra with SIM²

Full scan

Highest mobility resolution & sensitivity, good for targeted analysis and known compounds

Narrow mobility range, may require repeated injections, long ramp times (LC compatibility)

Large mobility range in a single acquisition

No mobility separation below 1.5% (moderate mobility resolution)