



## desorption – triple quadrupole mass spectrometry (LDTD-QqQMS)

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### Introduction

- ❖ Analysis of peptides using high-throughput techniques such as LDTD-QqQMS is of interest for quality control of peptide therapeutics and biological drugs in the pharmaceutical industry, monitoring of food allergens in the food industry, and detection of viruses, including SARS-CoV-2.
- ❖ **Objectives:** Identify the main ions generated by rapid thermal desorption and atmospheric pressure chemical ionization of target peptides in LDTD and determine if those ions can be used for quantitative analysis.

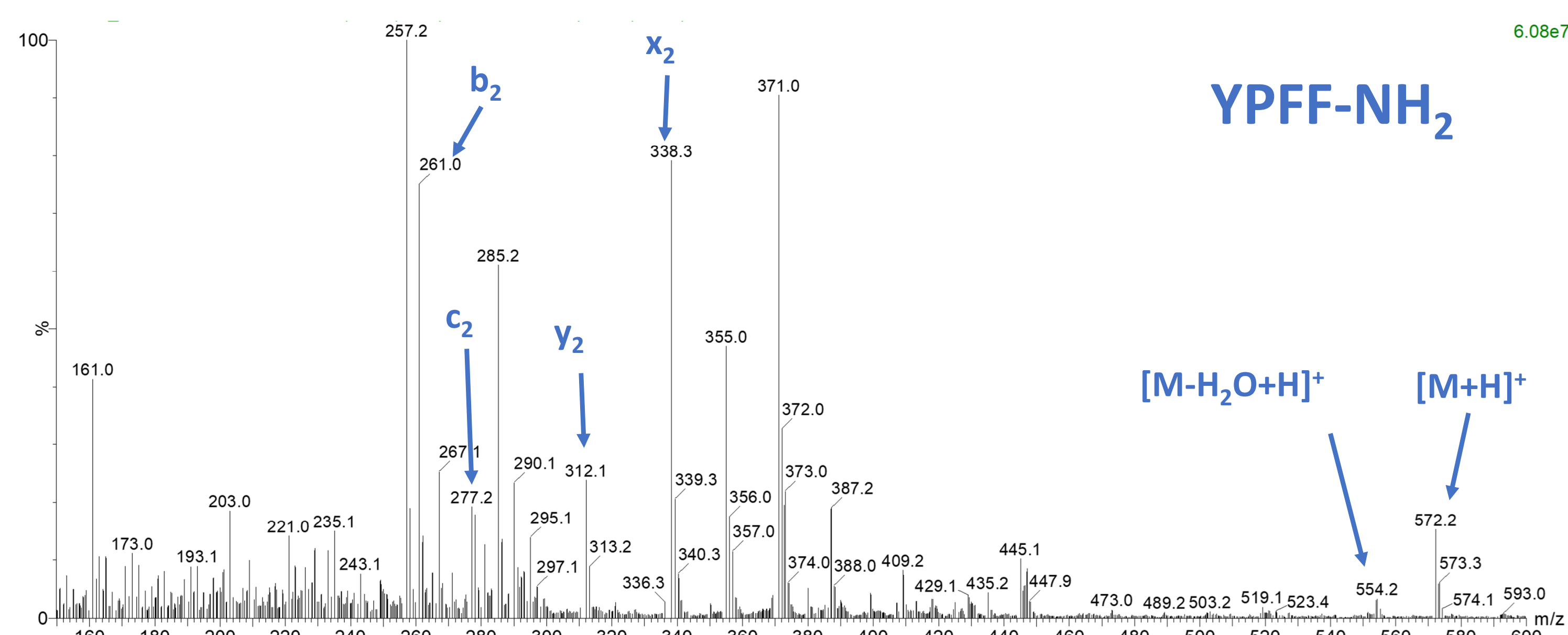
### Method

- ❖ **Target peptides:** endomorphin-2 (YPFF-NH<sub>2</sub>), leu-enkephalin (YGGFL), bradykinin (RPPGFSPFR) and representative peptides of the SARS-CoV-2 virus spike protein (GVYYPDK, IADYNY, QIAPGQTGK).
- ❖ **Sample preparation:** peptides were dissolved in water and mixed in 25% water and 75% methanol with 15 mM of dibasic phosphate buffer.
- ❖ **LDTD-QqQMS parameters:**
  - Ion source (Figure 1): LDTD model W-960 (Phytronix)
  - Laser pattern: 100% in 6 s then held for 4 s
  - Gas flow: 3 L/min
  - Corona needle current: 3µA
  - QqQMS: Xevo TSQ-micro triple quadrupole (Waters)
- ❖ **Quantification:** internal calibration using deuterated isotopologues of the target peptides

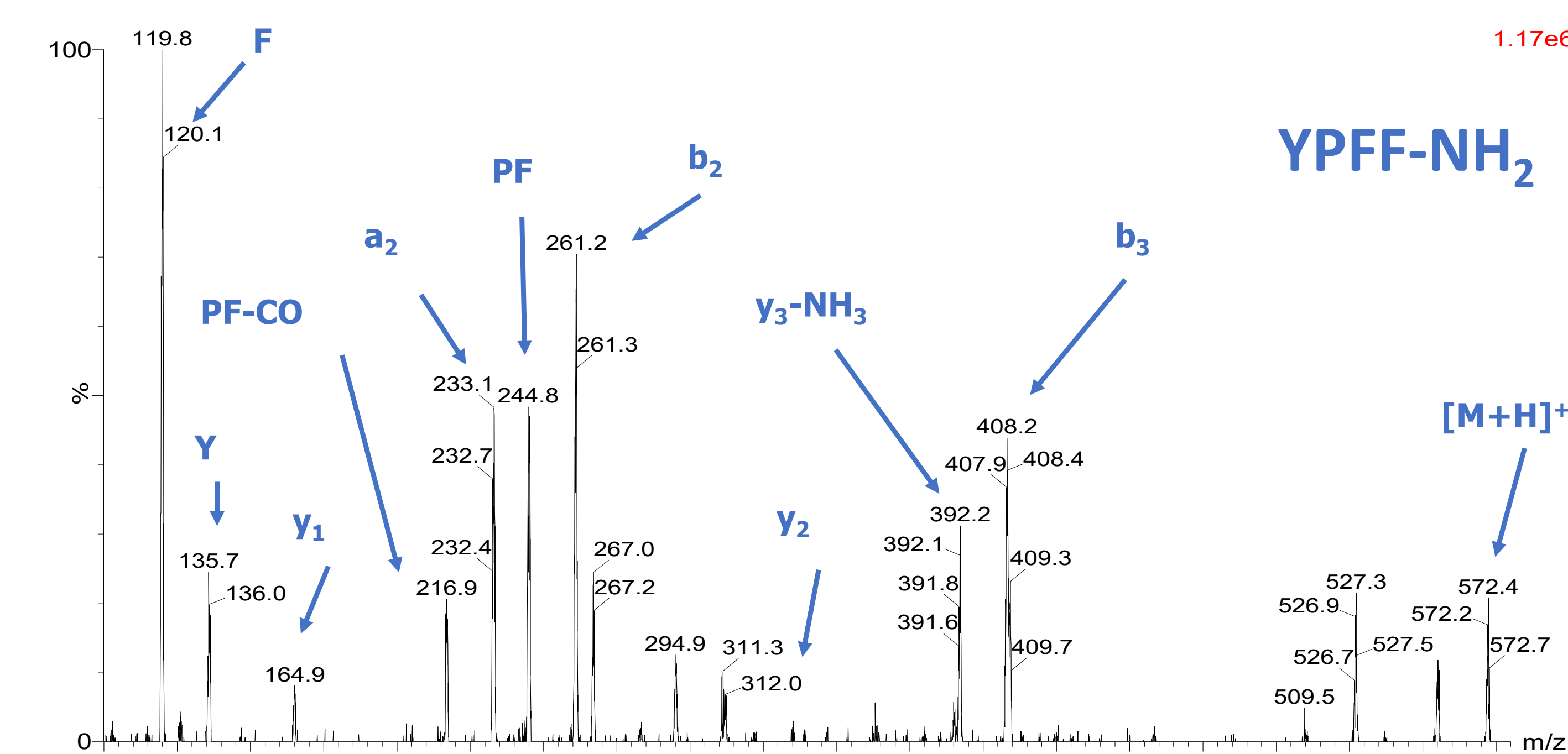
### Results

#### Detection of peptides

- ❖ [M+H]<sup>+</sup> and [M-H<sub>2</sub>O+H]<sup>+</sup> ions were observed for endomorphin-2 (Figure 2) and leu-enkephalin.
- ❖ a<sub>n</sub>, b<sub>n</sub>, c<sub>n</sub> and y<sub>n</sub>-ions are the most observed precursor and product ions.

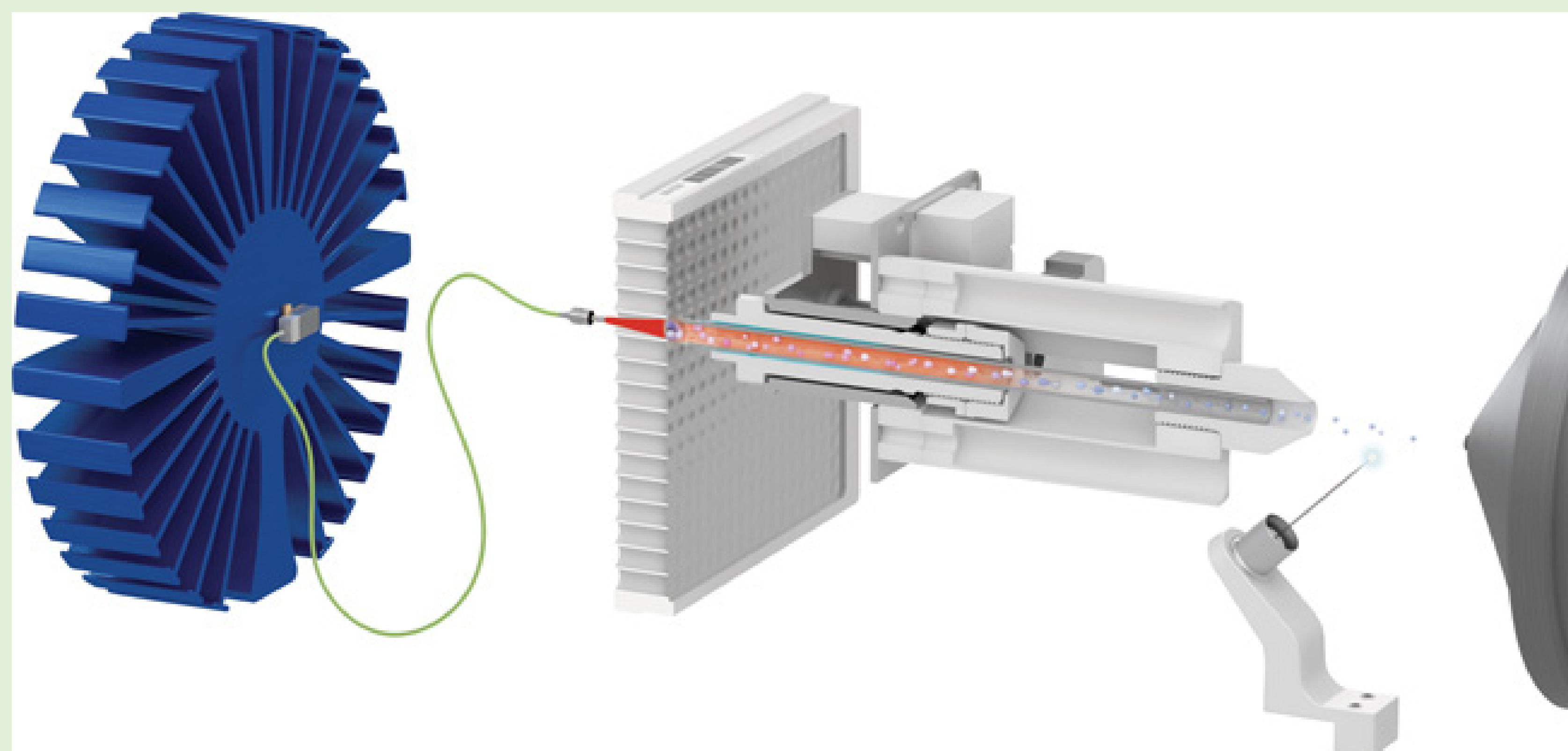


**Figure 2.** Full scan of endomorphin-2 generated by LDTD in the positive mode.



**Figure 3.** Product ion scan of  $m/z$  572 the [M+H]<sup>+</sup> ion of endomorphin-2 generated by LDTD in the positive mode.

Peptides can be  
detected and  
quantified in a  
few seconds  
using  
LDTD-QqQMS



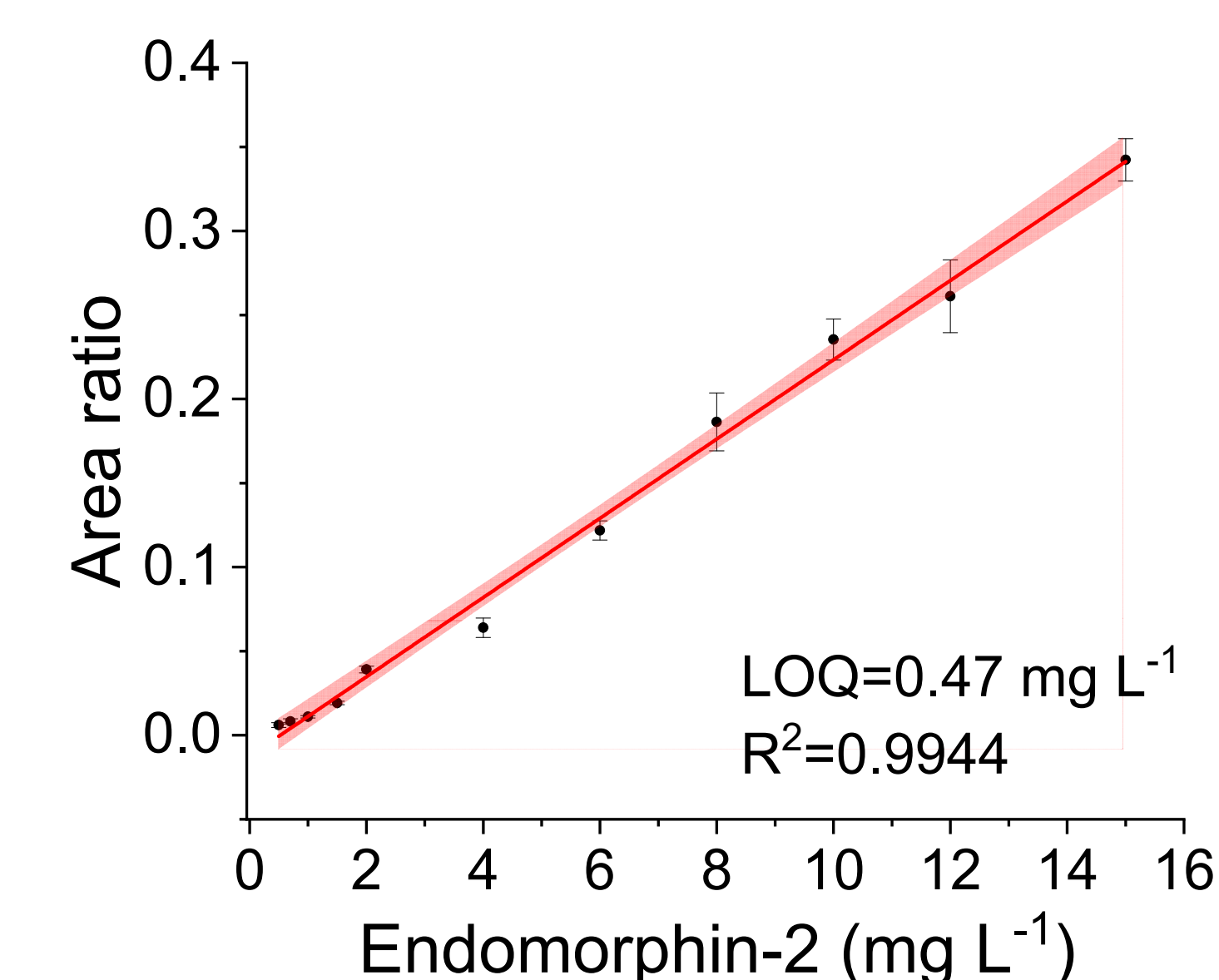
**Figure 1.** Diagram of the LDTD source.



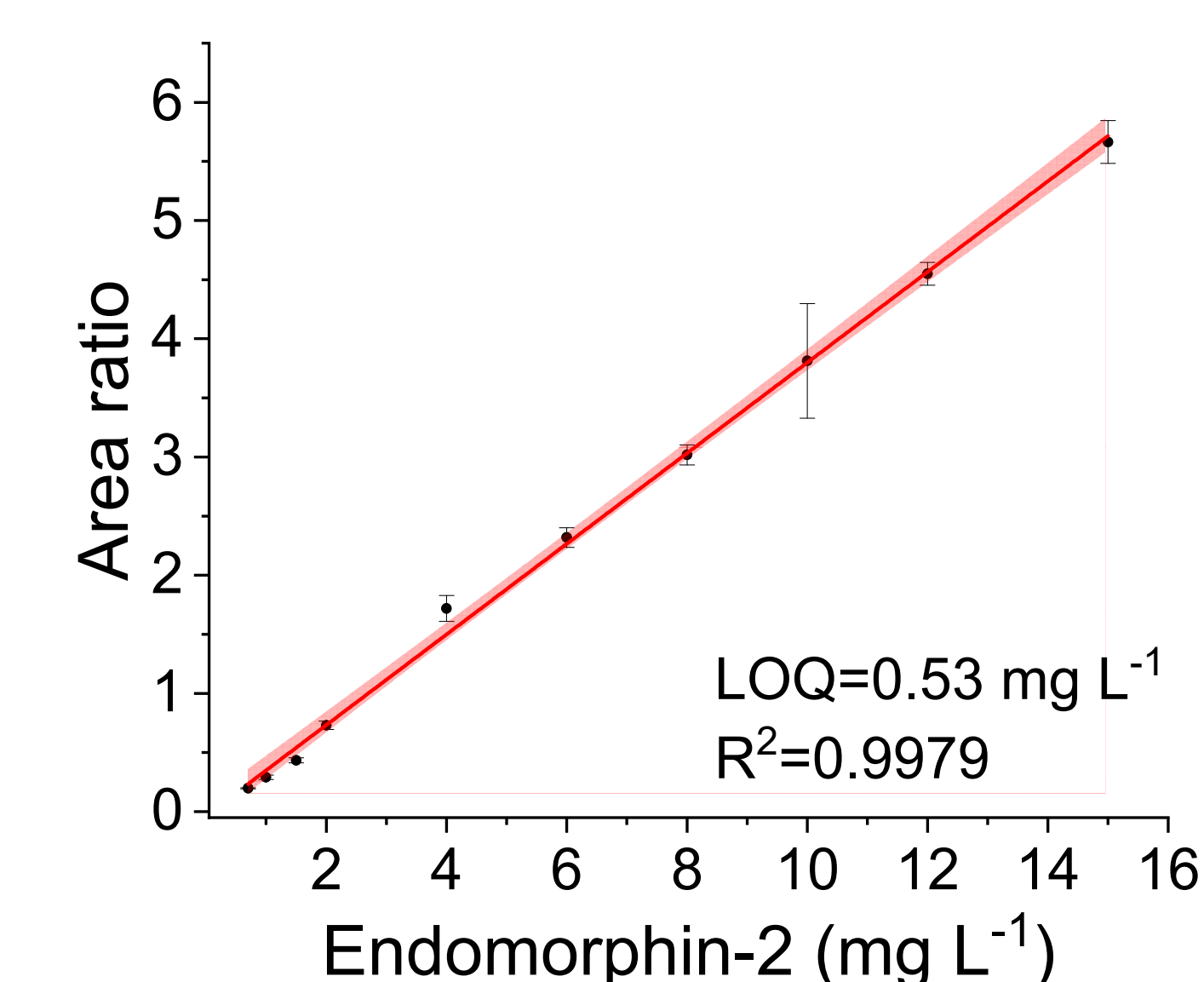
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#### Quantification of peptides

- ❖ Endomorphin-2, bradykinin, IADYNY and QIAPGQTGK can be quantified in the solvent (15 mM K<sub>2</sub>HPO<sub>4</sub> in H<sub>2</sub>O-MeOH 1:3) with a R<sup>2</sup> > 0.99.
- ❖ Endomorphin-2, IADYNY and QIAPGQTGK can be quantified in a 20 mg/L digested BSA matrix with R<sup>2</sup>>0.99.
- ❖ Calculated LOQ were between 0.4 and 2 mg/L depending on the peptide.



**Figure 4.** Calibration curve of endomorphin-2 in the solvent (MRM transitions used:  $m/z$  554 →  $m/z$  362 for endomorphin-2 and  $m/z$  577 →  $m/z$  408 for endomorphin-2-d<sub>5</sub>).



**Figure 5.** Calibration curve of endomorphin-2 spiked in a 20 mg/L digested BSA (MRM transitions used:  $m/z$  572 →  $m/z$  245 for endomorphin-2 and  $m/z$  577 →  $m/z$  233 for endomorphin-2-d<sub>5</sub>).

- ❖ Generally, coefficients of determination were higher when both peptide MRM transition and deuterated isotopologue MRM transition used isotopologue precursor ions to calculate areas ratios .

**Table 1.** Coefficients of determination obtained for endomorphin-2 calibration curves in a 20 mg/L digested BSA matrix (in green: R<sup>2</sup> when MRM transitions used isotopologue precursor ions).

	Endomorphin-2-d <sub>5</sub> MRM transitions					
	559→390	559→362	577→120	577→261	577→233	577→408
Endomorphin-2 MRM transitions	572→120	2-15 mg/L R <sup>2</sup> = 0.9615	2-15 mg/L R <sup>2</sup> = 0.9592	0.7-15 mg/L R <sup>2</sup> = 0.9977	0.7-15 mg/L R <sup>2</sup> = 0.9955	0.7-15 mg/L R <sup>2</sup> = 0.9966
	572→408	2-15 mg/L R <sup>2</sup> = 0.9506	2-15 mg/L R <sup>2</sup> = 0.9476	0.7-15 mg/L R <sup>2</sup> = 0.9974	0.7-15 mg/L R <sup>2</sup> = 0.9925	0.7-15 mg/L R <sup>2</sup> = 0.9942
	572→261	2-15 mg/L R <sup>2</sup> = 0.9636	2-15 mg/L R <sup>2</sup> = 0.9610	0.7-15 mg/L R <sup>2</sup> = 0.9976	0.7-15 mg/L R <sup>2</sup> = 0.9950	0.7-15 mg/L R <sup>2</sup> = 0.9969
	572→245	2-15 mg/L R <sup>2</sup> = 0.9644	2-15 mg/L R <sup>2</sup> = 0.9588	0.7-15 mg/L R <sup>2</sup> = 0.9966	0.7-15 mg/L R <sup>2</sup> = 0.9957	0.7-15 mg/L R <sup>2</sup> = 0.9979
	554→390	0.7-15 mg/L R <sup>2</sup> = 0.9951	0.7-15 mg/L R <sup>2</sup> = 0.9933	0.7-15 mg/L R <sup>2</sup> = 0.9827	0.7-15 mg/L R <sup>2</sup> = 0.9896	0.7-15 mg/L R <sup>2</sup> = 0.9910
	554→362	0.7-15 mg/L R <sup>2</sup> = 0.9966	0.7-15 mg/L R <sup>2</sup> = 0.9948	0.7-15 mg/L R <sup>2</sup> = 0.9835	0.7-15 mg/L R <sup>2</sup> = 0.9908	0.7-15 mg/L R <sup>2</sup> = 0.9918
	554→199	2-15 mg/L R <sup>2</sup> = 0.9933	2-15 mg/L R <sup>2</sup> = 0.9925	2-15 mg/L R <sup>2</sup> = 0.9896	2-15 mg/L R <sup>2</sup> = 0.9941	2-15 mg/L R <sup>2</sup> = 0.9963

### Acknowledgments

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