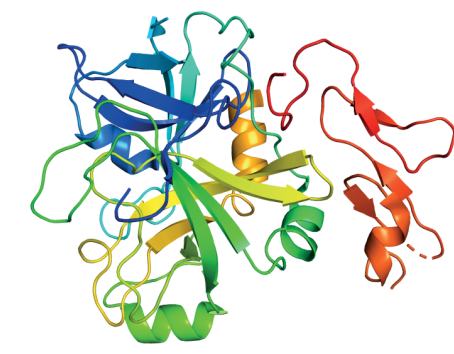


## Introduction

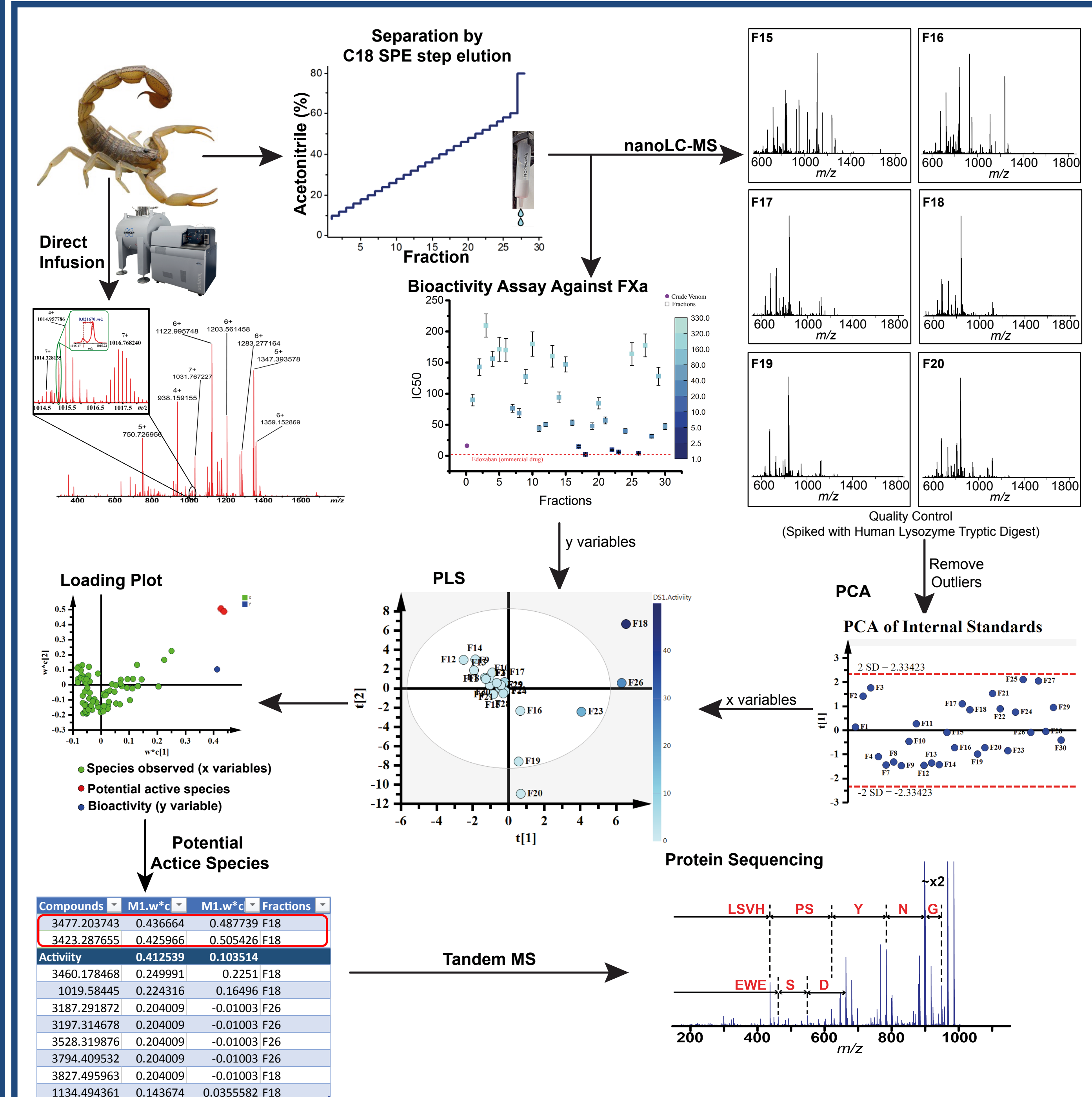
The scorpion *Mesobuthus Martensii*, is a species widely present in China and used in traditional Chinese medicines for thousands of years.<sup>1</sup> Venoms from this type of scorpions contain a highly complex mixture of proteins which have been proven to contain bioactive components.<sup>2,3</sup> These peptides show a diverse variety of pharmaceutical properties for the treatment of many conditions, such as cardiovascular problems, drug dependence, chronic pain, diabetes, and even tumors.<sup>4,5</sup>

Some proteins have shown in-vitro inhibition of the enzyme factor Xa, which catalyses the conversion of pro-thrombin to thrombin, causing blood coagulation, leading to thromboembolism. These proteins are highly varied in structure and often heavily modified and/or crosslinked with particularly high numbers of disulphide bonds, with only partial genome sequences available, sequencing and tandem MS of these species is extremely challenging.

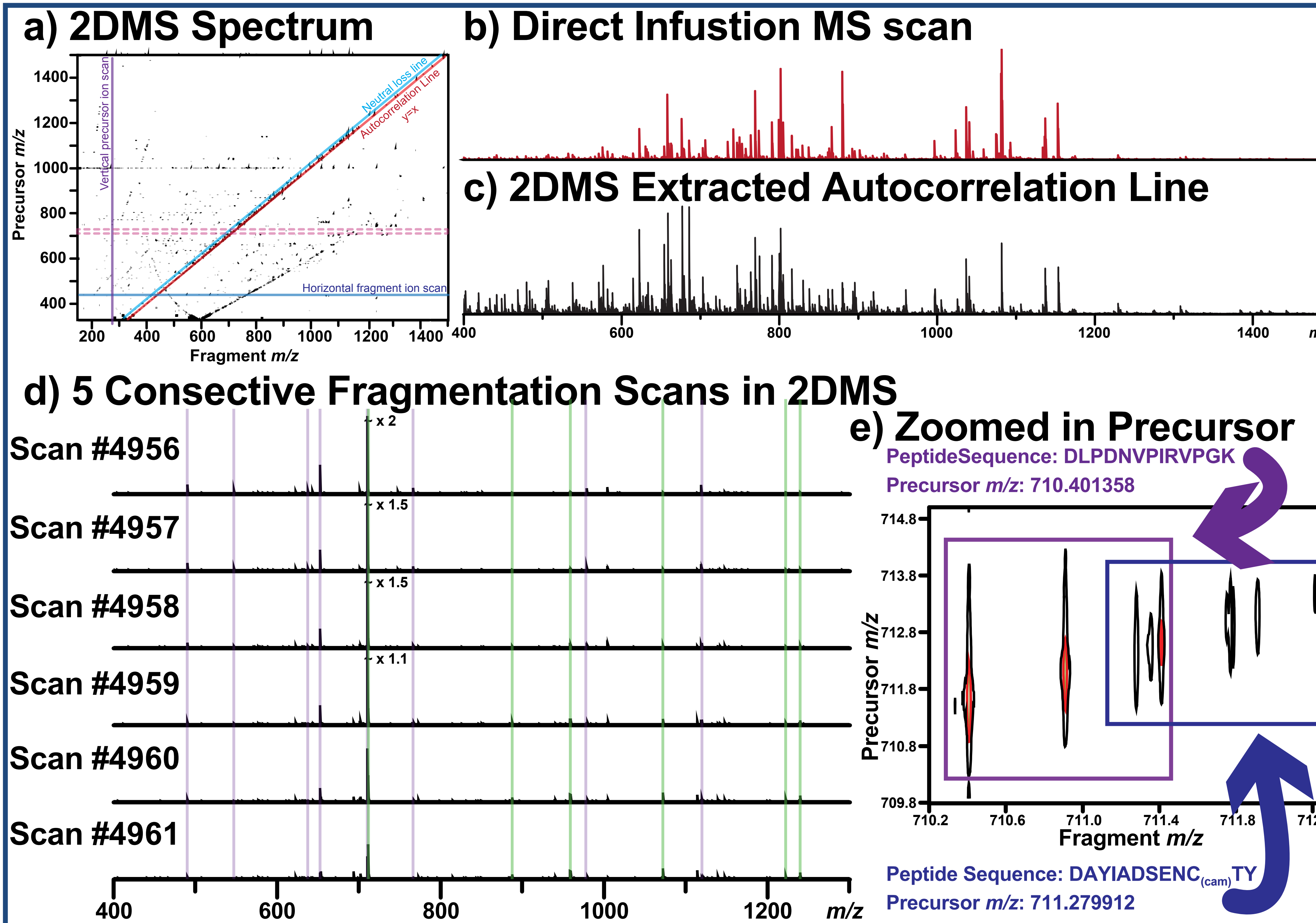


**Crystal Structure of Factor X**  
PDB:2BOK

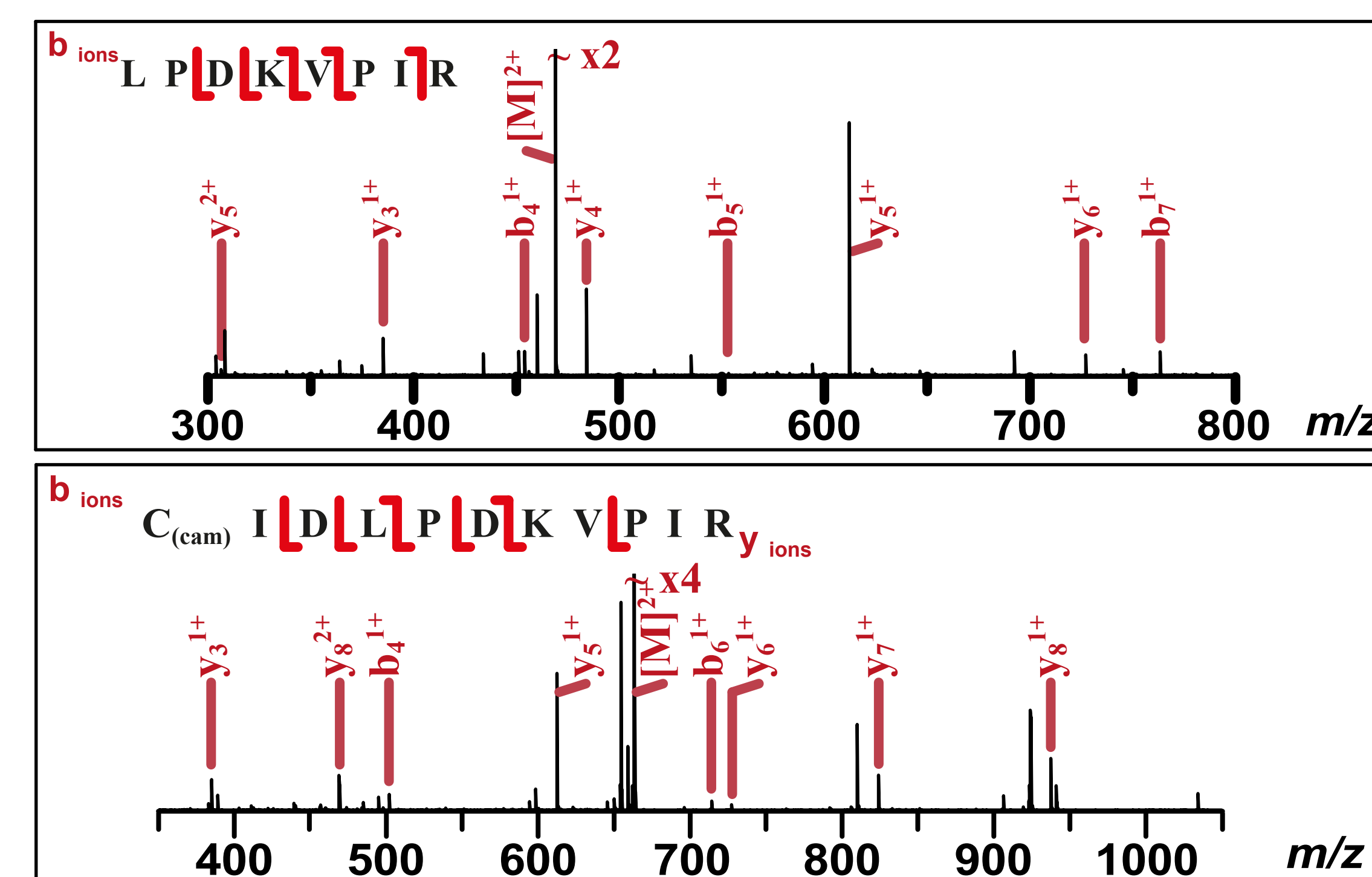
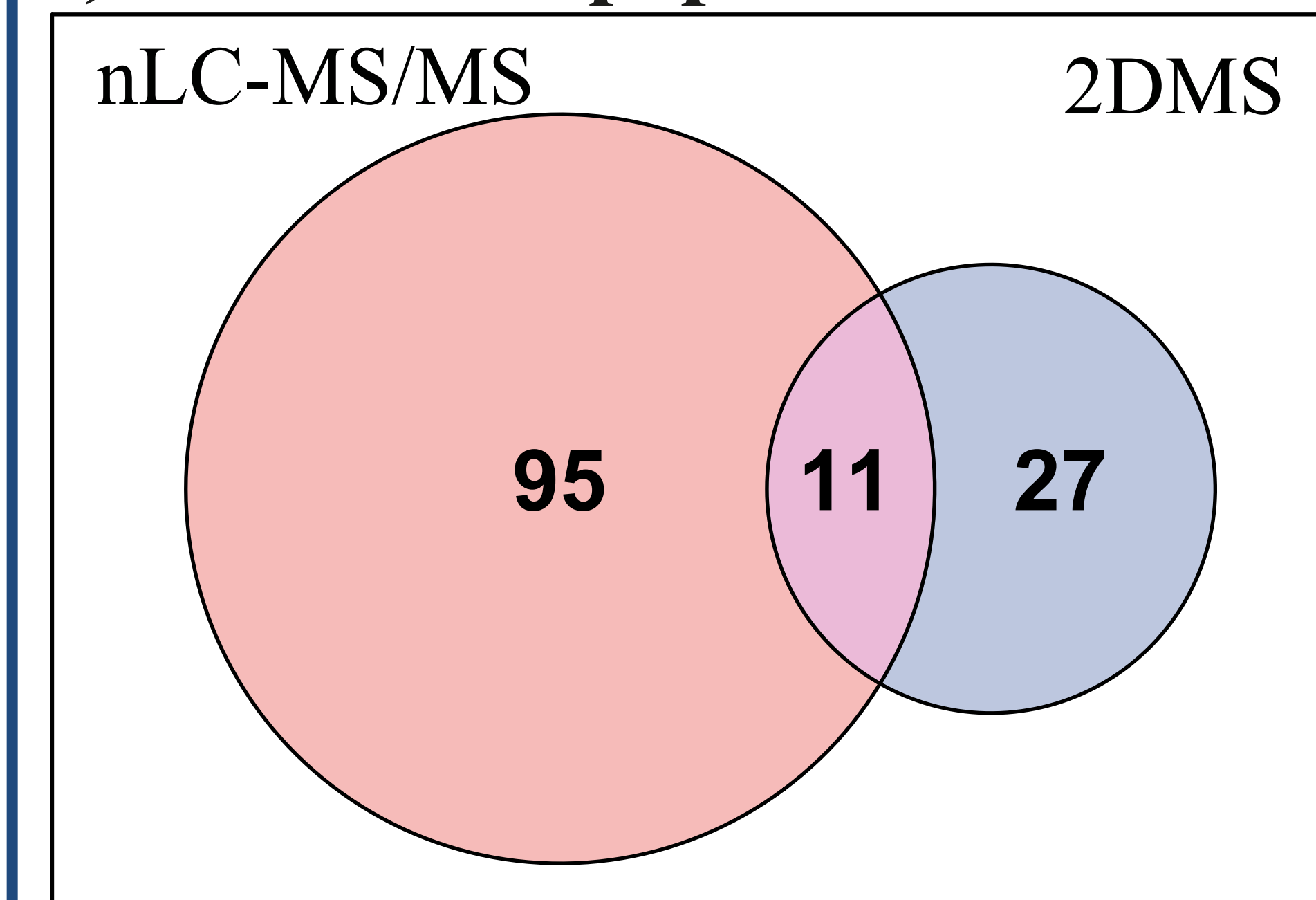
## Methods



## Results: 2D - FTICR-MS of Crude Venom Tryptic Digest



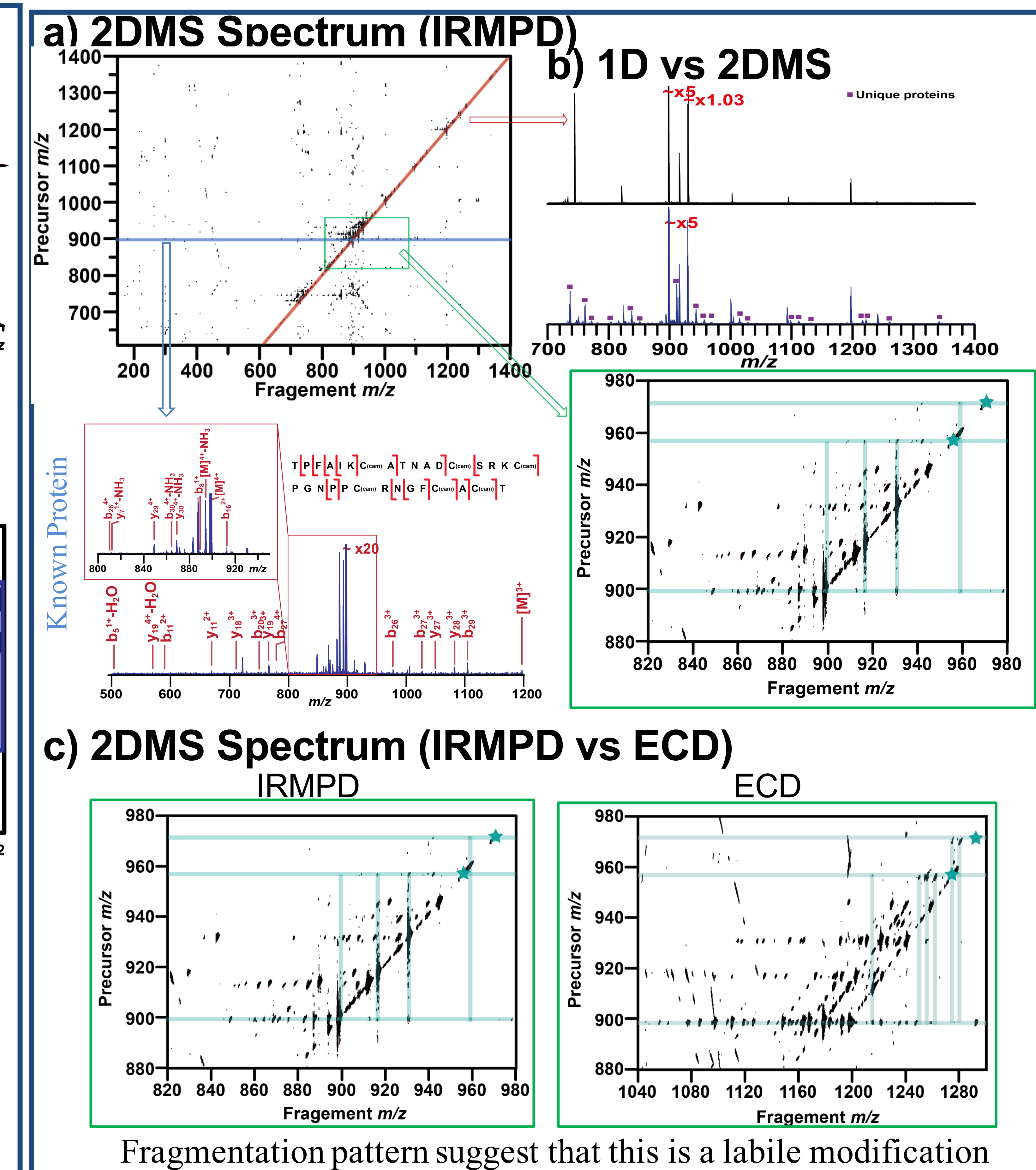
## f) Number of peptides identified



## Conclusions

- By utilising standard proteomics methods, it is difficult to find new potential pharmaceutical targets.
- 2D-FTICR-MS can provide additional information to nLC-MS/MS which is essential to de novo sequencing of unknown proteins and peptides.
- Bioactivity assays coupled with statistical methods helps to narrow down potential bioactive species
- Potential, novel FXa inhibitor protein has been sequenced.
- 2DMS allows for easy identification of labile modifications.
- The method is applicable to identifying potential pharmaceutical leads from other natural products.

## Results: 2DMS of Bioactive Species (Top-down)



## References

- Sridhara, S.; Chakravarthy, A. K.; Kalarani, V.; Reddy, D. C., Diversity and Ecology of Scorpions: Evolutionary Success Through Venom, Springer Singapore: 2016; pp 57-80
- Ortiz, E.; Gurrola, G. B.; Schwartz, E. F.; Possani, L. D., Toxicon 2015, 93, 125-135.
- D'Suze, G.; Rosales, A.; Salazar, V.; Sevcik, C., Toxicon 2010, 56 (8), 1497-1505.
- Xu, X.; Duan, Z.; Di, Z.; He, Y.; Li, J.; Li, Z.; Xie, C.; Zeng, X.; Cao, Z.; Wu, Y.; Liang, S.; Li, W., Journal of Proteomics 2014, 106, 162-180.
- Guan, R.-J.; Xiang, Y.; He, X.-L.; Wang, C.-G.; Wang, M.; Zhang, Y.; Sundberg, E. J.; Wang, D.-C., Journal of Molecular Biology 2004, 341 (5), 1189-1204.

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