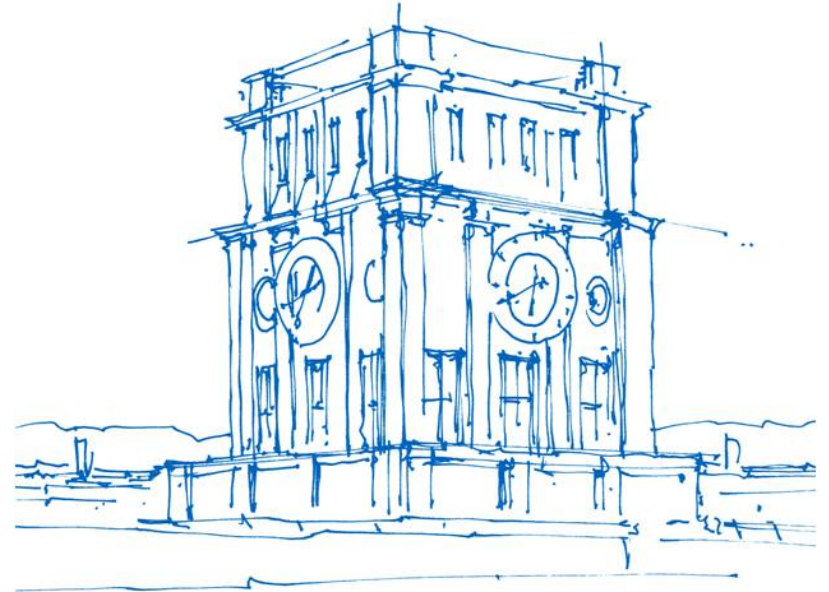# Real-time spectrum prediction in Skyline via ProteomicsDB's gRPC interface to Prosit

Tobias Schmidt

Technische Universität München

Uhrenturm der TUM

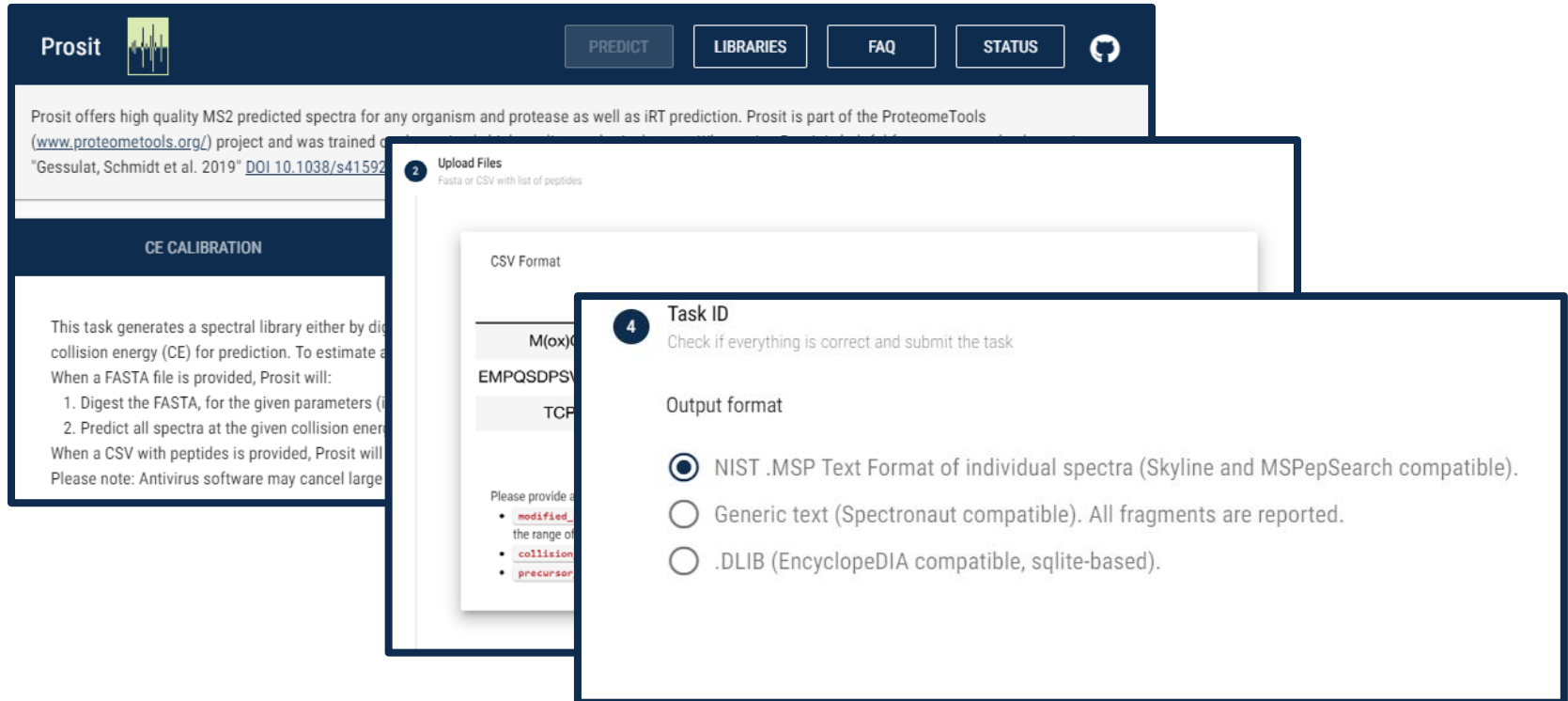# Real-time spectrum prediction in Skyline via ProteomicsDB's gRPC interface to **Prosit**

Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning

Siegfried Gessulat [1,2,7], Tobias Schmidt [1,7], Daniel Paul Zolg [1], Patroklos Samaras [1], Karsten Schnatbaum [3], Johannes Zerweck [3], Tobias Knaute [3], Julia Rechenberger [1], Bernard Delanghe [4], Andreas Huhmer [5], Ulf Reimer [3], Hans-Christian Ehrlich [2], Stephan Aiche [2], Bernhard Kuster [1,6]* and Mathias Wilhelm [1]*

Spectral libraries are just a click away

Real-time spectrum prediction in Skyline via **ProteomicsDB's gRPC interface** to Prosit

Tobias Rhode (a student at the MacCoss lab) was sent to our lab to evaluate with us how to become "real-time"

Real-time spectrum prediction in Skyline via ProteomicsDB's gRPC interface to Prosit
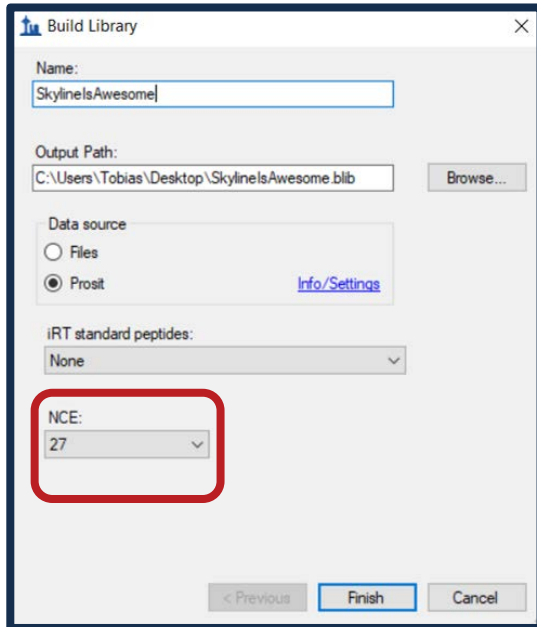
* Predicting the human Swiss-Prot database takes as long as listening to this slide (~30s)
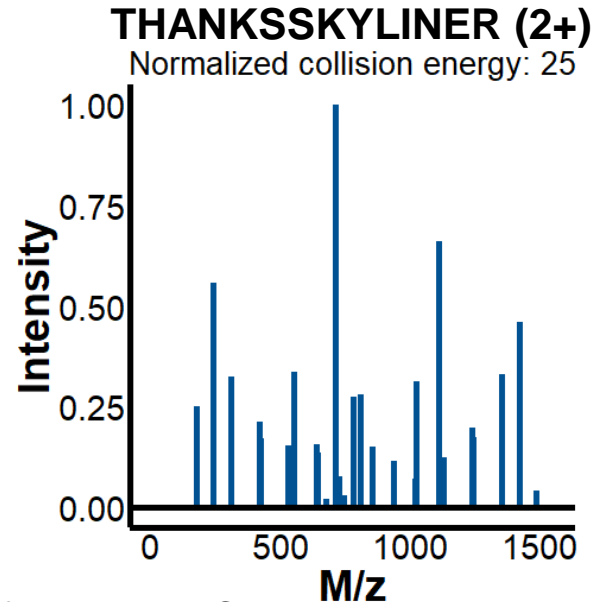
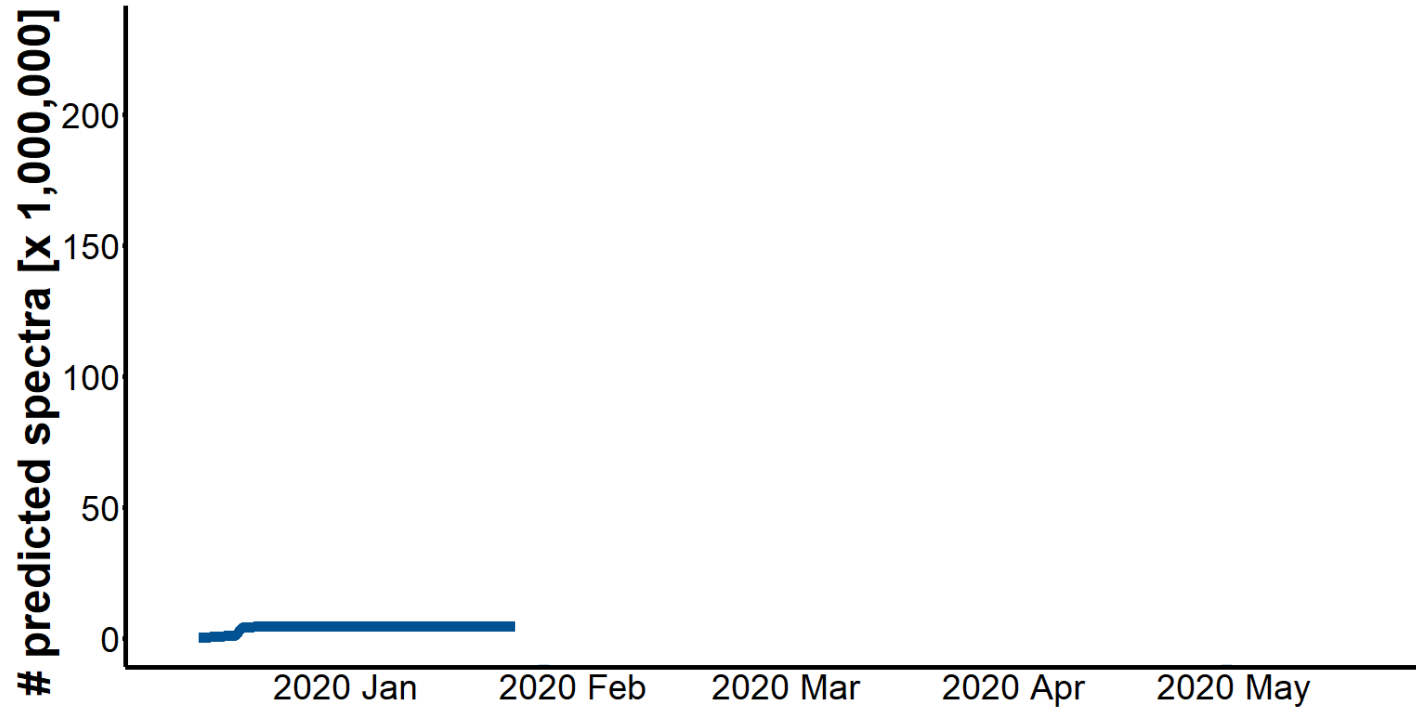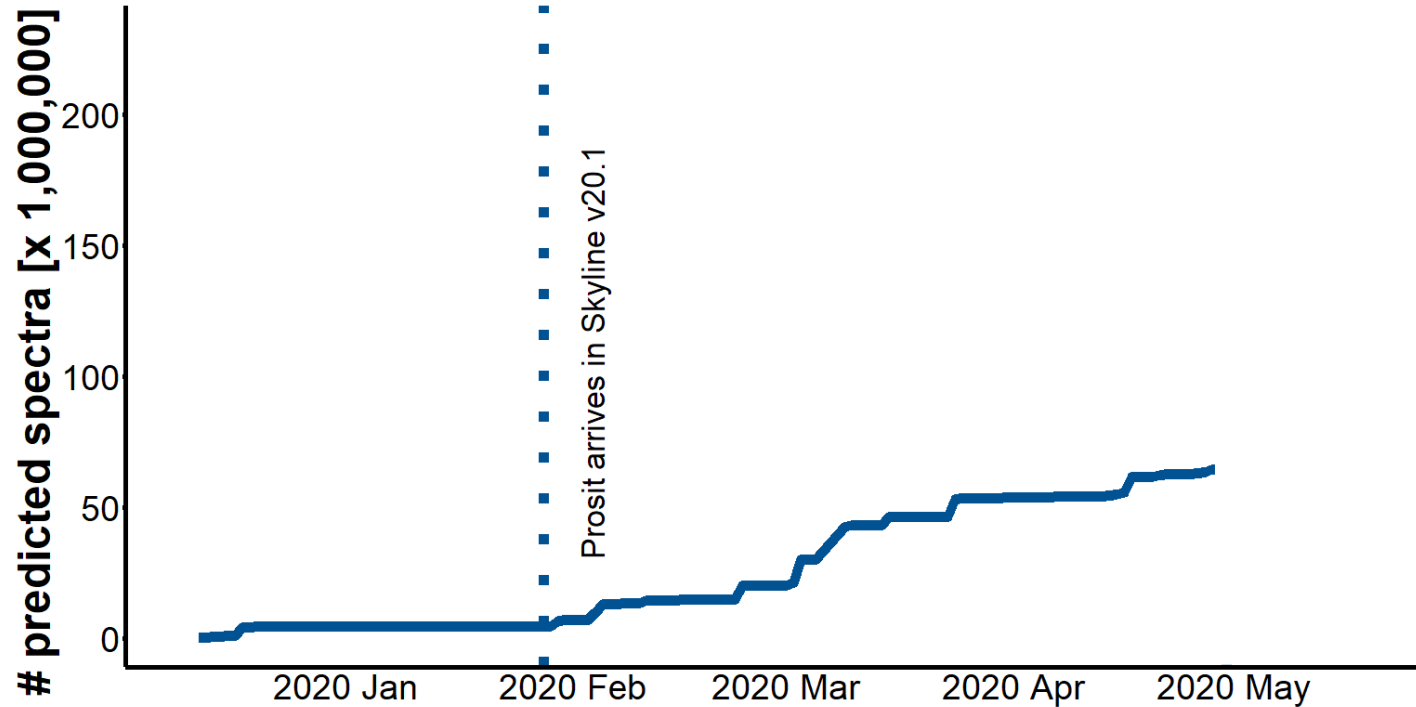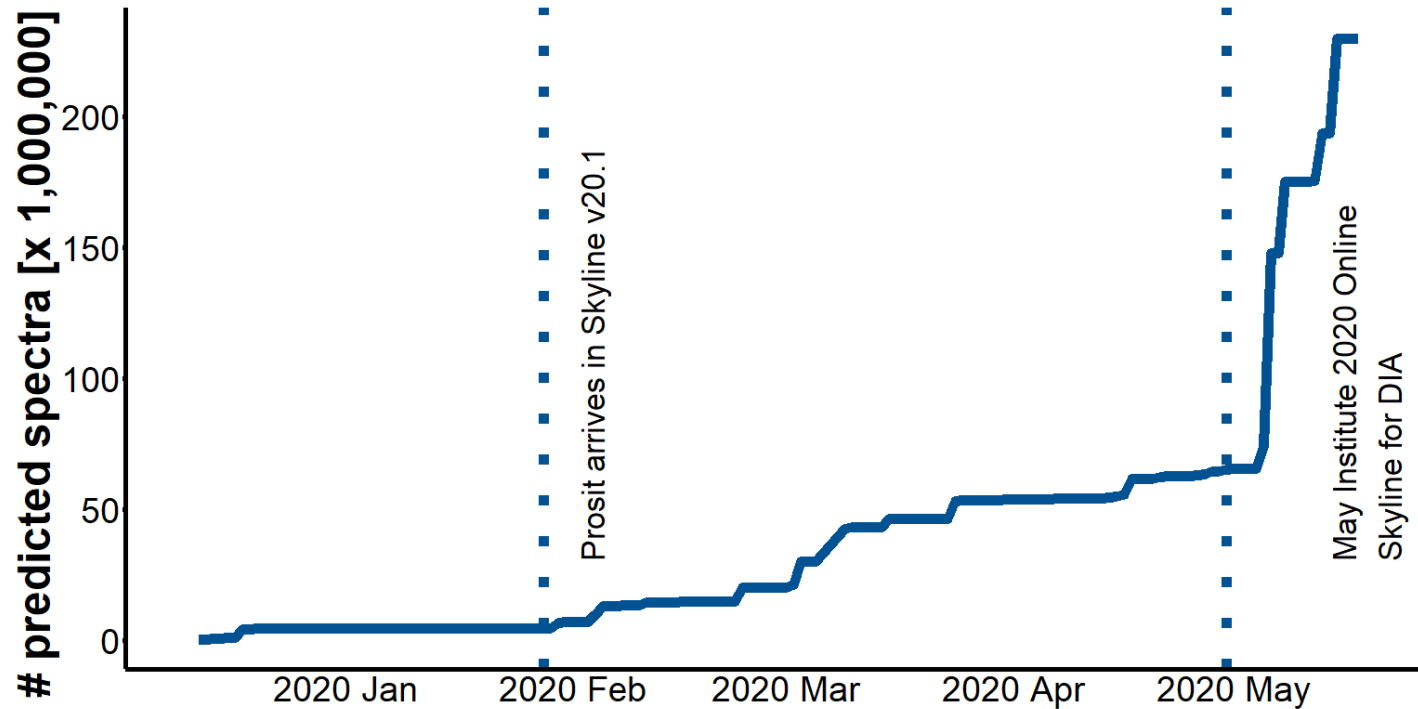Word of caution: for optimal NCE, please use our CE alignment tool at proteomicsdb.org/prosit
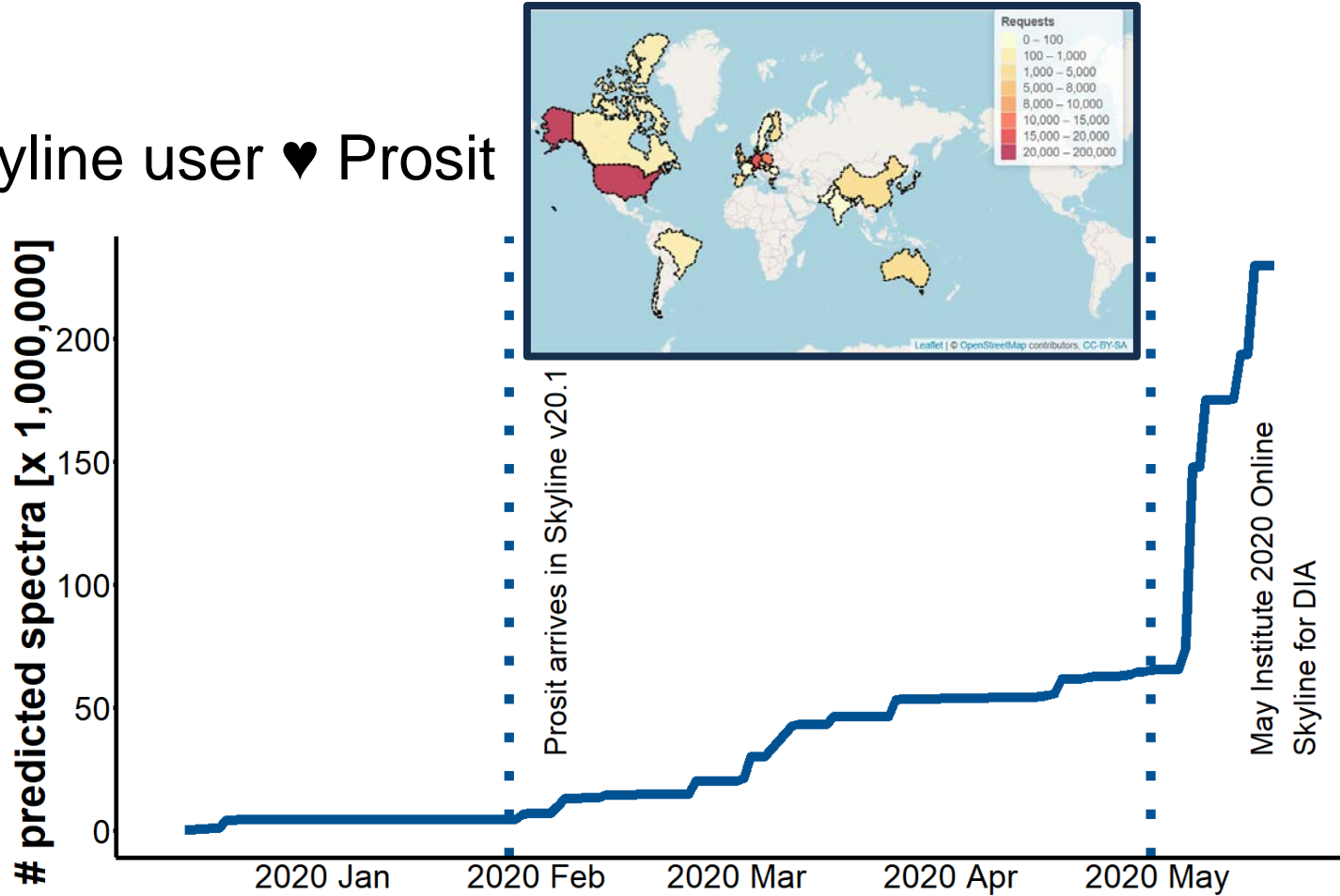
Skyline user ♥ Prosit
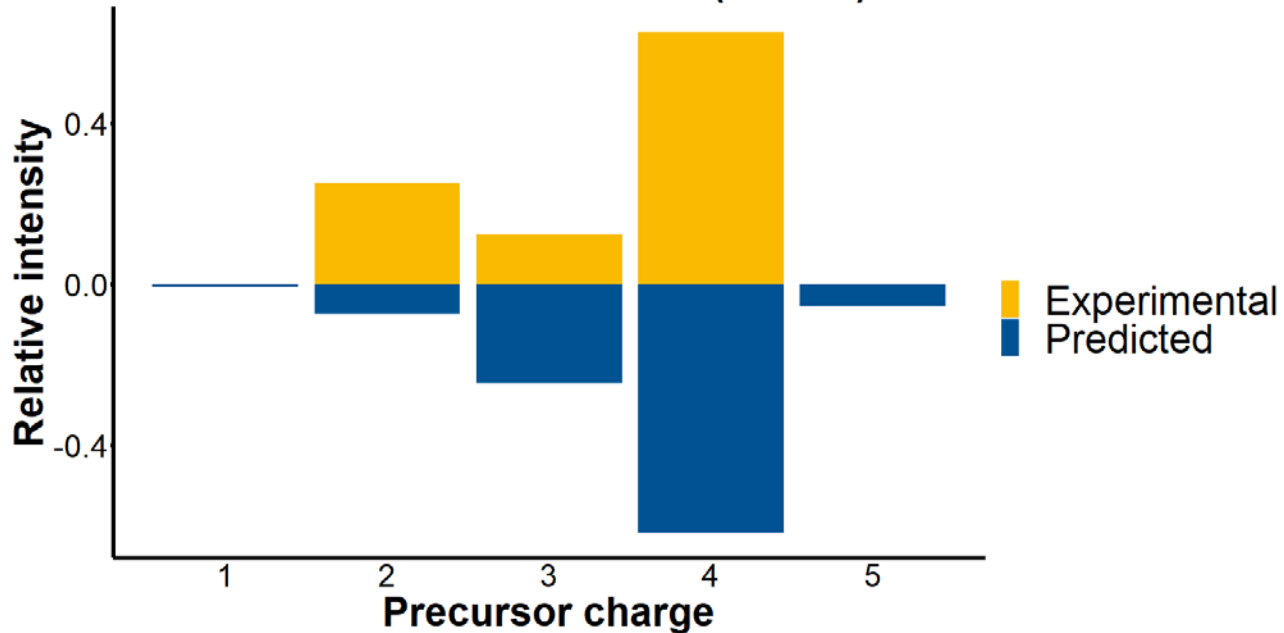
Skyline user ♥ Prosit

Skyline user ♥ Prosit

Skyline user ♥ Prosit

Outlook for more Prosit features in Skyline

Prosit keeps a common interface => new models will need minimal work for Skyline developers

GHYRGDPNWFMKKAQE (R=0.91)

TUM

Bernhard Kuster
Siegfried Gessulat
Patroklos Samaras
Miriam Abele
And all lab members

SAP UCC
University Competence Center

Johannes Rank
Marwin Shraideh
Helmut Krcmar

Skyline

Brendan McLean
Tobias Rhode
Brian Connolly

Want to learn more?

Brendan MacLean @ WOD am 09:30
Prosit meets Skyline

Mathias Wilhelm @ MOD am 10:10
Extending Prosit's predictions to proteotypicity, precursor ion charge and ion mobility collisional cross sections