

## Enhanced usage of top-down data for de novo sequencing of antibodies

*Thursday, August 28, 2025 4:50 PM (15 minutes)*

The Twister algorithm (Vyatkina et al., 2015, 2016, 2017), initially intended for de novo sequencing of antibodies from top-down MS/MS data supported with high-resolution bottom-up MS/MS spectra, is being developed further –currently aiming, at particular, at taking the maximum profit from internal fragment ions. In this talk, we will present the latest version of the Twister algorithm, along with the most recent results obtained.

### User consent

yes

**Author:** VYATKINA, Kira (Sechenov University)

**Presenter:** VYATKINA, Kira (Sechenov University)

**Session Classification:** Biopharmaceutical & Therapeutic Proteins