# Poster Proposal

* Exploring equine atypical myopathy through label-free proteomics

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In Europe, equine atypical myopathy (AM) is a seasonal intoxication linked to the ingestion and metabolization of toxins contained in seeds and seedlings of *Acer pseudoplatanus*. About 74% of intoxicated horses die within the first 72h following onset of an acute rhabdomyolysis syndrome. Since some co-grazing horses remain free of any abnormal clinical signs while blood testing confirms toxins’ ingestion, we aim at identifying potential causes of resistance whilst highlighting modified metabolic pathways.

For our preliminary studies, serum samples of two AM affected horses and two healthy co-grazing horses were assayed using Filter-Aided Sample Preparation before being analyzed using nano-LC-ESI-MS/MS timsTOF Pro coupled with an UHPLC nanoElute.

Two types of quantitative analyses were conducted through normalized t-testing and Benjamini-Hochberg correction. First, quantitative total spectral counting analysis in Scaffold showed a total of 168 differentially expressed proteins between both groups. Second, ion intensity-based label-free quantitative analysis was performed in PEAKS StudioXPro, which resulted in 252 differentially expressed proteins.

Interestingly, gene ontology analysis of these differentially expressed proteins point out *i.e.,* modifications in the coagulation cascade, the complement system and glycolysis.

This preliminary study sets the path for a more extensive investigation comparing AM affected horses, healthy co-grazing and reference horses.