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Mass spectrometry based serum glycoproteomic profiling: Challenges and opportunities

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Changes in glycosylation of serum proteins can be used as biomarkers for various diseases. However, profiling of the glycosylation patterns of these proteins presents a significant challenge due to the diversity of glycan structures and the overwhelming dynamic range of serum proteins concentrations. Moreover, simultaneous identification of the glycosylation site and glycan sequence is very challenging due to the labile nature of the glycans. New developments in mass spectrometry and bioinformatics enable high throughput identification of glycopeptides from the data generated by this mass spectrometer. We present proof of concept data to showcase a workflow that combines boronic acid enrichment of glycopeptides and glycoproteins, coupled with EThcD fragmentation technique, which is unique to the Orbitrap Fusion Lumos mass spectrometer. Combined with data processing using bionic and optimal experimental design, we can identify and quantify over 200 glycosylation forms and sites (O-linked and N-linked) from minute amount of human serum.

Biography

Yishai Levin has completed his PhD from the University of Cambridge, UK. He is Head of the de Botton Institute for Protein Profiling, which is one of the platforms at The Nancy and Stephen Grand Israel National Center for Personalized Medicine. He has published more than 40 papers in reputed journals and his greatest passion is applying proteomic technologies to clinical research.

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