

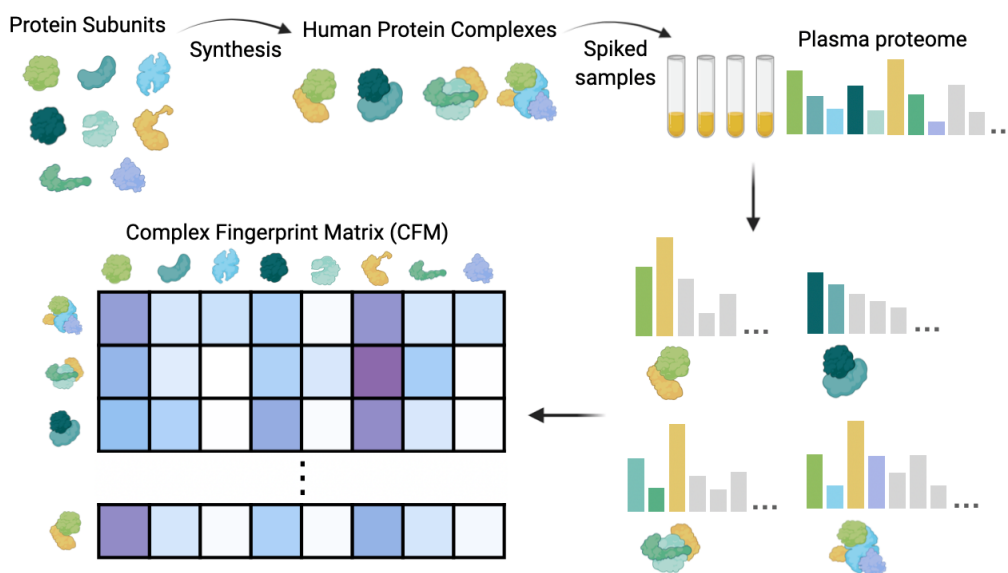
CONFIDENT

COMplexome Fingerprint DEconvolutioN Technology

Extending the Proteome
to complexome

- Breakthrough of protein complexes quantification
- Long-term fingerprint accumulation
- Utilization of established proteomics assays
- High-Dimensional Interdisciplinary landscape

Revolutionary Innovation of Complexome Profiling



High-throughput quantification:

Enabling large-scale quantification of protein complexes.

Innovative synthetic data:

Utilizing long-term accumulated Complex Fingerprint Matrix (CFM) for diverse and extensive complex measurements.

AI-based subunits connectivity:

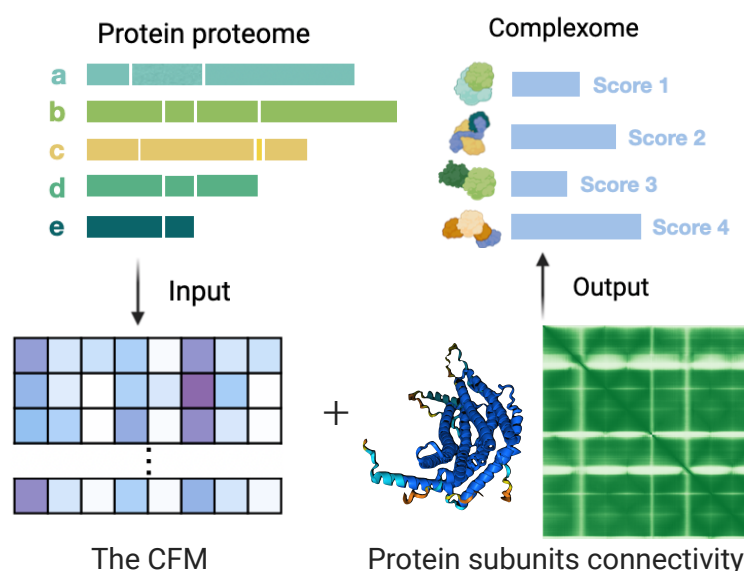
Taking advantage of AlphaFold's inference data of proteins connectivity

Advanced statistical modeling:

Utilize high-precision statistical modeling and deconvolution algorithms for accurate and comprehensive

Construct standard complex fingerprint matrix (CFM)

Add synthetic complexes into standard plasma samples, dividing them into aliquots for proteomics detection. Include a baseline reference sample for comparison. Complex interference during detection yield a unique Complex Fingerprint Matrix (CFM), portraying protein readout changes. Achieve CFM with abundant sample replicates, offering insights into natural complexome profiling.



Likelihood-based Deconvolution

Leverage the information encoded in the Complex Fingerprint Matrix (CFM) and the AI-based inference of protein subunits connectivity to establish a robust statistical model.

Dissect protein readout into distinct complexes, employing deconvolution algorithm to accurately estimate scores for each complex.

This streamlined approach provides a comprehensive and simplified insight into complex abundance patterns.

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Quantix BioSciences AB, org. nr. 559483-7428, Sareksvägen 13, SE-167 35 Bromma, Sweden

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