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Quantifying protein complexes with COMFIDENT

COMplex FIngerprint DEconvolutioN Technology (COMFIDENT) is a reference-guided deconvolution workflow that turns panel proteomics (e.g., SomaScan®/Olink®) into **complex-level abundance**.

It integrates two reference layers:

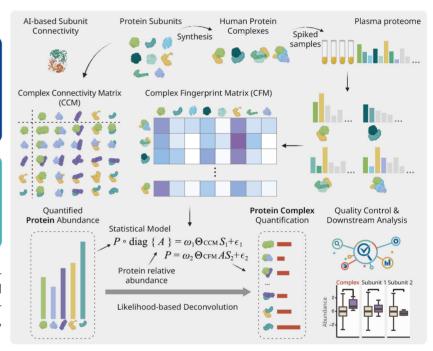
Complex Fingerprint Matrix (CFM)

curated human protein complexes profiled across >5,000 proteins and >2,000 complexes, capturing multi-subunit "fingerprints".

Complex Connectivity Matrix (CCM)

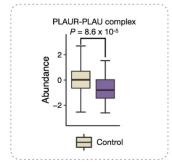
AI-based subunit connectivity scores (AlphaFold-driven) for millions of protein pairs.

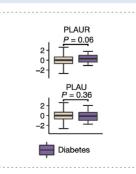
A likelihood-based statistical model combines **your protein abundances** with **CFM + CCM** to infer complex assembly/abundance, followed by QC, differential testing, and mechanism/biomarker interpretation.

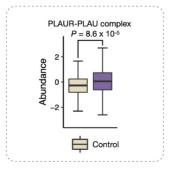


Example: Complex biomarkers for diseases (submitted & unpublished)

The results in the figure below demonstrate that the PLAUR-PLAU complex shows a significant difference in abundance between the control group and both the diabetes group and the calves pain group (N = 1,046). In contrast, individual components PLAUR and PLAU do not exhibit significant differences in abundance between the control group and the case groups. These findings suggest that the interaction between PLAUR and PLAU as a complex is more strongly associated with the tested conditions than the individual proteins alone. Meaning that the proteomic resources were not properly used to identify biomarkers.







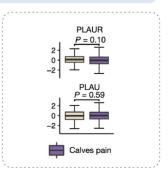


Figure: Association of the PLAUR-PLAU complex with type 2 diabetes and calves pain.