Olink Sessions



Industry Education Session

Proteomics at Population Scale: Insights from the UK Biobank Pharma Proteomics Project

Christopher Whelan, PhD
Director, Data Science, Neuropsychiatry, Johnson & Johnson

Moderated by Cindy Lawley, PhD Global Director, Population Health, Olink

Thursday, October 27 12:30 pm - 1:30 pm Room 306/South Building Lunch provided

CoLab Session

Considerations for integrating proteomics across 50,000+ sample population health genetic studies

Philippa Pettingill, PhD Director of Field Application Scientists, Olink

Klev Diamanti, PhD Data Scientist, Olink

Moderated by Cindy Lawley, PhD Global Director, Population Health, Olink

Thursday, October 27 3:00 pm - 3:30 pm CoLab Theater Assignment 1



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Olink Proteomics Inc., 130 Turner St, Building 2, Suite 230, Waltham, MA 02453, USA 1285, v1.0. 2022-10-11

Our technology is all over ASHG. List of talks and posters mentioning Olink technology.

Talks

Consequences of loss of function burden effects on the human plasma proteome in 54,306 UK Biobank participants C. Whelan | Program No. 632

Petree D/West Building | Tues. 7:00 pm - 7:30 pm

Mendelian randomization and colocalization characterize the impact of the plasma proteome on human complex diseases

D. Baird | Program No. 073 West Hall A/West Building | Wed. 8:45 am - 9:00 am

Proteogenomic analysis in UK Biobank identifies potential proteomic consequences of genetic susceptibility to Parkinson's disease

C. Robins | Program No. 274 Concourse Hall E/West Building | Thurs. 10:45 pm - 11:00 pm

Novel therapeutic target discovery using circulating proteins in up to 42,000 UK Biobank participants through systematic Mendelian randomization and genetic colocalization

L. Chen | Program No. 338

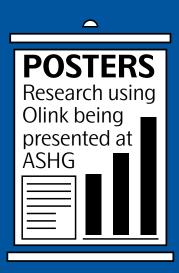
West Hall A/West Building | Thurs. 6:15 pm - 6:35 pm

An atlas of associations between plasma protein biomarkers and polygenic risk scores for complex human diseases D. Chasioti | Program No. 388

Concourse Hall E/West Building | Fri. 11:00 am - 11:15 pm

Characterising the circulating proteome of adiposity through use of weight loss interventions and Mendelian randomisation

L. Goudswaard | Program No. 502 Room 515 / West Building | Fri. 4:00 pm - 4:15 pm



Wed. 3:00 pm - 4:45 pm | Poster Hall South Building

Genome-wide association of NASH and Mendelian randomization with plasma protein levels identifies putative protein changes resulting from disease.

E. Smith | Board No. PB1426

Comprehensive signal identification highlights the contribution of protein QTLs to complex trait genetics

J. Chiou | Board No. PB2543

Consequences of loss of function burden effects on the human plasma proteome in 54,306 UK Biobank participants

C. Whelan | Board No. PB2547

Exome-wide association analyses of 1,463 proteins in 31k participants of the UK Biobank reveal the spectrum of coding variant effects on protein levels.

H. Kim | Board No. PB2579

The effect of rare protein-coding sequence variants on the human plasma proteome

B. Prins | Board No. PB2699

UK Biobank whole genome sequencing and large-scale proteomics identifies novel protein quantitative trait loci (pQTLs) contributing to human disease.

L. Hou | Board No. PB2711

Using an NGS readout for high-throughput proteome-wide analysis in large population health studies.

C. Lawley | Board No. PB3176

Mendelian randomization implicates GDF15 blood levels as a causal factor in inflammatory disease.

P. Timmers | Board No. PB3509

Proteome-Wide Association Analysis in the Women's Health

Initiative Study

B. Chen | Board No. PB3565

Systematic Integration of Multi-omics Data for the Study of Coronary Artery Disease and Subclinical Atherosclerosis C. Yang | Board No. PB3596

Thurs. 3:00 pm - 4:45 pm | Poster Hall South Building

Evidence of allelic series with fine-mapped protein quantitative trait loci across 1,470 protein abundance measurements and 30 biochemistry measurements in UK Biobank participants.

A. Cortes | Board No. PB1361

Genetic profiling and improved predictive capability with proteinbased risk scores for IBD and disease progression using UK Biobank data.

X. Zeng | Board No. PB1405

Integration of proteomics quantitative trait loci into genetic association analysis of stroke in the African American population Y. Cai | Board No. PB1498

Characterization of transthyretin TTR missense variants for associations with hereditary transthyretin-mediated (hATTR) amyloidosis and hallmark symptoms in 470,000 UK Biobank whole exome sequences

M. Plekan | Board No. PB1782

An updated genetic atlas of the plasma proteome: Findings from the UK Biobank Pharma Proteomics Project (UKB-PPP)

B. Sun | Board No. PB2516

Connecting rare variation to extremes of plasma protein levels X. Xie | Board No. PB2546

Elucidating genomic disease associations using transcriptomic, proteomic and metabolomic data in 4,732 individuals E. Persyn | Board No. PB2564

A demonstrated workflow to unleash the multiomic potential of a single blood draw.

B. Nui | Board No. PB2873

How UK Biobank is democratising access to large-scale genomic and phenotypic data for discovery science

B. Lacey | Board No. PB3217

Hand grip strength and its underlying genetics is associated with widespread protein changes revealed by population-based plasma proteomics.

Y. Huang | Board No. PB3428

Omics profiling in overweight and obese children in the California Bay Area during childhood development and the effects of a multimodal health intervention program tailored to a majority Latinx community

J. Li-Pook-Than | Board No. PB3532