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Thermo Fisher advances proteomics-enabled Parkinsonâ??s precision medicine

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Olinkâ?¢ Explore HT analysis of approximately 5,500 research samples completed, with data now available



Thermo Fisher Scientific Inc., the world leader in serving science, has announced the completion of Olink Explore HT proteomic analysis of approximately 5,500 research samples from The Michael J. Fox Foundation's (MJFF) landmark study, the Parkinson's Precision Medicine Initiative (PPMI). The resulting data are now in PPMI's data repository, where they are available to the global research community.

The project creates a large-scale proteomics resource designed to help researchers study Parkinson's disease at the protein level and investigate biological signals associated with disease progression, patient heterogeneity and potential biomarker development. By applying Olink technology to deeply characterised PPMI samples, Thermo Fisher is expanding access to MJFF's dataset that may help advance precision medicine approaches to Parkinson's research.

Olink, part of Thermo Fisher, enables high-throughput, affinity-based proteomic analysis using Proximity Extension Assay (PEA) technology. Olink's PEA-based platform is a scalable solution for protein biomarker analysis, supporting applications from discovery through translation and population-scale proteogenomics.

"Discovery is only the beginning in Parkinson's research," said Yan Zhang, president of proteomic sciences at Thermo Fisher. "The next challenge is determining which molecular signals are reproducible, clinically meaningful and useful for advancing Parkinson's precision medicine. Making these data available to the research community helps put that validation work into motion."