



Proteome Sciences is launching upgrades to its core proteomic services (SysQuant[®], TMTcalibrator[™] and Plasma Super Depletion) with increased multiplexing. Testing has shown that our new 16-plex reagents (TMTpro[™]) perform equivalently to the current 11-plex TMT[®] in terms of the numbers of quantified peptides and proteins, whilst providing a 50% increase in the number of samples that can be analysed in a single experiment.

“The realization of a 16plex reagent set for tandem mass tags represents a true milestone and a landmark development for the field of quantitative proteomics. In our hands, these are fantastic reagents which integrated into our TMT workflows seamlessly. Complex experimental designs including biological replicates as well as dose-response, time series, and rescue measurements can now be assembled into a single 16-plex analysis. Remarkably, there are no missing values across the 16 channels, facilitating expression and phosphorylation level profiling at true proteome-scale depth.” (Prof. Steve Gygi - Harvard Medical School)