

Human Protein Identification by 21 T FT-ICR Mass Spectrometry

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It is estimated that there are over a million structurally unique proteins (“proteoforms”) in human cells. Each proteoform has the potential to impact health and disease. However, limitations of commercial mass spectrometers (MS) require hundreds of experiments to obtain reasonable coverage of the human proteome. Furthermore, commercial MS is typically limited to molecular weights below 30 kDa, rendering half the human proteome inaccessible.

Researchers’ first experiments with the MagLab’s 21 Tesla FT-ICR mass spectrometer produced more detected proteins and proteoforms per experiment than any prior work (Figure 1A): the largest prior high-throughput human protein study had focused on smaller proteins of <30 kDa and identified 2.5 unique protein sequences per liquid chromatography mass spectrometry/mass spectrometry (LC-MS/MS) experiment. By contrast, we achieved more than 72 protein identifications per experiment, setting a new efficiency standard for intact protein analysis. Additionally, proteins identified ranged in size from 5 kDa all the way up to 55 kDa (Figure 1B), which is a two-fold higher mass range than the prior work.

The improved throughput, sequence coverage and molecular weight range available with the MagLab’s 21 Tesla FT-ICR mass spectrometer will facilitate discovery of potentially thousands of new proteoforms, a significant portion of which will have direct clinical relevance to human disease.

Facilities: Ion Cyclotron Resonance (21 T FT-ICR MS)

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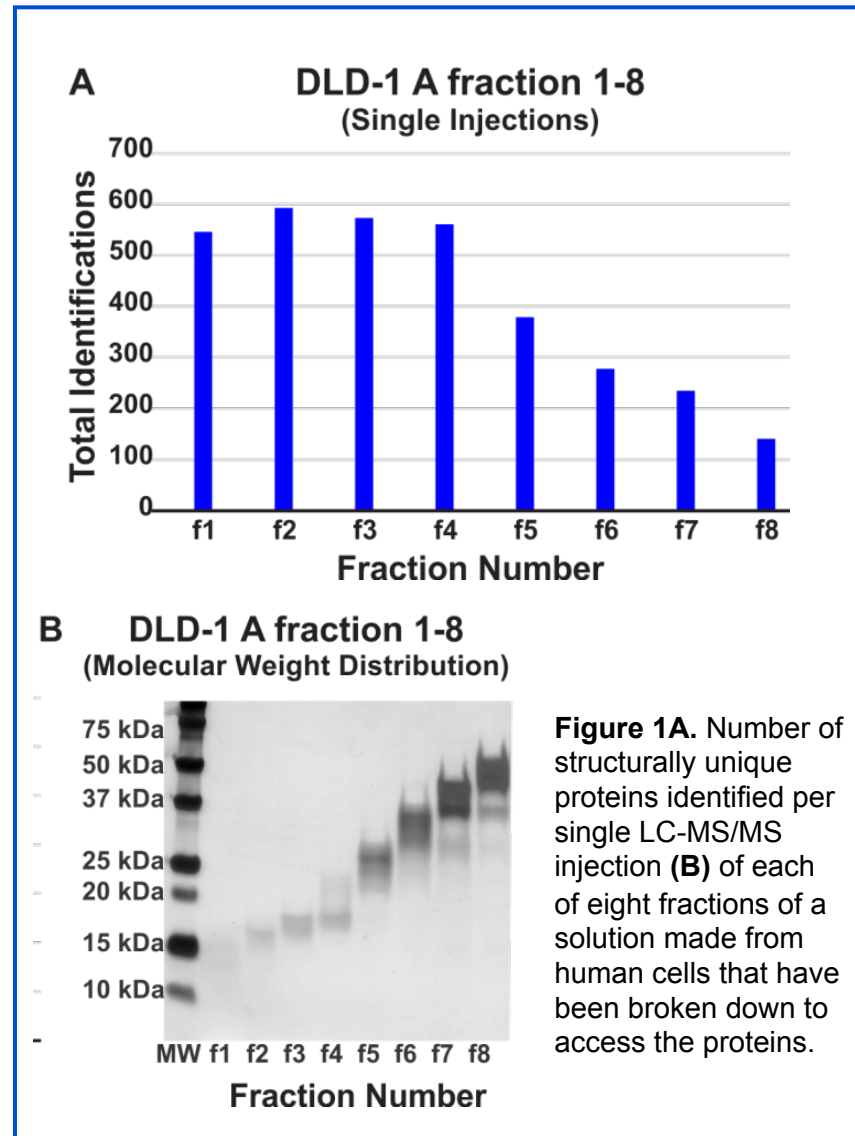


Figure 1A. Number of structurally unique proteins identified per single LC-MS/MS injection (**B**) of each of eight fractions of a solution made from human cells that have been broken down to access the proteins.