

# Proteomics: Finding the key ingredients of disease

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The winner of the chilli cook-off, usually has a key secret ingredient, which is hard to identify. Similarly, many diseases have crucial proteins, which change the dynamics of cells from benign to deadly.

New findings from an international collaboration, involving McGill University, the Research Institute of the McGill University Health Centre (MUHC) and the Human Proteome Organisation (HUPO) just made identifying these changes one step easier. Their findings published in [Nature Methods](#), show how to improve [protein](#) analysis to tease out relevant potential disease-causing molecules.

"Proteomics is the field that singles out the few significant proteins from the hundreds that may be present in a diagnostic sample," says co-author and recent new recruit of the Research Institute of the MUHC and of McGill University, Dr. Tommy Nilsson. "It is important to associate the correct proteins with the correct condition. This process is incredibly complex. The aim of our study was to benchmark current analysis techniques worldwide and to identify potential bottlenecks."

## Putting them to the test

Twenty-seven labs worldwide were sent a standard sample of proteins to analyse using their usual techniques. Only seven of the 27 participating labs were accurate in detecting all the proteins and in the more challenging part of the study, only one lab succeeded. However, further

analysis of their raw data, showed that all the proteins had been initially detected by all the labs involved but they had been rejected in later analyses.

"Our centralized analysis showed us the problems encountered while conducting this type of testing," says Dr. John Bergeron, senior author from McGill University and HUPO. "We found that a major contributing factor to erroneous reporting is at the [database](#) level. We expect once databases and search engines improve, the accuracy of reporting will as well."

## Importance of proteomics

The goal of proteomics is to characterise all the proteins that are encoded from human DNA, similar to how all genes were identified as a result of the Human Genome Project. It is expected that proteomics will accelerate the identification of cause of many human diseases and that improved diagnosis and therapy will emerge using proteomic techniques.

"The new technology described in our paper will potentially enable clinicians to determine the causes of disease," adds Dr. Bergeron.

Source: McGill University Health Centre ([news](#) : [web](#))

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