

New technique paves way for medical discoveries

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Researchers have previously been able to analyse which sugar structures are to be found on certain proteins, but not exactly where on the protein they are positioned. This is now possible thanks to a new technique developed at the Sahlgrenska Academy at the University of Gothenburg, Sweden.

The technique entails preparing samples in a new way and is a development of applied mass spectrometry. Presented in the latest issue of renowned journal *Nature Methods*, the technique will enable medical researchers to study the mechanisms behind diseases in more detail and, with luck, find new ways of treating them.

"When we developed the method, we were analysing cerebrospinal fluid from healthy subjects and could see that many proteins had sugar structures previously unknown to us," says Jonas Nilsson, a researcher at the Department of Clinical Chemistry and Transfusion Medicine at the Sahlgrenska Academy. "We know that some of these proteins play a role in diseases such as Alzheimer's disease, and now it's possible to study whether faults in these sugar structures are responsible for the development of the disease."

There are more than 20,000 proteins in the human body. These proteins ensure that the instructions from the [genes](#) are carried out. Around half of them have sugar structures on their surface consisting of chains of sugar molecules. These sugar structures mean that the [protein](#) can be recognised by other proteins. Some of these structures can act as a

locking mechanism when proteins bind to cells and other proteins. Sugar structures are also found on the surface of cells, where they determine, among other things, which blood group we belong to.

"Sugar structures often play an important role in how a cell or protein functions and how it affects different systems in the body," says Nilsson. "Being able to study them in more detail is a major step forward for biomedical research."

The chains of sugars in these structures are attached to the proteins at only one end. The new technique entails attaching a plastic bead to the loose end of these chains and separating the sugared proteins from those that do not have sugar structures. The proteins are then chopped into pieces and the sugar chain is released from the plastic bead, leaving the sugar chain attached to a chunk of protein known as a peptide. The researchers can then study the sugar structure on the peptide and see which protein the peptide belonged to and where on the protein it sat.

Mass spectrometry is an analytical method which can be used to determine the mass of positive or negative ions. The method can also be used to identify large molecules such as proteins and measure how much of a particular protein a sample contains. Mass spectrometry has been developed over a period of almost a century and is now one of the most important analytical techniques in modern biomedical research.

More information: [Nature Methods](#), Enrichment of Glycopeptides for Glycan Structure and Attachment Site Identification, Jonas Nilsson, Ulla Rüetschi, Adnan Halim, Camilla Hesse, Elisabet Carlsohn, Gunnar Brinkmalm and Göran Larson.

Source: University of Gothenburg ([news](#) : [web](#))

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