

METHOD FOR SELECTIVE PURIFICATION OF SIALIC ACID CONTAINING PEPTIDES

SDU 647- 41

25.01.08

Technological field

Biotechnology - health, medico-technical

The technology

Protein glycosylation is among the most common posttranslational modifications known in nature.

Glycosylation is difficult to analyze by biomedical methods due to chemically very similar monosaccharide building blocks and pronounced heterogeneity and micro heterogeneity of the carbohydrate chains with respect to branching patterns and monosaccharide composition.

Many extracellular glycoproteins contain sialic acid (SA) as the monosaccharide located on the end of the glycans. Changes in sialylation of cell surface or plasma proteins are often associated with various cancers and other disease conditions.

It has been demonstrated that cancers and cancer staging may be associated with a significant over-representation of SA on the surface glycoprotein of cancer cells compared to normal cells. Also it is well known that the amount of free SA and lipid bound SA is elevated in plasma from cancer patients compared to healthy individuals.

Here we report a simple, robust and very selective method for quantitative and qualitative assessment of SA containing peptides from complex peptide mixtures.

The method takes advantage of the extremely high affinity of titanium dioxide towards SA residues positioned in the reducing ends of glycans under specific buffer conditions.

Current state of the technology

The technology is ready for licensing

Applications

The method provides detection of biomarkers of conditions associated with a change in sialylation status

Intellectual property rights

IPRs are owned by the University of Southern Denmark. A PCT patent application has been filed. WO2007/124750 A2.

Inventor:



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Martin Røssel Larsen have worked in the area of mass spectrometry and proteomics for the last 12 years, in which he has completed his M.Sc., and Ph.D. degree under the supervision of Professor Peter Roepstorff.

The main focus in his research has been in the area of expression proteomics, development and application of methods for modification specific proteomics, membrane proteomics and lately also biomarker discovery using mass spectrometric methods.

He has coauthored 51 articles and 4 book chapters, and has held more than 70 international conference contributions or guest lectures, mostly invited.

Since the end of his Ph.D. education he has been largely self-financed through grants from the Danish Natural Science Research Council (postdoc and Steno stipend), European Foundation for the Study of Diabetes and lately he received a Young Investigator Award from the Danish Strategic Research Council and a Skou stipend from the Danish Natural Science Research Council. MRL is in addition member of the editorial board of the prestigious journal, journal of Biological Chemistry (JBC).

References:

Larsen MR, Jensen SS, Jakobsen LA, Heegaard NH. (2007) Exploring the sialome using titanium dioxide chromatography and mass spectrometry. *Mol Cell Proteomics*. 6(10), 1778-87.

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