QLUCORE

OVERVIEW

The Center for Interdisciplinary Cardiovascular Sciences (CICS).

CICS was created in 2009 by the Brigham and Women's Hospital in Boston and the Japanese pharmaceutical firm Kowa Company Ltd, and is located in Boston Massachusetts.

Founding Director: Masanori Aikawa, MD, PhD

CICS is looking into new ways to prevent and treat cardiovascular disease with a particular focus on proteomics.

Proteomics is the large-scale study of proteins (the proteome), contained within an organism, tissue, cell or organelle. Characterization of the proteome depends on mass spectrometry. As proteins are the primary effectors of cellular function, examining changes enables us to gain new insights into the cellular mechanisms and markers of disease.

CICS aims to use such novel discoveries in the development of first-in-class drugs that can modulate or regulate new protein targets responsible for the mechanisms for cardiovascular disease such as inflammation.

Using proteomics to understand cardiovascular disease

TECHNICAL SITUATION

The proteomics group at CICS, led by Dr. Sasha Singh, integrates the latest technologies in mass spectrometry and collaborates with the center's main research groups. These groups' studies focus on four major biological processes contributing to cardiovascular disease: macrophage biology, lipid metabolism, arterial and valvular calcification, and metabolic disorders such as type 2 diabetes.

"When any of the three groups wants to look at protein-related mechanisms involved in their particular disease models, we can use all major global proteomics quantitative strategies to analyze the changes in abundance of anywhere between 1000 to 5000 proteins across a particular experimental time course or across various conditions," Dr. Singh explains.

CICS' researchers work with the proteomics group to design experiments that minimize sources of variation due to experimental noise, thereby enhancing the biological variation they wish to pursue.

SOLUTION

Qlucore provides an ideal platform for data analysis and visualization of these changes in the proteome that can be flagged as trends of interest for follow-up studies.

BENEFITS

"Qlucore is fast, very intuitive and the graphical user interface is simple to use. It means that the biologists at CICS can now do fundamental statistical analyses independently, having more control of their own data. It also means that our informaticians can concentrate on very advanced bioinformatics on the wilder frontiers of statistical analyses." says Dr. Singh.
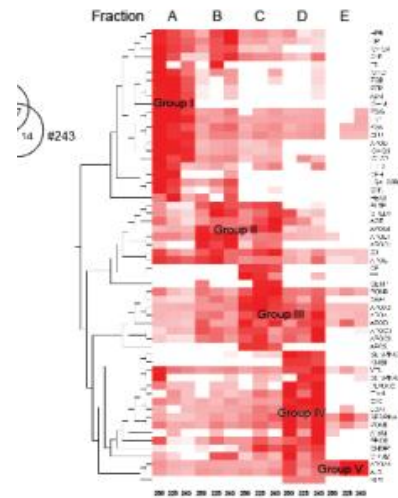
Hierarchical cluster analysis of the HDL proteome

"We have investigated the proteome across various HDL fractions and demonstrated, with the visual aid of Qlucore-generated hierarchical clustering or heat maps, that the proteome is split into sub-proteomes; each sub-proteome identifies with a specific subset of HDL fractions," she explains.

Approximately half of the research projects at CICS have generated large proteomics datasets (greater than 1000 proteins) and have incorporated Qlucore into the data analyses steps.

Since the first peer review process occurs in the laboratory itself, the researchers heavily depend on elements such as principle component analysis and hierarchical clustering to demonstrate to their peers in a group-meeting environment, the significance of their findings.

By doing so, the Qlucore has maintained itself as a permanent fixture at CICS for data analysis and representation, and communication of ideas and findings. The graphical and statistical outputs are also poised for publication-ready figures.

For More information Contact Qlucore at www.qlucore .com.

You can download a free trial version to try yourself.

US:
+1 310 945 3047

Europe and RoW:
+46 46 286 3110

For a list of agents, visit www.qlucore.com

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