

LC/MS, GC/MS Data Analysis Software

# Multi-omics Analysis Package



The Multi-omics Analysis Package is metabolic engineering software that can automatically generate metabolic maps and perform a variety of data analysis based on the vast amounts of mass spectrometry data generated in fields such as metabolomics, proteomics, and flux analysis. In conjunction with the various method packages and databases offered by Shimadzu for metabolomic analysis, the Multi-omics Analysis Package can help increase the efficiency of metabolomic data analysis work. The intuitive visualization of data provides powerful support for drug discovery, functionally-enhanced foods, bioengineering, and other life sciences research applications.

## Visualize Changes in Compound Quantities on a Metabolic Map Using Simple Operations

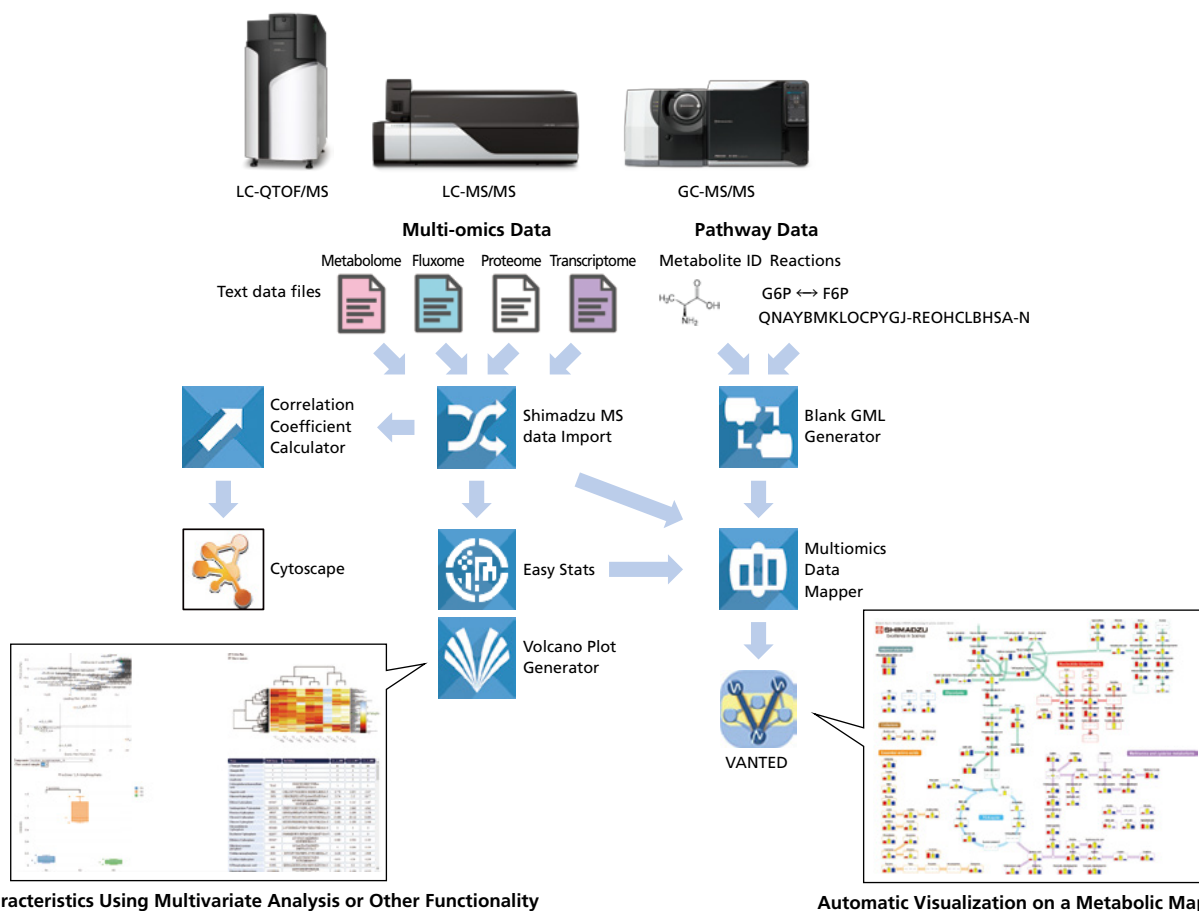
The software dramatically decreases the amount of work required for graphing measurement data or displaying it on a metabolic map.

## Identify Significant Compounds Using Simple Operations

It makes it easy to use volcano plots for comparing two groups, principal component analysis (PCA) for comparing multiple groups, hierarchical clustering analysis (HCA), and box plots. Linked PCA, HCA, and box plot results can be displayed in the same window to conveniently identify significant compounds. The metabolic map can be enlarged to confirm where identified compounds are located on the map and to support confirming and interpreting the data.

## Includes Visualization Template Files Compatible with a Variety of Method Packages

The templates are designed to work in combination with various Shimadzu method packages. These packages contain sample pretreatment methods and analytical conditions for use as "ready-to-use methods," which ensure the entire process, from mass spectrometry analysis to data analysis, can be performed with ease. In particular, these visualization templates (metabolic maps) are compatible with method packages for primary metabolites, cell culture profiling, lipid mediators, and bile acid. The templates can be used as-is or customized using simple operations.



Visualize Characteristics Using Multivariate Analysis or Other Functionality

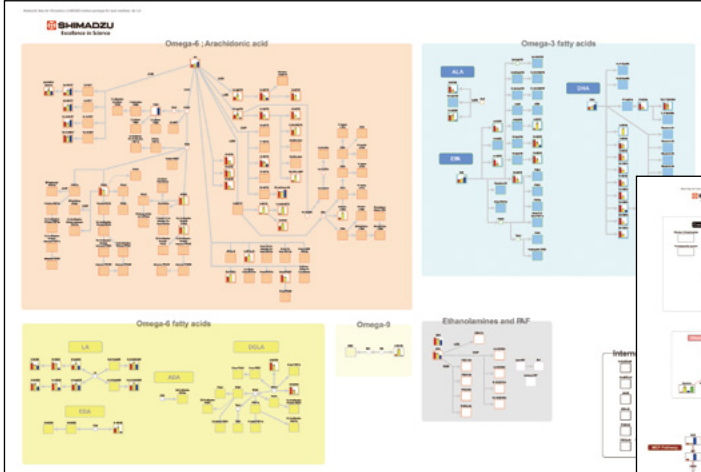
Automatic Visualization on a Metabolic Map

To view a video that describes the Multi-omics Analysis Package and how to operate the software, [click here](#).

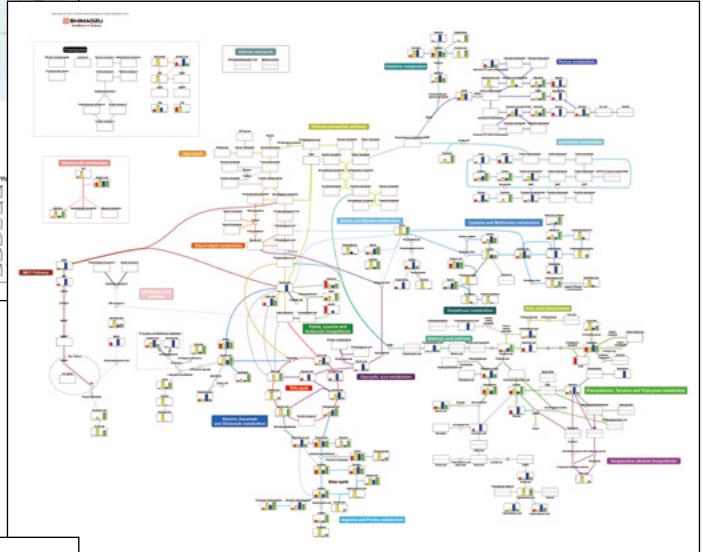


# Data Analysis Example

## Using the Lipid Mediator Method Package to Display Quantitative Changes in Human Plasma and Serum



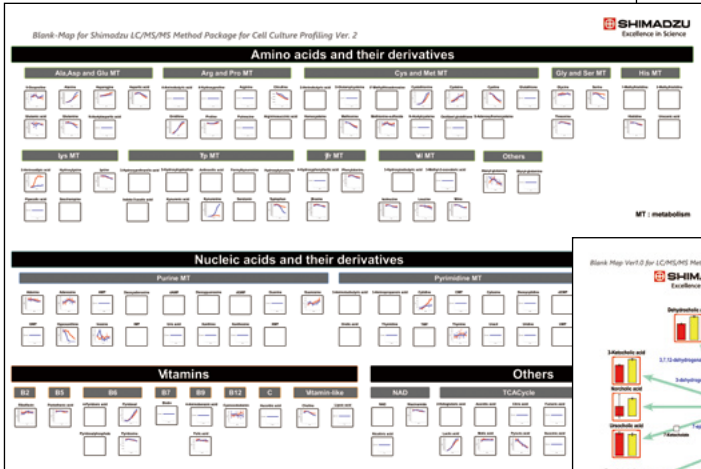
## Comprehensive Analysis of Cell-extracts and Culture Supernatants of *E. coli* and Yeast Using Primary Metabolites Method Package



The metabolic map above was developed in cooperation with the Department of Lipidomics at the Faculty of Medicine, The University of Tokyo. For more details, refer to Application News 01-00250.

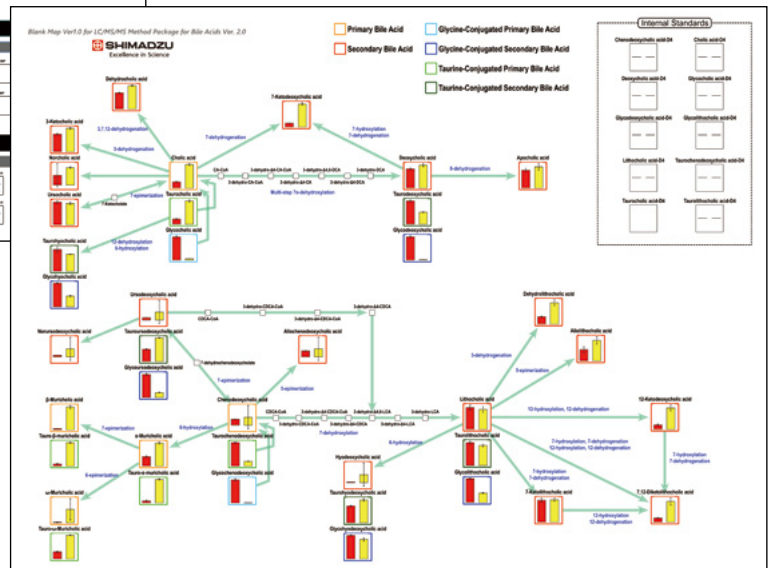


## Using the Cell Culture Profiling Method Package to Display the Time-Course Profile of Metabolites in iPS Cell Culture Supernatant



This data was provided by the Engineering Biology Research Center, Kobe University.

## Using the Bile Acid Method Package to Analyze Human Blood Plasma and Metabolites in Mouse Feces



This data was provided by the Research & Development Center for Cell Therapy, Foundation for Biomedical Research and Innovation, Kobe. For more details, refer to Application News C209.



For more details, refer to Application News 01-00196.



For the latest information about the Multi-omics Analysis Package, click here.

## Tools for Data Analysis

The Multi-omics Analysis Package is based on software tools (called gadgets) that have been released on the GARUDA platform - an open research platform developed by the GARUDA Alliance and led by The Systems Biology Institute, Japan (SBI).



<http://www.garuda-alliance.org/>

### Data Analysis Tools Used in the Multi-omics Analysis Package



#### Volcano Plot

A tool that combines a t-test (statistically significant difference) and a fold-change (example: difference in mean value such as 2 times or 1/2) to visualize the differences between the two groups. The Volcano Plot gadget developed by Shimadzu is included in the package.



#### EasyStats

This tool is for visualizing principal component analysis (PCA) or hierarchical cluster analysis (HCA) results on box plots (including t-test) of measurement data. It can display metabolite data analysis results in a single window to enable comprehensive determination of characteristic changes.



#### VANTED

Tool maintained at University of Konstanz, Germany, for visualization and analysis of networks across different data sets. (GARUDA support was developed at Monash University)



#### Cytoscape

Bioinformatics tool developed by the Cytoscape Consortium, used to visualize metabolic pathways, integrate gene expression profiles with related data, and so on. It is especially useful for analyzing networks and visualizing correlations.

### LC/MS/MS Method Packages Supported by Multi-omics Analysis Package

Product	Brochure code
Primary Metabolites	C146-E437
Cell Culture Profiling	C146-E408
Lipid Mediators	C146-E381
Bile Acids	C146-E428

\* The Multi-omics Analysis Package is included with the LC/MS/MS Method Package for Primary Metabolite, Cell Culture Profiling, and Metabolites Method Package Suite.

GARUDA is a trademark of The Systems Biology Institute.



Shimadzu Corporation  
[www.shimadzu.com/an/](http://www.shimadzu.com/an/)

#### For Research Use Only. Not for use in diagnostic procedures.

This publication may contain references to products that are not available in your country. Please contact us to check the availability of these products in your country.

Company names, products/service names and logos used in this publication are trademarks and trade names of Shimadzu Corporation, its subsidiaries or its affiliates, whether or not they are used with trademark symbol "TM" or "®". Third-party trademarks and trade names may be used in this publication to refer to either the entities or their products/services, whether or not they are used with trademark symbol "TM" or "®". Shimadzu disclaims any proprietary interest in trademarks and trade names other than its own.

The contents of this publication are provided to you "as is" without warranty of any kind, and are subject to change without notice. Shimadzu does not assume any responsibility or liability for any damage, whether direct or indirect, relating to the use of this publication.