KPSL
九州プロサーチLLP

Contract service

Proteomics specialists offer protein quantitative analysis of metabolic pathway-wide proteome profiling using the latest MS instrument & MRM Standard Mix (Page 2).

Available panel：Human major metabolic enzyme (338 proteins)

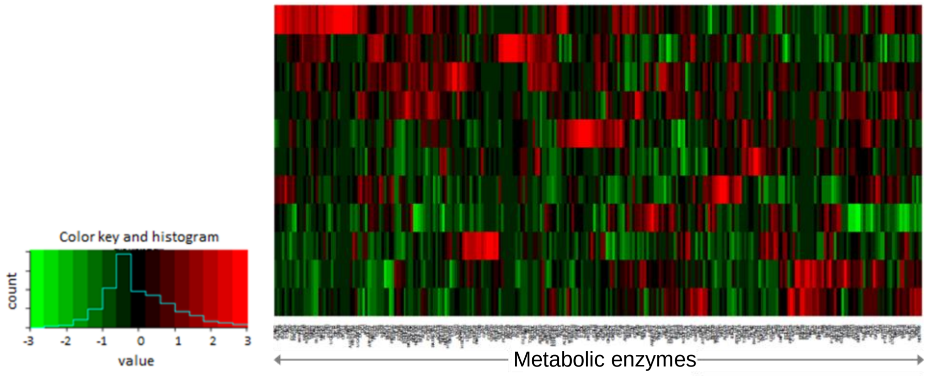
Sample preps：Frozen pellets of human cultured cells or frozen human tissue

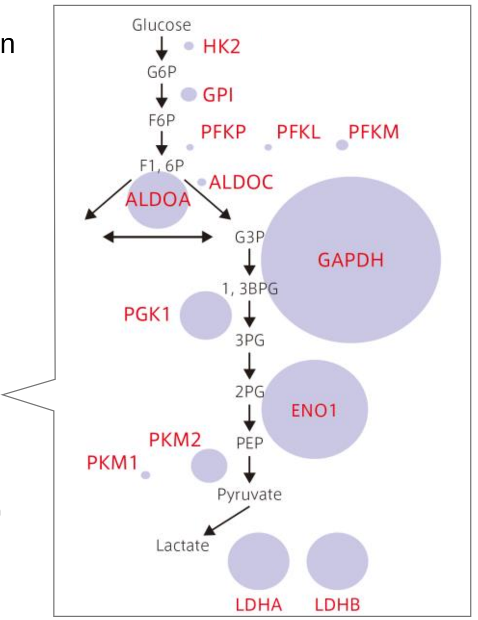
※Sample must be sent with serum free condition.

Example #1: Quantitative Analysis of Metabolic Enzymes in 11 Human Cancer Cell Lines

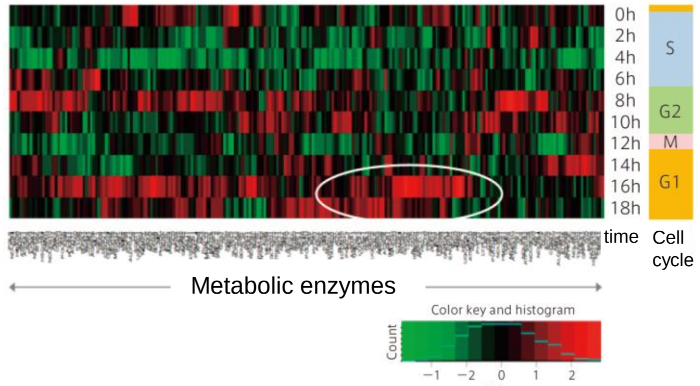
Bottom: Quantitative analysis was performed against 266 x human major metabolic enzymes in 11 human cancer cells. The expression levels were shown in the heat map below. Distinguished expression patterns among cell lines, which are clustered by the profile similarities. iMPAQT enables to show important factors on each pathway by calculating enzyme expression as quantitative value.

Right: Bubble charts of expression levels for glycolysis enzymes in HeLa cells. Expression levels of upstream enzymes were low, while those of downstream ones were high.





Example #2: Profiles of Human Metabolic Enzymes among Cell Cycles



After synchronizing cell division with thymidine block, HeLa cells were collected at every 2 hours and 236 x metabolic enzyme expressions were measured.

In S phase, expressions of many metabolic enzyme are suppressed (Green). In G1 phase, the expression level related to glycolysis and TCA cycle were greatly increased (Red).

※Please ask your local distributor about quote.

Note

This service uses synthetic peptides as standard, so obtained quantitative value is standardized by synthetic peptides (It does not reflect protein purification at pre-treatment and efficiency of enzyme digestion). Obtained quantitative value is calculated from concentration of inner standard peptide.

Your Local Distributor

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Singapore 738 960
TEL : +65-6555-9001
FAX : +65-6555-9030
Email: sales@bio-rev.com
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Address: 9-7 Hongo 2-Chome, Bunkyo-ku,
Tokyo 113-0033 JAPAN
Phone : +81-3-5684-6296
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Email : export@funakoshi.co.jp

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MRMplus

A new proteomics technology by LC-MS/MS/MRM

Quantitative proteomics tools & analysis service by iMPAQT method

More details: Web page No　Quantitative tools 81385

We offer product & service to quantify multiple proteins at one time by mass spectrometer (LC-MS/MS)

iMPAQT*1, New technology for Quantitative Proteomics

＊1 *in vitro* proteome-assisted MRM for Protein Absolute QuanTification
Matsumoto, M., *et al., Nat. Methods*, **14**(3), 251～258(2017).[PMID: 28267743]

- Developed by Drs. Nakayama & Matsumoto of Kyushu University.
- Highly ionized peptides by actual measurement of genome-wide human recombinant proteins
- Quantitative profiling of ~400 proteins/hour at once
- A powerful tool for pathway-wide proteomics, subtype clarification and no antibodies available targets

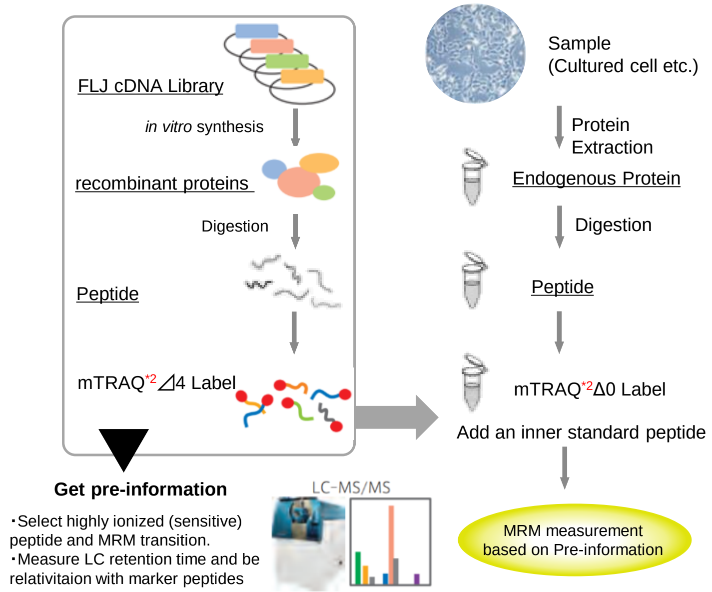
Technology Outline

1 **In vitro synthesis** of 18,000 recombinant human proteins, followed by digestion to peptides & mTRAQ*2 (heavy) labeling.

2 **Acquire pre-information** (MRM transition parameters, ionization values, relative retention time) of every peptides by LC-MS/MS.

3 **MRM-measurement based on the pre-information** for the samples & internal standards labeled with mTRAQ*2 (light for samples, heavy for standards)

＊2 mTRAQ reagent is product of AB Sciex.



Get pre-information
・Select highly ionized (sensitive) peptide and MRM transition.
・Measure LC retention time and be relativitaion with marker peptides

Funakoshi offer

✓Can perform LC-MS/MS analysis
Product available!

✓No compatible equipments…
✓No technitians/skills…
Service available!

funakoshi FRONTIERS IN LIFE SCIENCE MRMplus
Quantitative Proteomics tool for iMPAQT
MRMplus Standard Mix p.2
Mixture of standard peptides for human metabolic enzyme.

KPSL 九州プロサーチLLP
Quantitative Proteomics Service by iMPAQT p.4

funakoshi
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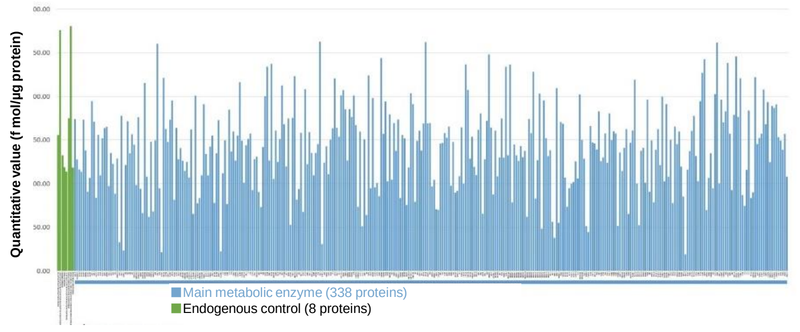
MRMplus

Standard peptides mixture for LC-MS/MS MRM
- 338x Human major metabolic enzymes can be quantified-

MRMplus Standard Mix

A standard peptides mixture of human major metabolic enzymes selected by iMPAQT.

Features



Expression level of human major metabolic enzymes in cultured cells

Measurable peptides in the Mix!

Total 338 of major human metabolic enzymes from carbohydrate metabolism, lipid metabolism, amino acids metabolism, nucleic acid metabolism.

Only 2 days !

(Sample prep.: 1 day + MS analysis: 1 day)
Expression level of 338x metabolic enzymes in one profile.

*This product is licensed from Kyushu university.
*This product requires triple-quadrupole (QqQ) mass spectrometry (AB Sciex 4000QTRAP or later).
*mTRAQ reagent (AB Sciex) is required but not provided.
*Compatible with conventional LC: Column inner diameter should be less than 2.1mm.

Other Features

- **Simple:** Well-validated 338 human major metabolic enzymes & 8 endogenous controls are pre-mixed, just mTRAQ-label & Go!
- **Easy:** Pre-set parameters (MRM transition, relative retention time) will be provided.

Application

- Visualization of up/down-regulations on whole metabolic pathway.
- Drug discovery/Pharmacology
- Basic research for proteomics

Discription Maker	Product code	Size
MRMplus Standard Mix, Metabolic Enzyme Deck		
FMI	FMI-METMIX	200μg
Content: peptide cocktail (lyophilized), method file, datasheet For 25 independent projects. ※To order, “letter of assurance” is needed.		

Related Products

■ Proteomics Sample Preparation Kit for Cultured Cell 2G

Cell lysis & peptide preparation for mass spectrometry by cultured cell sample, optimized for mTRAQ [*1] conjugation for LC-MS/MS MRM.

[*1] mTRAQ is a product from AB Sciex

■Protocol overview

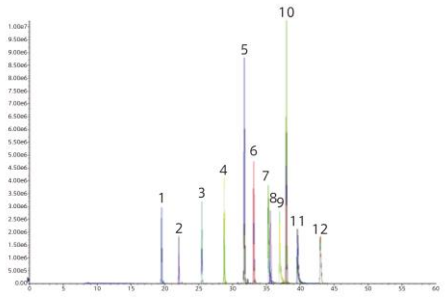
1. Cell lysis
2. BCA assay[*2]
3. Protease digestion & alkylation
4. mTRAQ [*2] Labeling.
5. Freeze-drying (-65oC).

[*2] BCA assay kit and mTRAQ reagents are not provided but required.

Discription Maker	Product code	Size
Proteomics Sample Preparation Kit for Cultured Cell 2G		
FMR	FMR-003	1 kit
Content: Tris HCl, SDS, urea, soluble buffer, protease, reagent A/B/C, store tube Enable to analyze 10 times . ※To order, “letter of assurance” is needed.		

■ MRMplus Retention Time Marker

A mixture of 12 synthetic peptides for calibration of retention times for each peptides in LC-MS/MS system. Compatible with MRMplus Standard Mix.



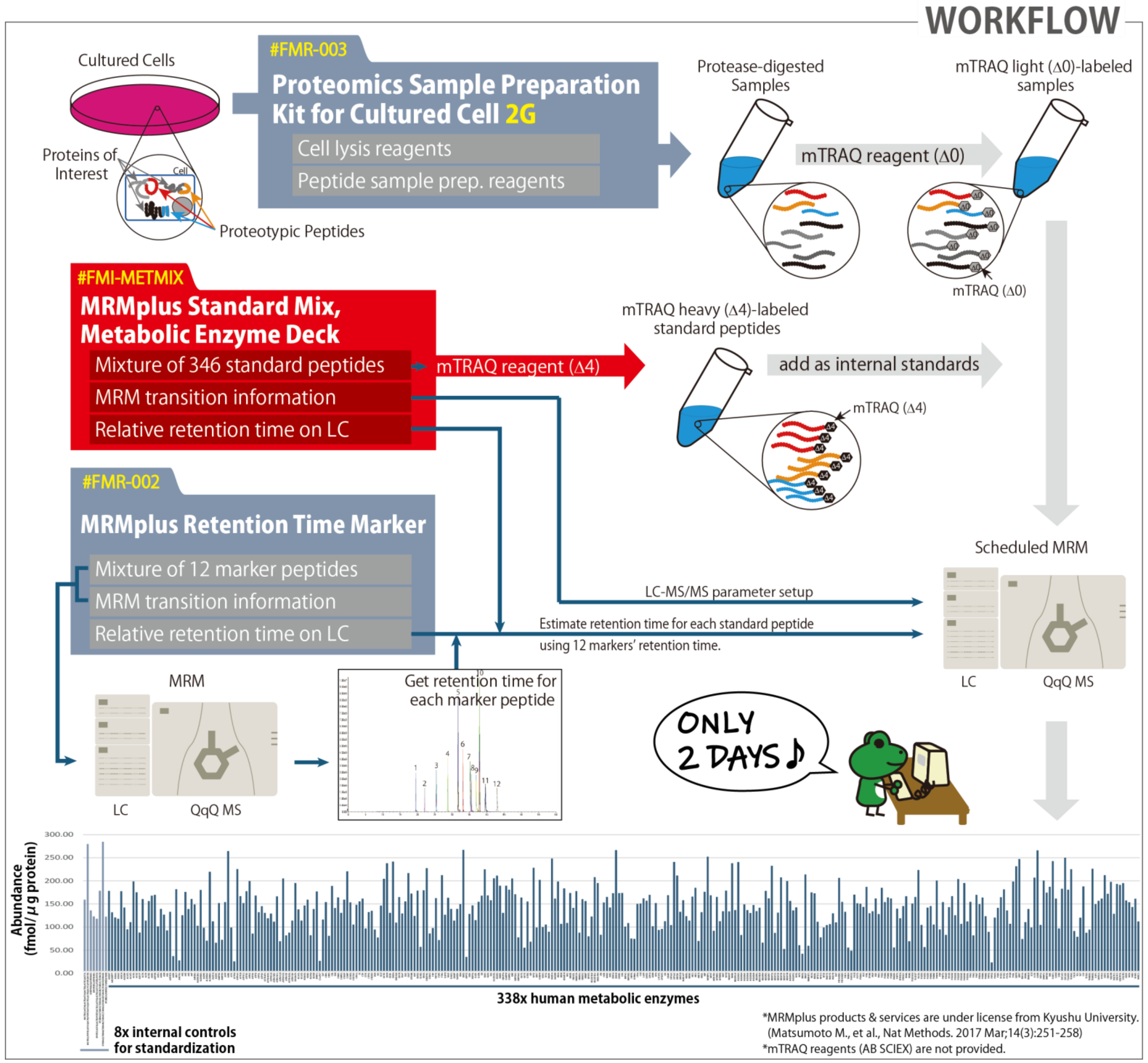
The result of LC-MS/MS MRM by this product

Web page No
80768
click

Discription Maker	Product code		Size
MRMplus Retention Time Marker			
FMR	FMR-002	-80℃	12μl
Content: 200×MRMplus Retention Time Marker Stock Solution (12μ l) ※To order, “letter of assurance” is needed.			

Workflow:
Preparation of Scheduled MRM by MRMplus®

MRM (Multiple Reaction Monitoring) and is one of the quantitative proteomics methods by mass spectrometry. MRM uses triple-quadrupole LC-MS/MS and enable us to distinguish peptides by their amino acid sequences specifically by detecting product/fragment ions of selected MS parameters (MRM transitions).
It is possible to quantify proteins of interest (POIs) by measuring MRM transitions of specific sequences (Proteotypic Peptides: PTPs) in samples along with internal standard peptides.



*MRMplus products & services are under license from Kyushu University. (Matsumoto M., et al., Nat Methods. 2017 Mar;14(3):251-258)
*mTRAQ reagents (AB SCIEX) are not provided.