

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)

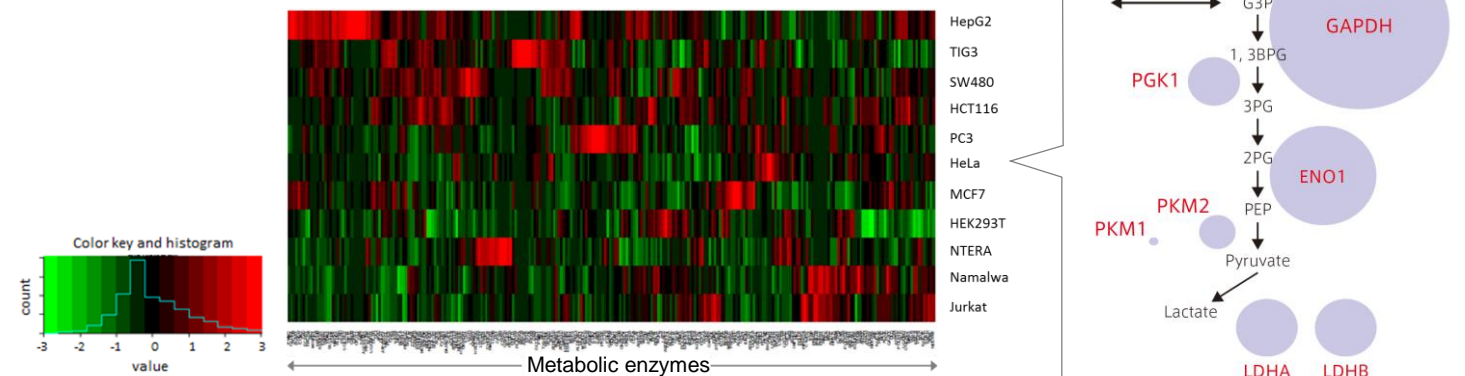
Sample preps : Frozen pellets of human cultured cells or frozen human tissue

※Sample must be sent with serum free condition.

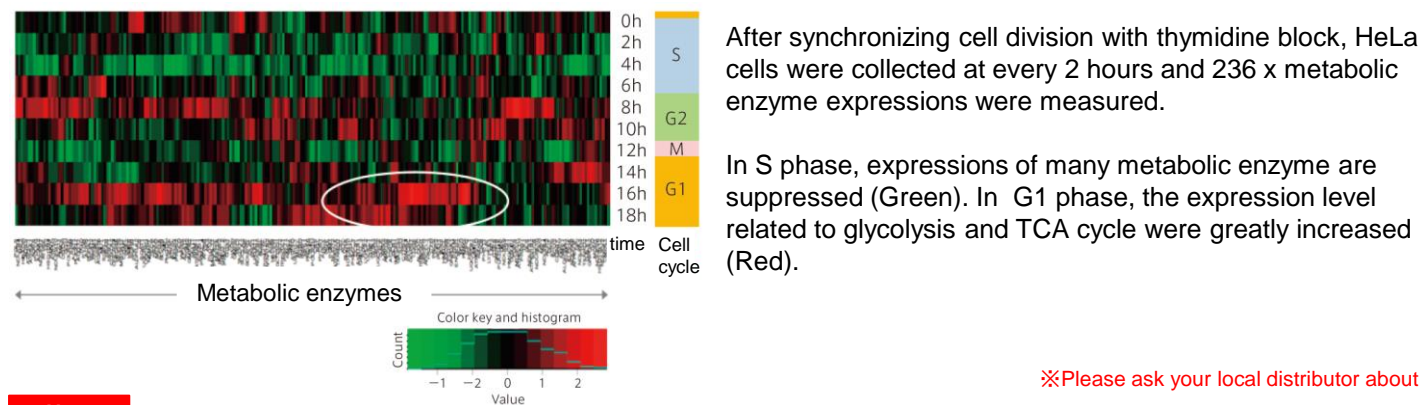
Example #1: Quantitative Analysis of Metabolic Enzymes in 11 Human Cancer Cell Lines

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



※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.

NOTE ※ All products here are research use only, not for diagnostic use. ※ Company name and product name are trademark or registered mark. ※ Specs might be changed for improvement without notice. ※ Please contact your local distributors for orders, quote request and inquiry.

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FMI-1912-F01



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

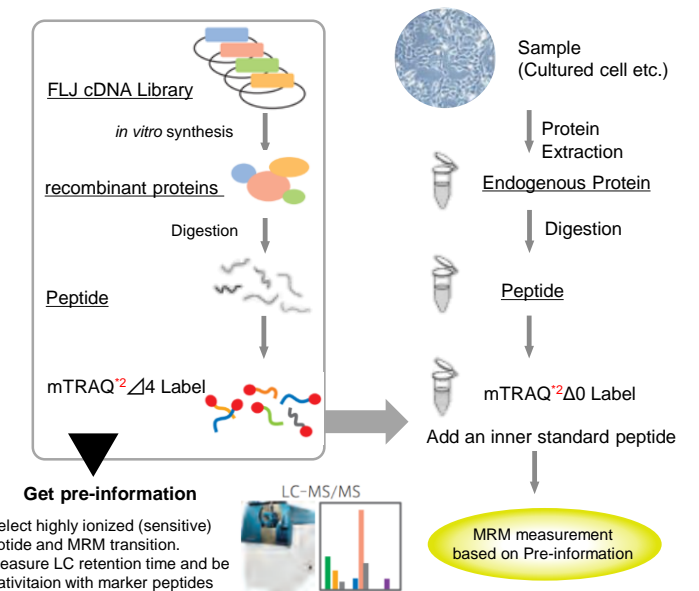
*1 *in vitro* proteome-assisted MRM for Protein Absolute Quantification
Matsumoto, M., et al., Nat. Methods, 14(3), 251~258(2017). [PMID: 28267743]

- 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.



Funakoshi offer



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

✓ No compatible equipments...
✓ No technicians/skills...
Service available!



Quantitative Proteomics tool for iMPAQT

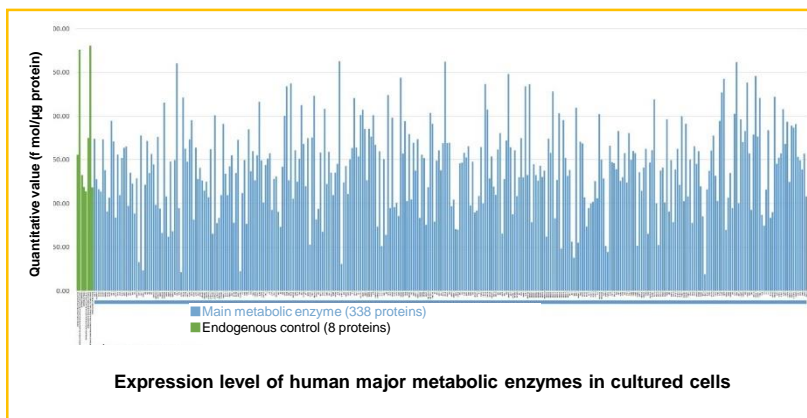
MRMplus Standard Mix p.2

Mixture of standard peptides for human metabolic enzyme.



**Quantitative Proteomics
Service by iMPAQT**

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



Features

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[®] conjugation for LC-MS/MS MRM.

*1: mTRAQ is a product from AB Sciex

Protocol overview

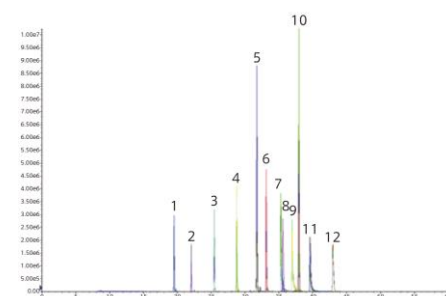
1. Cell lysis
2. BCA assay^{*2}
3. Protease digestion & alkylation
4. mTRAQ^{*2} Labeling.
5. Freeze-drying (-65oC).

*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

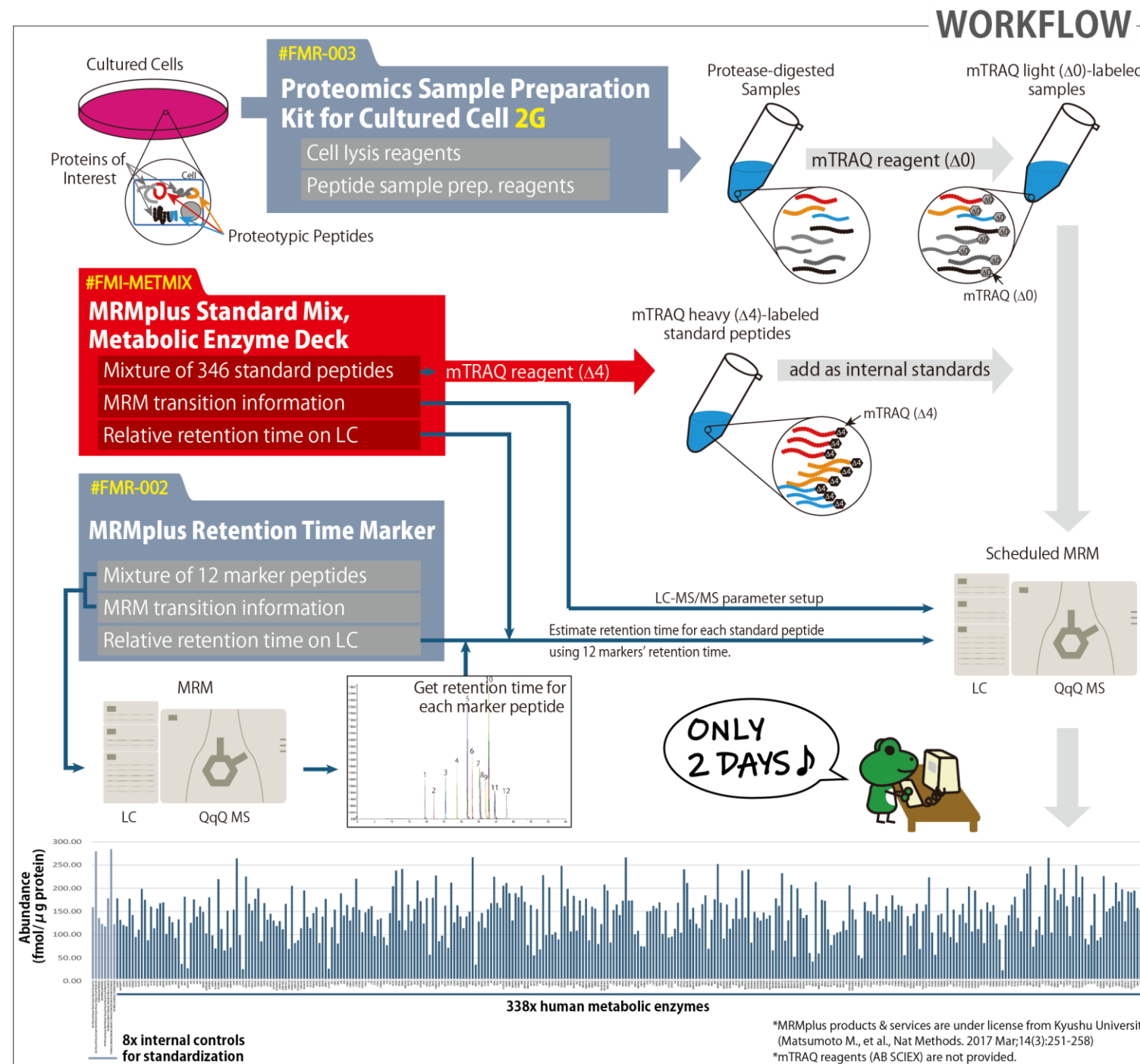
Discription	Maker	Product code	Size
MRMplus Retention Time Marker	FMR	FMR-002	12μl
Content: 200 x MRMplus Retention Time Marker Stock Solution (12μ l)			
※To order, "letter of assurance" is needed.			

Web page No
80768



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.