MASS SPECTROMETRY-BASED CUSTOMIZED OMICS ANALYSIS SERVICE

PASS

PAN-OMICS
ANALYSIS
SERVICE &
SOLUTION

BERTIS

MASS SPECTROMETRY-BASED
CUSTOMIZED OMICS ANALYSIS SERVICE
Bertis PASS

01

PASS

Pan-Omics Analysis Service & Solution

Bertis provides customized proteomics analysis services based on its extensive expertise in biomarker discovery and commercialization for cancer and major diseases, as well as state-of-the-art mass spectrometry platforms.

Cutting-edge Mass Spectrometry Instruments
The only company in Korea equipped with the latest instruments such as Astral and timsTOF.

Proteome Analysis Consulting
One-stop consulting from experimental design to result interpretation.

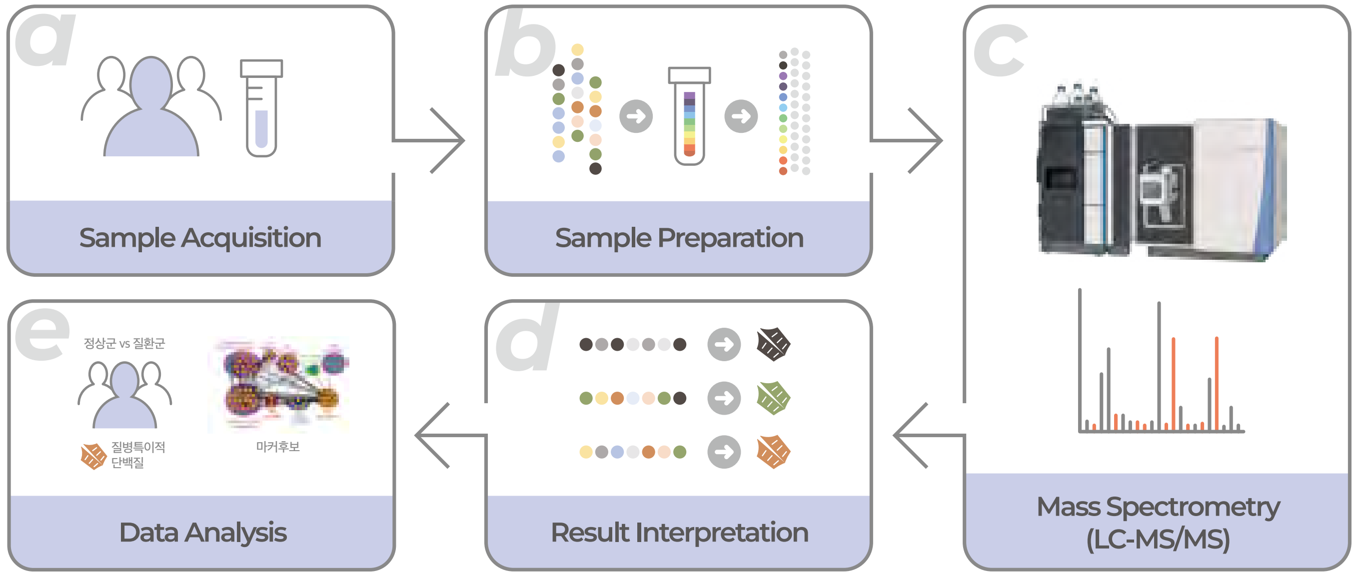
Wide Range of Sample Types
Expertise in analyzing blood, tissue, cell, exosome, and culture media.

Bioinformatics Analysis
Comprehensive proteomic data interpretation based on bioinformatics.

Drug Development Support
Tailored analyses for TPD, ADC, HCP, CMC, and other regulatory or research needs.

Advanced Proteomics Infrastructure

With extensive experience in mass spectrometry and biomarker discovery and validation, the PASS Center provides protein analysis services through standardized mass spectrometry workflows, data quality control, and advanced data interpretation platforms.



a **Sample Acquisition :** Collecting diverse specimens (biofluid, cell, tissue, EV, IP, etc.) from various organisms (human, mouse, plant, bacteria, etc.)

b **Sample Preparation :** Customized preprocessing depending on sample characteristics (in-solution/gel digestion, labeling, fractionation, lipid extraction, PTM enrichment, etc.)

c **Mass Spectrometry (LC-MS/MS) :** Using the latest instruments (Astral, timsTOF, etc.) and techniques (DDA, DIA, MRM, PRM)

d **Result Interpretation :** Delivering purpose-specific outcomes (identification, quantification, interactome, PTM analysis)

e **Data Analysis :** Providing tailored insights such as DEP, GO/Pathway analysis, and PPI analysis

---

High-Performance Mass Spectrometry

PASS services are powered by the most advanced mass spectrometry platforms, including Orbitrap Astral, Exploris 480, timsTOF SCP, and Qtrap 6500+

Thermo Fisher Scientific

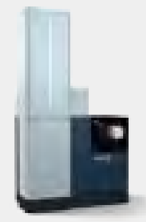
Orbitrap Astral

- Highest profiling capability
- Spatial single-cell proteomics

Thermo Fisher Scientific

Orbitrap Exploris 480

- Deep profiling with isotope labeling
- Post-translational modification (PTM)



Bruker

timsTOF SCP

- Ultra sensitive analysis for low abundant proteins
- Spatial single-cell proteomics

Sciex

QTRAP 6500+

- Highly reproducible peptide quantification through Multiple Reaction Monitoring (MRM)
- Quantifying over 100 specific biomarkers in a single analysis

02 OUR SERVICE

Customized to MFDS Guidelines   Customized to Academic Purposes (e.g., Publications)

RESEARCH SOLUTION

PASS DISCOVER

A customized proteome analysis solution designed to support research, performing protein analysis on various samples such as blood, tissue, and cells.

PROFILING (BLOOD / TISSUE / CELL)

- ✓ Deep Profiling
- ✓ Depletion
- ✓ PTM
- ✓ Spatial Single-Cell Proteomics
- ✓ Olink Reveal
- ✓ Interactome

TARGETED PROTEOMICS

- ✓ MRM / PRM
- ✓ Relative / Absolute Quantification

BIOINFORMATICS

- ✓ DEP
- ✓ GO / Pathway Analysis

TPD (TARGETED PROTEIN DEGRADATION)

Target Degradation / Off-Target Analysis

EXOSOME

Protein / Lipid / RNA Analysis

HCP (HOST CELL PROTEIN)

Individual HCP Quantification

ADC (ANTIBODY-DRUG CONJUGATE)

Multi-Enzyme *De Novo* Sequencing

INDUSTRIAL SERVICE

PASS DEVELOPER

Provides reliable and practical data throughout the entire process of biopharmaceutical product development, from target discovery and evaluation to quality control during production.

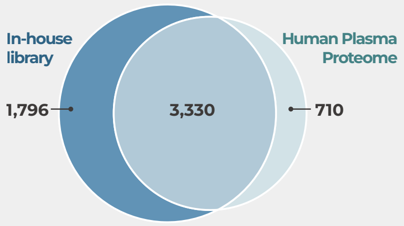
RESEARCH SOLUTION

PASS DISCOVER

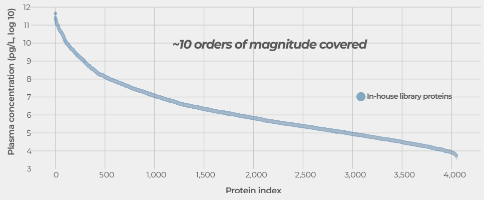
BLOOD PROTEOME

DEEP PROFILING

- An advanced analytical platform that enables in-depth interpretation of the blood proteome.



Blood dynamic range



DEPLETION

- Removes high-abundance proteins in blood to discover even low-abundance proteins in plasma or serum.

Antibody

Uses antibodies to remove high-abundance proteins (e.g., Albumin, IgG) for deeper detection.

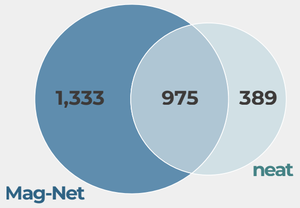
(Human: 14 proteins depletion, Mouse: 3 proteins depletion)

MARS Column

SAX magnetic bead

Automated low-abundance protein analysis using SAX (Strong Anion Exchange) magnetic beads.

Mag-Net enriched blood



OLINK REVEAL (PROXIMITY EXTENSION ASSAY)

- Olink Reveal enables discovery of over a thousand proteins from small blood volumes using a PEA-based (Proximity Extension Assay) platform.
- When combined with mass spectrometry-based profiling, it provides more comprehensive proteome information.

RESEARCH SOLUTION

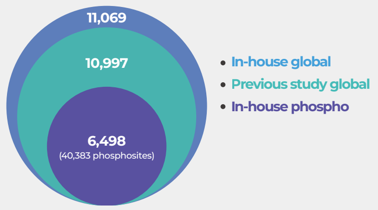
PASS DISCOVER

TISSUE/CELL PROTEOME

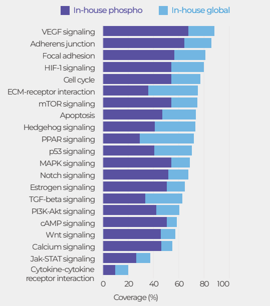
DEEP PROFILING

- Applies automated fractionation technology (COFFER) to evenly separate peptides, ensuring high reproducibility and sensitivity for deep profiling.

Deep Proteomic Profiling of Tumors



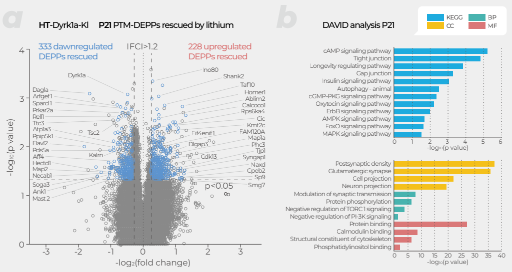
Cancer Pathway Coverage



PTM (POST-TRANSLATIONAL MODIFICATION)

- Provides analysis of diverse PTMs not detectable by RNA analysis, including phosphorylation, acetylation, methylation, ubiquitination, and glycosylation, offering both qualitative and quantitative results.

Phospho proteomics



(Roh et al., 2025, Mol Psychiatry)

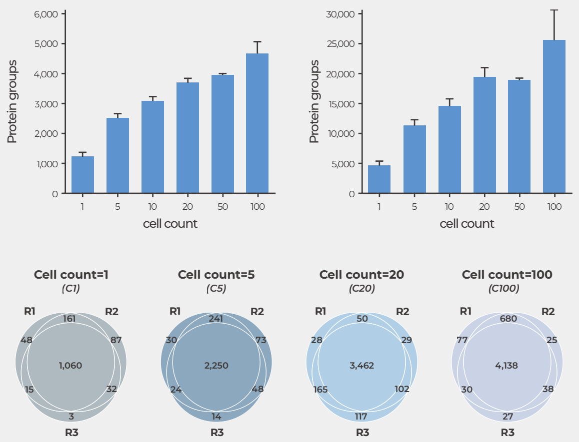
INTERACTOME

- Performs mass spectrometry on samples from various IP methods (antibody, tag, labeling, etc.) to identify and quantify proteins interacting with a target protein (bait).
- Essential for understanding biological mechanisms such as cell signaling, complex formation, and functional regulation.

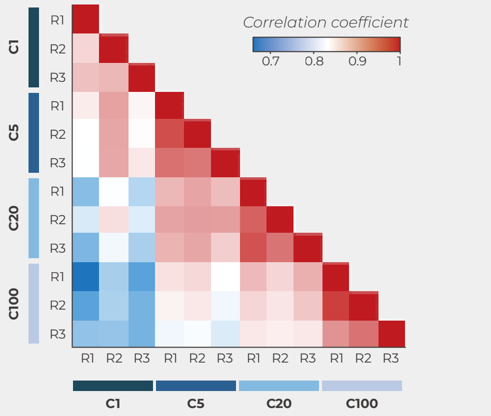
SPATIAL SINGLE-CELL PROTEOMICS

- ✓ PASS uniquely applies ultra-sensitive Astral and timsTOF SCP mass spectrometry technologies in Korea to provide single-cell level proteome analysis (>1,000 proteins).
- ✓ Applicable to cell lines, in-vitro samples, and clinical tissue samples (FFPE).

단일세포 단백질 분석 역량

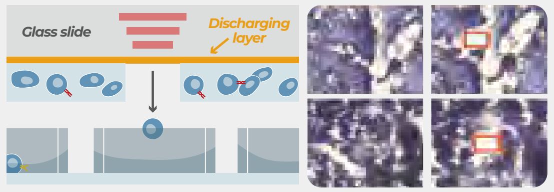


단일세포 단백질 분석 재현성



- ✓ In gastric cancer FFPE samples, over 1,500 proteins were reliably detected in precisely separated ROIs (Regions of Interest) at the single-cell level, clearly distinguishing protein expression differences between tumor and surrounding tissues.

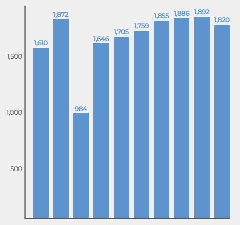
ROI isolation

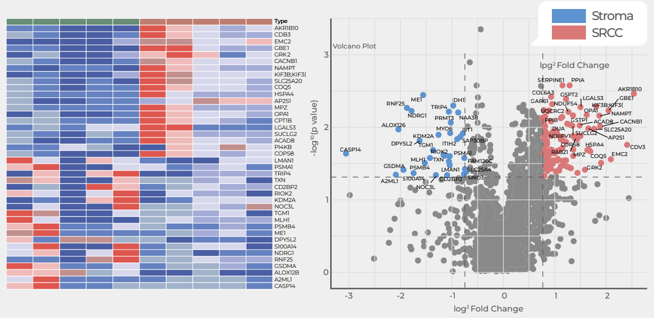


Ultra-sensitive LC/MS analysis

Ultimate 3000 linked to tims-TOF SCP

Number of detected protein IDs





Key effectors of ***metabolism*** *(NDUFV1, CPT1B, NAMPT),* ***ECM regulation*** *(MMP14, COL6A3, TGFBI), and signaling* ***pathways*** *(MARK3, GRK2, BCL9L, RBPJ) were upregulated in SRCC regions.*

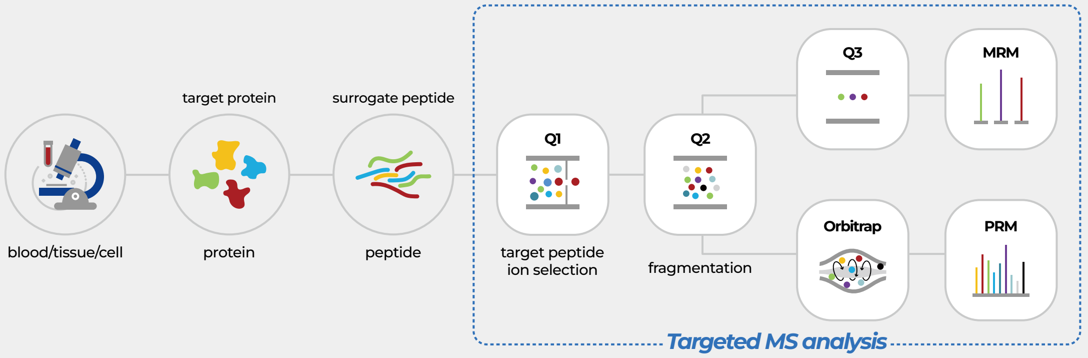
RESEARCH SOLUTION

PASS DISCOVER

TARGETED PROTEOMICS

TARGETED PROTEOMICS

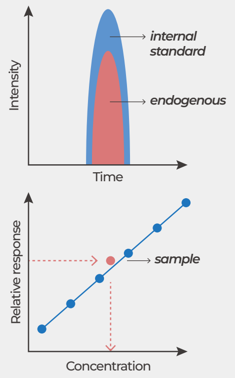
- ✓ A quantitative, mass spectrometry–based method that measures multiple target proteins simultaneously within a single sample, providing highly accurate quantification results using internal standards (IS) of target peptides.
- ✓ Based on MRM (Multiple Reaction Monitoring) and PRM (Parallel Reaction Monitoring) analyses, this service delivers reproducible results (CV < 15%) and validated methods that comply with the MFDS (Ministry of Food and Drug Safety) guidelines on validation of analytical methods for pharmaceuticals, etc.



WORKFLOW

- **01** Synthesis of Unique Peptides of Target Proteins (Light, 3 Peptides/ Protein)
- **02** Optimization (Optimization of retention time, gradient, and energy parameters)
- **03** Final Synthesis of Target Peptides (Heavy, 1 Peptide/ Protein)
- **04** Method Validation
- **05** Real Sample Analysis

Absolute quantification



Method validation

항목		Item
1	선택성	Selectivity
2	특이성	Specificity
3	검량선	Calibration curve
4	캐리오버	Carry-over
5	희석 타탕성	Dilution integrity
6	정확성 및 정밀성	Accuracy & Precision
7	생체시료 효과	Matrix effect
8	안정성	Stability

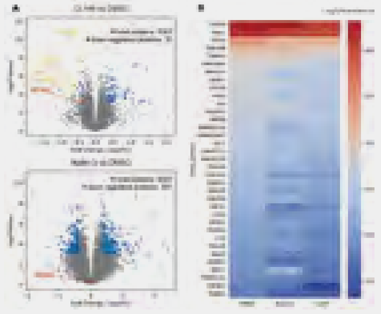
INDUSTRIAL SERVICE

PASS DEVELOPER

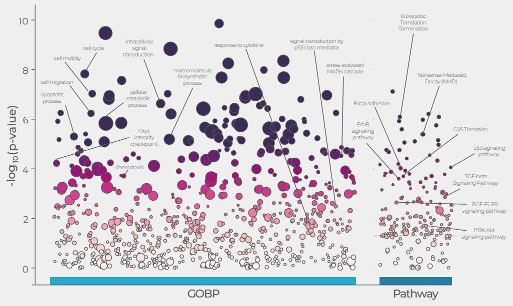
TPD / EXOSOME / HCP / ADC

TPD (TARGETED PROTEIN DEGRADATION)

- Using mass spectrometry, we quantitatively evaluate the extent of targeted protein degradation (TPD) and changes in downstream pathway proteins.
- By analyzing changes in off-target proteins, we generate the data needed to optimize TPD-based candidate molecules.



(Jeong et al., 2025, Adv Sci)



(in house data)

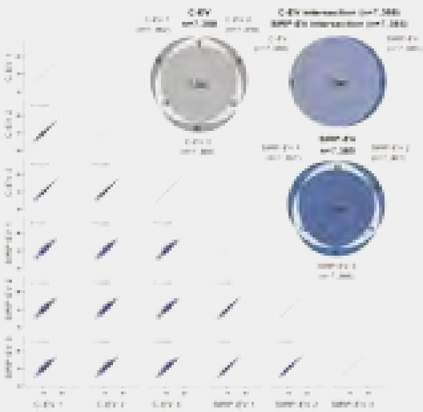
EXOSOME

MULTI-OMICS PACKAGE

Proteomics — Lipidomics — Transcriptomics

- An integrated analysis service designed to support quality control (CMC) for exosome therapeutics in compliance with MFDS (Ministry of Food and Drug Safety) guidelines.
- Through comprehensive package analysis, we provide data on equivalence verification, impurity assessment, and consistency validation across different manufacturing processes.

Proteomics

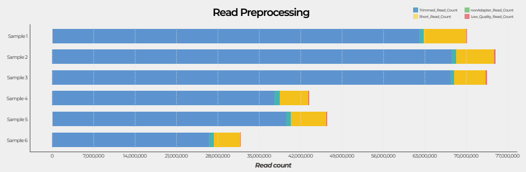


(Kim et al., 2025, Nat Commun)

Lipidomics

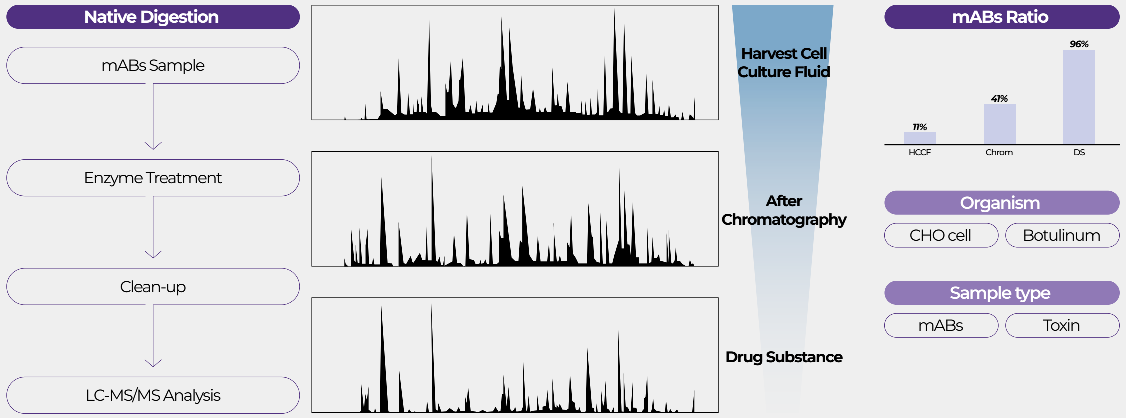
Lipid categories	Lipid classes	Lipid classes
Glycerolipid	Diacylglycerol (DG)	Triacylglycerol (TG)
Glycerophospholipid	Phosphatidylcholine (PC)	Lysophosphatidylcholine (LPC)
	Phosphatidylethanolamine (PE)	Lysophosphatidylethanolamine (LPE)
	Phosphatidic acid (PA)	Lysophosphatidylglycerol (LPG)
	Phosphatidylglycerol (PG)	Lysophosphatidylinositol (LPI)
	Phosphatidylinositol (PI)	Lysophosphatidylserine (LPS)
	Phosphatidylserine (PS)	
Sphingolipid	Sphingomeyelin (SM)	Ceramide (Cer)
	Hexosylceramide (HexCer)	
Cholesterol	Cholesterol ester (ChE)	

Transcriptomics



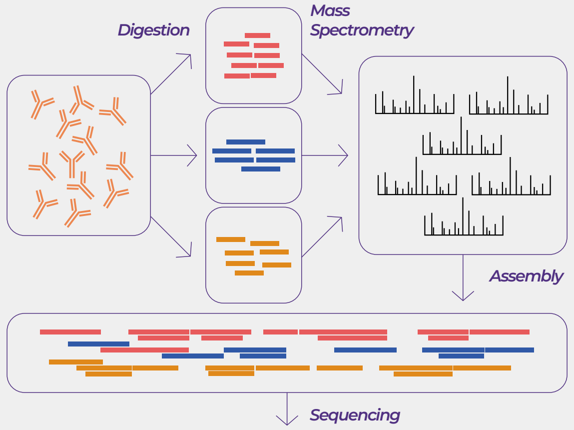
HCP (HOST CELL PROTEIN)

- We offer mass spectrometry–based quantitative analysis services essential for purity assessment in new drug manufacturing processes, such as ADC and cell therapy products.
- Unlike conventional antibody-based HCP quantification, Bertis' mass spectrometry–based semi- and absolute quantification identifies and quantifies individual HCPs, delivering highly reliable and precise data that fully comply with MFDS (Ministry of Food and Drug Safety) standards.



ADC (ANTIBODY-DRUG CONJUGATE)

- We offer a comprehensive analytical service that includes CDR (Complementarity Determining Region) sequence analysis and efficacy evaluation, both essential for the development of antibody therapeutics.
- Using multi-enzyme digestion (5 types), mass spectrometry capable of Ile/Leu differentiation, and specialized de novo sequencing software, PASS delivers highly precise and accurate data for ADC analysis.



QVKLQESGAELARPGASVKLSCKASCYTFTNYWMQWVKQRPGQGLDWIGAIYP · · ·

Peaks studio for de novo sequencing

03

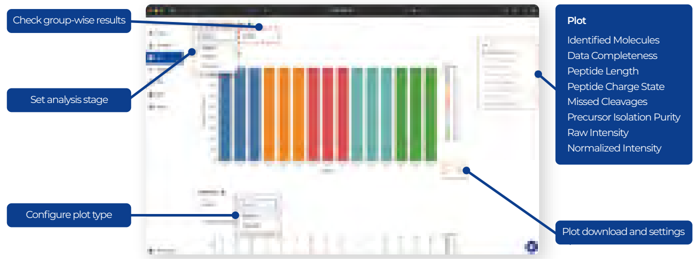
ANALYTICAL RESULT

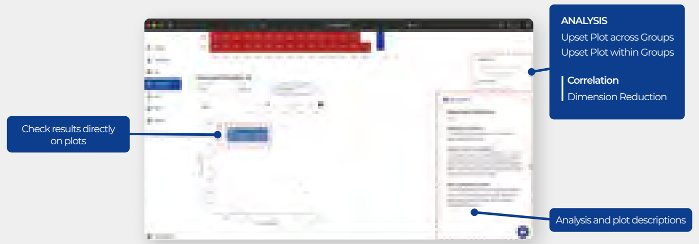
PASS REPORT

- ✓ Provides an integrated HTML report that can be viewed immediately without additional software installation
- ✓ Allows users to check key analysis results — including Data QC, Data Exploration, and DEA — all in one place
- ✓ Supports efficient data exploration with a user-friendly interactive interface
- ✓ Offers downloadable tables (.csv) and editable figures (.svg)

DATA QUALITY CONTROL

Instantly verify experimental and data quality with visualized QC results for each analysis stage.



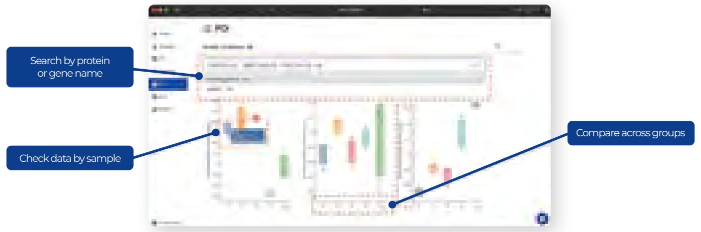


DATA EXPLORATION

Explore data characteristics quickly with analytical summaries.

PROTEIN EXPRESSION

View expression levels of proteins of interest.

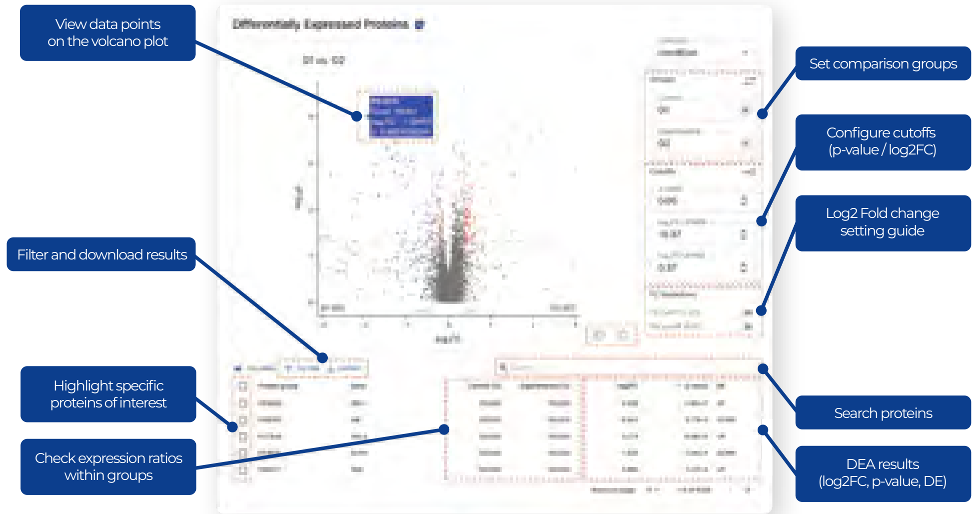


DOWNSTREAM ANALYSIS

Easily explore differential expression and related pathways through an intuitive interface.

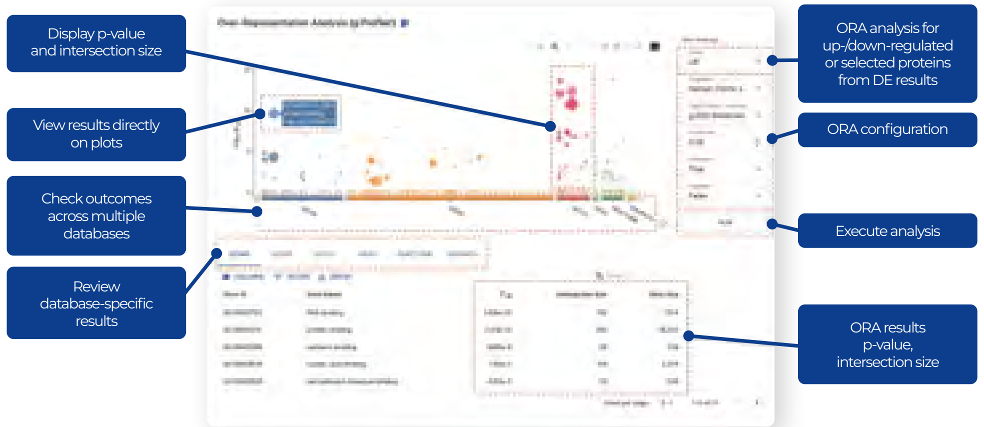
DIFFERENTIAL EXPRESSION ANALYSIS (DEA)

Visualize DEA results and adjust thresholds manually



OVER-REPRESENTATION ANALYSIS (ORA)

Perform GO and pathway analysis for proteins selected from DEA results using the integrated g:Profiler API.

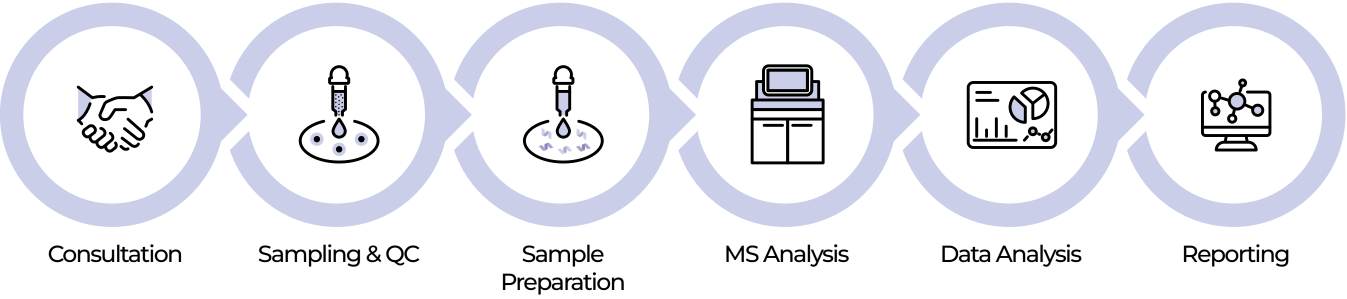


04

FAQ

SAMPLING & QC / SAMPLE PREPARATION

WORKFLOW



Q How much sample is required?

At least 100 µg of protein is required (with a concentration of ≥ 1 µg/µL).Because the required amount and condition of the sample may vary, prior consultation is essential.

Q How should I send my samples?

For cell, cell media, tissue, and serum/plasma, please ship the samples in a Styrofoam box with dry ice. For gel samples, please pack the gel and ship it with ice packs, ensuring that the gel does not dry out or warm up during transport.

Q How is QC for protein amount performed?

After lysis, we measure protein concentration using a BCA assay, and we measure again at the peptide stage after digestion.

Q Do I need to perform sample preparation myself?

In general, if you send samples in the forms listed below, the **PASS** Center will perform pre-processing suitable for mass spectrometry.

Sample type	Required amount	Storage condition	Remarks
Cell	1x10^6 cells	-20℃, -70℃	Prepare samples in cell pellet form. (Please consult us in advance if sending in lysate form.)
Cell media	≥ 20 ml	-20℃, -70℃	Concentration required (use FBS-free medium).
Tissue	≥ 20 mg	-20℃, -70℃	Expected yield: approximately 3-5 %.
Serum/Plasma	≥ 100 mg	-20℃, -70℃	Additional charge applies if depletion is required.
Gel	CBB, Silver staining	Refrigerated	Ensure that gels are neither dried nor frozen.
Exosome	1 x 10^{11} particles	-70℃	Please confirm the buffer volume.
IP sample	≥ Elute 15ug	-70℃	Please confirm the composition of the elution buffer.

FAQ

MS ANALYSIS / DATA ANALYSIS / REPORTING

Q How is LC-MS/MS analysis performed?

For profiling, the workflow is as follows :

01 Lysis : Protein denaturation using urea and guanidine
02 Reduction & Alkylation : DTT for reduction, IAA for alkylation
03 Digestion : Enzymatic digestion using trypsin and Lys-C
04 Labeling & Fractionation (for relative quantification) :
TMT labeling, followed by fractionation (12 or 24 fractions) to reduce complexity
05 LC-MS/MS analysis : 200 min/ 1 run
06 Data analysis

Thermo Scientific Orbitrap Exploris 480 & Orbitrap Astral	Thermo Scientific HF-X	Sciex Triple Quad 6500+	Thermo Scientific Orbitrap Astral & Bruker timsTOF
Profiling, TPD, Exosome	Interactome, HCP, PRM, Lipidomics	Targeted Proteomics	Single-Cell Proteomics

Q What types of results are provided?

Depending on your experimental objective, we provide the following.
Additional items can be discussed in advance if needed.

01 A matrix (Excel file) containing qualitative or quantitative protein information
02 A report (Word or PDF) including sample information, experimental methods, and summary of results
03 A data report (HTML file)
04 MS raw files, search results, and database (for publications, provided via cloud download)

Q How long does the analysis take?

- ✓ For standard analysis (deep profiling), the turnaround time is within 8 weeks after we receive the samples.
- ✓ Additional services such as pre-processing (depletion, PTM enrichment, etc.) require about 2 extra weeks.
- ✓ For MRM/PRM analysis, peptide synthesis is outsourced and takes about 4 additional weeks.
- ✓ The **PASS** Center always strives to deliver analysis results as quickly as possible.

CONTACT
FOR PASS SERVICE INQUIRIES
✉ pass@bertis.com
☎ 031-717-0511

Through **PASS** *to* **PATH**

PASS is a proteomics-based analysis solution developed by a team of experts with over 15 years of experience in proteomics and strong expertise in bioinformatics data analysis.

Bertis possesses advanced Pan-omics analysis technologies and integrated workflows, providing solutions applicable across all research fields that utilize omics data.

Through **PASS**, researchers can leverage Bertis's specialized expertise and cutting-edge instruments across every stage of their study—from experimental design and data acquisition to interpretation and publication.

PASS

Bertis PASS | 301-302, B Building, D-Tech Tower, 33 Gwacheon-daero 7-gil, Gwacheon-si, Gyeonggi-do, Republic of Korea