Solutions for Biopharmaceuticals Analysis
Shimadzu’s innovative and robust instruments to accelerate your workflow!

Shimadzu is an industry leader in providing innovative analytical solutions for the biopharmaceutical and pharmaceutical market segments. Working closely with global collaborators and partners in industry and academia, Shimadzu develops products that meet customer expectations for robustness, reproducibility, and versatility. You can depend on Shimadzu’s extensive range of analytical products to help you in your daily laboratory workflows in Drug Discovery and Development, Clinical Trials, and QA/QC.
Development

Clinical Trials

Production & Quality Assurance

Automated Sample Pre-treatment

Quantitative Proteomics

LC-MS

Co-sense BA

PPSQ Series

Edman Sequencing

Protein Sequencer

LCMS-8050 with Skyline

Skyline
Biomolecules Research

Ultimate performance in identification and structural characterization of biomolecules.

The MALDI-7090 sets a new standard in MS/MS acquisition. Several novel and exclusive technologies have been combined to create Hyper-MS².

Features of MALDI-7090

High-resolution ion gate

The MALDI-7090 is equipped with a dual wire-grid high-resolution ion gate. Compounds of similar nominal mass may produce MS/MS spectra that contain fragment ions from several precursors if not gated correctly. However, the high-resolution ion gate in the MALDI-7090 allows the individual gating of species close in nominal mass, thus producing distinct fragment ion spectra.

Ultrafast acquisition speed

Ultimate MS/MS resolution

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Ultrafast acquisition speed

Ultimate MS/MS resolution
Axial Spatial Distribution Focusing - ASDF

ASDF is a Shimadzu patented technology that enables unparalleled resolution in MS/MS acquisitions. Through correction of the axial spatial distribution of the ions generated, the mass resolution is significantly increased and becomes essentially independent of the laser power used to ionize the sample. With ASDF, the MALDI-7090 can achieve mass resolution of 10,000 FHWM – unobtainable through pulsed extraction and ion optics alone.

The result of applying ASDF in addition to pulsed extraction during an MS/MS acquisition is illustrated below. The full MS/MS spectrum shown in the inset demonstrates almost complete sequence coverage of the detected fragment ions. The detailed region (m/z 1190 - 1310) shows the high resolution achieved using ASDF (10000 FWHM) as well as the presence of high-energy w-type fragment ions characteristic of side chain fragmentation.
Peptide Mapping

Rapid on-line trypsin digestion

Peptide mapping is an essential analytical approach to confirm amino acid sequences and any modifications. This is useful for characterization and QC of biopharmaceuticals as well as in research fields. The reproducibility of the analysis is important to compare chromatograms.

Perfinity iDP

Features of Perfinity iDP

The Perfinity iDP (Integrated Digestion Platform) system digests proteins using a dedicated trypsin column. The peptide fragments obtained from digestion are separated in a reverse-phase column using HPLC. By fully automating the series of steps, the system is able to significantly reduce the time required for analysis. By linking directly to an LC/MS system, the resulting peptide fragments can be identified automatically online. Compared to manual methods, fully automating the process minimizes human error and provides reproducible results.

- Rapid online trypsin digestion using a high-efficiency trypsin column
- Dedicated software supports methods that extend from pretreatment to analysis
- Automatic online analysis results in high reproducibility and reliability
- Online connectivity to mass spectrometers provides broad applicability

Manual Method

Perfinity iDP reduces the entire sample preparation workflow down to 20 minutes

Perfinity iDP

Reduce trypsin digestion time to 1-4 minutes
Features of Nexera-i Series

Uniform graphical user interfaces between the system and workstation allow intuitive operations regardless of experience level and increase the operation availability of the i-Series. The browser functions in LabSolutions bring rapid processing of large amounts of data, real-time statistical calculation and easy confirmation of anomalous values, enabling more efficient data processing.

The i-Series saves lab operators time and energy. Combined with the LabSolutions automated functions, it reliably completes analyses under specified procedures.

Intra-Day Repeatability for Chromatograms of IgG Tryptic Digests
Accurate Protein Sequence Determination

Protein sequencer

N-terminal amino acid analysis is essential to confirm the type and uniformity of N-terminal amino acids. This analysis employs the Edman method (sequential cleaving of amino acids from the N-terminal of the protein to determine the amino acid sequence), which is the most reliable method available for determining amino acid sequences.

The PPSQ Protein Sequencer Systems automate the Edman reaction, LC separation, detection and data analysis to determine the amino acid sequence from the N-terminal.

Features of PPSQ Series

1. Easy-to-use and cost-effective solution.
2. Easy data analysis assisted.
3. Shimadzu provides full support.
The results show the N-terminus of the light chain is uniform and the identified amino sequence is Asp-Leu-Val-Met-Thr from N-terminus.
Ultra-Fast, Comprehensive Quantitative Proteomics

Shimadzu’s LCMS-8050 is the fastest triple quad on the market. Combination with the Skyline environmental significantly increases the throughput of quantitative proteomics.

Features

Quantitating the proteins and peptides in biological samples accurately and with high sensitivity is an important issue. Therefore, MRM (multiple reaction monitoring) currently has become a leading method in quantitative proteomics that offers high reliability. However, developing methods for quantitative proteomics requires comprehensively considering a large number of MRM transitions. Therefore, Skyline software was developed to assist with large-scale quantitative analysis of proteins by LCMS. By combining the Skyline software with the ultra fast MRM (UF-MRM®) capability offered by the LCMS-8050 and other models, the throughput of quantitative proteomics can be increased significantly.

LabSolutions

- Predict digest peptides
- Calculate precursor ions for each valence state
- Select product ion candidates (using measured or calculated product ions)

Select transitions
- Calculated retention time values
- Calculated CE values

Select peptides for quantitation
- Select product ions
- Evaluate results from considering CEs

Search for transitions by MRM (example: about 600 ch)

Determine analytical conditions using MRM (example: about 1500 ch)

Optimized analytical MRM method (example: about 4 ch)
Example of Determining Collision Energy Condition Using Trypsin Digestion Products of Bovine Serum Albumin (BSA)

For the 33 types of BSA trypsin digestion products, 50 precursor ions with different valence states were specified. In addition, three or four types of product ions were specified for each precursor ion, and nine levels of collision energy (3 V steps) were specified for each product ion (190 MRM transitions), for a total of 1710 transitions considered within eight minutes.

Even though the peptide HLVDEPQNLIK dissolves together with other high-intensity peptides, using UF-MRM® allowed determining conditions readily based on nine collision energy levels.
Precise Glycan Structural Analysis

As the glycans in glycoproteins such as antibody drugs are added by the actions of multiple enzymes after protein translation, the diversity and non-uniformity of the glycan structure is an unavoidable problem. Guidelines require analysis of the glycan structures to the maximum possible extent. Due to reports indicating the relationship between the existence of fucose (one component of glycans) and antibody-dependent cellular cytotoxicity (ADCC), for example, glycans in antibody drugs will become increasingly important for research and development in the future.

Features of Sugar Chain Structural Analysis System Using MALDI-TOF MS AXIMA Resonance

- AXIMA Resonance employs unique Quadrupole Ion Trap technology for highly sensitive and accurate MS® spectral measurements of the molecular ions produced by MALDI.
- Prominence nano Nanoflow LC permits highly sensitive sugar chain analysis. The unique reflux flow control system enhances separation reproducibility, and the Nano-Assist dedicated software simplifies automation and parameter settings.
- AccuSpot automatically performs spotting of the sugar chains separated by the Prominence nano system onto MALDI plates and matrix addition.
- Separation and purification of the sugar chain mixtures by Prominence nano reduces ion suppression by impurities.
- Analysis software provides powerful support for sugar chain structural analysis.

Separation and Purification of Glycans

Glycan Spotting onto MALDI Plates and Matrix Addition

Enables MS® Spectral Analysis

Highly Accurate Identification

Prediction of Glycan Structure

Client Software

Search Software* and Database**

AXIMA Resonance

MALDI Plate Spotter AccuSpot

* The search software is a product of Mitsui Knowledge Industry Co., Ltd.
** National Institute of Advanced Industrial Science and Technology (AIST) holds the copyright to the database.
Data

Analysis of Commercial IgG from Human Myeloma for Research

Fig. 1  LC Chromatograms of Sugar Chain Samples from Human Myeloma IgG

Table 1  List of m/z Values for Ions from Sugar Chains Extracted from Mass Spectra

<table>
<thead>
<tr>
<th>m/z Values for Ions from Extracted Sugar Chains</th>
</tr>
</thead>
<tbody>
<tr>
<td>1563.69</td>
</tr>
<tr>
<td>1725.75</td>
</tr>
<tr>
<td>1766.74</td>
</tr>
<tr>
<td>1887.68</td>
</tr>
<tr>
<td>1928.85</td>
</tr>
<tr>
<td>2030.87</td>
</tr>
<tr>
<td>2192.93</td>
</tr>
</tbody>
</table>

Fig. 2  Mass Spectra of Sugar Chain Samples from Human Myeloma IgG

Fig. 3  Predicted Structure of Sugar Chains from Human Myeloma IgG
Glycans in antibody drugs can contribute to a drug’s antigenicity, pharmacokinetics, stability of higher-order structures, and so on. Because they can affect the stability or efficacy of pharmaceuticals, it is necessary to investigate the types of sugar chains present in antibody drugs. In addition, since non-uniformity of the glycan content in antibody drugs due to variability in cultivation parameters is a concern, the ability to control their uniformity in manufacturing processes is also desired. Techniques for evaluating glycans are strongly desired.

The RF-20Axs fluorescence detector offers the highest sensitivity in the world and supports ultra-high-speed analyses. In addition, it provides superior reproducibility due to the ability to better control temperatures. Highly quantitative analyses are important to evaluate glycans, especially as it relates to QC of biopharmaceuticals. Shimadzu UHPLC systems with RF-20Axs detectors can offer highly quantitative analyses, due to their outstanding sensitivity and reproducibility.
Data

Analysis of 2-benzamide Labeled Glycans

Chromatogram of 40 fmol Each of 2-AB-labeled Glycans
(20 nmol/L each, 2 µL injection)

<table>
<thead>
<tr>
<th>Glycan standard</th>
<th>R.T. %RSD</th>
<th>Area %RSD</th>
</tr>
</thead>
<tbody>
<tr>
<td>2-AB Man5</td>
<td>0.273</td>
<td>0.743</td>
</tr>
<tr>
<td>2-AB G2</td>
<td>0.245</td>
<td>0.684</td>
</tr>
<tr>
<td>2-AB G2FS1</td>
<td>0.196</td>
<td>0.589</td>
</tr>
</tbody>
</table>

Chromatogram of 40 fmol Each of 2-AB-labeled Glycans (20 nmol/L each, 2 µL injection)

Linearity from 2 to 200 fmol (1-100 nmol/L, 2 µL injection)

Analysis of Glycans in Antibody Drugs

Procedure of sample preparation

- Sample (Antibody drugs)
- Ultrafiltration
- Typtic digestion
- Extraction of glycans by Glycopeptidase F
- Purification of glycans by Blot Glyco*
- Labeling (2-aminobenzamidation or Pyridylamination)
- UHPLC

*Blot Glyco: SUMITOMO BAKELITE CO., LTD.

Chromatograms of PA-Glycans from Antibody Drugs
Amino Acid Composition Analysis

Two systems are available, depending on the application and purpose of analysis.
- Pre-column HPLC for analysis that prioritizes quantitation
- UF-Amino Station LC/MS system for qualitative analysis, which can even be used for samples containing contaminants

1. Pre-Column HPLC

Features of Pre-column HPLC Analysis

- Fast analysis by UHPLC significantly shortens analysis time.
- Using the automatic pretreatment functionality of the SIL-30AC autosampler for the derivatization process provides data with high reproducibility.
- The RF-20Axs fluorescence detector offers the world’s highest sensitivity levels, enabling analysis with extremely high sensitivity.

Data

Chromatogram of a 10 µmol/L Standard Mixture Solution with 22 Amino Acid Components (1 µL injection)
2. UF-Amino Station (Fast LC-MS)

UF-Amino Station features a special-purpose, fast analysis column and an LCMS-2020 mass spectrometer, which supports ultra-fast analysis speeds, to achieve the simultaneous analysis of 38 amino acid and amino acid-related components* in just nine minutes.

Additionally, it automates the derivatization reaction to eliminate the need for cumbersome pretreatment procedures by manual operation. UF-Amino Station is an excellent tool for quantitatively analyzing culture fluids.

* Permits the analysis of 38 amino acid-related components, such as anserine, citrulline, taurine, and GABA (γ-aminobutyric acid), in addition to the 20 major amino acid components.
Polysorbates are popular detergents used as a stabilizer for biopharmaceuticals and the analysis of polysorbates is important for QC. This analysis can be performed without using a purification protocol.

**Co-Sense for BA with LCMS**

Automates complicated sample pretreatment steps online!
The Co-Sense for BA automatically and seamlessly performs all processes from sample pretreatment to analysis. This is achieved using a column-switching HPLC system equipped with the innovative Shimadzu Shim-pack MAYI-ODS pretreatment column and a unique on-line dilution bypass channel design.

MAYI-ODS column removes proteins quickly and reliably
Newly developed hydrophilic polymer coating technology quickly and reliably removes macromolecules, such as proteins, from injected biological samples to achieve high recovery rates for target components. In addition to ensuring analytical columns and LC/MS interfaces are protected, this also helps reduce the time required for finishing the analysis.

**Sample Pretreatment Process**

Automated processing by Co-Sense for BA eliminates manual steps, reduces analysis times, and avoids sample losses.
Data

Analysis of Polysorbates in Antibody Solutions

A 99% recovery rate and very good reproducibility results (0.034% for retention time and 1.11% for area) were obtained from a model sample consisting of 10 mmol/L phosphate buffer solution (pH 6.8) spiked with 20 mg/mL human immunoglobulin G (IgG) and 100 µg/mL Polysorbate-80. This is useful for monitoring the degradation status of polysorbates due to oxidation, hydrolysis, or other factors.

Quantitative Analysis of Polysorbates

Accurate results with excellent linearity (>0.999) were obtained for polysorbates.
Purity Testing

Powerful Aggregation Analysis
This system is able to measure sub-visible particle aggregates (0.1 to 10 µm), which are said to be potentially immunogenic, with a single measurement. This is the world’s first system able to analyze protein aggregates using the laser diffraction method.

Quick monitoring of aggregation processes can be accelerated by mechanical stimulus
Antibody drugs and other biopharmaceuticals have been identified as having the potential of forming sub-visible particle (SVP) aggregates, which can cause severe side-effects such as anaphylaxis. However, most SVP aggregates are currently not evaluated. Therefore, a new means of effectively analyzing them is required.

The ability to evaluate the aggregation characteristics during the early stages of biopharmaceutical development can significantly reduce both the time and cost of development by screening out proteins prone to aggregation.
Confirmation of Aggregation Inhibition Effects of L-Arginine in Bovine Serum Albumin (BSA)

Experiment and research flow
1. Add bovine serum albumin (BSA) to purified water to make 12 mg/mL and then add 50 mM Tris buffer solution adjusted to a pH of 5 with hydrochloric acid.
2. Add 100 mM of L-arginine.
3. Analyze the particle concentration and size distribution while mixing the solution in a batch cell (SLD-BC75).

Results
• The effectiveness of L-arginine added to a BSA dispersion in inhibiting the formation of aggregates was studied.
• The relationship between the measured total particle quantities and the stirring time shows that adding the L-arginine reduced the quantity of aggregates.
• Using the provided stirring mechanism reduces the time required for creating aggregates.

Relationship between the concentration of aggregations and stirring time

![Graph showing concentration vs. stirring time](image)

Without L-arginine addition

L-arginine addition 100 mM

![Graph showing concentration vs. particle diameter](image)

Batch Cell
SLD-BC75
Sample amount: 5 mL
Nanoparticles are being developed for a variety of biopharmaceutical products for drug delivery, including controlled release systems. Because of the inertness and biocompatibility of gold nanoparticles (Au-NPs), they show great promise for drug delivery. The majority of applications utilizing Au-NPs involve conjugation with proteins, DNA, or APIs. The conjunction with biologic molecule Au-NPs is mostly due to the electrostatic and hydrophobic interactions between the protein-Au-NP complexes. One of the critical factors in optimizing Au-NPs with proteins or DNA is selecting the optimal particle size and shape.

UV-Visible absorption spectra can be used to study the effectiveness of Au-NP conjugation. Fig. 1 shows the change in Au-NP absorption of approximately 20nm diameter particles with various Au-NP organic complexes.

FTIR absorption spectra can be used to study the formation of conjugation complexes. Analysis of Au-NP and API bonding and other structural characteristics can be investigated. Fig. 2 shows four characteristic absorption bands of the Au-NP complex. These bands are evident as distinct absorption bands in the conjugated complex or as shoulders of other complex characteristic bands.
TOC (Total Organic Carbon)

The USP specifies the use of Total Organic Carbon (TOC) for management of organic impurities in purified water, Water For Injection, and cleaning validation.

Features of TOC-L/TOC-V

- Two oxidation systems (types) are available. The combustion oxidation model offers superior organic matter detection, whereas the wet oxidation model is superior for high measurement sensitivity. In addition to water samples, TOC analyzer applications can be expanded to solid and gas samples.
- Both the combustion oxidation and wet oxidation models can be used in combination with a solid sample combustion unit to configure solid sample TOC analyzers, which enable cleaning validation using the direct combustion (swab/direct combustion carbon) measurement method.

Data – Results of TOC System Suitability

A TOC system suitability test was conducted using the Shimadzu TOC-L CPH combustion catalytic oxidation type analyzer by the procedure outlined in Table 1. According to the USP, the detection rate is to be evaluated using the analyzer response values, but here, the measured concentrations were used instead. The result indicated a 100.1 % detection rate with respect to the system suitability test. This result shows excellent robust oxidation.

Table 1  TOC System Suitability Test Procedure Specified in USP

<table>
<thead>
<tr>
<th>TOC System Suitability Test Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1) Measure the TOC in distilled water (distilled water used for preparing test solution). This value is indicated as r w .</td>
</tr>
<tr>
<td>(2) Measure the TOC in the sucrose standard solution (0.50 mg/L carbon concentration). This value is indicated as r s .</td>
</tr>
<tr>
<td>(3) Measure the TOC by the system suitability test (1,4-benzoquinone solution with 0.50 mg/L carbon concentration). This value is indicated as r ss .</td>
</tr>
<tr>
<td>(4) The system suitability test requirement is satisfied if: detection rate = 100 (r ss - r w ) / (r s - r w ) is 85% - 115%</td>
</tr>
</tbody>
</table>

Fig. 1  TOC system suitability test data
High-Sensitivity Analysis of Elemental Impurities

Elemental impurities in pharmaceuticals remain with the active pharmaceutical ingredients’ (APIs) raw materials or they are inadvertently introduced during the formulation and packaging processes. Their presence, even in small quantities, can influence the efficacy and safety of the product. Elemental impurity profiling is being emphasized by the various global regulatory pharmacopoeias and the International Conference on Harmonization (ICH). The United States Pharmacopoeia (USP) has revised elemental impurity limits and analysis techniques. These will be governed under USP <232>, <233>, <735>, and <2322>.

The new Shimadzu ICPE-9800 series is designed to help you meet the latest regulatory sensitivity guidelines for metal impurities in biopharmaceuticals using ICPE.

**Features of ICPE-9800**

A vertically oriented torch with dual view ensures a sensitive and robust system. Capable of analyzing tough organic matrices without the need of additional gases while achieving low operating costs with gas-saving features like a mini-torch, ECO mode and vacuum stabilized optics.

ICPESolution software utilizes Method Assistants in combination with All Wavelength Acquisition ability and a database with over 110,000 lines to develop and optimize data quickly, even allowing addition of elements and wavelengths without re-analysis.
The new EDX-7000/8000 is a highly sensitive Energy Dispersive XRF system combining easy-to-use software with minimal sample preparation for the investigation of metal impurities according to USP <232> & <735> requirements without the need for gases or chemicals.

**Features of EDX 7000/8000**

The EDX-7000/8000 combines a highly sensitive LN₂ – Free SDD detector with a sample positioning camera and graduated collimators of 1, 3, 5, & 10 mm diameter. This is used in combination with five built-in user-selectable primary filters. The sample image is automatically captured and incorporated into Pass/Fail results that are automatically reported using pre-loaded report templates. The addition of the optional 12-position sample turret enhances sample throughput. Sensitivity for low Z elements is enhanced with control of the sample chamber atmosphere using vacuum or helium environments.

The addition of the turret allows automated continuous measurements for improved sample throughput, especially for measurements in vacuum or helium atmospheres.
Metabolomics is a method to analyze various metabolomic substances cyclopaically. It is becoming widely used in the pharmaceutical field as a method to discover new biomarkers related to diseases.
Ready-to-use methods make it easy to perform everything from optimizing pretreatment protocols and analytical methods to using a database for highly precise identification.

**Cell cultures**

![Cell culture image]

**Measurement Results Using GC-MS**

<table>
<thead>
<tr>
<th>Intensity (x10,000,000)</th>
</tr>
</thead>
<tbody>
<tr>
<td>4.0</td>
</tr>
<tr>
<td>2.0</td>
</tr>
<tr>
<td>3.0</td>
</tr>
<tr>
<td>1.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Retention Time (Minutes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
</tr>
<tr>
<td>20</td>
</tr>
<tr>
<td>30</td>
</tr>
<tr>
<td>40</td>
</tr>
<tr>
<td>50</td>
</tr>
</tbody>
</table>

**Mouse tissue**

![Mouse tissue image]

**Model Mouse Liver Tissue**

(Non-ion pair method)

![Model Mouse Liver Tissue graph]

More than 80 hydrophilic metabolites, including amino acids and organic acids, can be verified.

LC-MS Data Sheet No. 49 (LAAN-J-LM018)

**Human serum**

![Human serum image]

**Human Standard Serum**

(TMS-derivated)

![Human Standard Serum graph]

106 metabolites, including amino acids, organic acids, fatty acids, and sugars, were identified.

GC-MS Data Sheet No. 89 (LAAN-J-MS089)
Imaging Mass Microscope

Imaging mass spectrometry helps identify what you see at the molecular level. The iMScope TRIO transforms your data from merely “observational” to “analytical”.

NOTICE: Sales area - All areas excluding North America

Features of iMScope TRIO

High-resolution imaging offered by optical microscopes is required not only for pharmacokinetic analysis, but also for toxicity testing and toxicity mechanism analysis. Analysis of the retina and skin requires imaging with high spatial resolution.

Section with chloroquine administered (retina)

In this experiment, a rat retina administered with chloroquine was measured. High spatial resolution imaging of the retina resulted in visualizing the distribution of chloroquine around the retinal pigment epithelium, which is about 10 µm thick. Therefore, evaluating the safety of phototoxic compounds requires performing detailed analysis near the retina.

Experiment Conditions

Sample: rat retina with chloroquine administered
Matrix: CHCA (vapor deposited)
Measurement points: 50 µm 81 × 81 (6,561 points)
10 µm 49 × 53 (2,597 points)
Measurement pitch: 50 µm/10 µm
Laser diameter: 50 µm/10 µm
Measurement time: about 18 minutes at 50 µm and about 7 minutes at 10 µm
in vivo Optical Imaging by functional Near-Infrared Spectroscopy (fNIRS)

LABNIRS can be applied to brain function research and drug development for research into mental illness, such as depression and schizophrenia. It is expected to be used for such applications as the prediction of drug efficacy based on brain function.

Features of LABNIRS

- Next-generation optical brain-function measurements start with multi-channel and high-density, high-speed sampling.
- Reliability of three wavelengths and photomultiplier tube achieve superb sensitivity.
- Comprehensive options provide powerful measurement support. Increase the number of channels according to the aim of the experiments.

NOTICE: LABNIRS is not a medical diagnostic device. It can only be used for Research purposes.
LABNIRS is not available in all regions. Please check with your local Shimadzu office or representative for availability.
SHIMADZU Presents PIC/S GMP / FDA 21 CFR Part 11 / Computerized Validation Total Solution

All Shimadzu network system products incorporate functions for the PIC/S GMP and the Part 11 compliance regulation, and computerized validation functions required by GxP. Shimadzu provides documentation including IQ/OQ, Certificates of Compliance, and Inspection Test Result Reports based on the Shimadzu ISO9001 certified system. Shimadzu’s accredited service personnel offer full support for validation of customers’ Shimadzu products. In addition, Shimadzu acquires information on PIC/S and FDA regulations through seminars and workshops, participates in vendor audits demanded by agencies, and actively assists customers to comply with new regulations.
Global Network

Network System Capable of Responding Quickly and Accurately to Regional Customer Needs

By being sensitive to regional market trends, we will supply solutions demanded by the market in a timely manner. We will respond quickly and accurately to the various needs of customers in regions around the world by taking maximum advantage of developing business operations in close cooperation with respective regions.

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