

Mass Spectrometry Service Overview

Biologics Characterization

Service Description

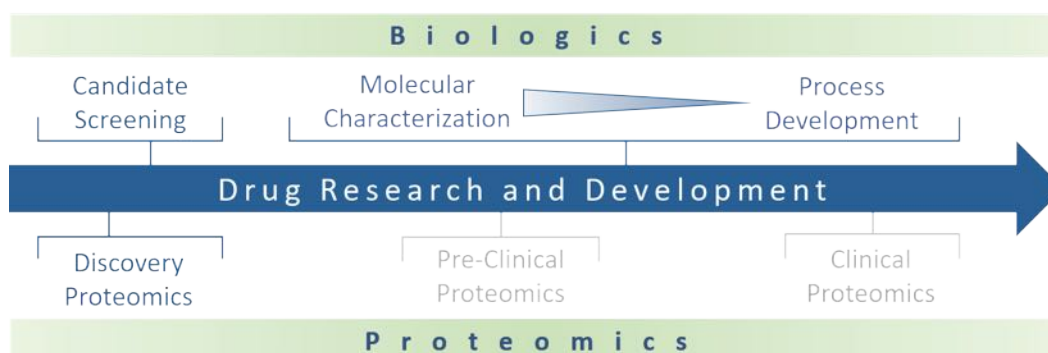
Innomics now offers proteomic and biologics characterization services to accelerate your life science research program. Our mass spectrometry service laboratory in San Jose, CA is staffed by scientists with extensive experience in liquid chromatography and mass spectrometry-based analytical methods. This state-of-the-art facility is designed to support a broad range of protein research applications.



Cutting Edge Solutions for Comprehensive Biologics Characterization

We provide analytical services and downstream support for biopharmaceutical and biotechnology industry customers. Our goal is to provide you with detailed knowledge about the molecular composition of your biologic sample using innovative analytical methods optimized for dynamic range and sensitivity.

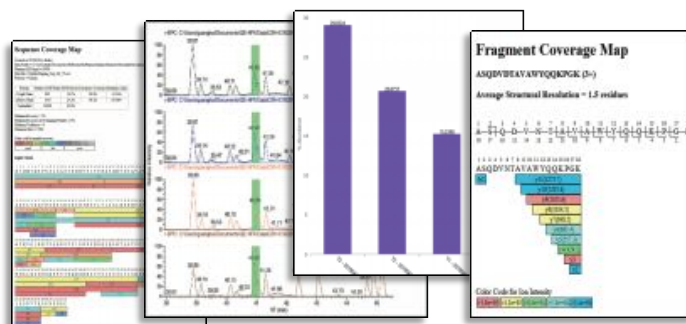
Our state-of-the-art LC-MS platform can support diverse biologics characterization projects, including highly complex samples such as bi-/multi-specific antibodies, ADCs, and Fc-fusion protein drugs. Additionally, our scientific team at the San Jose Mass Spectrometry Center have pioneered native LC-MS technology which can preserve non-covalent binding and is compatible with medium-high sample throughput ^{1,2,3}.



Biologics Characterization Service Overview

Peptide Mapping Services at Innomics

Innomics provides LC-MS/MS peptide mapping services to support biopharmaceutical and biotechnology applications. Our Peptide Mapping services are designed to characterize and monitor the molecular details of a therapeutic protein drug at each position in the amino acid sequence^{4,5}.



Sequence Verification

We provide amino acid sequence verification services and PTM mapping for purified proteins. Our service is useful for accurately validating expression of recombinant proteins or identifying process related PTMs on biologic drugs.

Individual samples



Molecular Assessment

We can help you characterize amino acid sequence liability. We provide a Molecular Assessment service to monitor specific amino acid modifications in response to a forced degradation treatment, which is customized to meet your project needs. Our service is optimized for high dynamic range peptide sequence coverage.

Sample batch

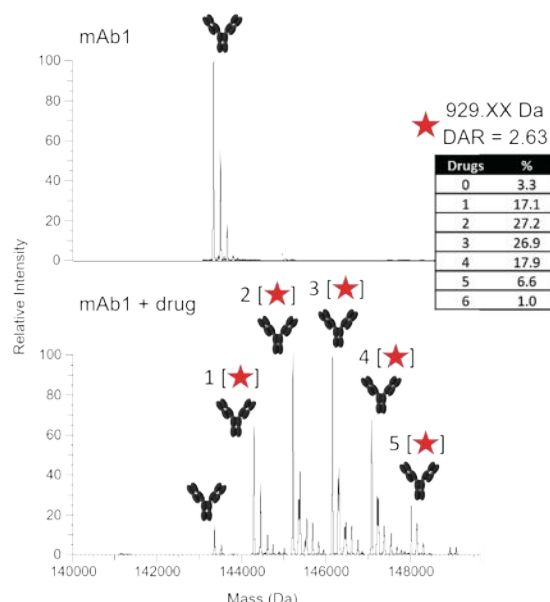


Biologics Characterization Service Overview

Intact Mass Services at Innomics

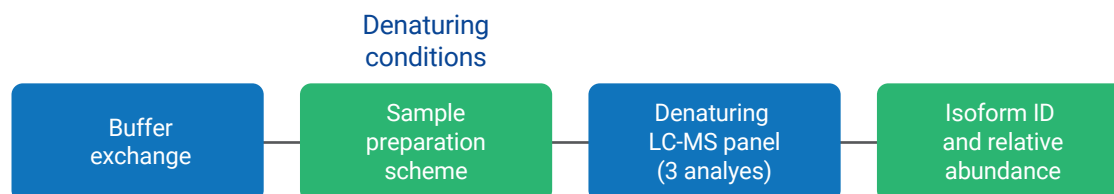
We can help you determine the whole intact mass of your recombinant protein or biologic sample. Intact Mass offers a “bird’s eye view” direct observation of mixtures of intact protein isoforms to monitor isoform heterogeneity and polydispersity.

Innomics scientists at the San Jose Mass Spec Center have developed cutting edge Intact Mass services utilizing multiple HPLC separation strategies combined with high resolution Orbitrap mass spectrometry^{1,2,3}.



Intact Mass

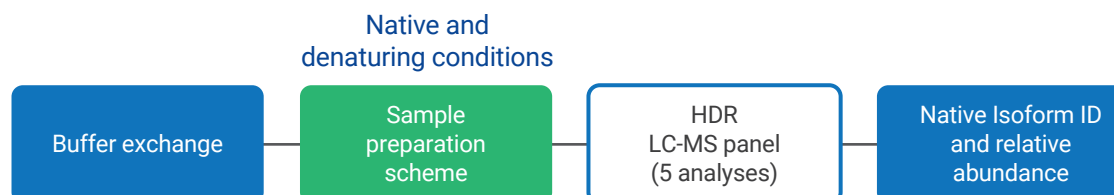
Our service incorporates a 3-way analysis of the untreated, deglycosylated, and reduced preparations of a biologic drug using reverse phase LC-MS. Our Intact Mass service is designed to accommodate screening and confirmation projects with large sample numbers¹.



High Dynamic Range (HDR) Intact Mass

High Dynamic Range (HDR) Intact Mass service combines data from both denaturing and native conditions. This service is based on size exclusion (SEC) LC-MS technology to directly measure masses using both denaturing and native conditions.

HDR Intact Mass service incorporates 5 key analyses, including native masses for (1) intact and (2) Ides-digested subunit (for antibody-related biologics) forms, and denatured masses for (3) intact, (4) deglycosylated, and (5) disulfide bond reduced form.



Biologics Characterization Service Overview

Mass Spectrometry Service Specification

Peptide Mapping and Intact Mass services are performed using analytical flow liquid chromatography, UV detection, and high resolution Orbitrap mass spectrometry

Sample Requirements

Service	Sample Type	Amount and Concentration		Minimum sample volume
Peptide Mapping and Intact Mass	Purified biologic sample in liquid solution	Recommended	1000 µg; 10 µg/µl	100 µl
		Required	10 µg; 1 µg/µl	10 µl

Data Analysis

Peptide Mapping

- Data analysis and validation performed with BioPharma Finder software
- Peptide mapping method for identifying sequence variants, unknown modification, and PTM co-occupancy
- Amino acid site PTM status and relative abundances

Intact Mass

- Peptide Mapping and Intact data analysis and validation performed with BioPharma Finder software
- Service allows protein isoforms to be identified by exact intact mass and quantified relative to other isoforms present

Sample Preparation and Services

Peptide Mapping

- Gentle digestion performed using sequencing-grade trypsin or alternative proteolysis designed to minimize sample preparation artifacts
- In-line UV detection also possible. Optimized for minimal sample oxidation
- Each fraction analyzed using 150 min analytical flow LC-MS/MS using a Q Exactive HF-X Orbitrap mass spectrometer

Intact Mass

- Includes buffer exchange and denaturing sample preparation panel including denatured intact, deglycosylation, and disulfide bond reduction
- Intact Mass service utilizes 20 min analytical flow reverse phase LC-MS/MS using Q Exactive HF-X BioPharma mass spectrometer
- High Dynamic Range (HDR) Intact Mass service utilizes 30 min SEC-MS performed using both denaturing and native MS-friendly mobile phase.
- HDR Intact Mass service includes native LC-MS measurement of intact and subunit masses

References

- [1] Schachner L, Han G, Dillon M, Zhou J, McCarty L, Ellerman D, Yin Y, Spiess C, Lill JR, Carter PJ, Sandoval W. Characterization of Chain Pairing Variants of Bispecific IgG Expressed in a Single Host Cell by High-Resolution Native and Denaturing Mass Spectrometry. *Anal Chem*. 2016 Dec 20;88(24):12122-12127. doi:10.1021/acs.analchem.6b02866.
- [2] Charge variant native mass spectrometry benefits mass precision and dynamic range of monoclonal antibody intact mass analysis. Bailey AO, Han G, Phung W, Gazis P, Sutton J, Josephs JL, Sandoval W. *MAbs*. 2018 Nov-Dec;10(8):1214-1225. doi: 10.1080/19420862.2018.1521131.
- [3] Ren C, Bailey AO, VanderPorten E, Oh A, Phung W, Mulvihill MM, Harris SF, Liu Y, Han G, Sandoval W. Quantitative Determination of Protein-Ligand Affinity by Size Exclusion Chromatography Directly Coupled to High-Resolution Native Mass Spectrometry. *Anal Chem*. 2019 Jan 2;91(1):903-911. doi:10.1021/acs.analchem.8b03829.
- [4] High-resolution peptide mapping separations with MS-friendly mobile phases and charge-surface-modified C18. Lauber MA, Koza SM, McCall SA, Alden BA, Iraneta PC, Fountain KJ. *Anal Chem*. 2013 Jul 16;85(14):6936-44. doi: 10.1021/ac401481z. Epub 2013 Jul 1.
- [5] Development of an LC-MS/MS peptide mapping protocol for the NISTmAb. Mouchahoir T, Schiel JE. *Anal Bioanal Chem*. 2018 Mar;410(8):2111-2126. doi: 10.1007/s00216-018-0848-6. Epub 2018 Feb 7.

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To learn more

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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