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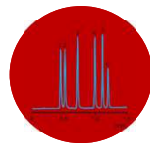
ZipChip™ System for Selected Thermo Scientific™ Mass Spectrometers
-- for CE/ESI-MS Analyses

The world leader in serving science

Content



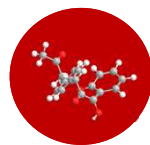
ZipChip System Introduction



ZipChip Separation Mechanism



Biopharmaceutical Application Examples



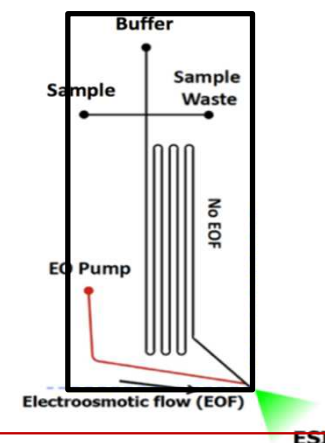
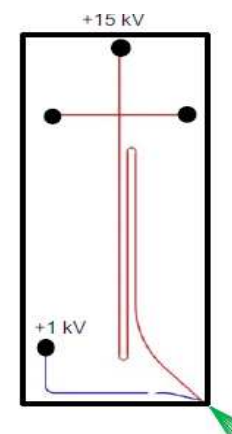
Metabolomics Application and System Test



Resources and Ordering Information

What is the ZipChip System?

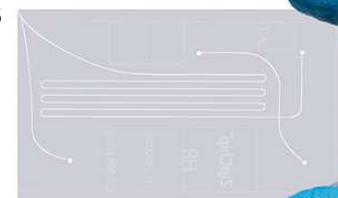
- The ZipChip system uses integrated microfluidic technology to prepare, separate samples by capillary electrophoresis (CE), and then electrospray (ESI) analytes directly into a mass spectrometer (MS)
- It is composed of the ZipChip interface and the microfluidic chip
- ZipChip Interface directly mounts onto the front end of a mass spectrometer
- The CE separation and ESI occur on the microfluidic chip
- ZipChip system is compatible with a broad range of biomatrices such as growth media, cell lysates, blood, plasma, and urine



	ZipChip HS	ZipChip HR
Separation channel length (cm)	10	22
Flowrate (nL/min)	150	150
Maximum # of injections per chip	125	125
On Chip De-salting capability	Yes	Yes
Integrated ESI Emitter	Yes	Yes
EEPROMS (recognize chip type and track usage)	Yes	Yes
Recommended use	Small molecules or simple sample mixture	Big molecules or complex sample mixture
Typical analysis time	Up to 3 min	Up to 15 min

Why the ZipChip System?

- Capillary Electrophoresis (CE) has unique advantages for certain analyses where traditional LC has its limitation
 - Separation of charge variants of intact antibodies/proteins
 - Effective separation of monosaccharides, glycans, and glycopeptides in a MS compatible condition
 - Separation of very hydrophilic molecules
 - Separation of amino acid isomers
 - Analyses of samples in high salt condition
- Other CE instruments that can be coupled with MS are bulky with cumbersome operations and take longer analysis time
- They are not specifically designed to be coupled with MS therefore requires additional interface
- There is a lack of convenient CE/ESI device that offers fast and good CE separation for mass spectrometry analysis
- ZipChip is the **ONLY** commercially available portable and integrated CE/ESI source designed for mass spectrometers



Fast CE separation • Nano Spray Sensitivity • HRAM Mass Spectrometry

Unique Values and Common Applications

Unique Values

- The only commercially available integrated and portable CE/ESI interface for MS
- Offers extremely rapid CE separations, nano-spray level sensitivity, and HRAM mass spectrometry in one platform
- Requires minimal sample preparation with on-chip desalting capability
- Consumes only picograms to nanograms of sample per analysis

Common Applications (not a full list)

- Intact mAb and ADC/biotherapeutics characterization
 - ✓ Native condition
 - ✓ Denatured condition
- mAb subunit analyses
- Glycomics and glycoproteomics
- Peptide mapping
- Metabolomics

Comprehensive Portfolio



ZipChip Interface

- Compatible with all Thermo Scientific™ Exactive, Q Exactive Orbitrap MS, and LTQ Orbitrap MS instruments
- Data collection, processing and reporting through Thermo Scientific™ Xcalibur and BioPharma Finder software
- Two versions: Autosampler operation version and manual operation version

ZipChip Autosampler

- Required to have for ZipChip Interface autosampler version
- Fully automated and controlled by the ZipChip software
- Conduct chip priming, sample and BGE loading, and chip flushing
- Compatible with both 48-vial plate and 96-well plate

DryDock

- A simply drying accessory
- No electrical component
- Utilize the MS gas to push air through the ZipChip channels removing residual fluid
- Dry 1 chip each time

ZipChips

- Disposable chips
- Good for up to 125 injections
- Two types: HR chip and HS chip
- Each chip is a single piece of glass similar as a microscope slide, housed in PEEK polymer
- Microfluidic channel and electrospray is integrated into both types of chips
- 5 chips per pack

ZipChip Assay Kits

- 3 types of pre-made assay kits are designed for intact antibody, peptides, and metabolites analyses, respectively
- Each box of assay kit contains 5 bottles of BGE and 5 bottles of sample diluents.
- Individual bottles can be directly loaded into ZipChip autosampler
- Each individual bottle contains enough volume for 100 runs
- Each box is good for 500 runs

ZipChip-MS Analysis Workflow

1



Select proper assay kit and ZipChip for your experiments

2



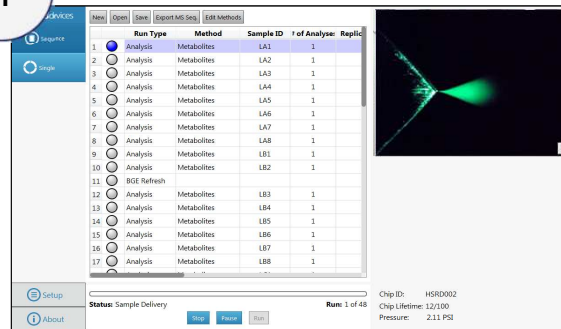
Simple Sample Prep

3



Place ZipChip and prepare the system

4



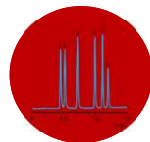
Set up sequence and collect CE-MS data



Content



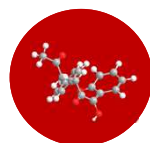
ZipChip System Introduction



ZipChip Separation Mechanism



Biopharmaceutical Application Examples

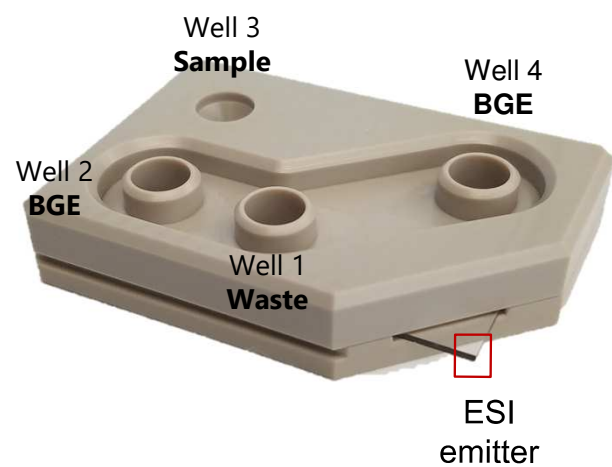


Metabolomics Application and System Test

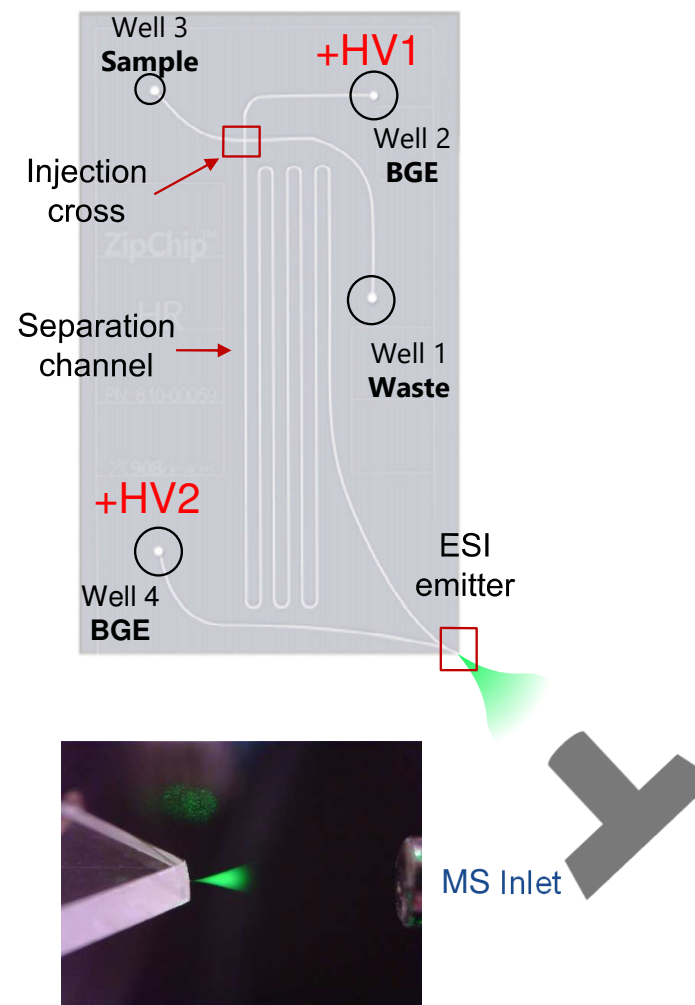


Resources and Ordering Information

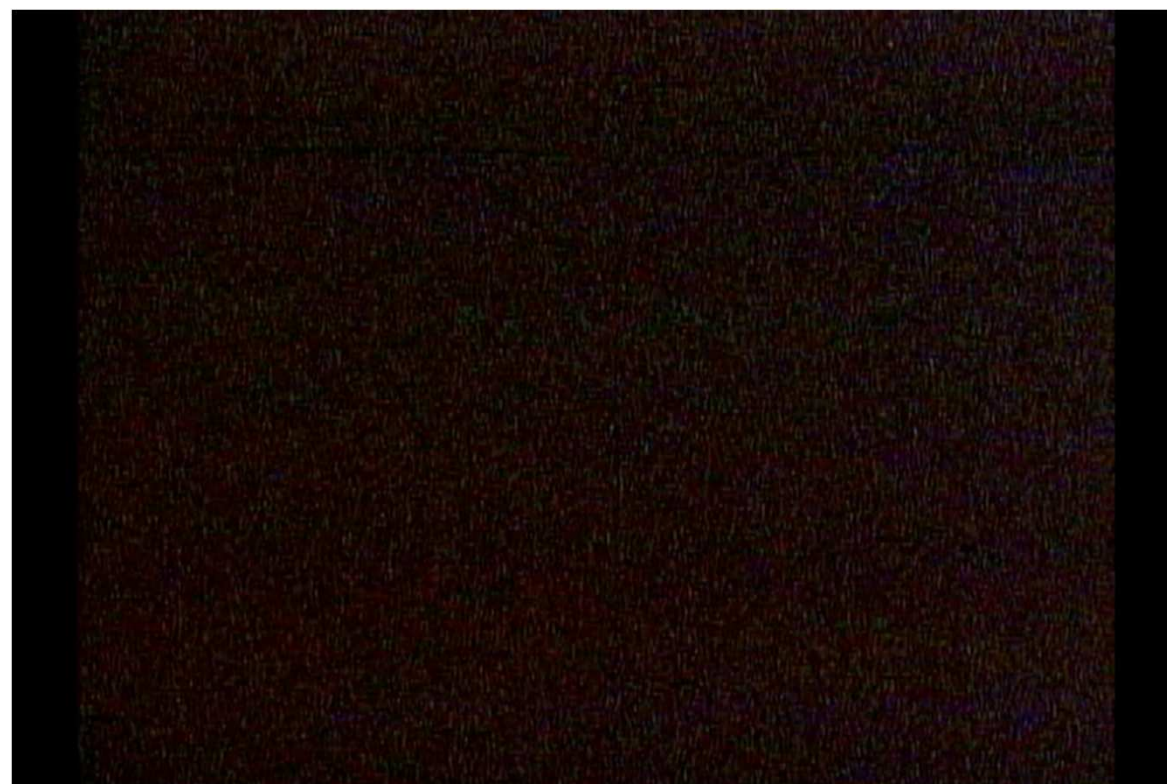
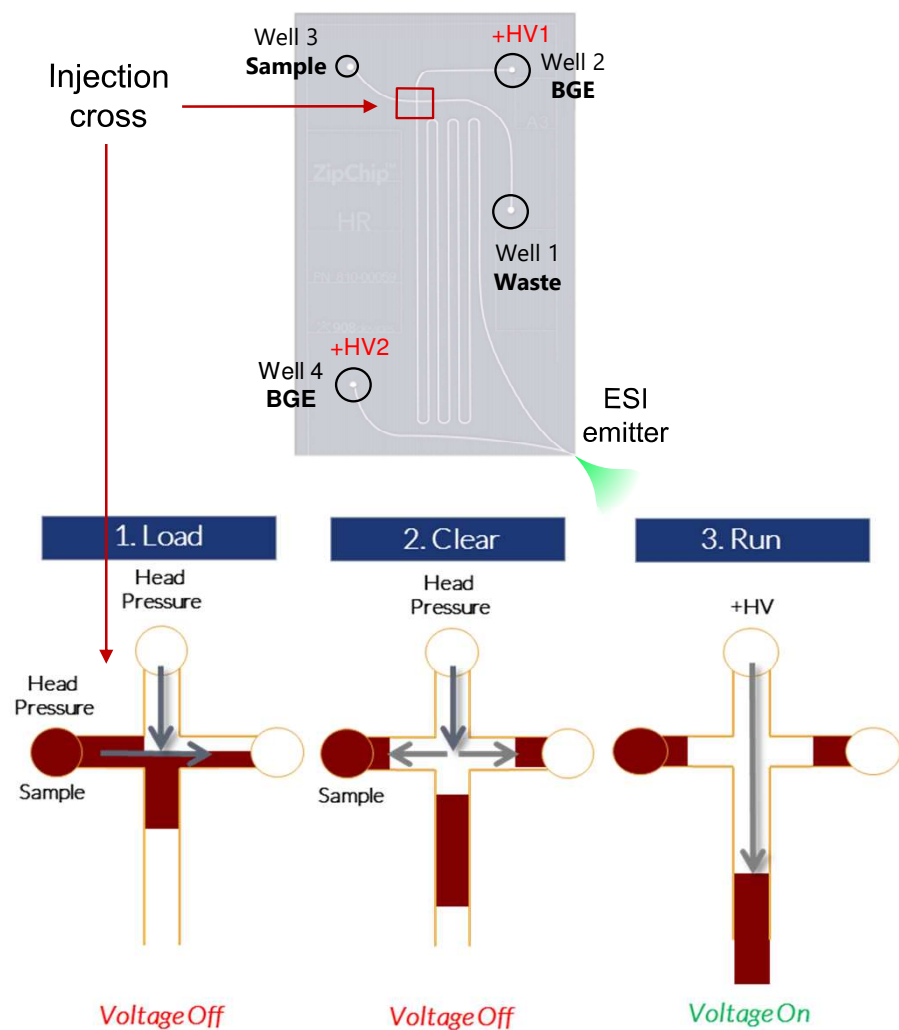
Anatomy of ZipChip



Glass microfluidic chip in PEEK housing



Sample Injection



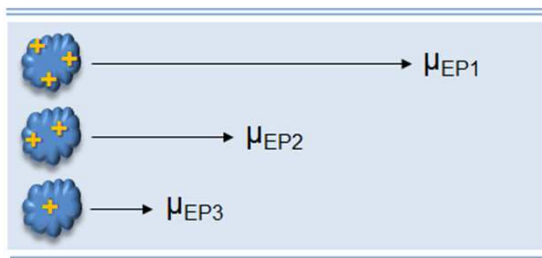
10 μ M rhodamine-6G in BGE + 100 mM ammonium acetate

Sample Separation

- High voltage applied to Wells 2 and 4
- HV1 and HV2 determine field strength

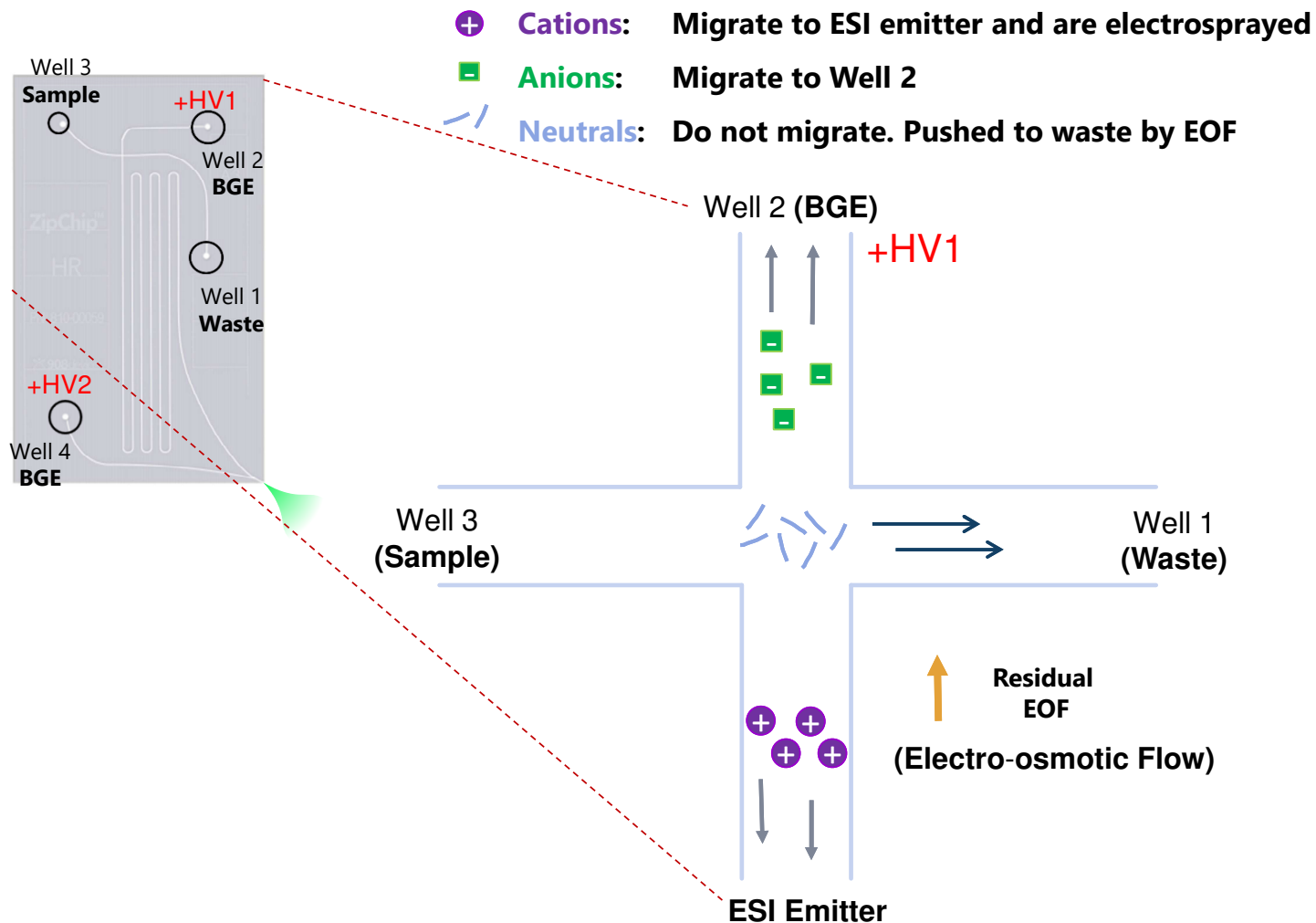
$$\text{Field Strength} = \frac{HV1 - HV2}{\text{Channel Length}}$$

- Field strength drives the ZipChip separation



$$\mu_{EP} = \frac{q}{6\pi\eta a}$$

q - charge
η - viscosity
a - hydrodynamic radius

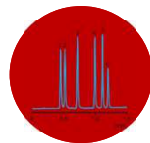


For ZipChip analysis analytes must be positively charged in solution

Content



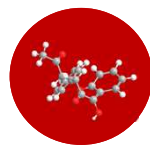
ZipChip System Introduction



ZipChip Separation Mechanism



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Resources and Ordering Information

The ZipChip System with Thermo Scientific™ Q Exactive™ BioPharma Platform



**High Mass Range (HMR) Mode
Intact mAb and
ADC Analysis**

Optimized intact protein analysis under both native and denaturing conditions assures the highest quality and most informative spectra for the widest range of therapeutic proteins.

**Protein Mode
Subunit Analysis**

Extreme resolving power of the Orbitrap™ mass analyzer ensures isotopic resolution of subunits

**Standard Mode
Peptide Mapping**

Perform peptide mapping with Orbitrap technology for unparalleled acquisition speed, mass accuracy, and spectral quality.

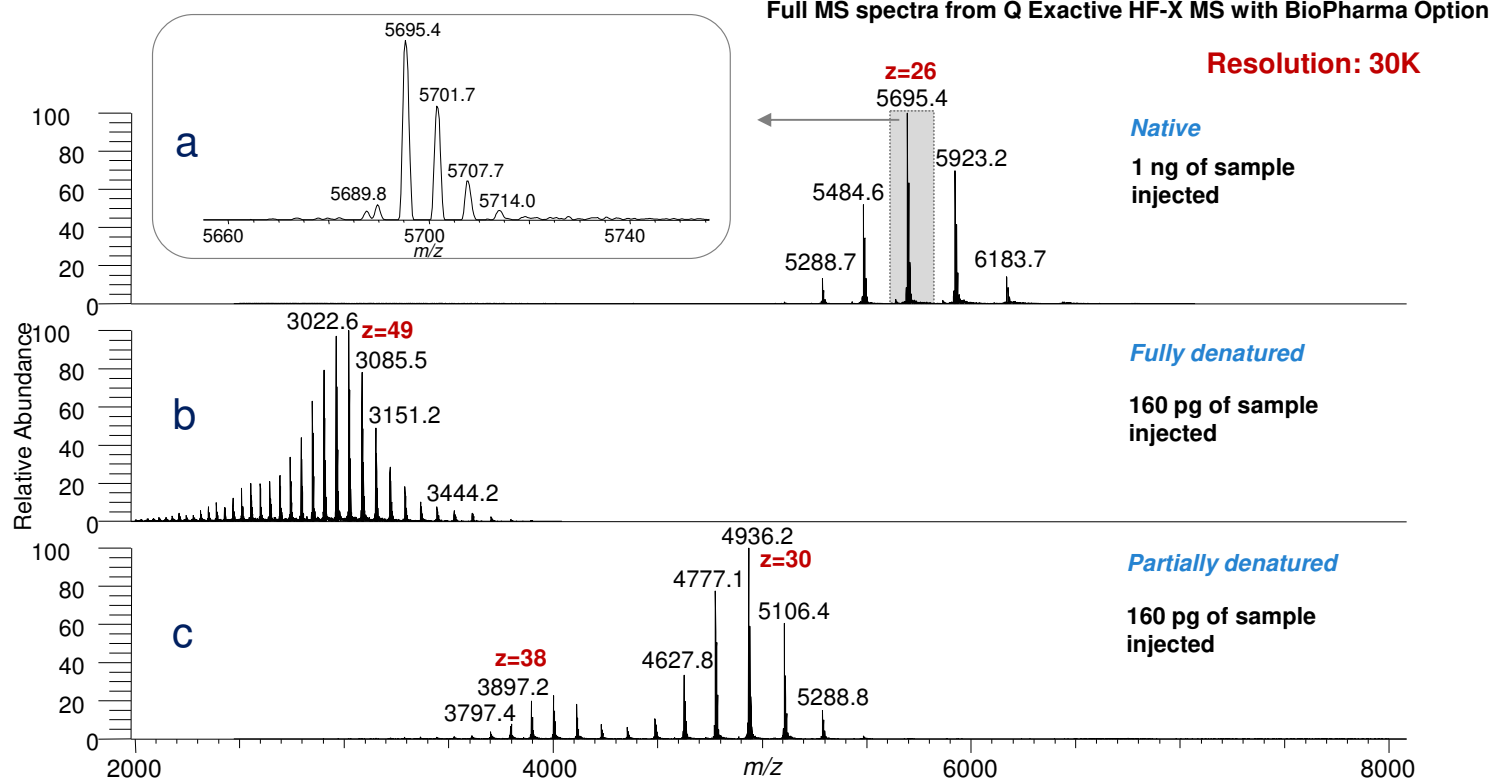
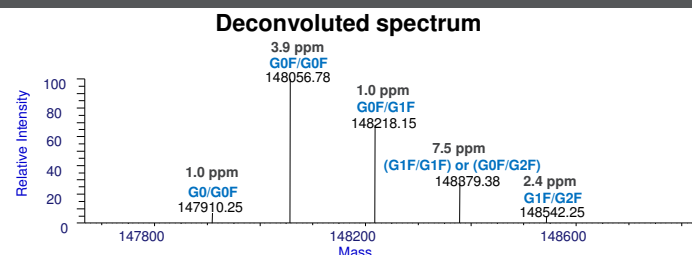
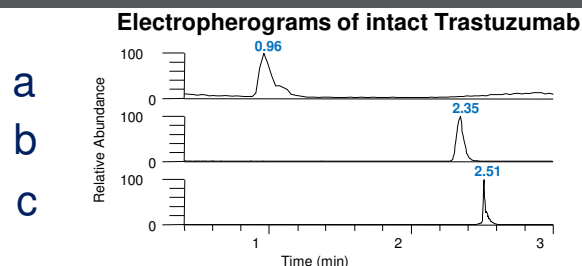
BioPharma Option is available for Q Exactive Plus, Q Exactive HF and Q Exactive HF-X mass spectrometers

Intact mAb - Trastuzumab Analysis in HMR mode

The ZipChip system coupled with the Q Exactive BioPharma platform can quickly analyze intact mAbs in native, partially denatured, and fully denatured conditions to support biotherapeutics characterizations under a diverse range of conditions

- CE/ESI-MS analysis can be completed within 3 minutes
- High resolution accurate mass spectra in intact native, partially denatured, and fully denatured states on the Q Exactive Plus/HF/HF-X MS with BioPharma option are confidently achieved
- Sample consumption can be as low as pico grams to nano grams
- Major glycoforms are identified by BioPharma Finder software

*MS data was acquired on a Q Exactive HF-X MS with BioPharma Option
 CE separation was achieved on ZipChip HR with 10mM Ammonium Acetate and 10% Isopropanol (native), Intact Antibody Assay kit (partially denatured), or Peptides Assay Kit (fully denatured)*

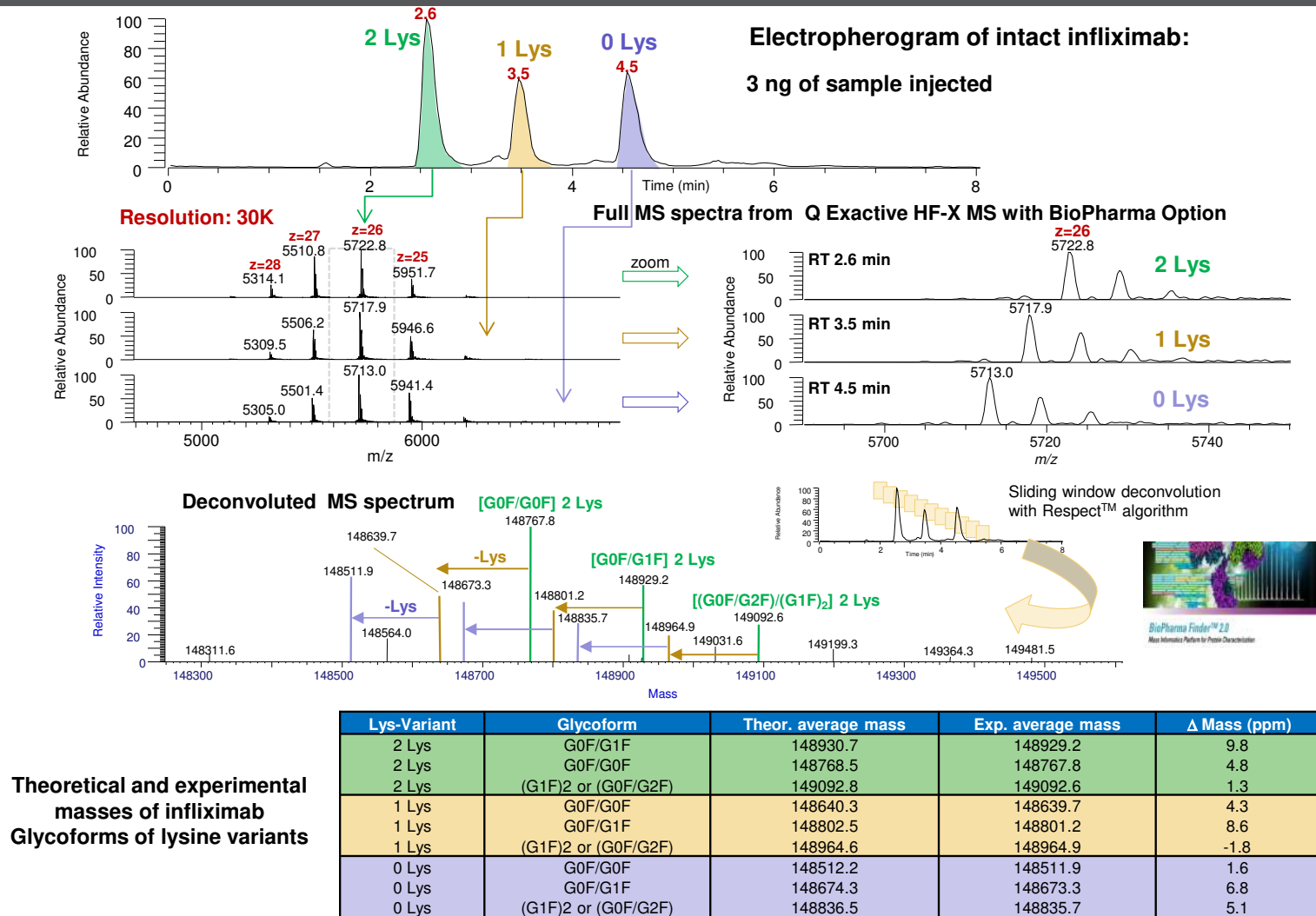


Intact mAb - Infliximab Analysis in HMR mode

The ZipChip system coupled with the Q Exactive MS BioPharma platform is unique and powerful to separate and identify different intact antibody charge variants in native and denatured conditions

- Baseline separation of intact mAb charge variants resulting from different levels of Lys-clipping can be achieved within three minutes by ZipChip system
- High resolution accurate mass spectra of all lysine variants are confidently detected on Q Exactive Plus/HF/HF-X MS with BioPharma option
- Three major glycoforms from each of the three lysine variants are identified by BioPharma Finder with mass accuracies better than 10 ppm

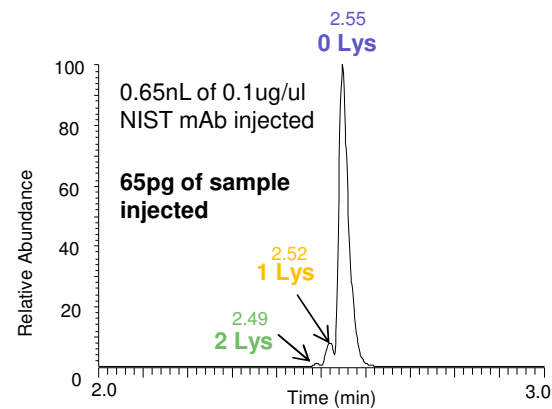
*MS data was acquired on a Q Exactive HF-X MS with BioPharma Option
CE separation was achieved on ZipChip HR with 10mM Ammonium Acetate in 10% Isopropanol as BGE*



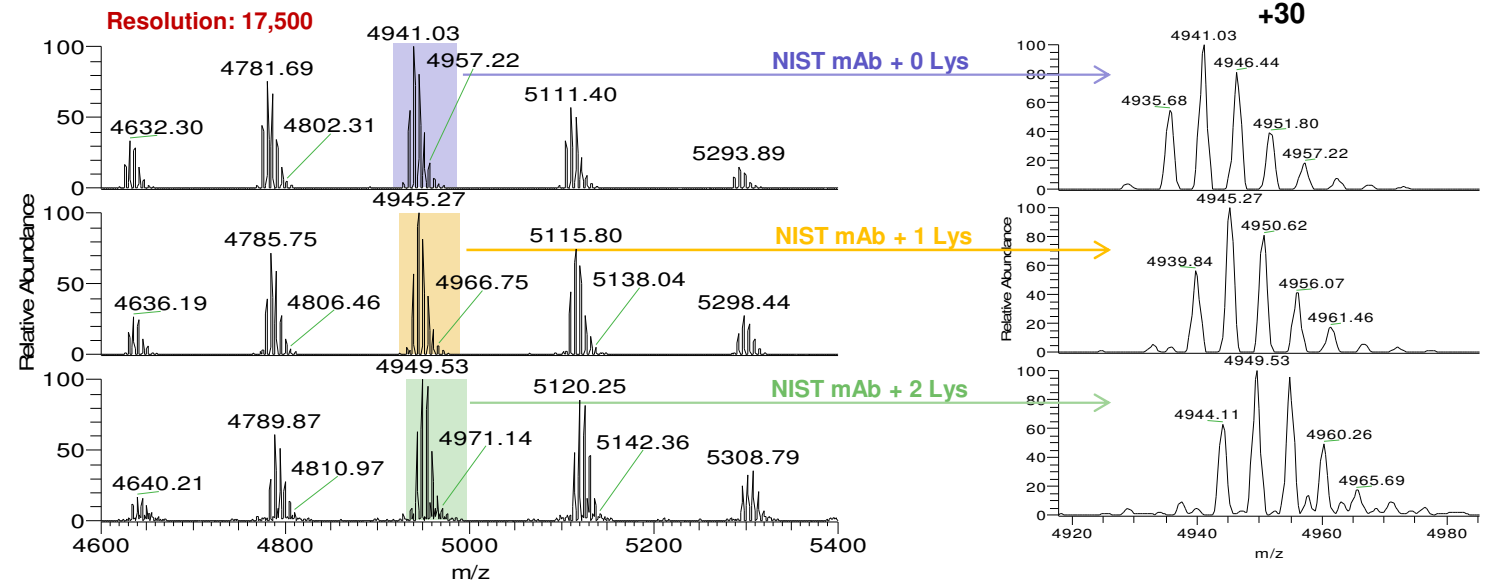
Intact NIST mAb Analysis in HMR Mode

The rapid separation and accurate identification of highly differently abundant charge variants can also be consistently achieved by the ZipChip system and Q Exactive BioPharma platform

- Near baseline separation of intact NIST mAb charge variants with abundance ranging over 2 orders of magnitudes can be achieved by the ZipChip system
- High resolution accurate mass data of each Lysine variant is confidently obtained on Q Exactive Plus/HF/HF-X MS
- Glycoform with abundance as low as 0.16% of the base peak can be detected and identified
- All 5 major glycoforms from each of the three different Lysine variants are identified by BioPharma Finder



Protein Name	Modification	Average Mass (Da)	Theoretical Mass (Da)	Matched Mass Error (ppm)	Intensity	Relative Abundance	RT (min)
NIST	1xG0F_G0F	148038.8	148037.1	11.5	1.28E+09	58.82	2.55
NIST	1xG0F_G1F	148200.0	148199.3	5.0	2.18E+09	100.00	
NIST	1xG1F_G1F	148362.1	148361.2	6.0	1.82E+09	83.26	
NIST	1xG1F_G2F	148522.7	148523.5	5.8	1.00E+09	46.00	
NIST	1xG2F_G2F	148684.6	148685.7	7.2	4.84E+08	22.21	
NIST_plus1K	1xG0F_G0F	148165.6	148165.3	1.9	7.66E+07	3.51	2.49
NIST_plus1K	1xG0F_G1F	148327.4	148327.4	0.1	1.39E+08	6.36	
NIST_plus1K	1xG1F_G1F	148489.7	148489.4	2.5	1.18E+08	5.40	
NIST_plus1K	1xG1F_G2F	148652.3	148651.7	3.6	5.97E+07	2.74	
NIST_plus1K	1xG2F_G2F	148811.9	148813.9	13.4	2.90E+07	1.33	
NIST_plus2K	1xG0F_G0F	148295.4	148293.5	13.1	1.04E+07	0.48	2.42
NIST_plus2K	1xG0F_G1F	148456.9	148455.6	9.0	1.56E+07	0.72	
NIST_plus2K	1xG1F_G1F	148618.4	148617.5	5.6	1.51E+07	0.69	
NIST_plus2K	1xG1F_G2F	148779.4	148779.9	3.1	8.07E+06	0.37	
NIST_plus2K	1xG2F_G2F	148942.0	148942.0	0.4	3.49E+06	0.16	



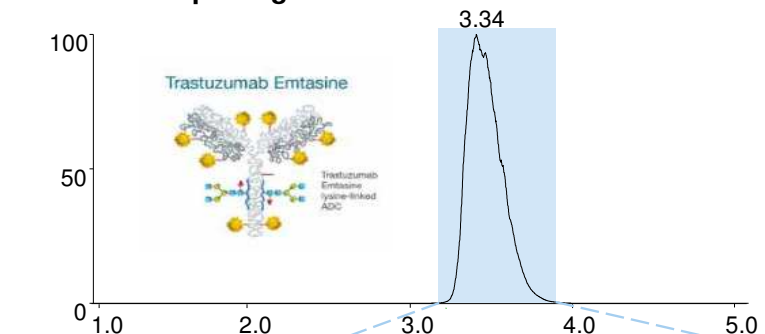
Similar MS data were obtained on both Q Exactive Plus MS and Q Exactive HF MS equipped with BioPharma Option CE separation was achieved on ZipChip HR with Intact Antibody Assay Kit

Antibody-Drug Conjugate (ADC) Analysis in HMR Mode

Heterogeneous ADCs can be successfully characterized within 1 minute without sample pre-treatment by the ZipChip system and Q Exactive BioPharma platform, and the powerful BioPharma Finder software

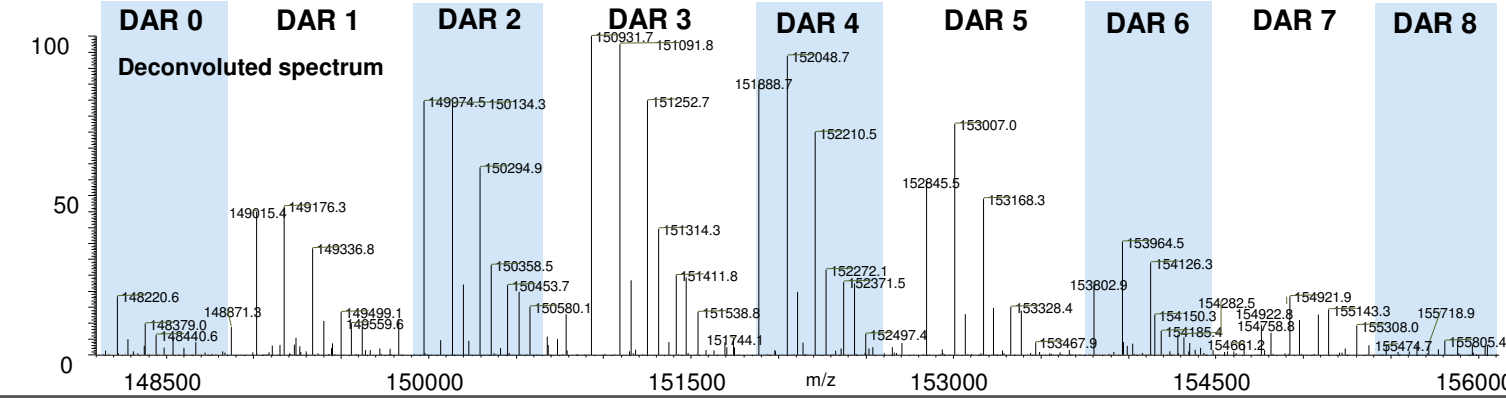
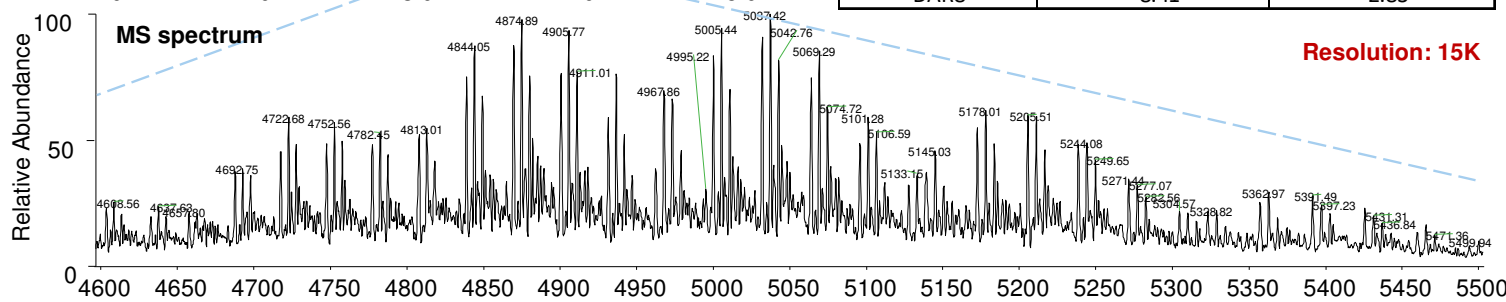
- Powerful sliding window capability enabled by BioPharma Finder software
- All of the different forms of Trastuzumab Emtansine can be analyzed in less than 40 seconds with only 3 nanograms of sample injected
- No sample pre-treatment required
- The calculated average DAR value is consistent with previous published data

Electropherogram of Trastuzumab Emtansine



Average Drug-to-Antibody Ratio (DAR) is 3.47

G0F/G1F DAR Form	Mass Accuracy (ppm)	Relative abundance
DAR0	10.72	9.95
DAR1	7.45	33.47
DAR2	1.23	58.97
DAR3	2.37	79.90
DAR4	5.63	69.92
DAR5	9.08	49.14
DAR6	13.89	28.97
DAR7	9.93	12.64
DAR8	8.41	2.83



MS data was acquired on a Q Exactive HF with BioPharma Option

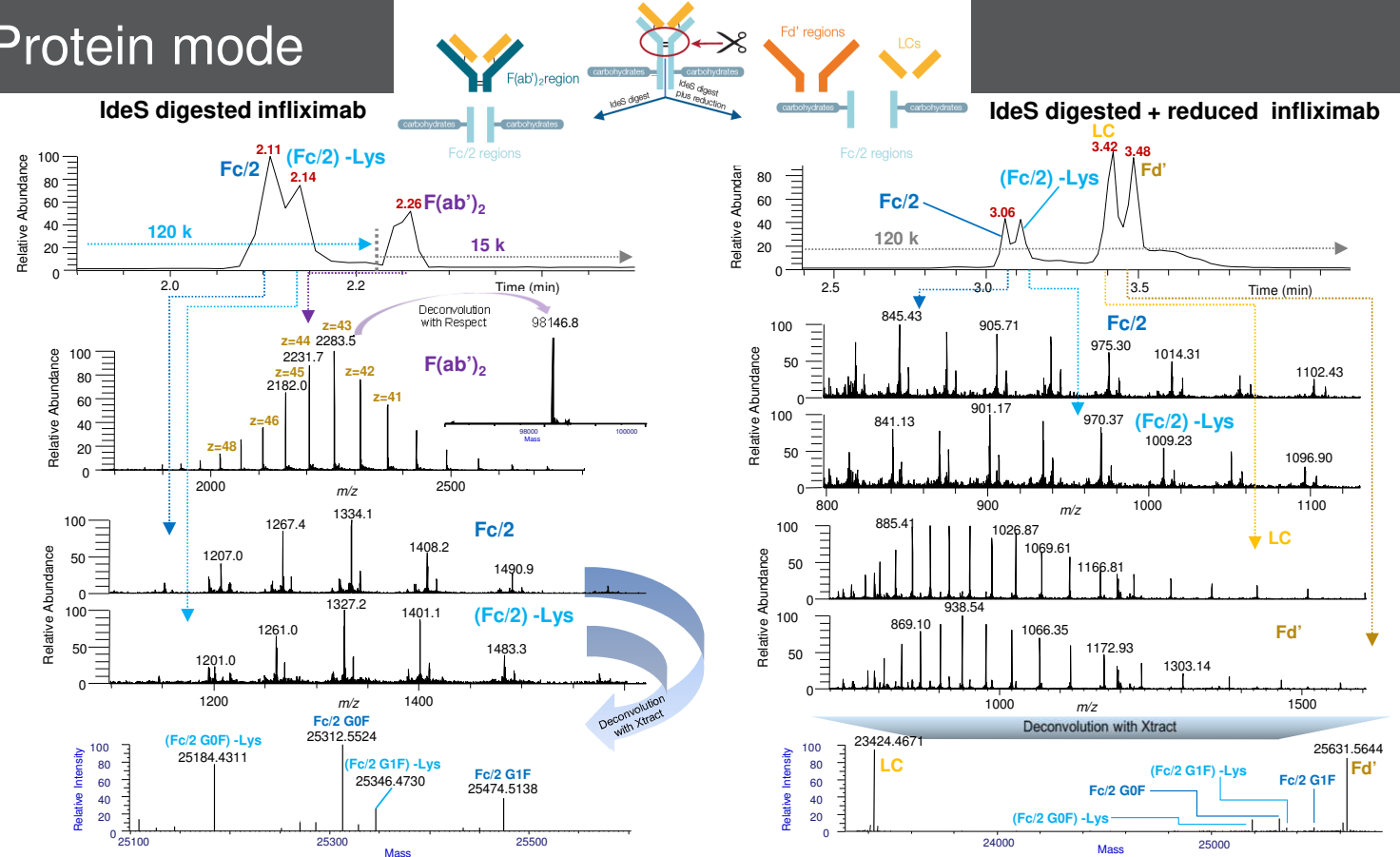
CE separation was achieved on ZipChip HR with Intact Antibody Assay Kit

mAb Subunits Analysis in Protein mode

Fast, sensitive, and accurate antibody subunit analysis can be accomplished by the ZipChip system and Thermo Scientific Q Exactive Plus/HF/HF-X MS platform

- Separation of infliximab mAb subunits can be achieved in 3 minutes by ZipChip system
- The sliding window method combined with Thermo Scientific™ Xtract™ deconvolution algorithm in BioPharma Finder software enables monoisotopic mass determination of each subunit
- Lysine variants and their major glycoforms of the subunits can be identified by BioPharma Finder software

*MS data was acquired on a Q Exactive HF-X MS with BioPharma Option
CE separation was achieved on ZipChip HR with Peptides Assay Kit*



	Subunit	Monoisotopic theo. mass	Experimental mass	Δ Mass (ppm)
IdeS digest plus reduction	Light chain	23424.3946	23424.4671	3.1
	Fd'	25631.5325	25631.5644	1.2
	Fc/2 G0F	25316.5863	25316.6345	1.9
	Fc/2 G1F	25478.6391	25478.5753	2.5
	(Fc/2 G0F)-Lys	25188.49131	25188.5763	3.3
	(Fc/2 G1F)-Lys	25350.54413	25350.5246	0.8
IdeS digest	F(ab)2	98146.3 (av.)	98146.8	-4.8
	Fc/2 G0F (2 SS bonds)	25312.5550	25312.5524	0.1
	Fc/2 G1F (2 SS bonds)	25474.6078	25474.5138	3.7
	(Fc/2 G0F)-Lys (2 SS bonds)	25184.4600	25184.4311	1.1
	(Fc/2 G1F)-Lys (2 SS bonds)	25346.5128	25346.4730	1.6

Peptide Mapping Analysis in Standard Mode

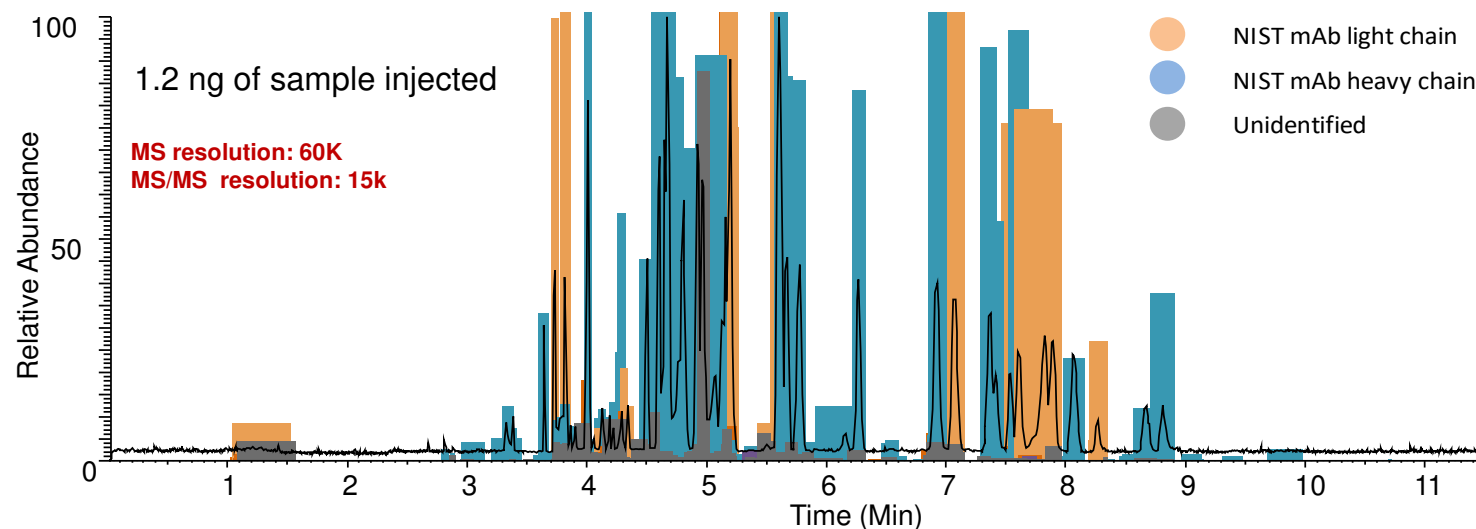
The combination of ZipChip sample separation, Q Exactive Plus/HF/HF-X MS platform produced HRAM MS and MS/MS spectra, and BioPharma Finder software enables fast and accurate peptide identification

- Plug and play ZipChip delivers stable nano spray and nano spray level sensitivity
- CE-MS/MS analysis can be completed in 10 minutes
- Only a few nanograms of sample are sufficient for the analysis
- 98% sequence coverage based on MS/MS data for the light chain and heavy chain is confidently achieved

MS data was acquired on a Q Exactive Plus MS with BioPharma Option

CE separation was achieved on ZipChip HR with Peptides Assay kit

Electropherogram of Digested NIST mAb

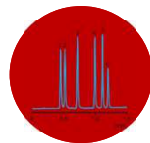


Proteins	Number of MS Peaks	MS Peak Area	Sequence Coverage	Abundance
NIST mAb light chain	141	26.4%	100.0%	41.67%
NIST mAb heavy chain	339	60.5%	97.6%	56.35%
Unidentified	1441	12.6%		

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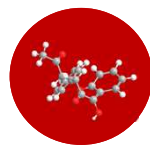
ZipChip System Introduction



ZipChip Separation Mechanism



Biopharmaceutical Application Examples



Metabolomics Application and System Test



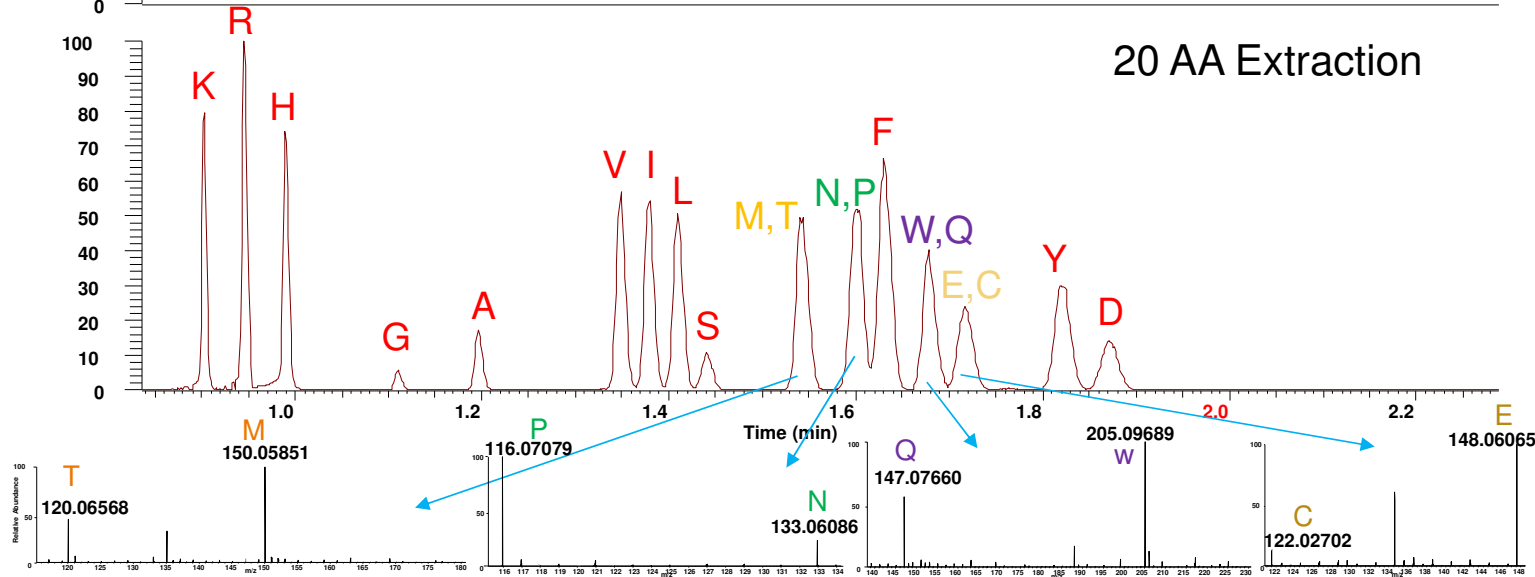
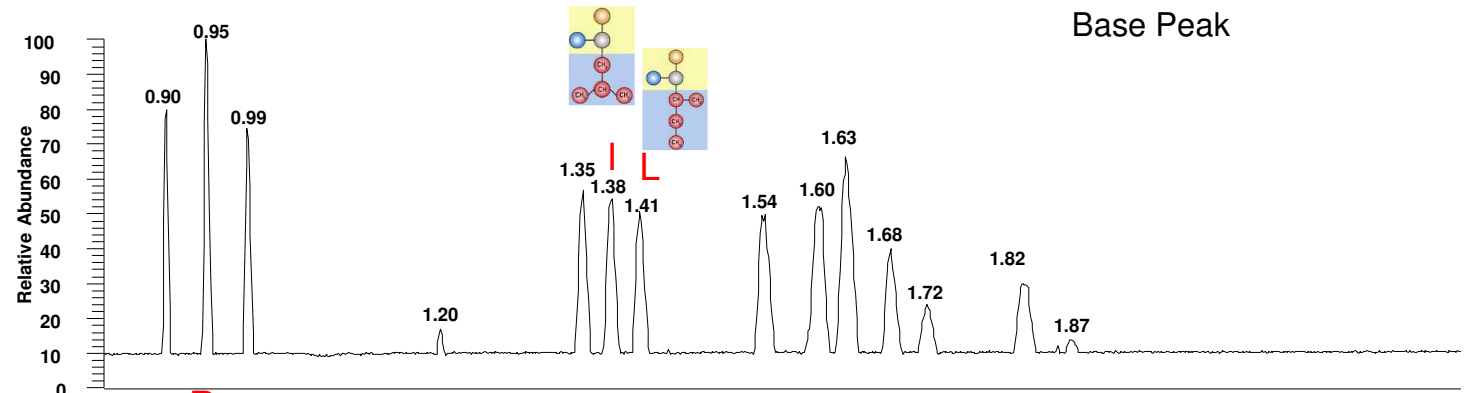
Resources and Ordering Information

Complete 20 Amino Acids Analysis

Extremely rapid separation and accurate identification of all 20 amino acid mix can be confidently achieved by the ZipChip system and Thermo Scientific Q Exactive /Focus/Plus/HF/HF-X MS platform

- Separation of 20 amino acids can be completed in 2 minutes by the ZipChip system
- Isomers, Leucine(L) and Isoleucine(I), can be baseline separated
- Co-eluted amino acids can be identified with HRAM mass spectrometry
- Femto grams level of sample is sufficient for each analysis

Electropherogram of 10uM Promega 20 AA Mix



MS data was acquired on a Q Exactive MS

CE separation was achieved on ZipChip HS with Metabolites Assay kit

Linear Dynamic Range Test of Arginine and Valine

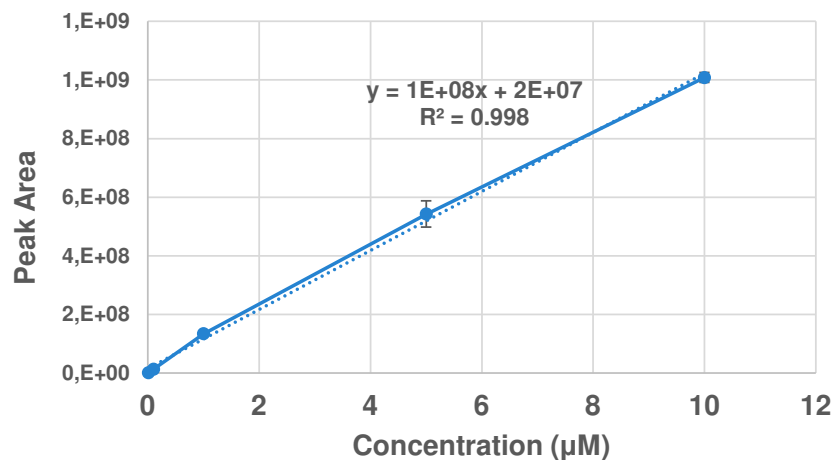
Minimum sample loading of 40 attomole Arginine and Valine can be achieved by the ZipChip system and Thermo Scientific Q Exactive /Focus/Plus/HF/HF-X MS platform

- Arginine and Valine calibration curves provide good linearity over the range of 10 nM to 10 μ M
- Lowest sample injection amount on the linear curve is 40 attomoles (4nL of 10 nM sample injected)

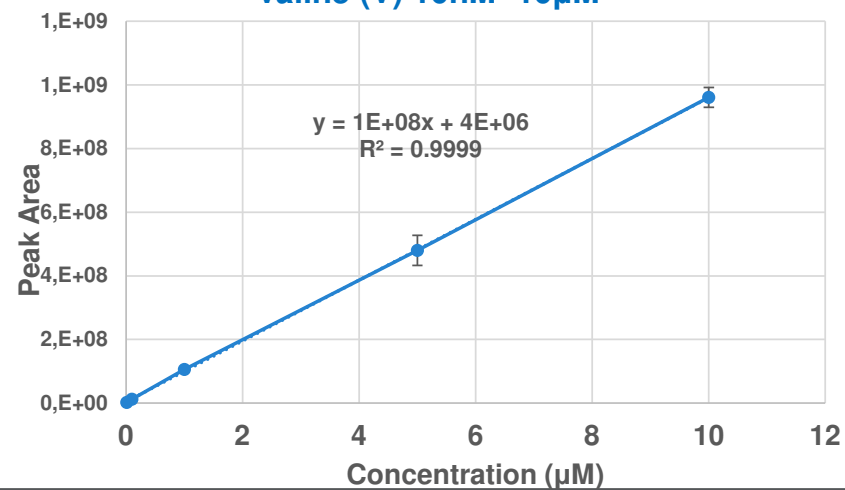
MS data was acquired on a Q Exactive MS

CE separation was achieved on ZipChip HS with Metabolites Assay kit

Arginine (R) 10nM~10 μ M



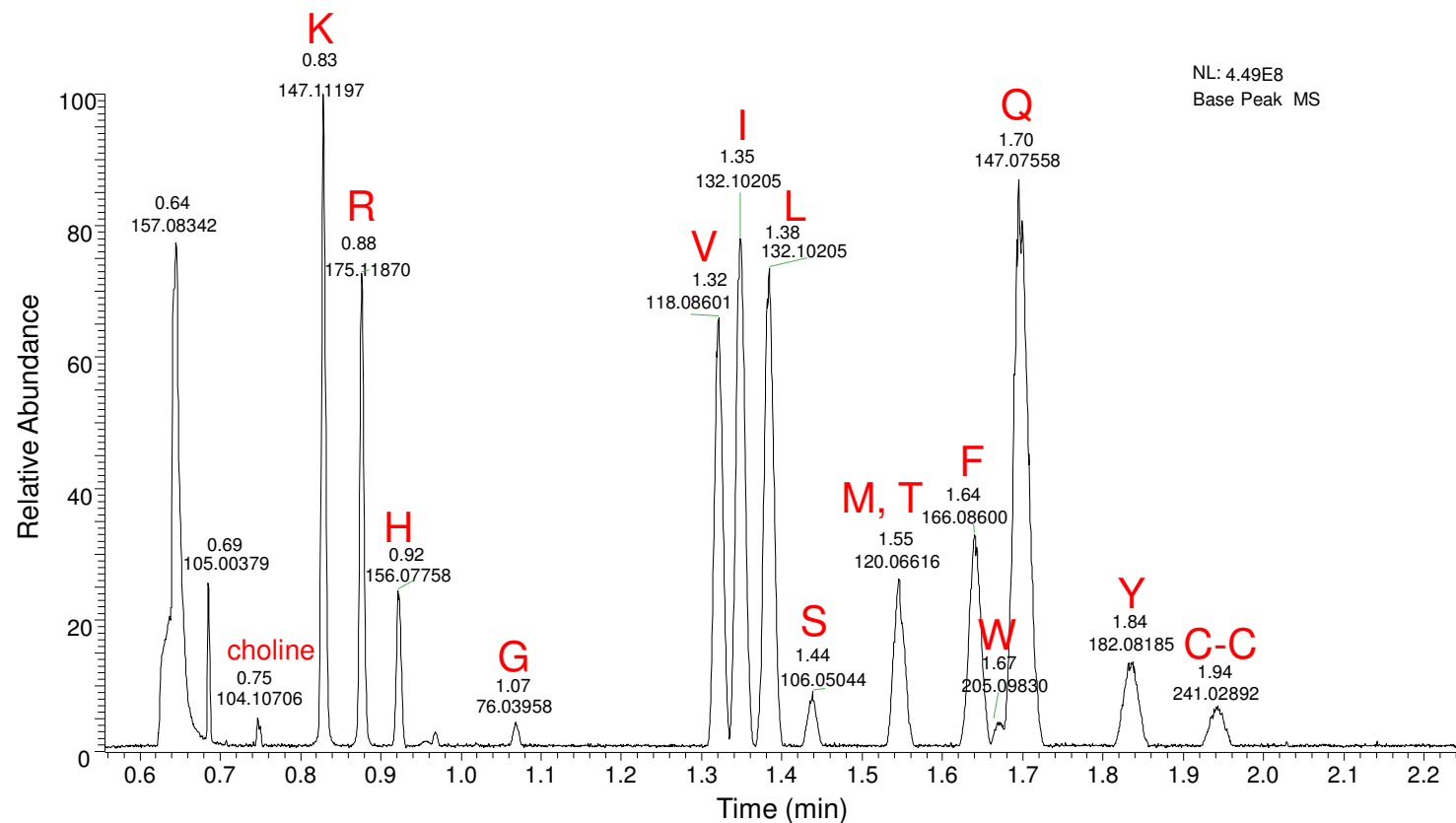
Valine (V) 10nM~10 μ M



Quick Analysis of Amino Acids in Gibco™ DMEM Cell Culture Media

The ZipChip system and Thermo Scientific Q Exactive /Focus/Plus/HF/HF-X MS platform can rapidly separate and identify the amino acids presented in cell culture media

- Sample can be directly analyzed after simple filtration and dilution
- On chip desalting capability allows direct analysis of samples in high salt condition without pre-treatment
- Separation can be completed in 2 minutes by the ZipChip system
- All 15 amino acids presented in the cell culture media are identified and results match up with the aa composition indicated in the commercial sample spec sheet



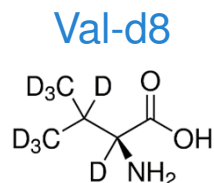
MS data was acquired on a Q Exactive MS

CE separation was achieved on ZipChip HS with Metabolites Assay kit

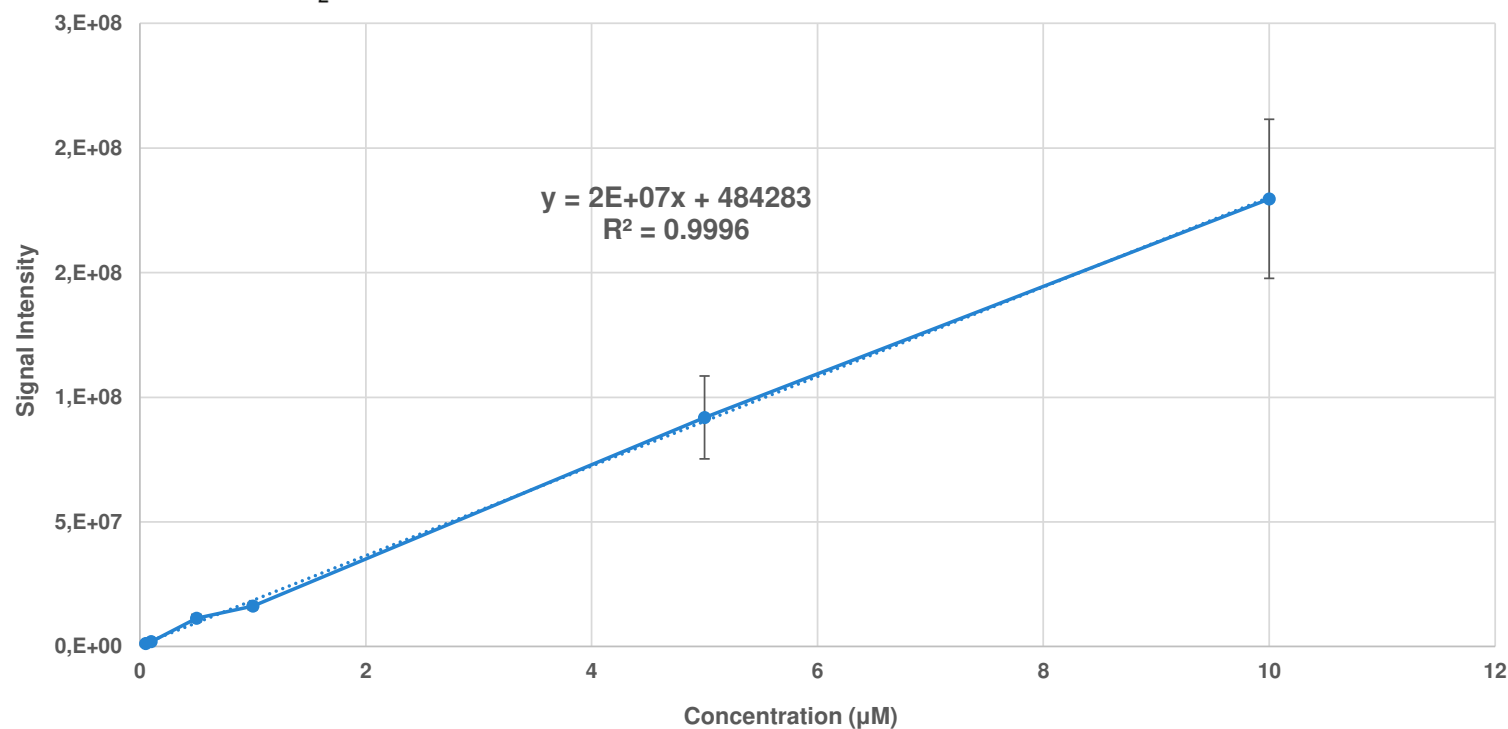
Calibration Curve of Internal Standard in Cell Culture Media

Accurate quantification of amino acids in cell culture media with stable isotope labeled internal standard can be achieved by the ZipChip system and Thermo Scientific Q Exactive /Focus/Plus/HF/HF-X platform

- Deuterated Valine standard, Valine-d8, was spiked into the crude cell culture media
- High linearity calibration curve with concentration range from 50nM to 10µM can be established.



Concentration range: 50 nM to 10µM



MS data was acquired on a Q Exactive Classic MS

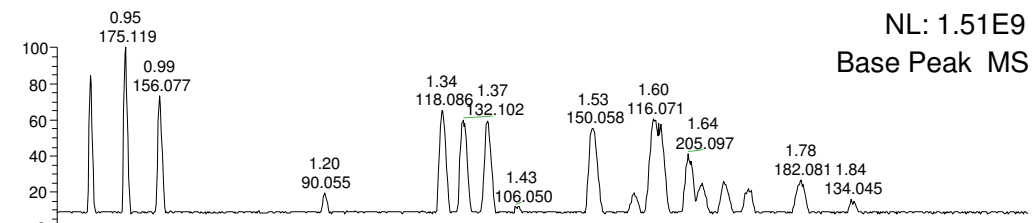
CE separation was achieved on ZipChip HS with Metabolites Assay kit

Carryover Test by Monitoring Arginine

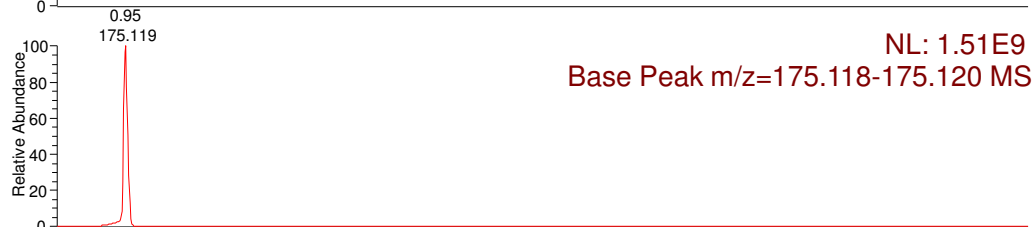
The ZipChip system has extremely low carryover

- Blank injections interleaved between 10 μ M AA mix injections
- Extracted ion electropherogram of Arginine from sample injection and blank injection were used to calculate the carryover
- Observed carryover of Arginine is only 0.054% or less

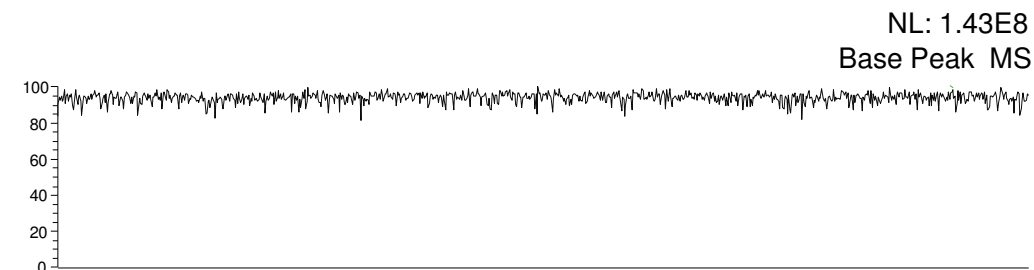
10 μ M AA mix



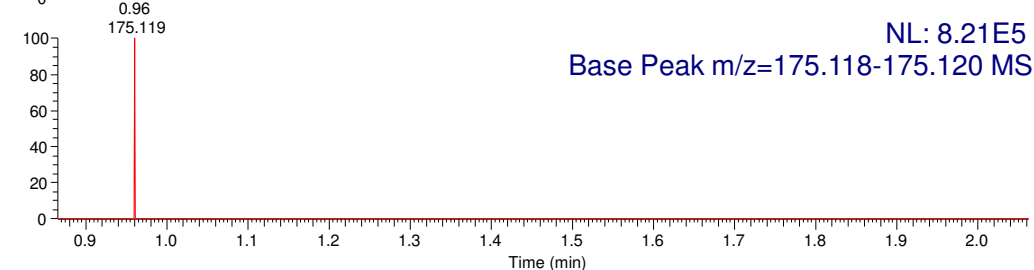
Extraction of Arg



Blank



Extraction of Arg



MS data was acquired on a Q Exactive Classic MS

CE separation was achieved on ZipChip HS with Metabolites Assay kit

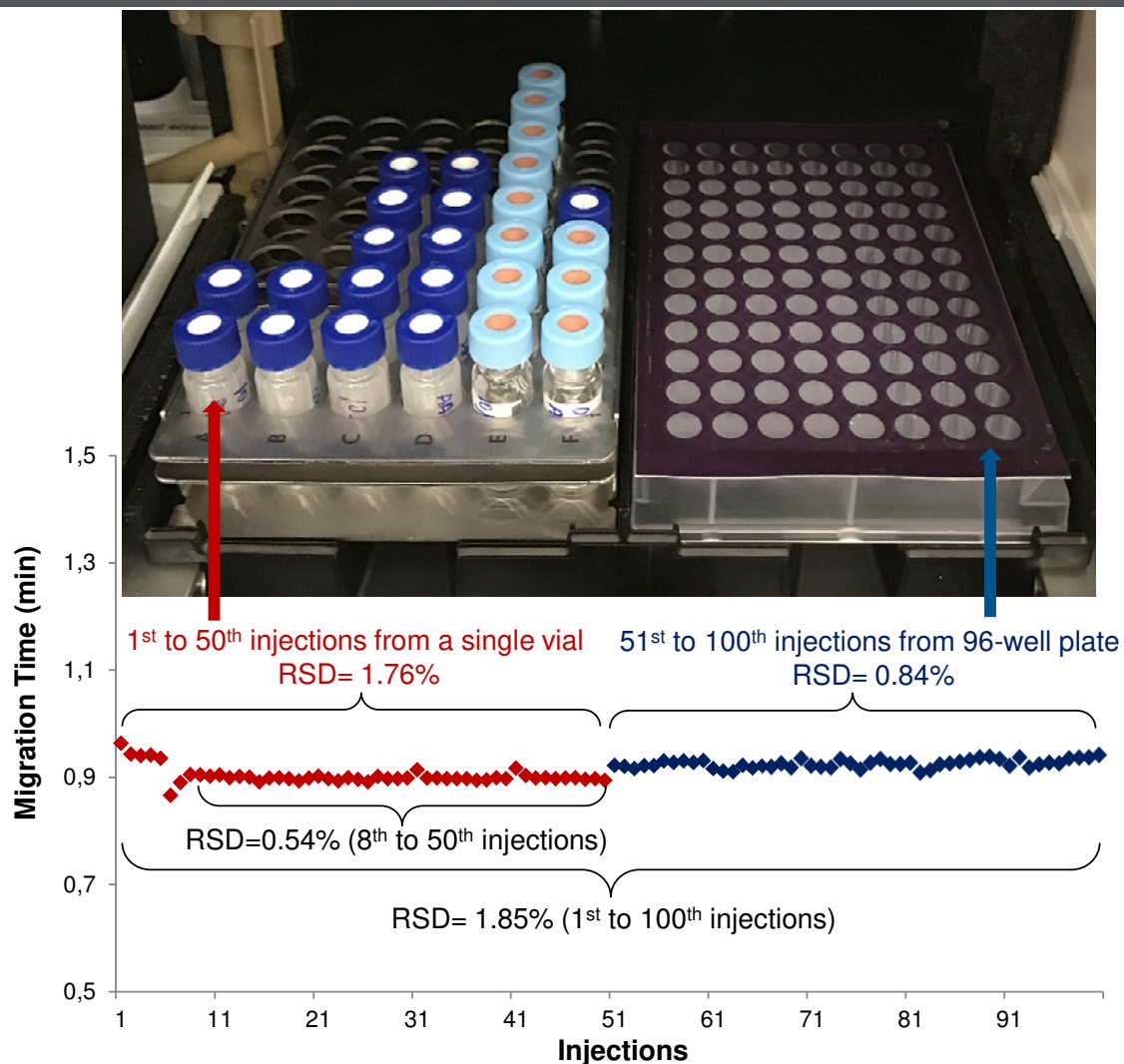
Migration Time Reproducibility Test Using Arginine (R) Standard

Operation of the ZipChip system through ZipChip autosampler can achieve good reproducibility

- The migration time of Arginine was monitored throughout 100 runs; the overall RSD value of the migration time is 1.85%
- It takes 5-10 injections for the system to get stabilized
- First 50 injections are from the same sample vial; the RSD value of the migration time is 1.76%; the RSD value dropped to 0.54% if excludes the first 7 injections
- Last 50 injections are from 50 different sample wells; the RSD value of the migration time is only 0.84%

MS data was acquired on a Q Exactive MS

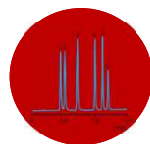
CE separation was achieved on ZipChip HS with Metabolites Assay kit



Content



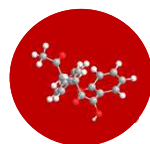
ZipChip System Introduction



ZipChip Separation Mechanism



Biopharmaceutical Application Examples



Metabolomics Application and System Test



Resources and Ordering Information

Available Resources

CE/ESI-MS Brochure

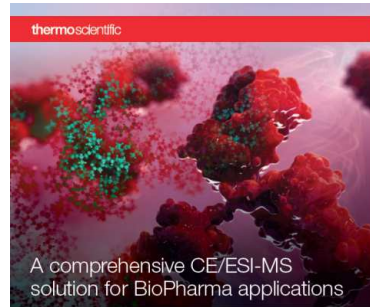
Hardware Spec Sheets

Consumable Spec sheet

Application Note

www.thermofisher.com/zipchip

908devices.com/products/zipchip



Thermo Scientific Q Exactive hybrid quadrupole-Orbitrap mass spectrometers with ZipChip system



Authors: Chien-Hsun Alex Chen, Stephanie Houck, Terry Zheng, Brian J. Agnew, Stephanie Gu, Yuh Zhou, Jonathan Joseph, Alan Peake, and Andrew E. Hahnley

Goal: Rapid screening of the heterogeneity of monoclonal antibodies and antibody-drug conjugates by an integrated microfluidic capillary electrophoresis (CE) and mass spectrometry (MS) workflow.

Introduction: Monoclonal antibodies (mAbs) and antibody-drug conjugates (ADCs) constitute two of the most important biopharmaceuticals within the class of biopharmaceutical drugs. During drug development and manufacturing, uncharacterized molecules and/or site modifications may introduce sample heterogeneity, causing changes to the protein structure that may lead to the loss of drug efficacy.¹⁻³ Therefore, the availability of a rapid screening method of the intact protein level to detect and assess any variability that might occur during drug development is attractive. Multiple analytical methods such as high-resolution liquid chromatography (HPLC), capillary electrophoresis (CE), and mass spectrometry (MS) have been used separately or together to characterize monoclonal antibodies.

Keywords: CE/MS, ZipChip, Q Exactive, BioPharma mass spectrometer, BioPharma Protein antibody, Monoclonal antibody, Antibody-drug conjugates.

Introduced here is an integrated CE-MS solution achieved by coupling the ZipChip™ (MS) system and the Thermo Scientific™ Q Exactive™ Orbitrap™ MS with the BioPharma option to rapidly assess the heterogeneity

Home > Industrial & Applied Science > Mass Spectrometry > Liquid Chromatography Mass Spectrometry (LC-MS) > LC-MS Accessories > ZipChip Interface for Mass Spectrometry

ZipChip Interface for Mass Spectrometry

LC-MS Accessories

ZipChip Interface for Mass Spectrometry



ZipChip Interface—seamless workflow for MS analysis of biological samples

Integrate capillary electrophoresis (CE) and electrospray ionization (ESI) into a single microfluidic device to rapidly prepare, separate, and electrospray biological samples directly into your Thermo Scientific mass spectrometer. The portable size ZipChip™ Interface directly mounts onto select models of Thermo Scientific mass spectrometers, and creates a seamless CE-MS workflow that offers fast CE separation, nano-spray level sensitivity, and HRAM spectrometry for the characterization of intact proteins, antibody drug conjugates (ADCs), antibody subunits, peptides, and metabolites.

The ZipChip Interface is a Class 1 laser product in compliance with 21 CFR 1040.10 and 1040.11 except for deviations pursuant to laser notice No. 50.

Featured ZipChip products



ZipChip™ Interface for Mass Spectrometry



ZipChip™ HR and HS Chips



ZipChip™ Assay Kits

SPEC SHEET ZipChip Hardware



Interface Specifications

Mounting Configuration: All Thermo Scientific

Operation: Fully automatic

Software: ZipChip™ interface software

Dimensions: 8.0x10.0x10.0

Weight: 7 lbs

Power Requirements: 110V/24V



Autosampler Specifications

Sample Format: Vials and plates

Sample Capacity: 100 vials and plates

Sample Tray Counting: 100 vials and plates

Software: ZipChip™ interface software



ZipChip provides unique microfluidic of Bio-compounds for mass spectrometry

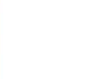
- High Precision CE/ESI-MS
- CE/ESI-MS
- Auto-MS/MS
- Auto-MS/MS
- Auto-MS/MS



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SPEC SHEET ZipChip Consumables



ZipChip Specifications

	ZipChip HR	ZipChip HS
Separation channel length (mm)	50	22
ZipChip media	Yes	Yes
Integrated CE	Yes	Yes
Electrospray Capillary	Yes	Yes
MS/MS capability	Yes	Yes
Autosampler	Yes	Yes
Autosampler tray	Yes	Yes
Autosampler tray	Yes	Yes
Autosampler tray	Yes	Yes
Autosampler tray	Yes	Yes

ZipChip Assay Kit Specifications

Available Kits: ZipChip Assay Kit (HR/HS), ZipChip Assay Kit (HR/HS), ZipChip Assay Kit (HR/HS), ZipChip Assay Kit (HR/HS)

Capacity: 100 samples (400 per kit)

Storage Conditions: Room temperature, 20-40°C

Quality Assurance: High purity, low background

Autosampler: Fully automatic, no-dead-end

The ZipChip system provides unique microfluidic preparation and separation of Bio-compounds for mass spectrometry:

- Fast analysis: < 30 min per sample
- Low sample volume: 100 nL
- Minimal sample preparation, no-dead-end
- Single measurement capability: antibodies and ADCs
- Autosampler for unattended operation

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Evaluation of a microfluidic electrophoresis device coupled to an Orbitrap mass spectrometer for the characterization of biotherapeutics proteins.

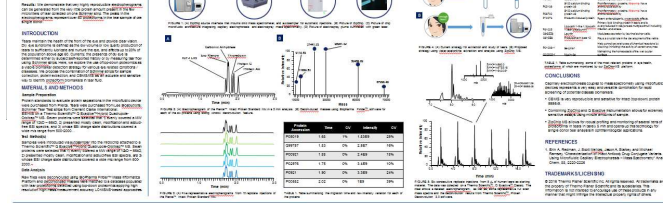
Abstract: The ZipChip™ interface for mass spectrometry (MS) provides a seamless workflow for the analysis of biological samples. This study evaluates the performance of the ZipChip™ interface for the analysis of intact antibodies and antibody-drug conjugates (ADCs) using an Orbitrap mass spectrometer.

Capillary Electrophoresis – Mass Spectrometry for Intact Mass Analysis of Antibodies and Antibody-Drug-Conjugates

Abstract: The ZipChip™ interface for mass spectrometry (MS) provides a seamless workflow for the analysis of biological samples. This study evaluates the performance of the ZipChip™ interface for the analysis of intact antibodies and antibody-drug conjugates (ADCs) using an Orbitrap mass spectrometer.

Profiling Of Clinically Relevant Proteoforms in Human Tears Using Chip-Based Capillary Electrophoresis Coupled To Mass Spectrometry

Abstract: The ZipChip™ interface for mass spectrometry (MS) provides a seamless workflow for the analysis of biological samples. This study evaluates the performance of the ZipChip™ interface for the analysis of intact antibodies and antibody-drug conjugates (ADCs) using an Orbitrap mass spectrometer.



Empowering Traditional Mass Spec

The ZipChip™ separations platform uses integrated microfluidic technology to prepare, separate and electrospray biological samples directly into traditional mass spectrometers (MS). In less than 3 minutes per sample, the cost-effective ZipChip system enables analysis of a broad range of matrices from growth media to cell lysates, blood, plasma, urine, and biopharma products. Each chip provides answers on analytes from small molecules up to intact proteins, antibodies and antibody drug conjugates (ADCs). This platform provides better separation quality than most liquid chromatography (LC) instruments – in a fraction of the time – all with full MS identification behind every separation peak.



Ordering Information

Product	P/N
Hardware	
ZipChip Interface (Autosampler version)	00950-01-00492
ZipChip Interface (Manual version)	00950-01-00493
ZipChip Autosampler	00950-01-00494
DryDock	00950-01-00518
Consumables	
Installation Test Kit	00950-01-00510
ZipChip HS	00950-01-00498
ZipChip HR	00950-01-00499
ZipChip Metabolites Assay Kit	00950-01-00500
ZipChip Peptides Assay Kit	00950-01-00501
ZipChip Intact Antibody Assay Kit	00950-01-00502

Thank you!

Any Questions?