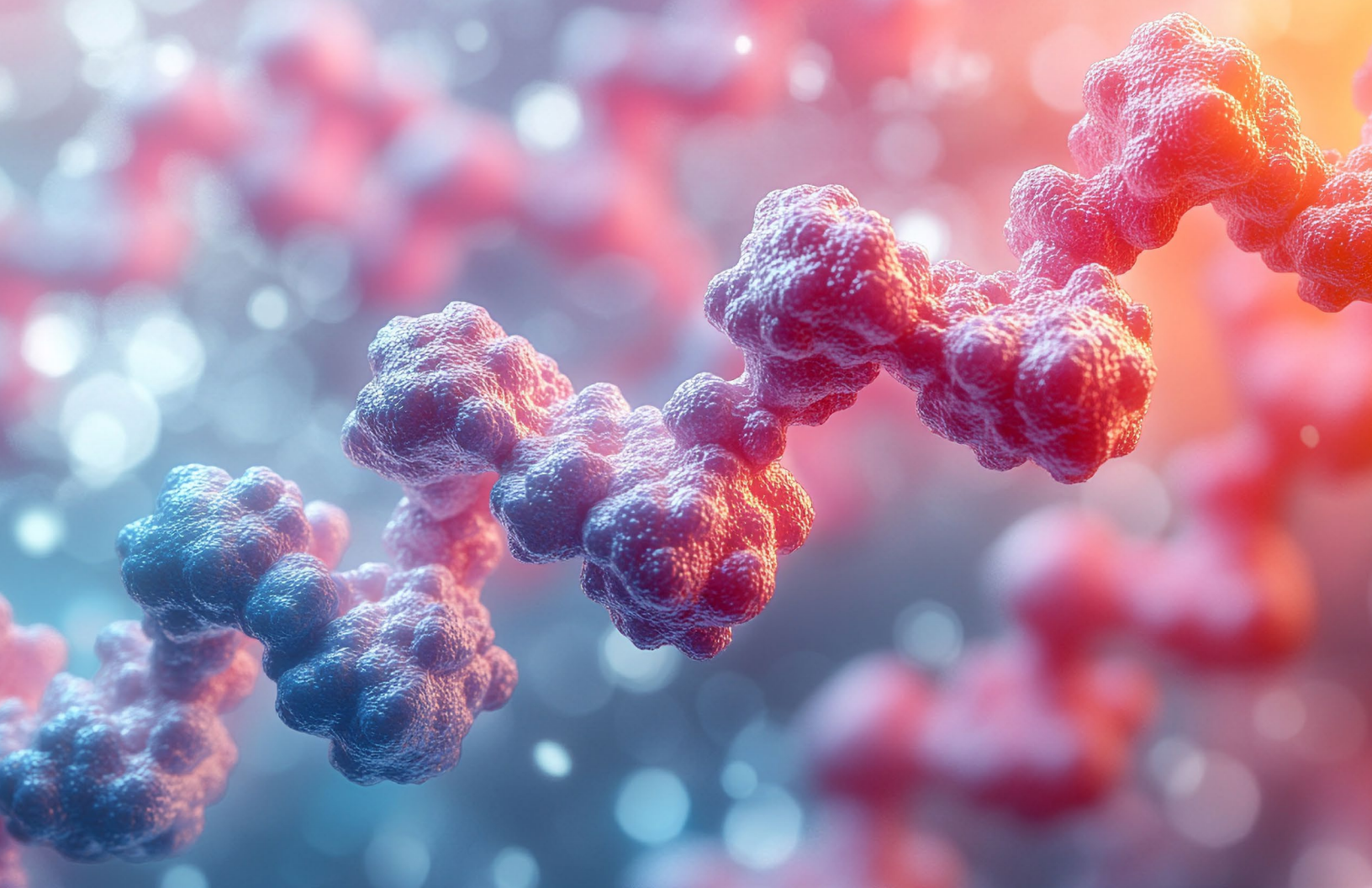




Waters™

Analysis and Characterization of GLP-1 Receptor Agonists

Your guide to precise and robust separation methods

Introduction

Glucagon-like peptide-1 receptor agonists (GLP-1 RAs) are widely used to treat type 2 diabetes and obesity.¹ The success of the latter has resulted in an increase in product demand, which significantly strains both supply chains and manufacturers. As a result, customers are increasingly turning to compounded drugs, which are not regulated by global regulatory authorities and pose an elevated risk to consumer safety.

Drug manufacturers need reliable and robust methods to perform raw material screening, in-process control, lot release, and stability monitoring to ensure drug safety and efficacy. Analytical solutions must be capable of efficiently detecting anomalies and supporting risk-based decisions to ensure that manufacturers can meet regulatory standards and drug product safety while improving productivity.

This guidebook provides a comprehensive overview of Waters™ analytical technologies that support critical quality attribute (CQA) analysis of GLP-1 receptor agonists. It features our reliable LC systems, high-performance columns, and advanced MS and MALS detectors, as well as compliance-ready software and informatics to ensure accurate characterization of these peptide therapeutics. Waters is committed to ongoing innovation and collaboration, delivering proven analytical solutions backed by application notes, implementation guides, and peer-reviewed articles.

Explore our comprehensive guide and visit [waters.com/GLP-1](https://www.waters.com/GLP-1) to stay up to date with the latest publications.



References

1. Yu, M. et al. Battle of GLP-1 Delivery Technologies. Advanced drug delivery reviews. (2018) 130:113-130. DOI: 10.1016/j.addr.2018.07.009.

Critical Quality Attributes

Complexity	Structure	Quality Attributes
Low		<ul style="list-style-type: none">■ Oxidation■ Deamidation■ Isomerization■ Deletion/Insertion
Medium		<ul style="list-style-type: none">■ Purity■ Excipients■ Raw material
High		<ul style="list-style-type: none">■ Truncation■ Glycosylation■ Charge variants■ Sequence variants

Structures of GLP-1 peptide (top), Semaglutide (middle), and Dulaglutide (bottom) with corresponding analytical complexity and potential modifications of concern that can adversely affect biological drug safety or efficacy.

Synthetic peptides navigate a complex regulatory landscape shaped by factors such as molecular size, therapeutic application, and production methodology. Notably, peptides manufactured via recombinant DNA technology are subject to distinct approval pathways and may require different considerations for critical quality attributes (CQAs) compared to their chemically synthesized counterparts. Despite the absence of a unified global standard, several CQAs, such as identity, purity, stability, and safety, are consistently emphasized by major regulatory bodies and pharmacopoeias. These attributes are fundamental to ensuring product consistency, therapeutic efficacy, and patient safety.

Critical Quality Attributes of GLP-1 RAs

Identity	Ensures that the drug substance consists of the intended substance with the correct amino acid sequence and structure.
Purity	<p>Ensures the absence of impurities that can arise from the manufacturing process or degradation. Impurities can potentially reduce efficacy, trigger immune responses, or be toxic. Some notable impurities in GLP-1 RAs include:</p> <ul style="list-style-type: none">■ Truncated peptides with incomplete peptide chains.■ Degradation products from the breakdown of the GLP-1 RA, which can compromise its stability and effectiveness.■ Process-related impurities: residual solvents, buffers, and other chemicals used during manufacturing that might interact with the molecule.
Stability	Ensures that the drug substance maintains its structural integrity and effectiveness throughout its shelf-life and under various storage and handling conditions.
Safety	This is a fundamental CQA encompassing the overall safety profile of the GLP-1 RA, including potential adverse effects and immunogenicity that can result from covalent aggregates or impurities.

CQAs Addressed by RPLC-MS

Reversed-Phase Liquid Chromatography for GLP-1 RA Analysis

Reversed-Phase Liquid Chromatography (RPLC) coupled with Mass Spectrometry (MS), commonly referred to as RPLC-MS, is a broadly adopted, powerful technique for peptide characterization. RPLC-MS is particularly useful for separating structurally similar peptides, including those that have undergone subtle changes due to degradation.



BioResolve™ Peptide Phenyl-Hexyl+ Columns with MaxPeak™ Premier Technology

- 1st choice for peptide RPLC and RPLC-MS
- 230Å pore size produces up to 2x higher resolution of critical impurities
- Superficially porous particle provides kinetic advantages
- Optimal peak capacity and peak shape in FA for impurity analysis
- QC batch tested with GLP-1 and insulin standards to ensure column performance consistency



XSelect™ Premier Peptide CSH Columns

- Incorporates a low-level positive surface charge.
- Good peak shape with formic acid for MS-based applications
- Achieve greater peptide mass loads for detection of low-level impurities
- Scalable offerings (1.7 µm–10 µm)
- QC tested with protein digests to ensure column-to-column performance consistency



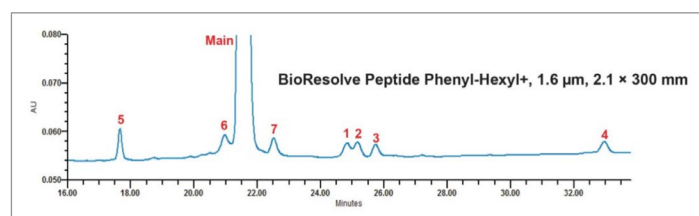
XBridge Premier Peptide BEH C₁₈ Columns

- Best suited for reversed-phase analysis of hydrophobic and hydrophilic peptides at low and high pH
- Scalable Offerings (1.7 µm–10 µm)
- QC tested with protein digests to ensure column-to-column performance consistency

CQAs that can be studied with RPLC-MS are:

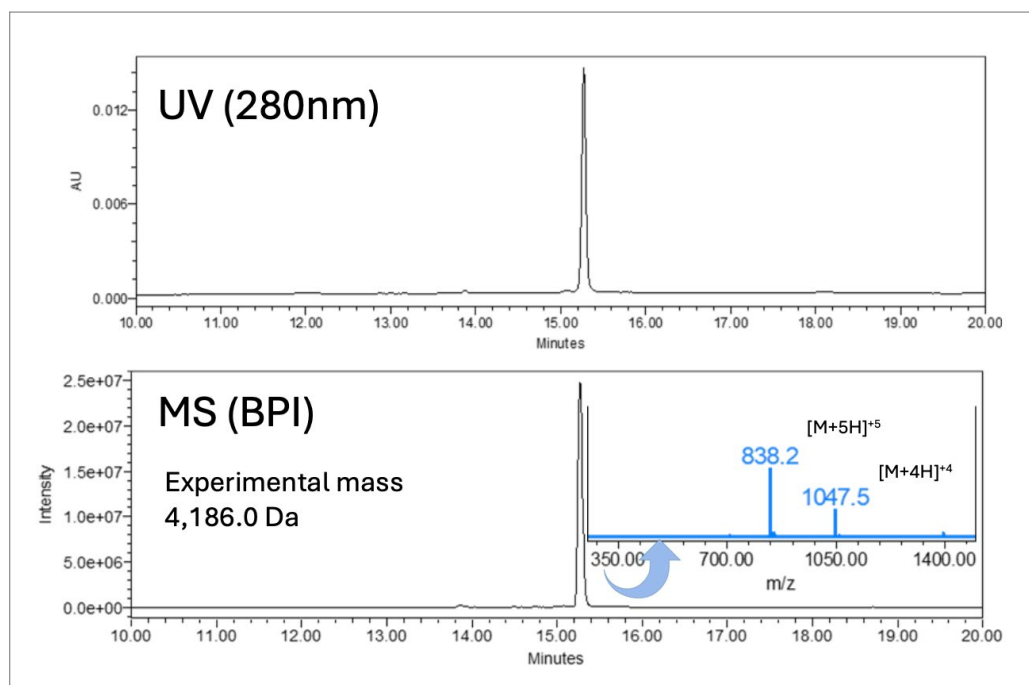
- Identity
- Purity
- Stability

Waters offers a variety of solutions designed to obtain high-quality, reproducible GLP-1 RA separations.



High resolution impurity profiling of Tirzepatide using a 2.1 x 300 mm BioResolve Peptide Phenyl-Hexyl+ Column.

Confirming Identity of GLP-1 RAs Using RPLC-MS

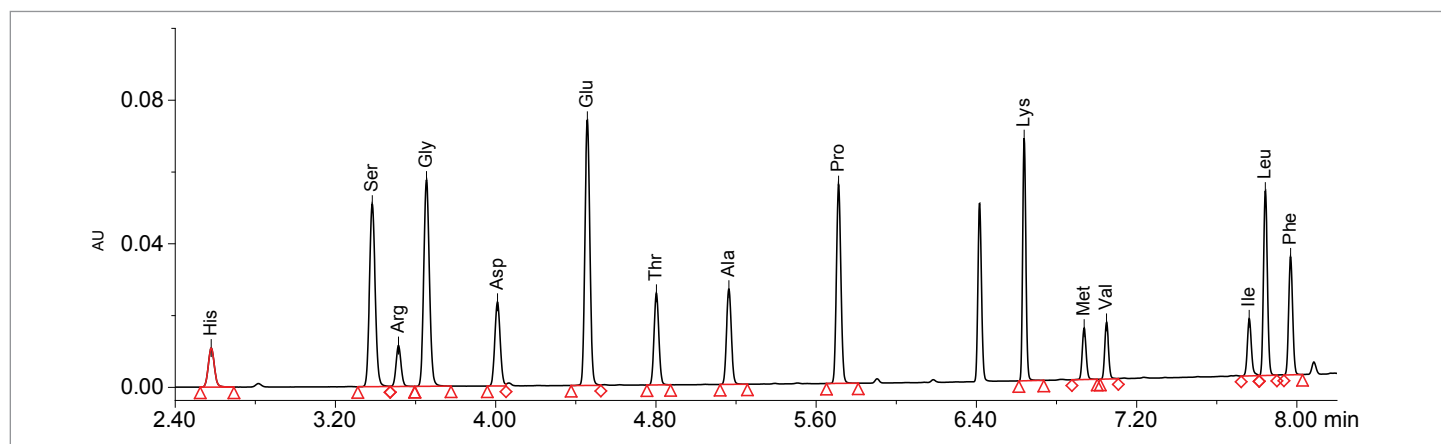


RPLC-UV and MS profile of Exenatide (Eli Lilly & Company), a GLP-1 RA. Observed mass from spectral data confirms peptide identity by molecular weight.

RPLC coupled with orthogonal mass detection offers a streamlined and effective method for confirming the identity of GLP-1 receptor agonists. This approach combines retention time and mass confirmation for dual verification of identity, suitable for routine testing in research, development or QC environments.

System Component	Details
LC system	ACQUITY™ Premier System (BSM)
Column	ACQUITY UPLC™ Premier CSH C ₁₈ 130 Å, 1.7 µm, 2.1 x 100 mm (P/N: 186009908)
Mobile phase A	0.1% formic acid in water
Mobile phase B	0.1% formic acid in acetonitrile
Column temp.	60 °C
Optical detector	PDA, λ = 210–400 nm
Mass detector	ACQUITY QDa™ II Mass Detector = ESI+, Full scan, 250–1500 m/z, Scan rate: 5 Hz, Capillary voltage: 1.5 kV, Cone voltage: 15 V Probe temperature; 600 °C
Chromatography software:	Empower™ Chromatography Data System (CDS) 3.8.1

Confirming Identity of GLP-1 RAs Using Amino Acid Analysis



AccQ-Tag™ derivatized amino acids from Exenatide separated under reversed-phase LC conditions within a 10-minute method.

Confirmation of GLP-1 receptor agonist identity can also be achieved through direct amino acid residue analysis of the hydrolyzed peptide. In this example, Exenatide was subjected to microwave-assisted acid hydrolysis then derivatized using the AccQ-Tag Ultra Derivatization Method. The measured molar ratios of amino acids are compared to the theoretical amino acid composition based on the known sequence of the GLP-1 RA. Deviations may indicate sequence variants or product degradation.

Advantages:

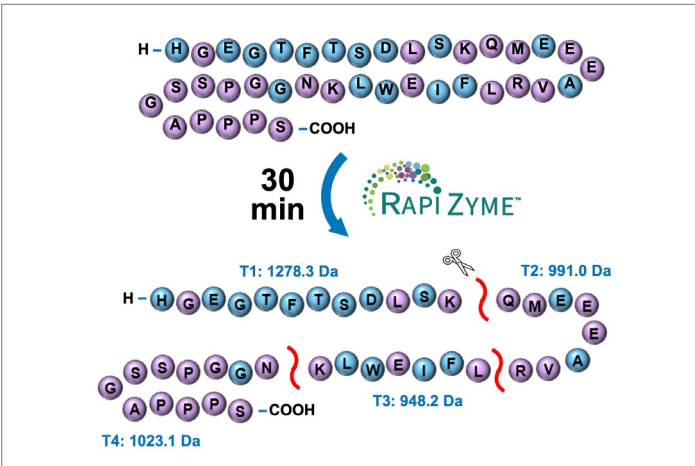
- Confirms amino acid composition without relying on intact peptide mass determinations.
- Detects unexpected modifications or truncations.
- Useful for batch-to-batch consistency

Amino Acid	Theoretical Residues	Observed Residues
Histidine	1	1.08 ± 0.01
Serine	5	4.84 ± 0.01
Arginine	1	0.94 ± 0.01
Glycine	5	5.48 ± 0.01
Aspartic acid	2	2.28 ± 0.01
Glutamic acid	6	6.64 ± 0.01
Threonine	2	2.00 ± 0.01
Alanine	2	2.20 ± 0.01
Proline	4	4.41 ± 0.01
Lysine	2	2.16 ± 0.01
Methionine	1	0.96 ± 0.01
Valine	1	1.00 ± 0.01
Isoleucine	1	0.99 ± 0.01
Leucine	3	3.28 ± 0.01
Phenylalanine	2	2.07 ± 0.01

Summary of calculated amino acid residues compared to the theoretical residue count of Exenatide.

System Component	Details
LC system	ACQUITY Premier System (Binary Solvent Manager) equipped with a column heater (CH-A) and flow-through needle (FTN) sample manager
Detection	TUV, $\lambda = 260 \text{ nm}$ @ 10 Hz
Detector inlet tubing	0.0025" x 8.5" PEEK (P/N: 700009971)
Column	AccQ-Tag Ultra Column 130 Å, 1.7 μm , 2.1 x 100 mm (P/N: 186003837), with ACQUITY Column In-Line Filter (P/N: 205000343)
Column temp.	45 °C
Sample temp.	20 °C
Injection volume	1 μL
Flow rate	0.70 mL/min
Mobile phase A	1:20 dilution of AccQ-Tag Ultra Eluent A Concentrate (P/N 186003838) with water (LC-MS grade)
Mobile phase B	AccQ-Tag Ultra Eluent B (P/N: 186003839)
Wash	Needle wash: 95:5 water:acetonitrile Seal wash: 50:50 water:acetonitrile
Chromatography software	Empower CDS 3.6.1

Identity and Impurity Characterization of a GLP-1 RA Using RPLC-MS Peptide Mapping



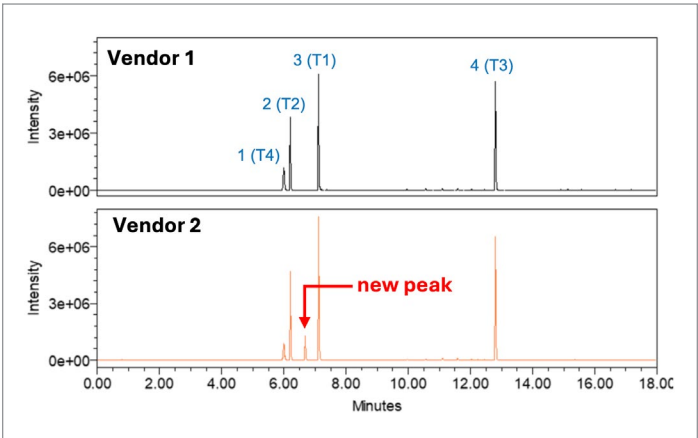
Exenatide, a GLP-1 RA, is digested with RapiZyme™ Trypsin, yielding predictable peptide fragments with unique masses in a 30-minute digestion protocol.

Peptide mapping is especially powerful for comparing impurities between different vendors or batches of a GLP-1 receptor agonist, as it provides high-resolution, site-specific insights into the molecular makeup of each sample and its impurities. This workflow can pinpoint exact locations of modifications, truncations, or unexpected residues. In a study comparing Exenatide from two manufacturers, a new peak was detected and identified as a sequence variant representing a proline insertion in the proline-rich region of the C-terminus.

Fragment T4		New peak	
b Name	b m/z (Monoisotopic)	b Name	b m/z (Monoisotopic)
N	1/b1 115.0502	N	1/b1 115.0502
G	1/b2 172.0717	G	1/b2 172.0717
G	1/b3 229.0931	G	1/b3 229.0931
P	1/b4 326.1459	P	1/b4 326.1459
S	1/b5 413.1779	S	1/b5 413.1779
S	1/b6 500.2100	S	1/b6 500.2100
G	1/b7 557.2314	G	1/b7 557.2314
A	1/b8 628.2685	A	1/b8 628.2685
P	1/b9 725.3213	P	1/b9 725.3213
P	1/b10 822.3741	P	1/b10 822.3741
S	1/b11 919.4268	P	1/b11 919.4268
		S	1/b12 1016.4796

Summary table comparing the monoisotopic mass of fragment ions detected from peptide fragment T4 compared to the new peak, highlighting a proline insertion.

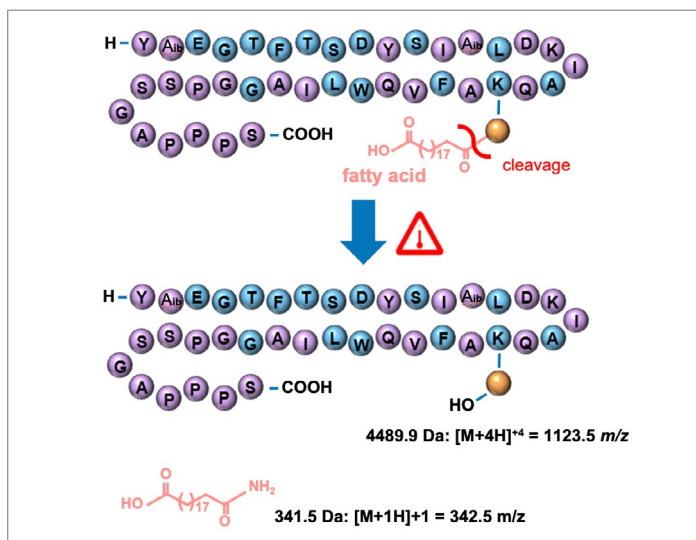
Peptide mapping is an industry-standard technique for confirming the identity of peptides and proteins. This is accomplished by combining enzymatic digestion, reversed-phase liquid chromatography (RPLC), and high-resolution mass spectrometry (HRMS) to achieve detailed identification and localization of impurities. Waters RapiZyme Trypsin, a chemically optimized, recombinant trypsin, provides gold-standard performance while cutting lengthy digestion times from over three hours to just 30 minutes. Through the analysis of fragment ions from digested peptide chains, automated workflows can provide both amino acid-level confirmation of the desired product sequence as well as the detection of impurities from sequence variants and post-translational modifications that can occur during recombinant DNA peptide manufacturing processes.



Comparison of Exenatide RPLC-MS profiles highlighting a unique fragment present in the sample from vendor 2.

System Component	Details
LC system	ACQUITY Premier System (BSM)
Column	ACQUITY UPLC Premier CSH C ₁₈ 130 Å, 2.1 x 100 mm, 1.7 µm (P/N: 186009488)
Mobile phase A	0.1% formic acid in water
Mobile phase B	0.1% formic acid in acetonitrile
Column temp.	60 °C
Optical detector	TUV, λ = 214
Mass detector	Xevo™ G3 QTof Mass Spectrometer
Chromatography software	waters_connect™, UNIFI™ Scientific Information System

Stability Testing of GLP-1 RAs Using RPLC-MS



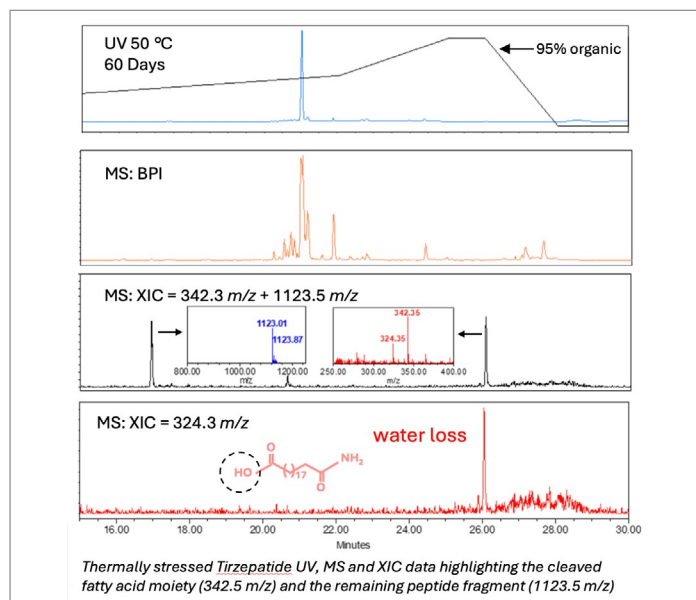
Thermally stressed Tirzepatide can undergo cleavage of the fatty acid from the peptide which can impact pharmacokinetics and binding

RPLC-UV/MS-enabled workflows offer a unique advantage of specificity when compared to UV-based workflows alone. This can prove useful when investigating stability-indicating impurities that may exhibit unique properties, as is the case with fatty acid-conjugated GLP-1 receptor agonists. Fatty acids increase the complexity of profiling experiments through the introduction of non-native linkers and potentially more hydrophobic conjugates, as demonstrated by the longer retention and elution occurring above 50% organic.

Identification of the fatty acid using UV data alone would be challenging in the absence of a synthetic standard to compare against. However, MS data can be used to confirm the fatty acid conjugate, which was observed at 26 minutes (342.5 *m/z*), along with the remaining peptide fragment (1123.5 *m/z*) at 17 minutes.

Stability testing is a critical step in the development and quality assurance of peptide therapeutics, particularly for GLP-1 receptor agonists like Tirzepatide (Eli Lilly and Company). While the peptide-based structure is inherently susceptible to chemical and physical degradation, including deamidation, oxidation, and hydrolysis, there is an additional layer of complexity due to its fatty acid modification.

This lipid moiety enhances pharmacokinetics by promoting albumin binding and extending half-life, but it also presents unique degradation risks. Under thermal and oxidative stress, the fatty acid chain and its linker are vulnerable to hydrolysis, lipid peroxidation, and conformational rearrangements, which can alter the drug's stability profile and therapeutic performance.



Thermally stressed Tirzepatide UV, MS and XIC data highlighting the cleaved fatty acid moiety (342.5 m/z) and the remaining peptide fragment (1123.5 m/z).

System Component	Details
LC system	Arc™ Premier System (QSM)
Column	XSelect™ Premier Peptide CSH C ₁₈ Column, 130 Å, 2.5 µm, 4.6 x 100 mm (P/N: 186009908)
Mobile phase A	0.1% formic acid in water
Mobile phase B	0.1% formic acid in acetonitrile
Column temp.	60 °C
Optical detector	TUV, λ = 220
Mass detector	ACQUITY QDa II Mass Detector = ESI+, Full scan, 250–1500 <i>m/z</i> , Scan rate: 5 Hz, Capillary voltage: 1.5 kV, Cone voltage: 15 V Probe temperature; 600 °C
Chromatography software	Empower CDS 3.8.1

CQAs Addressed by SEC-MALS

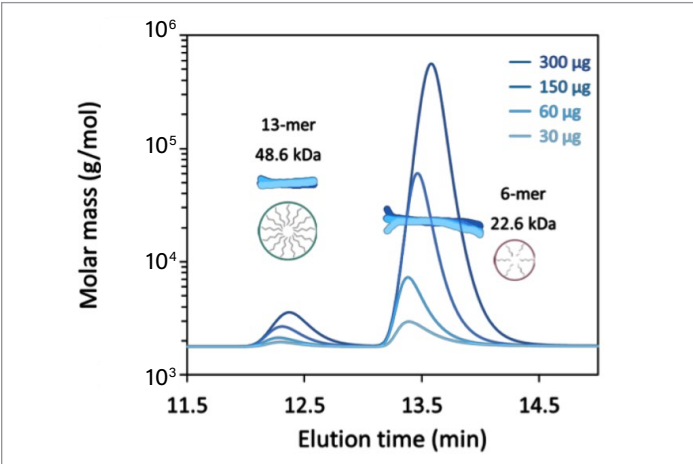
Size-Exclusion Chromatography for GLP-1 RA Analysis

Size-Exclusion Chromatography (SEC) is a valuable technique for characterizing GLP-1 RAs including their monomeric, oligomeric, and aggregated states. When coupled with multi-angled light scattering detection (SEC-MALS), this technique enables the identification of undesirable high-order structures that can impact safety and efficacy. SEC can also be used to identify stable, low-molecular-weight oligomers that may represent off-pathway aggregation in GLP-1 RAs.

SEC-MALS is particularly useful when addressing:

- Stability
- Identity
- Purity

Aggregate Identity and Stability Testing Using Non-Denaturing SEC-MALS



SEC-MALS analysis of liraglutide drug substance in its native formulation buffer reveals two distinct oligomeric states, corresponding to 13-mers and hexamers.

System Component	Details
LC system	Arc Premier HPLC
Column	XBridge™ Premier SEC 250 Å, 2.5 µm, 7.8 mm x 300 mm (P/N: 186009962)
Native buffer mobile phase	10 mM Na ₂ HPO ₄ , pH 8.1 (liraglutide)
MALS detector	DAWN™ MALS Detector
Column temp.	40 °C
Optical detector	PDA, λ = 280
RI detector	Optilab™ dRI Detector
Chromatography software	ASTRA™ MALS analysis software or Empower CDS 3.10.0



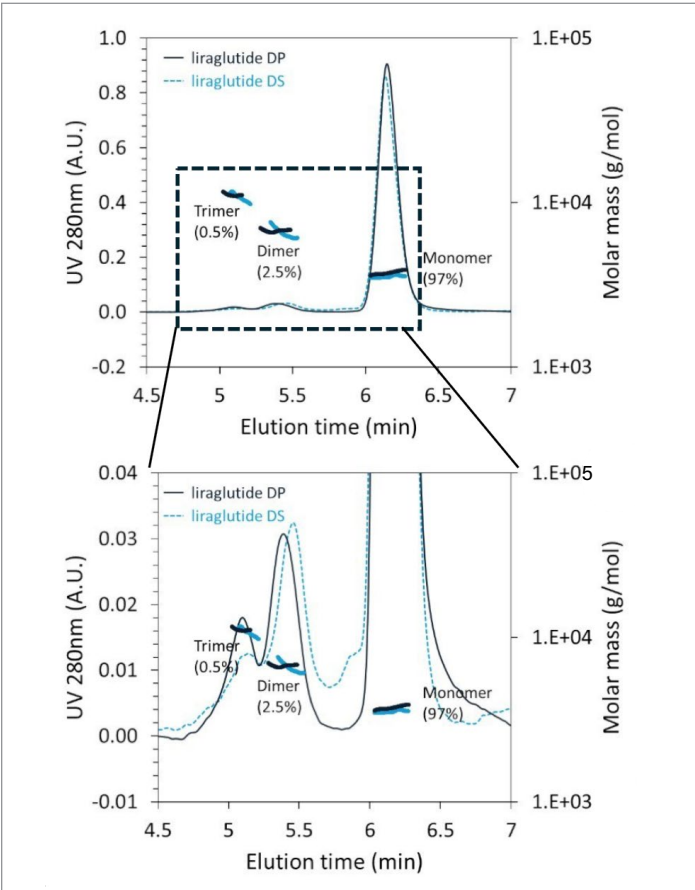
MaxPeak Premier SEC Peptide and Protein Columns 125 Å and 250 Å provide:

- BEH-based SEC Columns (1.7 µm or 2.5 µm particles) for high quality data on UHPLC or HPLCs.
- High resolution separations over an extended molecular weight range.
- MaxPeak Premier High Performance Surfaces minimize unwanted ionic interactions.
- QC batch tested for reproducibility and reliability.

Regulatory agencies require detailed characterization of oligomers and aggregates in peptide therapeutics because of their tendency to form fibrils. SEC-MALS provides non-destructive, absolute molar mass measurements directly in solution, enabling unambiguous identification of native oligomeric states. Unlike mass spectrometry, which is incompatible with the inorganic salts commonly present in formulation buffers, SEC-MALS delivers accurate determinations of molar mass and oligomerization across virtually all buffer and salt conditions.

For example, SEC-MALS demonstrates that liraglutide forms distinct oligomeric states: hexamers (22.6 kDa) and 13-mers (48.6 kDa). Studies have shown that a high proportion of hexamers is closely linked to fibril formation under mechanical stress, whereas a higher percentage of 13-mer species is less susceptible to fibril formation. These insights can be applied to confirm the identity of oligomers and aggregates, as well as to evaluate the impact of formulation and processing methods.

Identity Testing of Covalent Aggregates Using Denaturing SEC-MALS



Denaturing SEC-MALS of liraglutide shows a main monomer peak with low-level covalent dimer (2.5%) and trimer (0.5%) impurities.

Regulatory agencies emphasize the need to detect covalent aggregates in peptide therapeutics, as their presence can increase immunogenic risk upon repeated exposure. Denaturing SEC-MALS provides absolute molecular weight measurements while distinguishing between reversible oligomers and covalently linked species. By using a mobile phase containing acetonitrile, n-propanol, and isopropanol, reversible associations are disrupted, leaving only covalently interacting species for analysis. Denaturing SEC-MALS of liraglutide drug substance and drug product reveals a predominant monomeric peak, with two low-level impurities identified as covalent dimers (2.5% relative mass) and trimers (0.5% relative mass) based on MALS-derived molar mass.

System Component	Details
LC system	ACQUITY Premier UPLC System
Column	ACQUITY Premier SEC 125 Å, 1.7 µm, 4.6 mm x 150 mm (P/N: 186009963)
Denaturing mobile phase	(40% v/v), acetonitrile (50% v/v), n-propanol (5% v/v), IPA (5% v/v), TFA (0.04% v/v), and 17 mM NaCl
MALS detector	DAWN MALS Detector
Column temp.	40 °C
Optical detector	PDA λ = 280
RI detector	Optilab dRI Detector
Chromatography software	ASTRA MALS analysis software or Empower CDS 3.10.0

Closing Considerations

To achieve precise and robust reversed-phase and size-exclusion separations for GLP-1 RA analysis and characterization, the right systems, software, and column technologies are essential. By partnering with Waters, you gain access to the advanced tools and expertise to confidently tackle GLP-1 RA analysis. Whether you're supporting early-stage research or advancing through clinical development, Waters solutions help you streamline workflows, meet regulatory requirements, and stay ahead of the evolving GLP-1 therapeutics landscape.

For more information, visit [waters.com/GLP-1](https://www.waters.com/GLP-1)

Recommended System Configurations

Attribute Characterization



ACQUITY Premier System with Xevo G3 QTof MS

- BioResolve Peptide Phenyl-Hexyl/C₁₈ + RP
- Maximize sensitivity with MaxPeak HPS Technology.
- Get peak chromatographic performance for complex applications with sub-2.0 μm particle columns.
- Confirm sequence variants and low-level impurity analysis with MS/MS fragmentation.

Attribute Monitoring & Method Development



Arc Premier System with ACQUITY QDa II Mass Detector

- BioResolve Peptide Phenyl-Hexyl/C₁₈ + RP
- Simplify HPLC and UHPLC separations with an all-in-one platform that includes MaxPeak HPS technology.
- Increase productivity with a compliant-ready solution while enabling the acquisition of orthogonal MS data.
- Streamline workflows with seamless integration to Empower 3 CDS.

Reversed-Phase and Size Exclusion Chromatography Columns

Sub 2 μm particles for UHPLC-based separations

- ACQUITY Premier BEH SEC 125/250 $\text{\AA}$
- ACQUITY Premier Peptide BEH C₁₈
- ACQUITY Premier Peptide CSH C₁₈



2.5 μm particles for HPLC-based separations

- XBridge Premier BEH SEC 125/250 $\text{\AA}$
- XBridge Premier Peptide BEH C₁₈
- XBridge Premier Peptide CSH C₁₈

For more information on recommended columns for your application, please contact your local Waters representative.

Biophysical Characterization



Arc Premier System with DAWN MALS Detector

- Perform native and denaturing SEC-MALS analysis and obtain oligomers and aggregates identify.
- Leverage ASTRA Software for research and discovery.
- Compliant-ready Empower Software for routine analysis and quality control.

Quality Control



Alliance™ iS Bio System

- Multiply the productivity and efficiency of your QC lab by reducing human error.
- At-instrument guided workflows for system start-up, shutdown, and priming.

Waters Application Notes



- [Characterization and Impurity Profiling of Combined Amylin and GLP-1 Analogs with RapiZyme Trypsin | Waters](#)



- [Application of LC-UV/MS Workflows to Increase Efficiency in Impurity Profiling of GLP-1 Analogs](#)



- [Column Selection for RPLC-UV Impurity Analysis of Fatty Acid Modified GLP-1 Receptor Agonists](#)



- [Reversed-Phase LC-MS Analysis of Low-Abundance Impurities in a GLP-1 a Therapeutic Using a Charged Surface 230 Å Superficially Porous Phenyl-Hexyl Column](#)



- [Development of Separation Methods for GLP-1 Synthetic Peptides Utilizing a Systematic Protocol and MaxPeak High Performance Surface Technology](#)



- [Separation of a GLP-1 Receptor Agonist and Structurally Similar Impurities Using BioResolve Peptide Phenyl-Hexyl+ and C₁₈+ Columns](#)



- [Temperature Dependence on Reversed-Phase Separations of Fatty Acid Modified GLP-1 Receptor Agonists and Their Impurities](#)



- [Unlocking Robust, Reproducible Separations for Modern Peptide Therapeutics with BioResolve Peptide Phenyl Hexyl+ Columns](#)



- [Identification of GLP-1 analog oligomeric states using SEC-MALS](#)



- [Accelerating Method Development and Manufacturing of GLP-1 Analogs with LC-UV/MS](#)

GLP-1 RA and Synthetic Peptide Method Development Posters



- [GLP-1 Analogs: Accelerating method development and manufacturing with LC-UV/MS](#)



- [Characterizing Quality Attributes of GLP-1 Analogs by Light Scattering](#)



- [Principles and Practice Using SEC for Reliable Biotherapeutic Peptide Analysis](#)

Ordering Information

Recommended reversed-phase and size exclusion chromatography columns for GLP-1 RA analysis.

Column Configurations

BioResolve Peptide Phenyl-Hexyl+ RP Columns with MaxPeak Premier Technology		
Particle Size: 1.6 μ m		
SPP, 230 Å	Dimension	Part Number
	2.1 x 50 mm	186011725
	2.1 x 100 mm	186011726
	2.1 x 150 mm	186011727
	2.1 x 300 mm	186011835
	2.1 x 150 mm, 3/pk	186011741

Particle Size: 2.7 μ m		
SPP, 230 Å	Dimension	Part Number
	2.1 x 50 mm	186011728
	2.1 x 100 mm	186011729
	2.1 x 150 mm	186011730
	2.1 x 300 mm	186011876
	2.1 x 150 mm, 3/pk	186011742
	4.6 x 50 mm	186011731
	4.6 x 100 mm	186011732
	4.6 x 150 mm	186011733
	4.6 x 150 mm, 3/pk	186011743

XBridge Premier Peptide Columns		
Particle Size: 2.5 μ m		
BEH C ₁₈ , 130 Å	Dimension	Part Number
	2.1 x 50 mm	186009733
	2.1 x 100 mm	186009734
	2.1 x 150 mm	186009835
	4.6 x 50 mm	186009898
	4.6 x 100 mm	186009899
	4.6 x 150 mm	186009900

ACQUITY Premier Peptide Columns		
Particle Size: 1.7 μ m		
BEH C ₁₈ , 130 Å	Dimension	Part Number
	2.1 x 50 mm	186009481
	2.1 x 100 mm	186009482
	2.1 x 150 mm	186009483

XSelect Premier Peptide Columns		
Particle Size: 2.5 μ m		
CSH C ₁₈ , 130 Å	Dimension	Part Number
	2.1 x 50 mm	186009904
	2.1 x 100 mm	186009905
	2.1 x 150 mm	186009906
	4.6 x 50 mm	186009907
	4.6 x 100 mm	186009908
	4.6 x 150 mm	186009909

ACQUITY Premier Peptide Columns		
Particle Size: 1.7 μ m		
CSH C ₁₈ , 130 Å	Dimension	Part Number
	2.1 x 50 mm	186009487
	2.1 x 100 mm	186009488
	2.1 x 150 mm	186009489

Columns	Pore size	Molecular weight range	Particle size	4.6 x 30mm Guard	4.6 x 150 mm Column	4.6 x 300 mm Column	7.8 x 150 mm Column	7.8 x 300 mm Column
ACQUITY 125 Å SEC Columns with MaxPeak Premier	125 Å	Approx. 1K – 80K Daltons	1.7 µm	–	186011350	186011351	–	–
XBridge 125 Å SEC Columns with MaxPeak Premier			2.5 µm	186011356	186011352	186011353	186011354	186011355
ACQUITY 250 Å SEC Columns with MaxPeak Premier	250 Å	Approx. 10K – 650K Daltons	1.7 µm	–	186009963	186009964	–	–
XBridge 250 Å SEC with MaxPeak Premier			2.5 µm	186009969	186009959	186009960	186009961	186009962

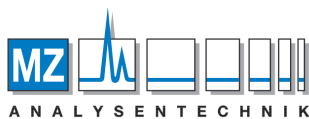
MaxPeak Premier Peptide Reversed-Phase Column Method Development Screening Kit

Product Description	Part Number
MaxPeak Premier Peptide RP Columns and Method Development Kit	176005408

Kit Components	
XSelect Premier Peptide CSH C ₁₈ Column, 130 Å, 2.5 µm, 4.6 x 150 mm	186009909
XBridge Premier Peptide BEH C ₁₈ Column, 130 Å, 2.5 µm, 4.6 x 150 mm	186009900
MassPREP Peptide Mixture	186002337
Step-by-Step Peptide Separation Method Development Guide	

Peptide and Protein SEC Connections		
0.005 x 1.75 inch UPLC SEC Connection Tubing (2 pack)		186006613
Short rigid column connector (1 pack)		WAT022681
U-shaped column connector (1 pack)		WAT084080

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