

Pharma and Biopharma

Biotherapeutic Peptide Mapping Information Independent SWATH[®] Acquisition Method

Routine biotherapeutic accurate mass peptide mapping analysis on the X500B QTOF System

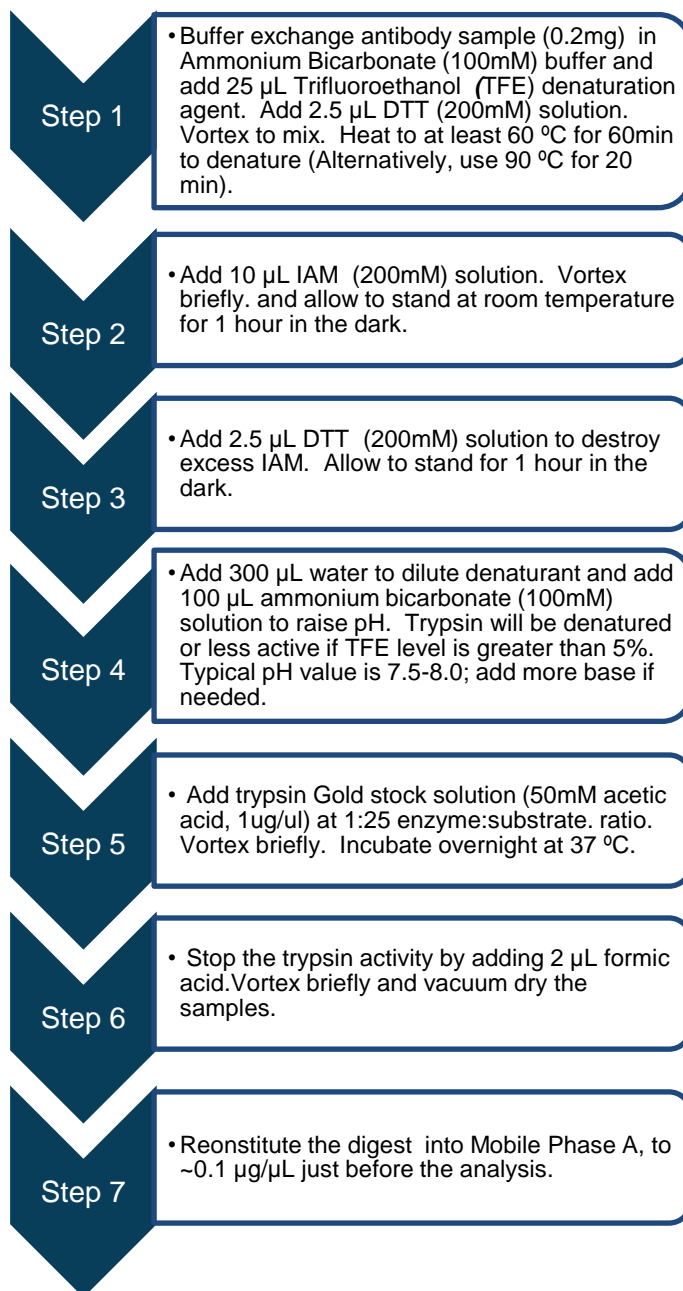
Method details for the routine peptide mapping of a biotherapeutic monoclonal antibody (mAb) protein by high-resolution accurate mass analysis on the X500B QTOF System, powered by SCIEX OS Software. An information independent SWATH Acquisition method was employed to acquire high-resolution MS and MS/MS level data on the digested biologic protein product.

SWATH Acquisition utilizes either fixed or variable Q1 mass isolation window, transmitting all precursor ions in the defined Q1 window through to the collision cell. Transmitted ions are fragmented and analyzed at high-resolution. The Q1 isolation window is stepped across the entire mass range, with an LC compatible cycle time, resulting in the comprehensive acquisition of high-resolution MS/MS spectra for every precursor ion in a sample. This unbiased data acquisition approach ensures data completeness is maximized, and enables detection of low abundance peptides and modifications.



Sample Prep

A generic sample preparation strategy is shown for reduction and tryptic digestion of an antibody biotherapeutic prior to LC-MS analysis.



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LC Method

<i>Column</i>	Waters Acquity UPLC BEH C18 Column, 130 1.7 μ m, 2.1 mm X 100 mm
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<i>Mobile Phase A</i>	Water, 0.1% Formic acid
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<i>Mobile Phase B</i>	Acetonitrile, 0.1% Formic acid
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<i>Flow rate</i>	200 μ L/min
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<i>Column temperature</i>	40 ^o C
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<i>Injection volume</i>	10 μ L, 1 μ g total protein
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<i>Gradient profile</i>	Time (min)	% B
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	8.0	2
--	-----	---

	40.0	30
--	------	----

	60.0	50
--	------	----

	62.0	90
--	------	----

	66.0	90
--	------	----

	66.5	2
--	------	---

	75.0	2
--	------	---

MS Method

Suggested starting MS and MS/MS method parameters for routine SWATH based peptide mapping analysis as displayed in SCIEX OS user interface. The SWATH acquisition criteria are shown with a 50Da fixed SWATH window from 350-2000 m/z acquiring high-resolution MS/MS in each cycle. For best sequence coverage and sensitivity, the specific SWATH parameters should be optimized for the length of HPLC separation used.

Generic SWATH

Method Overview

Device: X500 QTOF
Ion Source: TurboSpray

SWATH
(TOF MSMS Scans: 33)
0 min - 75 min

Method duration: 75 min
Total scan time: 1.11322 sec

Estimated cycles: 4042

Source and Gas Parameters

Ion source gas 1: 40 psi	Curtain gas: 35	Temperature: 450 °C
Ion source gas 2: 40 psi	CAD gas: 7	

Experiment SWATH

Polarity: Positive

TOF MS

TOF start mass: 350 Da
TOF stop mass: 2000 Da
Accumulation time: 0.125 s

TOF MSMS

TOF start mass: 50 Da
Accumulation time: 0.025 s

Mass Table [Autofill SWATH windows...](#)

	Precursor ion st...	Precursor ion st...	Declusteri...	DP spread (V)	Collision energy (V)	CE spread (V)
1	350.0000	400.0000	80	0	19	15
2	399.0000	450.0000	80	0	22	15
3	449.0000	500.0000	80	0	26	15
4	499.0000	550.0000	80	0	29	15
5	549.0000	600.0000	80	0	32	15
6	599.0000	650.0000	80	0	35	15
7	649.0000	700.0000	80	0	38	15
8	699.0000	750.0000	80	0	41	15
9	749.0000	800.0000	80	0	44	15

Autofill SWATH Windows

Generate an initial set of SWATH windows and then use the windows to autofill the MSMS mass table

Precursor start mass: 350 Da Window width: 50 Da

Precursor stop mass: 2000 Da Windows per cycle: 33

Populate the MSMS table

Append to existing list

Overwrite the existing list

Apply Cancel

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Batch

In the Batch setup, open the 'Automated Calibration Editor' window in order to select the use of the autocalibration function. Designate use of the 'X500 ESI Positive Calibration Solution', and then determine how often you would like the system to perform a fast, automated calibration. These short calibrations will be added automatically to your queue once you have submitted a sample batch.

The screenshot shows the 'Batch' software interface. At the top, there is a menu bar with options like 'Auto-Calibrate...', 'Plate Layout...', 'New', 'Open', 'Save', 'Print...', 'Manage', and 'Submit'. Below the menu bar is a table with columns: 'Sample Name', 'MS Method', 'LC Method', 'Rack code', 'Vial position', and 'Data File'. The first row contains 'Intact protein', 'intact protein analysis MS', 'Intact_10min', '1.5mL (105 vial)', '1', and 'Intact protein file'. Overlaid on the table is the 'Batch - Automatic Calibration Editor' dialog box. The dialog box has a title bar and a close button. The main text reads: 'Provide ion reference and calibrant delivery settings to be applied automatically, at the correct frequency during acquisition'. There are three main settings: 'Ion reference table' with a dropdown menu showing a list of calibration solutions (including 'X500 ESI Positive Calibration Solution' which is highlighted), 'Calibrate every' with a dropdown menu set to '3' samples, and 'Calibrant delivery' with a dropdown menu set to 'CDS'. There is also a 'CDS channel' dropdown set to '1'. An 'Edit...' button is next to the 'Ion reference table' dropdown. At the bottom of the dialog box are 'OK' and 'Cancel' buttons.

This is a close-up view of the 'Batch - Automatic Calibration Editor' dialog box. The 'Calibrate every' field is highlighted with a dashed border, showing the value '3' samples. The other settings are: 'Ion reference table' set to 'X500 ESI Positive Calibration Solu...', 'Calibrant delivery' set to 'CDS', and 'CDS channel' set to '1'. The 'Edit...' button is visible next to the 'Ion reference table' dropdown. The 'OK' and 'Cancel' buttons are at the bottom.

Data Processing

Process SWATH® biotherapeutic peptide mapping data in BioPharmaView™ Software 2.0.

Input the protein sequence, and assign potential modifications in the 'Assay Information' window.

Assay Information | Sequence Features | Intact Protein | Peptide Mapping

Protein Sequence

Protein Type: **Antibody** | **Add Chain** | Unmodified Protein MWs: | Monoisotopic: 144195.3139 | Average: 144286.27

Chain 1: **Light Chain1** | **Delete Chain**

AA Indexes:

```

1-100 QIVLSQSPAILSASPGKEVMTTCRASSSVSYIHWFOQKPGSSPKFWIYATSNLASGVPVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
101-200 TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKHRYACEVTHQGL
201-213 SSPVTKSFNRGEC
    
```

Chain 2: **Heavy Chain 1** | **Delete Chain**

AA Indexes:

```

1-100 QVQLQPGAEELVQPGASVKMSCKASGYTFTSYNMHWKQTPGRGLEWIGAIYPNGDTSYNQKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARST
101-200 YYGGDWYFNVWGAGTTVTVAASATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQ
201-300 TYICNVNHKPSNTKVDKRAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
301-400 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP
401-450 VLDSDGSPFLYSLKLTVDKSRWQQGNVFCVMHEALHNYHTOKSLSLSPG
    
```

Chain 3: **Heavy Chain 2** | **Delete Chain**

AA Indexes:

```

1-100 QVQLQPGAEELVQPGASVKMSCKASGYTFTSYNMHWKQTPGRGLEWIGAIYPNGDTSYNQKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARST
101-200 YYGGDWYFNVWGAGTTVTVAASATKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQ
201-300 TYICNVNHKPSNTKVDKRAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
301-400 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP
401-450 VLDSDGSPFLYSLKLTVDKSRWQQGNVFCVMHEALHNYHTOKSLSLSPG
    
```

Chain 4: **Light chain 2** | **Delete Chain**

AA Indexes:

```

1-100 QIVLSQSPAILSASPGKEVMTTCRASSSVSYIHWFOQKPGSSPKFWIYATSNLASGVPVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
101-200 TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKHRYACEVTHQGL
201-213 SSPVTKSFNRGEC
    
```

Modifications | Cysteine Modifications Can Replace Disulfide Bonds | **Disulfide Bonds - (16)** | **Import** | **Export...**

Chains	Type	Name	Position	Modified AA	Applies To	Workflow Usage	Mass Shift
1	1-4 N-terminal	Gln->pyro-Glu	-	Q	Q	Both	-17.0265
2	1-4 Internal	Deamidated	*	n/a	NQR	Peptide Mapping	0.9840
3	1-4 Internal	Oxidation	*	n/a	MWHCDNYFKPR	Peptide Mapping	15.9949
4	2-3 Internal	G1F	301	N	N	Both	1606.5867
5	2-3 Internal	G2F	301	N	N	Both	1768.6395
6	2-3 Internal	G0	301	N	N	Both	1298.4760
7	2-3 Internal	G0F-GlcNAc	301	N	N	Both	1241.4545
8	2-3 Internal	G0-HexNAc	301	N	N	Both	1095.3966
9	2-3 Internal	G0F	301	N	N	Both	1444.5339

From Chain	To Chain	From Cysteine	To Cysteine
1	1	1	23
2	1	1	133
3	1	2	213
4	2	2	22
5	2	2	148
6	2	2	265
7	2	2	371
8	4	4	23
9	4	4	133
10	4	3	213
11	3	3	22
12	3	3	148
13	3	3	265
14	3	3	371
15	2	3	230
16	2	3	233

Add modifications... | **Delete selected modifications** | **Edit bond...** | **Add bonds...** | **Delete selected bonds**

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Navigate to the 'Peptide Mapping' tab complete processing parameters and to generate all peptide forms for matching.

Rituximab

Create Open Save Save As Close

Project

Assay Information

Intact Protein

Characterize Standard

Create Batch

Review Results

Peptide Mapping

Characterize Standard

Create Batch

Review Results

System

View Queue

Create Report

Assay Information

Sequence Features

Intact Protein

Peptide Mapping

Processing Parameters

m/z Tolerance, ppm:	± 5.0 ppm	RT Range Processing: Time Selection	Retention Time Tolerance:	± 0.50 min
Minimum Score for Auto-Validation:	3.0	Start RT: 0.00 min		
MS/MS Matching Tolerance:	0.03 Da	Stop RT: 58.36 min		

Batch Processing Parameters

Batch Processing Pass / Fail Criteria	
<input type="checkbox"/> XIC Area Limits:	± 10.0 %
<input type="checkbox"/> Minimum Sequence Coverage:	≥ 85.0 %
<input type="checkbox"/> Required Form Minimum:	≥ 80 %
<input type="checkbox"/> Restricted Form Maximum:	≤ 120 %

Annotated Protein Sequence

Chain 1 - Light Chain1

```
QIVLSQSPAILLSASPGKEVTMTCRASSSVSYIHWFPQKPGSSPKPWYATSNLNSAGVVPVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSLTLLSKADYKHKHYACEVTHQGL
SSPVTKSFNRGEC
```

Chain 2 - Heavy Chain 1

```
QVQLQPGAEIVKPGASVKMSCKASGYFTFSYNMHVWQVTPGRGLEWIGAIYFGNGDTSYQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARST
YYGGDWYFNVGAGTTVTVAASATKGPSVFLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQ
TYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYVLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGCPENNYKTTTPP
VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKLSLSLSPG
```

Chain 3 - Heavy Chain 2

```
QVQLQPGAEIVKPGASVKMSCKASGYFTFSYNMHVWQVTPGRGLEWIGAIYFGNGDTSYQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARST
YYGGDWYFNVGAGTTVTVAASATKGPSVFLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQ
TYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYVLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGCPENNYKTTTPP
VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKLSLSLSPG
```

Chain 4 - Light chain 2

```
QIVLSQSPAILLSASPGKEVTMTCRASSSVSYIHWFPQKPGSSPKPWYATSNLNSAGVVPVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSLTLLSKADYKHKHYACEVTHQGL
SSPVTKSFNRGEC
```

Peptide Mapping

Cysteine Alkylation: Iodoacetamide Maximum Number of Combined Modifications per Peptide: 4

Digest Agent: Trypsin Maximum Missed Cleavages: 4

Peptides Reduced Protein Form Sequence coverage of 0 Matched peptides = 0.0 % Filter | Digest

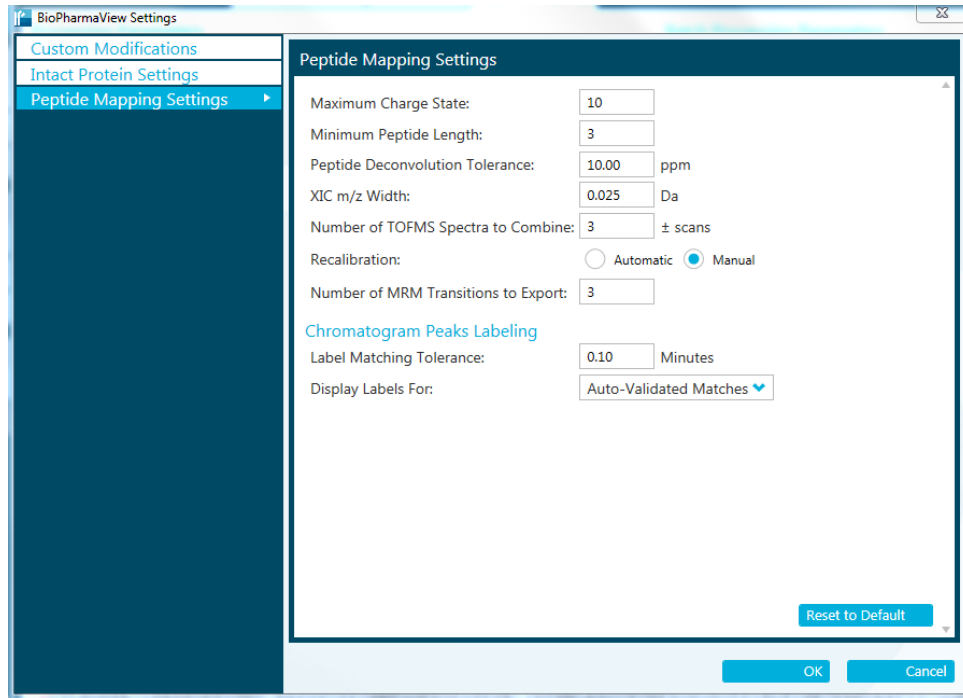
Chains	Peptide	AA Index	Sequence	Modifications	Disulfide Bonds	Mono. Mass	Mono. m/z	Charge	XIC Area	Retention Time
1, 1,4	T1	1-18	QIVLSQSPAILLSASPGKE			1823.9993	-	-	-	-
2, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4594.3570	-	-	-	-
3, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Oxidation@*		4553.3305	-	-	-	-
4, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4593.3730	-	-	-	-
5, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Oxidation@*		4552.3465	-	-	-	-
6, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4085.0456	-	-	-	-
7, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4070.0347	-	-	-	-
8, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Deamidate		4029.0081	-	-	-	-
9, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4084.0616	-	-	-	-
10, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4069.0507	-	-	-	-
11, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Oxidation@*		4028.0241	-	-	-	-
12, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4054.0398	-	-	-	-
13, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Deamidate		4013.0132	-	-	-	-
14, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4068.0667	-	-	-	-
15, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Oxidation@*, Oxidation@*		4027.0401	-	-	-	-
16, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4053.0558	-	-	-	-
17, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Oxidation@*, Oxidation@*		4568.3414	-	-	-	-
18, 1,4	T8-10	108-144	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Oxidation@*		4012.0292	-	-	-	-
19, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4609.3679	-	-	-	-
20, 1,4	T8-11	108-148	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		4595.3410	-	-	-	-
21, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Oxidation@*		6686.2763	-	-	-	-
22, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		6712.2919	-	-	-	-
23, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Deamidated@*, Deamidate		6671.2654	-	-	-	-
24, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		6726.3188	-	-	-	-
25, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Oxidation@*, Oxidation@*		6685.2923	-	-	-	-
26, 1,4	T8-12	108-168	TVAAPSVFIFPPSDEQLK...	Carbamidomethyl@26(133)		6711.3079	-	-	-	-

Settings Help About

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Pharma and Biopharma

Navigate to the 'Settings' icon and review your global 'Peptide Mapping Settings'



Data extraction, including peptide matching can be performed in minutes, on either a single datafile, or on multiple samples using the batch processing function. Review your peptide mapping results in the BioPharmaView Software window. Full sequence coverage of matched peptides can be viewed by clicking 'View Sequence'. Peptide matches can be reviewed in the 'Peptide Results' window. For each selected peptide, corresponding TOF-MS raw spectrum (lower left) and high-resolution, annotated MS/MS spectrum (lower right) are shown for easy confirmation.

BioPharmaView Create Open Save Save As Close

Rituximab

Project

Assay Information

Intact Protein

Characterize Standard

Create Batch

Review Results

Peptide Mapping

Characterize Standard

Create Batch

Review Results

System

View Queue

Create Report

Characterize Standard for Peptide Mapping

Open File... 20160713-Ritu_R_SWATH01.wiff2 Process

Sample # 1 Experiment # 1

Processing Parameters

m/z Tolerance, ppm: ± 5.0 ppm

Minimum Score for Auto-Validation: 3.0

MS/MS Matching Tolerance: 0.03 Da

RT Range Processing

Automatic

Time Selection - to - min

BPC/TIC/XIC Graph

● BPC from 20160713-Ritu_R_SWATH01.wiff2 (sample 1) - 20160713-Ritu_R_SWATH, Experiment 1, +SWATH TOF MS (400 - 1500)

Peptide Results Filter P...99.1% View Sequence Optimize Matching Parameters Update Assay Information

RT	Sequence	Modifications	Disulfide Bonds	Theoretical Mono m/z	Observed Mono m/z	Error (PPM)	Score	Charge	XIC Area
178	20.02 VDNALQSGNSQESVTEQDSK			712.6611	712.6587	-3.3	14.936	3	2.034
179	20.02 VDNALQSGNSQESVTEQDSK			534.7476	534.7466	-2.0	5.445	4	3.597
180	19.48 TISK			448.2766	448.2779	3.0	0.718	1	2.5574

TOF MS Graph

● +SWATH TOF MS (400 - 1500) from 20160713-Ri... Mono m/z: 712.6587 from 19.90 to 20.15 min

MS/MS Graph Fragments

● +MS/MS (50 - 1500) from 20160713-Ritu_R_SWA... Experiment 14 @ 20.04 min. (699 - 725 Da)

Sequence Coverage 99.1%

All Matched Peptides Auto-Validated Used for IDs Selected Peptides

Chain 1 - Light Chain1. Sequence Coverage 100.0%

```

QIVLSQSFALLSASFGKVTMTCRASSSVYIHWFOQKPGSSPKFWIYATSNLASGVVPRFSGSGSTSYSLTISRVEAE
DARTYICQWTSNPFPGGQTKLEIRRYAAPSVFIFPSPDEQLKSGTASVCLLNFFPREARQVWVDNALQSGNSQES
SVTEQDSKSTYSLSLSTLSDYERKRVYACEVTHQGLSSFPVTKSINRGE
    
```

Chain 2 - Heavy Chain 1. Sequence Coverage 98.7%

```

QVLOQPGAEALVPGASVVMKSCASGYTFTSYNMHWKQTPGRGLEWIGAIYFGNGDTSYNGKFKGRATLADKSSSTAY
MQLSSLTSEDAVYICARSTYGGDWYFNWAGTITVTSAASTGKPSVPLAPSKSTSGGTAALGCLVKDYFPEPVTV
SRNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDRAEPEKSCDKTHTCPPCPAPPELLG
GFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTRFREEQNSTYRVYVSLVPLRQDNLNG
REYKCKVSNKALPAPIEKTIISKAKGQFPREVITLPSRDELTKNGVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKLSLSPG
    
```

Chain 3 - Heavy Chain 2. Sequence Coverage 98.7%

```

QVLOQPGAEALVPGASVVMKSCASGYTFTSYNMHWKQTPGRGLEWIGAIYFGNGDTSYNGKFKGRATLADKSSSTAY
MQLSSLTSEDAVYICARSTYGGDWYFNWAGTITVTSAASTGKPSVPLAPSKSTSGGTAALGCLVKDYFPEPVTV
SRNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDRAEPEKSCDKTHTCPPCPAPPELLG
GFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTRFREEQNSTYRVYVSLVPLRQDNLNG
REYKCKVSNKALPAPIEKTIISKAKGQFPREVITLPSRDELTKNGVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKLSLSPG
    
```

Chain 4 - Light chain 2. Sequence Coverage 100.0%

```

QIVLSQSFALLSASFGKVTMTCRASSSVYIHWFOQKPGSSPKFWIYATSNLASGVVPRFSGSGSTSYSLTISRVEAE
DARTYICQWTSNPFPGGQTKLEIRRYAAPSVFIFPSPDEQLKSGTASVCLLNFFPREARQVWVDNALQSGNSQES
SVTEQDSKSTYSLSLSTLSDYERKRVYACEVTHQGLSSFPVTKSINRGE
    
```

Displaying 106 unique peptides

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