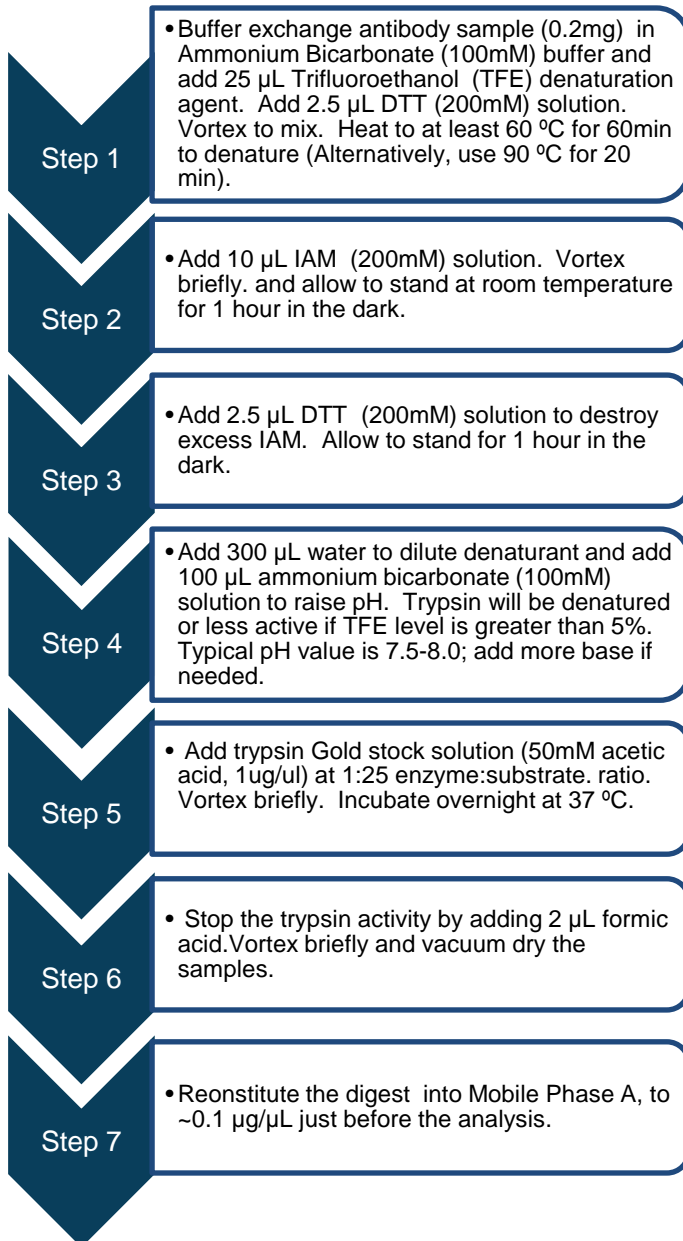


Pharma and Biopharma

Biotherapeutic Peptide Mapping Information Dependent Acquisition (IDA) 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 dependent acquisition (IDA) method was employed to acquire high-resolution MS and MS/MS level data on the digested biologic protein product.



Sample Prep

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

Pharma and Biopharma



LC Method

<i>Column</i>	Waters Acquity UPLC BEH C18 Column, 130 1.7 μ m, 2.1 mm X 100 mm	
<i>Mobile Phase A</i>	Water, 0.1% Formic acid	
<i>Mobile Phase B</i>	Acetonitrile, 0.1% Formic acid	
<i>Flow rate</i>	200 μ L/min	
<i>Column temperature</i>	40° C	
<i>Injection volume</i>	10 μ L, 1 μ g total protein	
<i>Gradient profile</i>	Time (min)	% B
	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 peptide mapping analysis as displayed in SCIEX OS user interface. The information dependent acquisition (IDA) method criteria is shown for selecting the top 15 precursor ions for high-resolution MS/MS in each cycle. For best sequence coverage and sensitivity, the specific IDA criteria parameters should be optimized for each individual biotherapeutic and HPLC separation used.

Peptide Map_IDA_75min
Add Experiment

Method Overview

Device: X500 QTOF
Ion Source: TurboSpray

Method duration: 75 min Total scan time: 0.953434 sec
Estimated cycles: 4719

Source and Gas Parameters

Ion source gas 1: 40 psi	Curtain gas: 30	Temperature: 450 °C
Ion source gas 2: 40 psi	CAD gas: 7	

Experiment IDA

Polarity: Positive V Spray voltage: 5500 V

TOF MS

TOF start mass: 350 Da	Declustering potential: 100 V	Collision energy: 10 V
TOF stop mass: 2000 Da	DP spread: 0 V	CE spread: 0 V
Accumulation time: 0.125 sec		

IDA Criteria Peptide

Maximum candidate ions: 15	<input checked="" type="checkbox"/> Dynamic background subtraction	<input checked="" type="checkbox"/> Dynamic CE for MS/MS
Intensity threshold exceeds: 100 cps	<input checked="" type="checkbox"/> Exclude former candidate ions	<input checked="" type="checkbox"/> Charge state: 1
	For: 6 sec	to: 7
	After: 2 occurrences	

TOF MSMS

Precursor ion: 830 Da	Declustering potential: 100 V	Collision energy: 35 V
TOF start mass: 50 Da	DP spread: 0 V	CE spread: 15 V
TOF stop mass: 2000 Da	Accumulation time: 0.05 sec	

Pharma and Biopharma

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's a navigation bar with 'Batch' and 'Running' indicators. Below it is a menu bar with options like 'Auto-Calibrate...', 'Plate Layout...', 'New', 'Open', 'Save', 'Print...', 'Manage', and 'Submit'. The main area contains a table with columns: Sample Name, MS Method, LC Method, Rack code, Vial position, and Data File. The first row is populated with 'Intact protein', 'intact protein analysis MS', 'Intact_10min', '1.5mL (105 vial)', '1', and 'Intact protein file'. Overlaid on this is the 'Batch - Automatic Calibration Editor' dialog box. The dialog has a title bar and a close button. The main text says 'Provide ion reference and calibrant delivery settings to be applied automatically, at the correct frequency during acquisition'. It contains several fields: 'Ion reference table' with a dropdown menu currently open showing a list of calibration solutions (including 'X500 ESI Positive Calibration Solution' which is highlighted), 'Calibrate every' with a numeric input field set to '3' and the unit 'samples', 'Calibrant delivery' with a dropdown menu set to 'CDS', and 'CDS channel' with a dropdown menu set to '1'. There are 'Edit...', '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' and the unit 'samples'. The 'Ion reference table' dropdown is set to 'X500 ESI Positive Calibration Solu...', and the 'Calibrant delivery' dropdown is set to 'CDS'. The 'CDS channel' dropdown is set to '1'. The 'Edit...' button is visible to the right of the 'Ion reference table' dropdown. The 'OK' and 'Cancel' buttons are at the bottom right.

Data Processing

Process biotherapeutic peptide mapping data in BioPharmaView™ Software 2.0.

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

Project: Rituximab

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 Chain 1 | AA Indexes: | Delete Chain

```

1-100 QIVLSQSPAILSASPGKVTMTCRASSVSYSIHWFQOKPGSSPKPWIYATSNLASGVVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
101-200 TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKHYACEVTHOGL
201-213 SSPVTKSFNRGEC
    
```

Chain 2: Heavy Chain 1 | AA Indexes: | Delete Chain

```

1-100 QVQLQQGAEELVKGASVKMSCKASGYTFTSYNMHWKQTPGRGLEWIGAIYPNGDTSYNQRFKGRATLTADKSSSTAYMQLSSTLSEDSAVYYCARST
101-200 YYGGDNYFNWVAGTITVSAASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVEVPSSSLGTQ
201-300 TYICNVNHPKSNKVDKRAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
301-400 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP
401-450 VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQKLSLSFG
    
```

Chain 3: Heavy Chain 2 | AA Indexes: | Delete Chain

```

1-100 QVQLQQGAEELVKGASVKMSCKASGYTFTSYNMHWKQTPGRGLEWIGAIYPNGDTSYNQRFKGRATLTADKSSSTAYMQLSSTLSEDSAVYYCARST
101-200 YYGGDNYFNWVAGTITVSAASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVEVPSSSLGTQ
201-300 TYICNVNHPKSNKVDKRAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
301-400 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP
401-450 VLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQKLSLSFG
    
```

Chain 4: Light chain 2 | AA Indexes: | Delete Chain

```

1-100 QIVLSQSPAILSASPGKVTMTCRASSVSYSIHWFQOKPGSSPKPWIYATSNLASGVVRFSGSGSGTYSYSLTISRVEAEDAATYYCQQWTSNPPTFGGG
101-200 TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKHYACEVTHOGL
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	G0F-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
1	1	23	87
2	1	1	133
2	1	133	193
3	1	2	213
3	1	213	224
4	2	2	22
4	2	22	96
5	2	2	148
5	2	148	204
6	2	2	265
6	2	265	325
7	2	2	371
7	2	371	429
8	4	4	23
8	4	23	87
9	4	4	133
9	4	133	193
10	4	3	213
10	4	213	224
11	3	3	22
11	3	22	96
12	3	3	148
12	3	148	204
13	3	3	265
13	3	265	325
14	3	3	371
14	3	371	429
15	2	3	230
15	2	230	230
16	2	3	233
16	2	233	233

Buttons: Add modifications... | Delete selected modifications | Edit bond... | Add bonds... | Delete selected bonds

Pharma and Biopharma

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

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

Retention Time Tolerance: ± 0.50 min

Batch Processing Pass / Fail Criteria

XIC Area Limits: ± 10.0 %

Minimum Sequence Coverage: ≥ 85.0 %

Required Form Minimum: ≥ 80 %

Restricted Form Maximum: ≤ 120 %

Annotated Protein Sequence

Chain 1 - Light Chain1

QIVLSQSPAILLSASPGKVTMTCRASSVSYSIHWPOQKPGSSPKPWVYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQWTSNPPTFGGG
TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKHVAACEVTHQGL
SSPVTKSFNRGEC

Chain 2 - Heavy Chain 1

QVQLQQPGAEELVKPGASVKMSCKASGYFTFSYMHVVKQTPGRGLEWIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARST
YGGDWYFNWVAGTFTVSAASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQ
TYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYRTPFP
VLDSDGSFFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKLSLSLSPG

Chain 3 - Heavy Chain 2

QVQLQQPGAEELVKPGASVKMSCKASGYFTFSYMHVVKQTPGRGLEWIGAIYPNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARST
YGGDWYFNWVAGTFTVSAASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQ
TYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYDGVGEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYRTPFP
VLDSDGSFFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKLSLSLSPG

Chain 4 - Light chain 2

QIVLSQSPAILLSASPGKVTMTCRASSVSYSIHWPOQKPGSSPKPWVYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQWTSNPPTFGGG
TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKHVAACEVTHQGL
SSPVTKSFNRGEC

Peptide Mapping

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

Digest Agent: Trypsin Maximum Missed Cleavages: 4

Reduced Protein Form Sequence coverage of 0 Matched peptides = 0.0 %

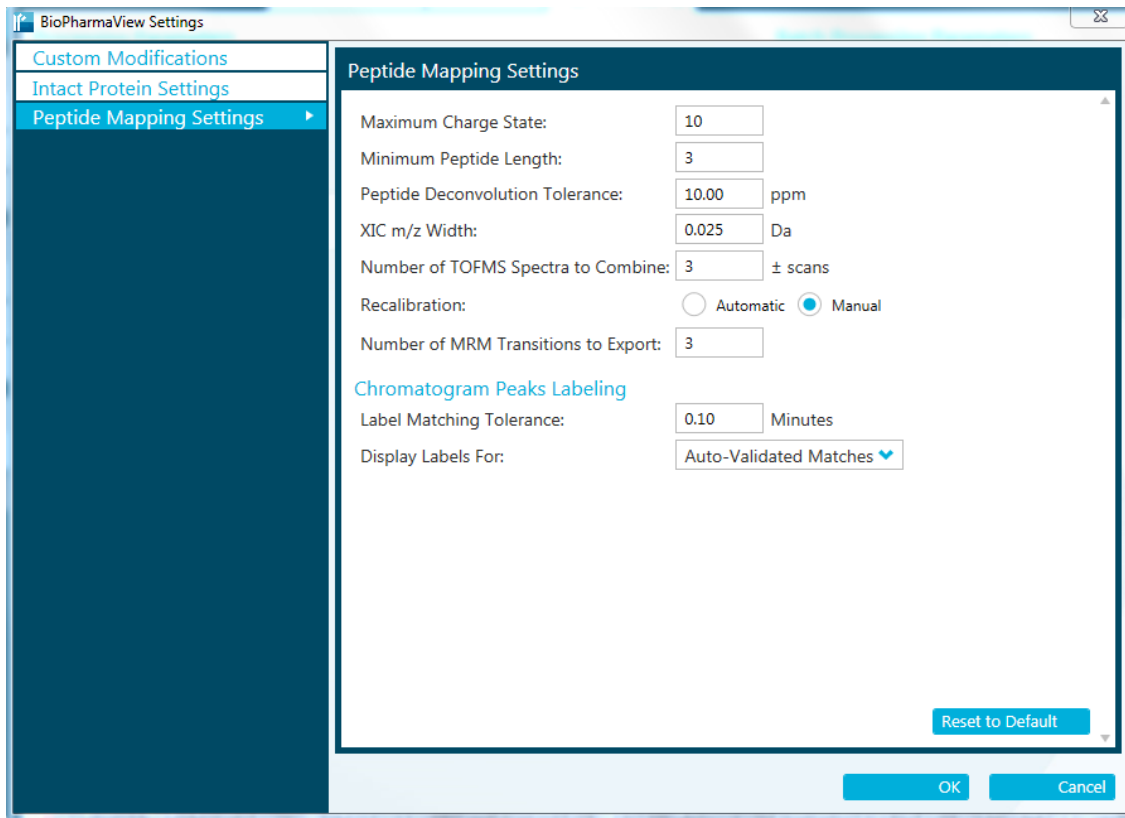
Filter Digest

Chains	Peptide	AA Index	Sequence	Modifications	Disulfide Bonds	Mono. Mass	Mono. m/z	Charge	XIC Area	Retention Time
1 1.4	T1	1-18	QIVLSQSPAILLSASPGK			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
?
!

p6

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.

Project: Rituximab

Assay Information: 20160713-Ritu_R_IDA01.wiff2

Processing Parameters: m/z Tolerance: ± 5.0 ppm; Minimum Score for Auto-Validation: 3.0; MS/MS Matching Tolerance: 0.03 Da

Peptide Results Table:

RT	Sequence	Disulfide Bonds	Theoretical Mono m/z	Observed Mono m/z	Error (PPM)	Score	Charge	XIC Area	Peptide	Chains	User Defin
30.70	FNWYYDGVVHNAK		839.4046	839.4034	-1.5	24.037	2	2.7105e6	T21	2,3	
40.41	VVSVLTVLHQDWLNGK		904.9989	904.9994	0.5	23.852	2	3.7501e5	T24	2,3	
24.22	VYACEVTHQGLSSPVTK		625.9805	625.9791	-2.2	23.325	3	4.8263e6	T16	1,4	

Sequence Coverage 100.0 %

All Matched Peptides Auto-Validated Used for IDs Selected Peptides

Chain 1 - Light Chain1 Sequence Coverage 100.0 %

QIVLSQSPAILSASPGKVTMTCRASSSVSIHWFQKPGSSPKPWIYATSNLAGVVPVRFSGSGSSTYSYSLTISRVEAEDAATYYCQQW
 TSNPPTFGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWIKVDNALQSGNSQESVTEQDSKDSYISLSSTLT
 SKADYERKRVYACEVTHQGLSSPVTKSFNRGEC

Chain 2 - Heavy Chain 1 Sequence Coverage 100.0 %

QVQLQPGAEELVPGASVRMSCKASGYTFTSYNHMHWKQTPGRLGLEWIGAIYPNGDTSYKQKFKGKATLTADKSSSTAYMQLSSLTSED
 SAVYYCARSTYYGGDWYFNWVAGTFTVTSAASTRKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQS
 SGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKRAEPKSCDKHTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
 SHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNYTKRSLSLSPG

Chain 3 - Heavy Chain 2 Sequence Coverage 100.0 %

QVQLQPGAEELVPGASVRMSCKASGYTFTSYNHMHWKQTPGRLGLEWIGAIYPNGDTSYKQKFKGKATLTADKSSSTAYMQLSSLTSED
 SAVYYCARSTYYGGDWYFNWVAGTFTVTSAASTRKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQS
 SGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKRAEPKSCDKHTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
 SHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNYTKRSLSLSPG

Chain 4 - Light chain 2 Sequence Coverage 100.0 %

QIVLSQSPAILSASPGKVTMTCRASSSVSIHWFQKPGSSPKPWIYATSNLAGVVPVRFSGSGSSTYSYSLTISRVEAEDAATYYCQQW
 TSNPPTFGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWIKVDNALQSGNSQESVTEQDSKDSYISLSSTLT
 SKADYERKRVYACEVTHQGLSSPVTKSFNRGEC

Displaying 105 unique peptides

For more information, please visit sciex.com/X500B

AB Sciex is doing business as SCIEX.

© 2016 AB Sciex. For Research Use Only. Not for use in diagnostic procedures. The trademarks mentioned herein are the property of AB Sciex Pte. Ltd. or their respective owners. AB SCIEX™ is being used under license.

Document number: RUO-MKT-02-4637-A



Headquarters
 500 Old Connecticut Path | Framingham, MA 01701 USA
 Phone 508-383-7700
sciex.com

International Sales
 For our office locations please call the division
 headquarters or refer to our website at
sciex.com/offices