

APPLICATIONS

Lys-C Protease for Improvements in Peptide Mapping Workflows

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Overview

Peptide mapping is a ubiguitous method within protein characterization. The general workflow includes the isolation of a protein, followed by insolution digest using a serine protease to yield peptides, which are subsequently separated by LC and analyzed by UV and/or MS techniques. Because of its specificity and the general size of peptides generated, trypsin is most commonly However, trypsin can have missed used. cleavages, particularly with lysine. Therefore, a common approach is to supplement the digestion with Lys-C, another serine protease. In this application note, we demonstrate the sequence coverage results for NIST mAb digestion between standard in-solution trypsin when compared to a trypsin/Lys-C digest.

The number of unique peptides yielded from the trypsin-only digestion was 267, when compared to the trypsin/Lys-C digestion with 288 (full peptide maps shown in **Figure 1**). Importantly, the DMIF peptide, as shown in **Figure 2**, is recovered significantly more with the trypsin/Lys-C digestion. This result allowed for the DMIF peptide to be identified by the information-dependent acquisition (IDA) MS/MS experiment. As such, sequence coverage of 91.6% for the heavy chain for the trypsin/Lys-C digestion, whereas trypsin-only yielded an 85.8% sequence coverage.

In summary, peptide mapping workflows should be optimized to improve digestion efficiency and reproducibility, and one strategy is to use the serine protease Lys-C to overcome any missed cleavages or digestion inefficiencies.

Digestion Procedure:

Step	Details
Denaturation	To sample, add 1:1 (v:v) of 5 M Guanidine
Reduction	1:10 (v:v) 200 mM DTT:Protein
	Incubate at 57 °C for 30 min, shaking at 1000 rpm
Alkylation	1:2 (v:v) 400 mM iodoacetamide (IAM): DTT
	Incubate in the dark 45 min Quench, 1:2 (v:v) 200 mM DTT: IAM
Buffer Exchange	100 mM Ammonium Bicarbonate, overnight
Digestion	1:20 (w/w) Trypsin:Sample or 1:20 (w/w) Trypsin/Lys-C:Sample
	Incubate 37 °C for 6 h, shaking at 1000 rpm
Reaction Quench	Formic acid
	SpeedVac to dryness, resuspend in mobile phase prior to analysis

LC Conditions

Column:	bioZen [™] 2.6 µm Peptide XB-C18
Dimension:	150 x 2.1 mm
Part No.:	00F-4768-AN
Recommended Guard:	SecurityGuard™ ULTRA
Guard Cartridge Part No.:	<u>AJ0-9806</u>
Guard Holder Part No.:	<u>AJ0-9000</u>
Mobile Phase:	A: 0.1 % Formic Acid in Water
	B: 0.1 % Formic Acid in Acetonitrile
Flow Rate:	0.3 mL/min
Gradient:	1-50% B in 50 minutes
Temperature:	40 °C
Detector:	Q-TOF (SCIEX [®] X500B)
Sample:	Digested NIST mAb



Figure 1. Comparison of TICs- Trypsin vs Trypsin/Lys-C



Figure 2. XIC Comparison, DMIF Peptide



Comparison of Sequence Coverage Trypsin/Lys-C Digested NIST mAb

Heavy Chain Sequence Coverage 91.6% QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVG WIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISKD TSKNQVVLKVTNMDPADTATYYCARDMIFNFYFDVWG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK

Trypsin Digested NIST mAb

Heavy Chain Sequence Coverage 85.8% QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVG WIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISKD TSKNQVVLKVTNMDPADTATYYCARDMIFNFYFDVWG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK



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