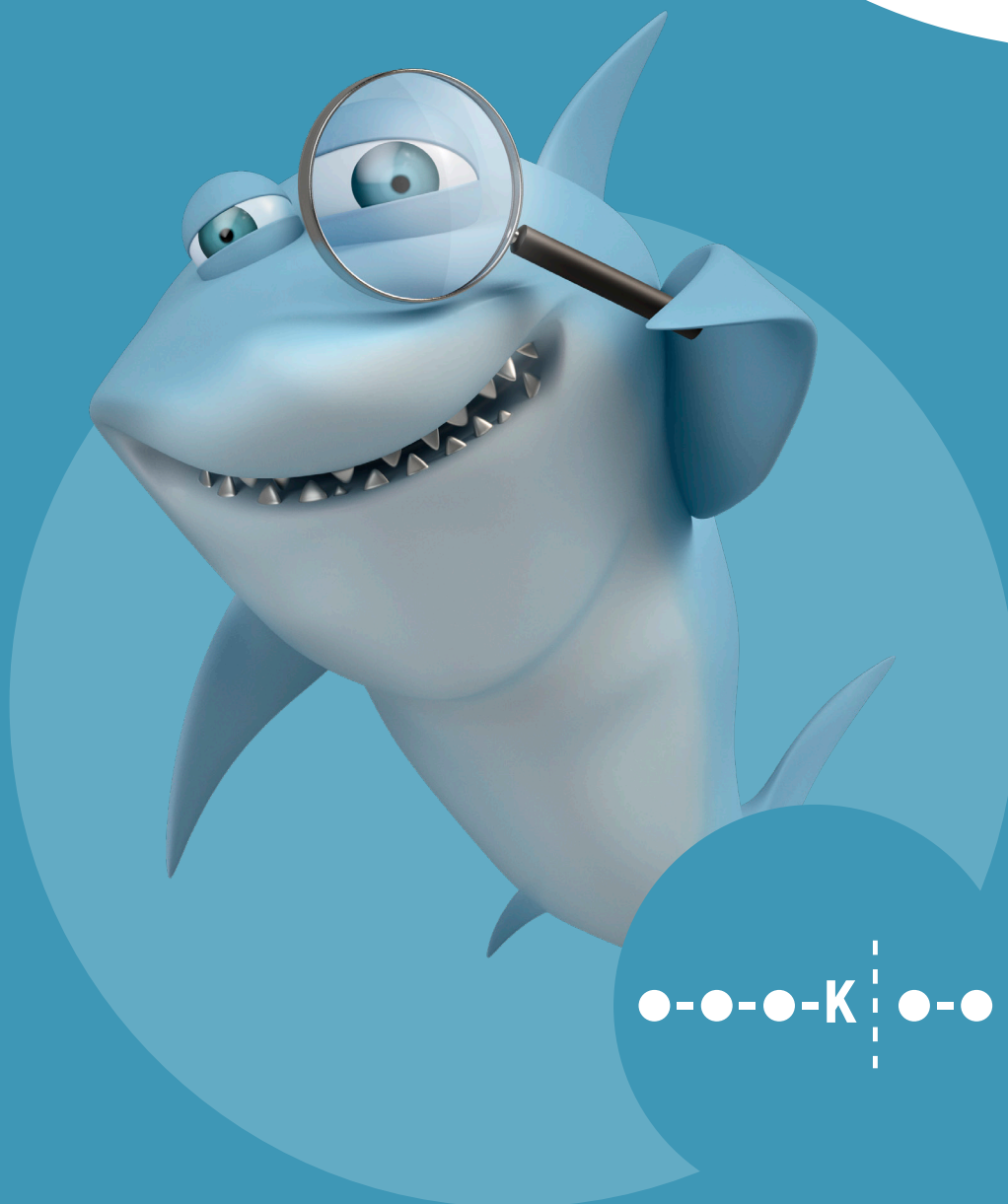




LysCERATOR™

Lysine-specific Protein Digestion

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LysCERATOR (Lys-C) is a lysine-specific endopeptidase that digests proteins C-terminally of lysine residues, including at lysine-proline linkages.

LysCERATOR is recombinantly produced to high purity and is ideally suited for mass spectrometry-based proteomics applications. Additionally, the enzyme supports peptide mapping, *de novo* sequencing and characterization of post-translational modifications.

- 

Digests peptides or proteins containing lysine residues, including at Lys-Pro motifs
- 

Digests C-terminally of Lys residues
- 

1–18 h reaction
- 

Active in up to 8 M urea and 2 M guanidine hydrochloride

Protein Digestion Workflow



LysCERATOR is a recombinantly produced lysyl endopeptidase that specifically digests peptide bonds C-terminally to lysine residues, including at lysine-proline linkages.

LysCERATOR is a highly efficient enzyme and ensures consistent and specific peptide cleavage whilst minimizing missed cleavages. By generating longer peptides than trypsin, LysCERATOR provides a complementary approach for peptide

mapping experiments and can help improve overall sequence coverage. The enzyme is active in a pH range of 7.0–9.0 and retains high activity under denaturing conditions up to 8 M urea and 2 M guanidine hydrochloride.

Product Formats



LysCERATOR™ Lyophilized
Lyophilized enzyme for lysine-specific protein digestion

LysCERATOR™ Lyophilized

PRODUCT	DESCRIPTION	ID
LysCERATOR Lyophilized 20 µg	Process 0.4–2 mg protein	B0-LC1-020
LysCERATOR Lyophilized 5 × 20 µg	Process 5 × 0.4–2 mg protein	B0-LC1-100



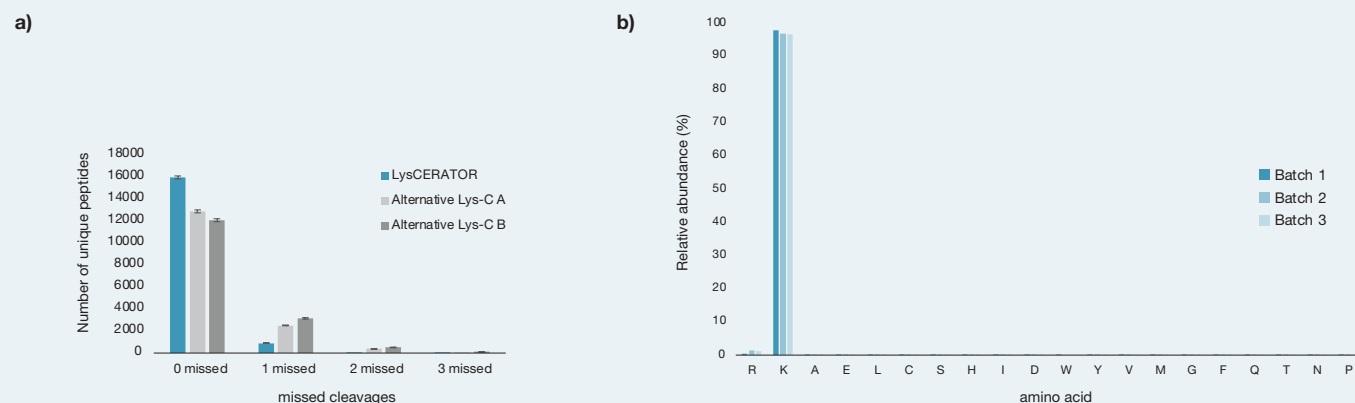
Superior Digestion Performance of LysCERATOR™



LysCERATOR demonstrates superior digestion performance in complex samples, as shown in HeLa cell lysate experiments. Compared to two alternative Lys-C enzymes, LysCERATOR generated the highest number of unique peptides

and the largest proportion of fully digested peptides with zero missed cleavages, resulting in a more informative peptide pool for LC-MS analysis. In addition, LysCERATOR showed consistently high lysine specificity (~97–98%) across multiple

batches, highlighting its robustness and reproducibility. Together, these features enable cleaner spectra, increased confidence in protein identification, and more reliable data analysis of complex biological samples.



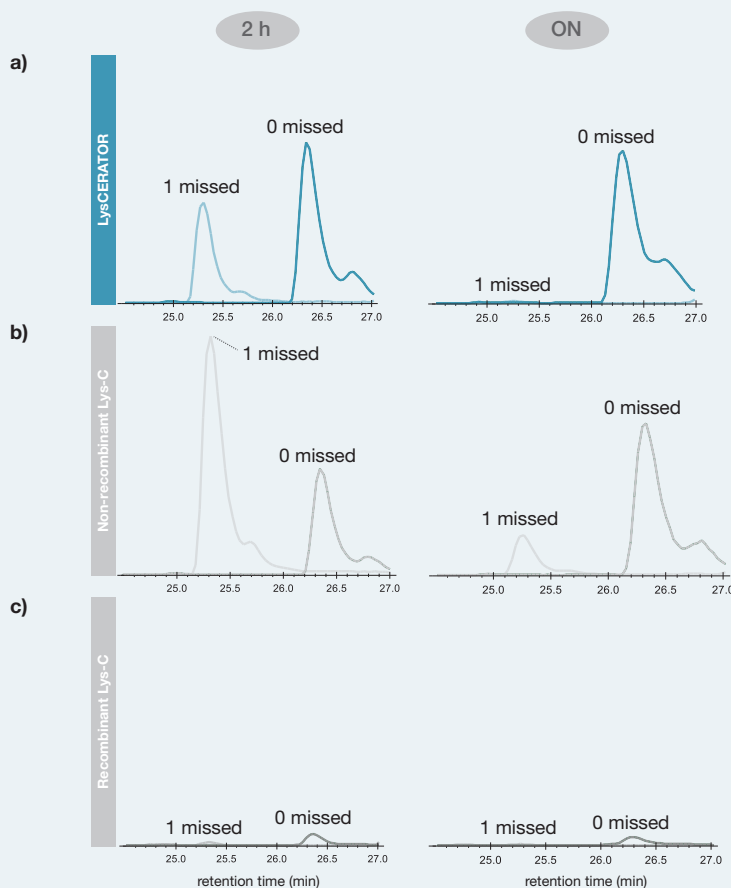
Performance of LysCERATOR in HeLa Cell Digestion. **a)** HeLa cell lysates were digested with LysCERATOR or alternative Lys-C enzymes (1:100, 50 mM HEPES pH 8.5, overnight at 37 °C) and analyzed by LC-MS after PAC clean-up. Bars show the number of unique peptides identified grouped by the number of missed cleavages (mean $\pm$ SD, $n=3$). **b)** Lysine specificity across three LysCERATOR batches, determined from C-terminal amino acid frequencies.

Fewer Missed Cleavages at Challenging K-P Sites



LysCERATOR demonstrates superior digestion efficiency at challenging lysine-proline (K-P) sites, a known limitation for many Lys-C enzymes. LysCERATOR achieves more efficient digestion at K-P sites with fewer missed cleavages compared to both recombinant and non-recombinant alternative Lys-C enzymes, demonstrated at the K39/P40 site in the trastuzumab light chain. Even after short digestion times, LysCERATOR favored fully cleaved peptides, and near-complete digestion was achieved after overnight incubation. This improved performance at difficult digestion sites enables more complete proteolytic processing and higher-quality peptide data.

Comparison of Lys-C digestion efficiency at K-P sites. Relative intensities of trastuzumab light chain peptides aa 1–39 (fully cleaved) and aa 1–42 (missed cleavage at K39/P40) following digestion with **a)** LysCERATOR, **b)** non-recombinant alternative Lys-C, or **c)** recombinant alternative Lys-C. Digestion was performed in 2 M urea (1:50, 0.1 M Tris pH 8.0) for 2 h or overnight at 37 °C, followed by LC-MS analysis.



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