

Active Recombinant *Achromobacter lyticus* Lys-C

Cat. No. Lys-C-20 **Lot. No.** (See product label)

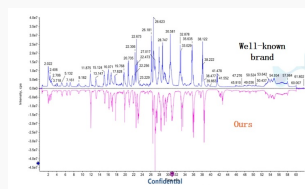
SPECIFICATION

Product Overview	Recombinant Lysyl Endopeptidase (Lys-C) is derived from <i>Achromobacter lyticus</i> and recombinantly expressed in <i>E.coli</i> .
Species	<i>Achromobacter lyticus</i>
Source	<i>E.coli</i>
Description	This product is a serine protease that can highly specifically hydrolyze amide, ester, and peptide bonds on the carboxyl side of lysine. The optimal reaction pH ranges from 9.0 to 9.5, and the optimal reaction temperature is between 30 centigrade and 37 centigrade. It can still maintain relatively high enzymatic activity in the presence of 4M urea or 0.1% SDS.
Form	Lyophilized
Purity	≥ 95% by SDS-PAGE
Bio-activity	≥ 3.0AU/mg
Protein Content	≥ 50 µg
Unit definition	In a 25 mmol/L Tris-HCl buffer at pH 9.0, under the condition of 37 centigrade, the amount of enzyme that catalyzes the formation of 1 µmol of AC-Lys-pNA in 1 minute is defined as one unit (AU).

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Usage	1. It is recommended to reconstitute this product with ultrapure water to a final concentration of 1 mg/mL. Once reconstituted, it can be directly used for protein digestion. Incubate the protein with Lys-C at a protease: protein ratio of 1: 100 to 1: 20. 2. Digest at 37 centigrade overnight.																					
Applications	1. Protein sequence analysis 2. Synthesis of lysine-related derivatives																					
Note	1. After reconstitution, this product should be stored at -20 centigrade, where it can remain stable for 6 months. Repeated freeze-thaw cycles should be avoided as much as possible; 2. Please wear lab coat and disposable gloves when using; 3. This product should not be used directly for clinical diagnosis and treatment.																					
Stability	This product should be stored at 2-8 centigrade, where it can be preserved for at least 12 months.																					
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Storage Buffer	5mM NaAc, 10mM EDTA, pH=5.5.																					
Shipping	Ice pack																					
Performance Tests	<table><thead><tr><th>Type of PTMs</th><th>Well-known brand</th><th>Ours</th></tr></thead><tbody><tr><td>Et+Glu</td><td>0.8</td><td>0.8</td></tr><tr><td>D-Isoomerization</td><td>5.0</td><td>5.0</td></tr><tr><td>M338+Oxidation</td><td>2.2</td><td>2.3</td></tr><tr><td>M434+Oxidation</td><td>0.7</td><td>0.8</td></tr><tr><td>N-Deamidation</td><td>0.53</td><td>0.52</td></tr><tr><td>D-Succinimide D</td><td>0.7</td><td>0.7</td></tr></tbody></table> Compared with the peptide maps resulting from digestion by Lys-C of a well-known brand, those from our Lys-C are essentially the same. Additionally, there are virtually no differences in common PTMs.	Type of PTMs	Well-known brand	Ours	Et+Glu	0.8	0.8	D-Isoomerization	5.0	5.0	M338+Oxidation	2.2	2.3	M434+Oxidation	0.7	0.8	N-Deamidation	0.53	0.52	D-Succinimide D	0.7	0.7
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	Digestion time	Number of Protein	Number of Peptide	Missed cleavage rate
①	3h	9068	64842	9.2%
②	12h	8972	64734	10.9%

Trypsin/Lys-C combined digestion

Design: Trypsin/Lys-C co-digestio: Trypsin:Protein=1: 50 and Lys-C:Protein=1: 100 were added to the sample, and then digested at 37 centigrade for 3h; Trypsin digestion: Trypsin:Protein=1: 50, digested at 37 centigrade overnight.

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