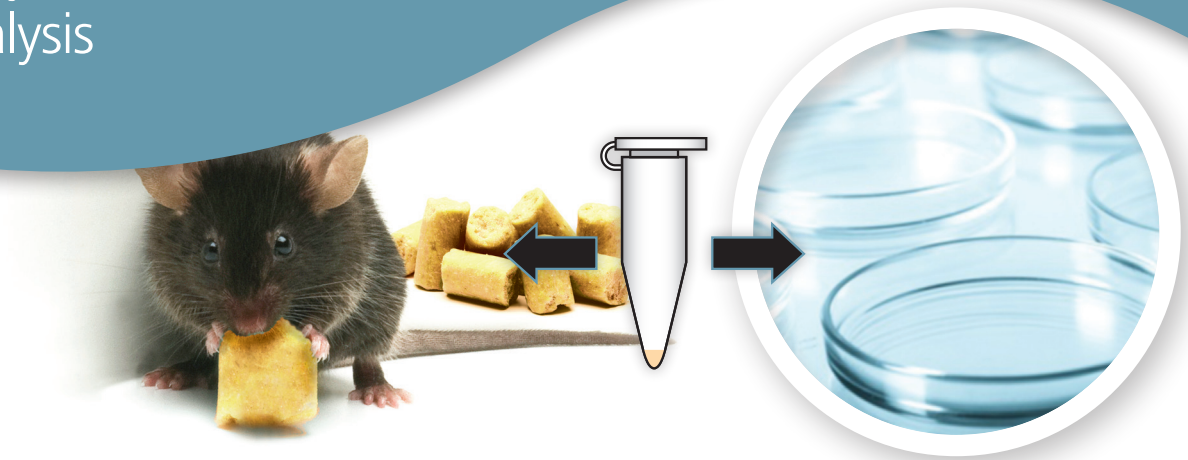
Eurisotop
A CAMBRIDGE ISOTOPE LABORATORIES COMPANY

RESEARCH PRODUCTS

L-Azidohomoalanine·HCl

For Newly Synthesized Protein Analysis



Azidohomoalanine (AHA) is a stable, non-toxic, non-canonical amino acid. This substrate readily replaces methionine during protein synthesis and is therefore ideally suited for evaluating newly synthesized proteins (NSPs) in cell culture and *in vivo*. NSPs are of importance as they have the potential to identify regulatory or expression changes associated with disease states or perturbations. To date, unlabeled AHA has been successfully incorporated into proteins of cells,[1] tissues,[2-4] and organisms.[5-7] However, isotopically labeled AHA opens the door to expanded research opportunities.

Cambridge Isotope Laboratories, Inc. (CIL) is pleased to offer stable isotope-labeled and unlabeled L-azidohomoalanine·HCL for targeted and untargeted, MS-based proteomics. The unlabeled and labeled AHA (see **Figure 1**) are available for cell culture and rodent feed. Please inquire for pricing.

Catalog No.	Description
CNLM-9461	L-Azidohomoalanine·HCl (1,2,3,4-$^{13}C_4$, 99%; 2,4-$^{15}N_2$, 98%)
ULM-9460	L-Azidohomoalanine·HCl (unlabeled)

Overview

Labeled AHA can be used to:

- probe protein synthesis
- evaluate rates of protein degradation
- study proteome-based expression changes

Labeled AHA enables:

- reduced labeling time
- selective separation and enrichment
- improved NSP identification

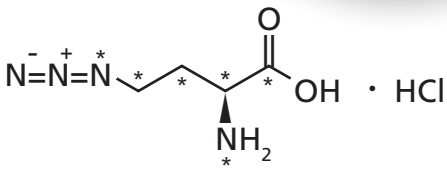


Figure 1. Chemical structure of labeled AHA. The asterisks represent isotope labels (1,2,3,4-$^{13}C_4$, 99%; 2,4-$^{15}N_2$, 98%; chemical purity ≥98%).

AHA for protein synthesis and turnover analysis

AHA is used to evaluate the rate and extent of NSPs. Experimentally, in a recent application example,[2] following a defined labeling period in mice (e.g., 4 days at 2 g AHA per kg feed), the mice are sacrificed and the tissue(s) extracted. Through click chemistry (e.g., biotinylation), biotin-alkynes can be covalently attached to the azido group of AHA-labeled proteins in the tissue homogenate(s). This modification enables the low abundance NSPs to be enriched (at the protein and/or peptide level) before LC-MS/MS analysis.

References

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5. Shen, W. et al. **2014**. *Cell Rep, 6(4),* 737-747.
6. Ullrich, M. et al. **2014**. *Nat Protoc, 9(9),* 2237-2255.
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