



SILAC Reagents

Stable Isotope Labeling with Amino Acids in Cell Culture

Stable isotope incorporation into protein has proven to be a powerful technology for quantitatively comparing the proteomes of multiple samples. Although isotopes can be incorporated metabolically or chemically, the SILAC method (utilizes metabolic incorporation) has emerged as one of the most powerful techniques for MS-based quantitative applications (see references on reverse).

Cambridge Isotope Laboratories, Inc. (CIL) is pleased to offer the following products for SILAC-based, quantitative proteomic studies.

Amino Acids

L-Arginine (L-Arg)

Catalog No.	Description	Shift from Unlabeled
CLM-2265-H*	L-Arginine-HCl ($^{13}\text{C}_6$, 99%)	+6 Da
CNLM-539-H*	L-Arginine-HCl ($^{13}\text{C}_6$, 99%; $^{15}\text{N}_4$, 99%)	+10 Da
ULM-8347	L-Arginine-HCl (unlabeled)	N/A

L-Lysine (L-Lys)

Catalog No.	Description	Shift from Unlabeled
CLM-2247-H*	L-Lysine-2HCl ($^{13}\text{C}_6$, 99%)	+6 Da
DLM-2640	L-Lysine-2HCl (4,4,5,5- D_4 , 96-98%)	+4 Da
DLM-2641	L-Lysine-2HCl (3,3,4,4,5,5,6,6- D_8 , 98%)	+8 Da
CNLM-291-H*	L-Lysine-2HCl ($^{13}\text{C}_6$, 99%; $^{15}\text{N}_2$, 99%)	+8 Da
ULM-8766	L-Lysine-2HCl (unlabeled)	N/A

*H denotes highly enriched amino acid (i.e., 99%, as revealed by GC-MS).

Tabulated below are typical compounds used in 3-plex (triple) SILAC-MS experiments. Only the light and heavy reagents would be employed in 2-plex (double) SILAC experiments.

Type	Typical Compounds and Catalog Numbers
Light (L)	Unlabeled L-Arg (ULM-8347) and Unlabeled L-Lys (ULM-8766)
Medium (M)	$^{13}\text{C}_6$ L-Arg (CLM-2265) and D_4 L-Lys (DLM-2640)
Heavy (H)	$^{13}\text{C}_6$, $^{15}\text{N}_4$ L-Arg (CNLM-539-H) and $^{13}\text{C}_6$, $^{15}\text{N}_2$ L-Lys (CNLM-291-H)

Chemical purity (CP) is 98% or greater, unless otherwise indicated.



Applications

- Peptide/protein identification
- Protein expression profiling (i.e., normal vs. disease cells)
- Signaling pathway evaluation
- Relative protein quantification

L-Leucine (L-Leu)

Catalog No.	Description	Shift from Unlabeled
CLM-2262-H*	L-Leucine ($^{13}\text{C}_6$, 99%)	+6 Da
DLM-1259	L-Leucine (5,5,5- D_3 , 99%)	+3 Da
CNLM-281-H*	L-Leucine ($^{13}\text{C}_6$, 99%; ^{15}N , 99%)	+7 Da
ULM-8203	L-Leucine (unlabeled)	N/A

L-Phenylalanine (L-Phe)

Catalog No.	Description	Shift from Unlabeled
DLM-372	L-Phenylalanine (D_8 , 98%)	+8 Da
CNLM-575-H*	L-Phenylalanine ($^{13}\text{C}_9$, 99%; ^{15}N , 99%)	+10 Da
ULM-8205	L-Phenylalanine (unlabeled)	N/A

L-Valine (L-Val)

Catalog No.	Description	Shift from Unlabeled
CLM-2249-H*	L-Valine ($^{13}\text{C}_9$, 99%)	+5 Da
DLM-488	L-Valine (D_8 , 98%)	+8 Da
ULM-8202	L-Valine (unlabeled)	N/A

*H denotes highly enriched amino acid (i.e., 99%, as revealed by GC-MS).

Visit isotope.com
for additional
amino acids.

Please see other side for additional products of interest ►

Other Products of Interest

Methionine (Met) Surrogates

L-Azidohomoalanine·HCl (light, AHA; heavy, hAHA) and L-azidonorleucine·HCl (ANL) can be used to evaluate the synthesis and turnover of newly synthesized proteins *in vivo* through targeted or untargeted MS analysis (e.g., Yates JR et al. JPR 2015). CIL is pleased to offer AHA, hAHA, and ANL for use in SILAC applications. 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)
ULM-10989	L-Azidonorleucine·HCl (unlabeled) CP 97%

Chemical purity (CP) is 98% or greater, unless otherwise specified.

References

- Itzhak, D.N.; Sacco, F.; Nagaraj, N.; et al. **2019**. SILAC-based quantitative proteomics using mass spectrometry quantifies endoplasmic reticulum stress in whole HeLa cells. *Dis Model Mech*, 12(11).
- Shin, J.; Rhim, J.; Kwon, Y.; et al. **2019**. Comparative analysis of differentially secreted proteins in serum-free and serum-containing media by using BONCAT and pulsed SILAC. *Sci Rep*, 9(1), 3096.
- Itzhak, D.N.; Sacco, F.; Nagaraj, N.; et al. **2019**. SILAC-based quantitative proteomics using mass spectrometry quantifies endoplasmic reticulum stress in whole HeLa cells. *Dis Model Mech*, 12(11).
- Shin, J.; Rhim, J.; Kwon, Y.; et al. **2019**. Comparative analysis of differentially secreted proteins in serum-free and serum-containing media by using BONCAT and pulsed SILAC. *Sci Rep*, 9(1), 3096.
- Han, J.; Yi, S.; Zhao, X.; et al. **2019**. Improved SILAC method for double labeling of bacterial proteome. *J Proteomics*, 1(194), 89-98.
- Duan, Q.; Li, D.; Xiong, L.; et al. **2019**. SILAC quantitative proteomics and biochemical analyses reveal a novel molecular mechanism by which ADAM12S promotes the proliferation, migration, and invasion of small cell lung cancer cells through upregulating hexokinase 1. *J Proteome Res*, 18(7), 2903-2914.
- Han, J.; Yi, S.; Zhao, X.; et al. **2019**. Improved SILAC method for double labeling of bacterial proteome. *J Proteomics*, 194, 89-98.
- McMillan, L.J.; Hwang, S.; Farah, R.E.; et al. **2018**. Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. *Environ Microbiol*, 20(1), 385-401.
- Heo, S.; Diering, G.H.; Na, C.H.; et al. **2018**. Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. *Proc Natl Acad Sci U S A*, 115(16), E3827-E3836.
- Ma, Y.; McClatchy, D.B.; Barkallah, S.; et al. **2018**. Quantitative analysis of newly synthesized proteins. *Nat Protoc*, 13(8), 1744-1762.
- Ma, Y.; McClatchy, D.B.; Barkallah, S.; et al. **2017**. HILAC: A novel strategy for newly synthesized protein quantification. *J Proteome Res*, 16(6), 2213-2220.
- Moody, L.R.; Barrett-Wilt, G.A.; Sussman, M.R.; et al. **2017**. Glial fibrillary acidic protein exhibits altered turnover kinetics in a mouse model of Alzheimer disease. *J Biol Chem*, 292(14), 5814-5824.
- Luo, Y.; Mok, T.S.; Lin, X.; et al. **2017**. SWATH-based proteomics identified carbonic anhydrase 2 as a potential diagnosis biomarker for nasopharyngeal carcinoma. *Sci Rep*, 7, 41191.
- Mondello, P.; Derenzini, E.; Asgari, Z.; et al. **2017**. Dual inhibition of histone deacetylases and phosphoinositide 3-kinase enhances therapeutic activity against B cell lymphoma. *Oncotarget*, 8(8), 14017-14028.
- Ji, Y.; Wei, S.; Hou, J.; et al. **2017**. Integrated proteomic and N-glycoproteomic analyses of doxorubicin sensitive and resistant ovarian cancer cells reveal glycoprotein alteration in protein abundance and glycosylation. *Oncotarget*, 8(8), 13413-13427.
- Diaz-Vera, J.; Palmer, S.; Hernandez-Fernaund, J.R.; et al. **2017**. A proteomic approach to identify endosomal cargoes controlling cancer invasiveness. *J Cell Sci*, 130(4), 697-711.
- Gonneaud, A.; Jones, C.; Turgeon, N.; et al. **2016**. A SILAC-based method for quantitative proteomic analysis of intestinal organoids. *Sci Rep*, 6, 38195.
- Gong, J.; Körner, R.; Gaitanos, L.; et al. **2016**. Exosomes mediate cell contact-independent ephrin-Eph signaling during axon guidance. *J Cell Biol*, 214(1), 35-44.
- McClatchy, D.B.; Ma, Y.; Liu, C.; et al. **2015**. Pulsed azidohomoalanine labeling in mammals (PALM) detects changes in liver-specific LKB1 knockout mice. *J Proteome Res*, 14(11), 4815-4822.
- Bell-Temin, H.; Culver-Cochran, A.E.; Chaput, D.; et al. **2015**. Novel molecular insights into classical and alternative activation states of microglia as revealed by stable isotope labeling by amino acids in cell culture (SILAC)-based proteomics. *Mol Cell Proteomics*, 14(12), 3173-3184.
- Harel, M.; Oren-Giladi, P.; Kaidar-Person, O.; et al. **2015**. Proteomics of microparticles with SILAC quantification (PROMIS-Quan): a novel proteomic method for plasma biomarker quantification. *Mol Cell Proteomics*, 14(4), 1127-1136.
- Edfors, F.; Boström, T.; Forsström, B.; et al. **2014**. Immunoproteomics using polyclonal antibodies and stable isotope-labeled affinity-purified recombinant proteins. *Mol Cell Proteomics*, 13(6), 1611-1624.
- Bagert, J.D.; Xie, Y.J.; Sweredoski, M.J.; et al. **2014**. Quantitative, time-resolved proteomic analysis by combining bioorthogonal noncanonical amino acid tagging and pulsed stable isotope labeling by amino acids in cell culture. *Mol Cell Proteomics*, 13(5), 1352-1358.
- Ong, S.E.; Mann, M. **2006**. A practical recipe for stable isotope labeling by amino acids in cell culture (SILAC). *Nat Protoc*, 1(6), 2650-2660.

Please visit isotope.com/applications →
Proteomics → Metabolic Labeling → SILAC
for more information.

