Resource Summary Report

Generated by RRID on Aug 5, 2026

Stable Isotope Labeling with Amino Acids in Cell Culture

RRID:SCR_001873
Type: Tool

Proper Citation

Stable Isotope Labeling with Amino Acids in Cell Culture (RRID:SCR_001873)

Resource Information

URL: http://silac.org/

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Description: Stable isotope labeling with amino acids in cell culture (SILAC) is a simple and straightforward approach for in vivo incorporation of a label into proteins for mass spectrometry (MS)-based quantitative proteomics. SILAC relies on metabolic incorporation of a given "light" or "heavy" form of the amino acid into the proteins. The method relies on the incorporation of amino acids with substituted stable isotopic nuclei (e.g. deuterium, 13C, 15N). In an experiment, two cell populations are grown in culture media that are identical except that one of them contains a "light" and the other a "heavy" form of a particular amino acid (e.g. 12C and 13C labeled L-lysine, respectively). When the labeled analog of an amino acid is supplied to cells in culture instead of the natural amino acid, it is incorporated into all newly synthesized proteins. After a number of cell divisions, each instance of this particular amino acid will be replaced by its isotope labeled analog. Since there is hardly any chemical difference between the labeled amino acid and the natural amino acid isotopes, the cells behave exactly like the control cell population grown in the presence of normal amino acid. It is efficient and reproducible as the incorporation of the isotope label is 100%. SILAC Applications: - Differential expression of proteins and identification of disease biomarkers - Cell signaling dynamics - Analysis of yeast pheromone signaling pathway - Identification of methylation sites - Identification of protease substrates - Study of protein complexes/protein interactions - Analysis of signaling pathways and effect of pharmacological inhibitors - Subcellular proteomics Sponsors: Supported in part by an NIH Roadmap grant Technology Center for Networks & Pathways of Lysine Modification.

Synonyms: SILAC

Resource Type: topical portal, portal, data or information resource

Keywords: amino acid, analog, biomarker, cell culture, cell division, cell signal, chemical, deuterium, disease, inhibitor, in vivo, isotope, labeling, lysine, mass spectrometry, media, metabolic, methylation site, nucleus, pharmacological, protease, protein, protein complex, protein interaction, proteomics, signaling pathway, subcellular, substrate, yeast pheromone

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Stable Isotope Labeling with Amino Acids in Cell Culture

Resource ID: SCR_001873

Alternate IDs: nif-0000-10435

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260805T044029+0000

Ratings and Alerts

No rating or validation information has been found for Stable Isotope Labeling with Amino Acids in Cell Culture.

No alerts have been found for Stable Isotope Labeling with Amino Acids in Cell Culture.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 650 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Seifert S, et al. (2026) A step-by-step guide to performing cancer metabolism research using custom-made media. Life science alliance, 9(2).

Gomez-Artiguez L, et al. (2025) Candida albicans: a comprehensive view of the proteome. bioRxiv : the preprint server for biology.

Ryan MM, et al. (2025) A signaling inspired synthetic toolkit for efficient production of tyrosine phosphorylated proteins. bioRxiv : the preprint server for biology.

Gao J, et al. (2025) Aspirin inhibits proteasomal degradation and promotes ?-synuclein aggregate clearance through K63 ubiquitination. Nature communications, 16(1), 1438.

Leduc A, et al. (2025) Impact of protein degradation and cell growth on mammalian proteomes. bioRxiv : the preprint server for biology.

Bahr J, et al. (2025) A secretome atlas of cardiac fibroblasts from healthy and infarcted mouse hearts. Communications biology, 8(1), 675.

Kugapreethan R, et al. (2025) Complex II assembly drives metabolic adaptation to OXPHOS dysfunction. Science advances, 11(33), eadr6012.

Sun Y, et al. (2025) Targeting CXCR2 in prostate cancer cells can block CD47-SIRP? interaction and reverse M2 macrophage polarization in the TME. Molecular cancer, 24(1), 273.

Carlos AJ, et al. (2025) Spatially-resolved Photoproximity Profiling of MYC Identifies a MYC-BAF Liability in Cancer Cells. bioRxiv : the preprint server for biology.

Yarbro JM, et al. (2025) Human and mouse proteomics reveals the shared pathways in Alzheimer's disease and delayed protein turnover in the amyloidome. Nature communications, 16(1), 1533.

Zhao Z, et al. (2025) YibN, a bona fide interactor of the bacterial YidC insertase with effects on membrane protein insertion and membrane lipid production. The Journal of biological chemistry, 301(4), 108395.

Paumier JM, et al. (2025) Neurofilament accumulation disrupts autophagy in giant axonal neuropathy. JCI insight, 10(5).

Luteijn MJ, et al. (2025) High-throughput screen of 100 000 small molecules in C9ORF72 ALS neurons identifies spliceosome modulators that mobilize G4C2 repeat RNA into nuclear export and repeat associated non-canonical translation. Nucleic acids research, 53(7).

Tan C, et al. (2025) Intracellular diffusion in the cytoplasm increases with cell size in fission yeast. Molecular biology of the cell, 36(4), ar51.

Vrooman LA, et al. (2025) Effect of Brief Maternal Exposure to Bisphenol A on the Fetal Female Germline in a Mouse Model. Environmental health perspectives, 133(3-4), 47002.

Sun M, et al. (2025) Utilizing a Negative Enrichment Strategy to Profile Protein Methylation, Leveraging the Orthogonality of LysargiNase and Trypsin. Molecular & cellular proteomics : MCP, 24(7), 100970.

Aval SF, et al. (2025) Role of the sarcin-ricin loop of 23S rRNA in biogenesis of the 50S ribosomal subunit. RNA (New York, N.Y.), 31(4), 585.

van Bentum M, et al. (2025) Spike-in enhanced phosphoproteomics uncovers synergistic signaling responses to MEK inhibition in colon cancer cells. Nature communications, 16(1), 4884.

Guldner IH, et al. (2025) Synaptic proteins that aggregate and degrade slower with aging accumulate in microglia. bioRxiv : the preprint server for biology.

Vandenbulcke S, et al. (2025) msqrob2TMT: Robust Linear Mixed Models for Inferring Differential Abundant Proteins in Labeled Experiments With Arbitrarily Complex Design. Molecular & cellular proteomics : MCP, 24(7), 101002.