Resource Summary Report

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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: data or information resource, portal, topical portal

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: 20260903T234511+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 673 mentions in open access literature.

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

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

Niotis G, et al. (2026) DNA damage in macrophages drives immune autoreactivity via nuclear antigen presentation. Nature aging, 6(2), 393.

Callahan A, et al. (2026) Phosphotyrosine proteomics reveals novel Zap70 and Itk pathway targets downstream of TCR and CAR in Jurkat T cells. Scientific reports, 16(1).

Chen L, et al. (2026) Peroxisome-derived ether lipids regulate lysosomal exocytosis. The EMBO journal, 45(11), 3699.

Adumeau L, et al. (2026) Condensate corona-nanoparticle complexes transfer functional biomolecules between cells. Nature materials, 25(6), 1045.

Sauer T, et al. (2026) Proteomic remodeling during tumor cell-induced platelet aggregation unveils metastatic drivers in colorectal cancer. Cancer cell international, 26(1).

Orellana EA, et al. (2026) Targeting tRNA-Arg-TCT-4-1 suppresses cancer cell growth and tumorigenesis. bioRxiv : the preprint server for biology.

Deutsch EW, et al. (2026) Expanding the human proteome with microproteins and peptideins. Nature, 654(8119), 813.

Clements J, et al. (2026) HDAC11 Regulates RNA Splicing via De-Fatty Acylation of SF3B2. bioRxiv : the preprint server for biology.

Franciosa G, et al. (2026) The proteomics and phosphoproteomics landscape of melanoma under T cell attack. Cell reports. Medicine, 7(6), 102829.

Xue Y, et al. (2026) Translation in proximity to forming autophagosomes during sustained autophagy. Nature communications, 17(1).

Jiang H, et al. (2026) Systematic characterisation of site-specific proline hydroxylation using hydrophilic interaction chromatography and mass spectrometry. eLife, 14.

Schooley A, et al. (2026) Interphase chromosome conformation is specified by distinct folding programmes inherited through mitotic chromosomes or the cytoplasm. Nature cell biology, 28(1), 82.

Hanel A, et al. (2026) Mathematical analysis of G1/S sub-networks in hematopoietic proliferation: Sequential and lineage-specific activation. iScience, 29(2), 114291.

Guldner IH, et al. (2026) Ageing promotes microglial accumulation of slow-degrading synaptic proteins. Nature, 650(8103), 930.

Mu C, et al. (2026) Noncanonical function of epigenetic reader YTHDF1 inhibits MASLD progression by maintaining peroxisomes and mitochondrial homeostasis. Experimental & molecular medicine, 58(4), 1172.

Ferrick JM, et al. (2026) Tollip antagonizes ESCRT-III-mediated plasma membrane repair and cell recovery. Cell regeneration (London, England), 15(1).

Chen W, et al. (2026) Coenzyme A is a redox sensing cofactor for malic enzyme 2 regulating oxidative stress and mitochondrial metabolism. bioRxiv : the preprint server for biology.

Kohlhause D, et al. (2026) The nuclear envelope protein TMEM209 is an integral component of the nuclear pore complex and interacts with Nup210. Journal of cell science, 139(12).

Xu T, et al. (2026) Calcineurin-NFAT-DSCR1.4 signaling as druggable axis in G??q-R183Q-driven capillary malformations. Angiogenesis, 29(2), 16.