Silantes
Stable Isotope Labeled Biomolecules

Product Information

U-15N-SILAM-Mouse Diet
U-14N-SILAM-Mouse Diet

A mouse feed (Harlan Laboratories) which is composed of a conventional protein-free diet, supplemented with a ^{15}N- or unlabeled *Ralstonia*-based protein hydrolysate.

Background

Stable isotopic labeling is the most reliable and accurate method for quantitative proteomics and metabolomics.

In cooperation with Prof. Chris Turck's group at the *Max Planck Institute of Psychiatry* Silantes has developed a ^{15}N-diet specifically designed for mouse uniform metabolic labeling. The diet is made of a *Ralstonia eutropha* bacteria hydrolysate as ^{15}N protein source. When labeling is started *in utero* and offspring continued to be fed for 2 months, only 1 mouse generation is needed to achieve greater than 90% ^{15}N incorporation rates in all tissues (Figs. 1 and 2) (*Frank E, et al. 2009*).

Almost every nitrogen atom in the organism is present as ^{15}N isotope. This includes proteins, metabolites and DNA/RNA.

Tissue including adrenal gland, brain sections, heart, kidney, liver, lung, muscle, pancreas, plasma, red blood cells, spleen and thymus has been retrieved, snap frozen in liquid nitrogen, stored at -80°C and is available upon request.

Fig. 1

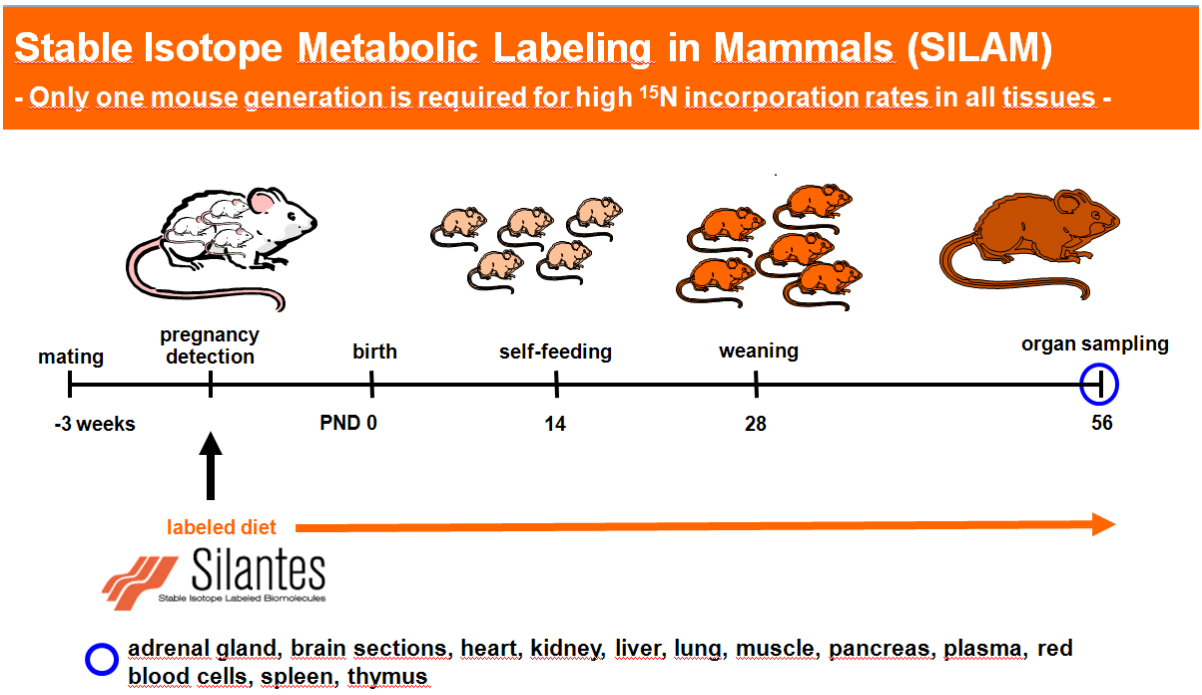

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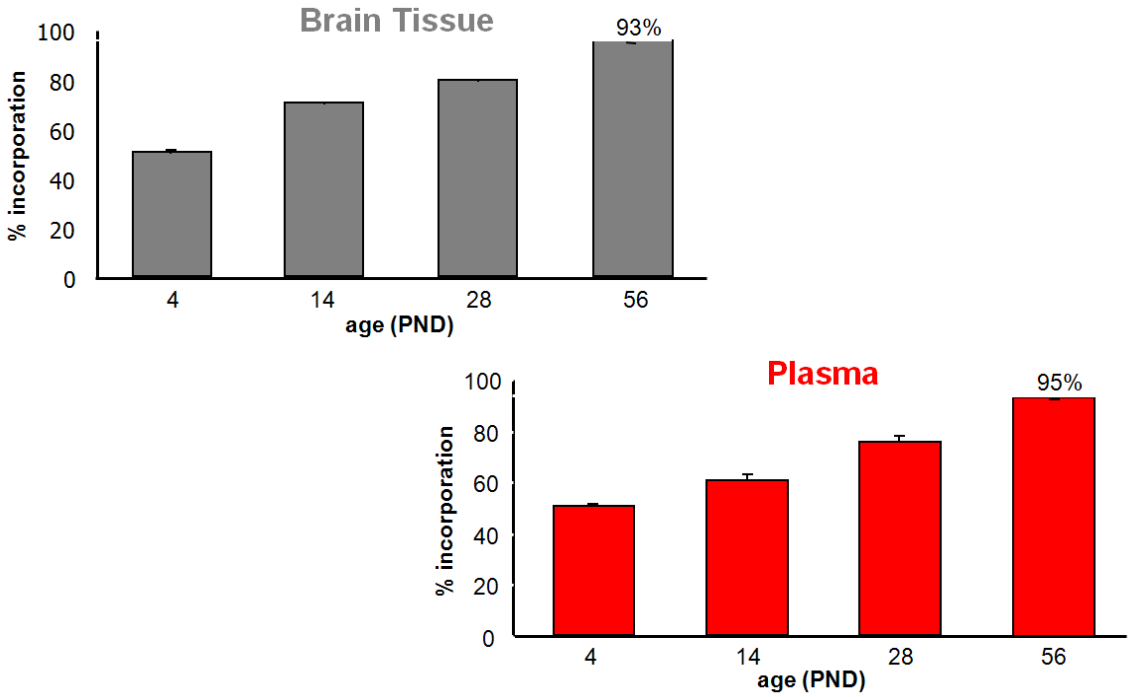
Fig. 2

Stable Isotope Metabolic Labeling in Mammals (SILAM)

- Only one mouse generation is required for high ^{15}N incorporation rates in all tissues -



Applications

Proteomics:

- Completely labeled mouse specimens as reference material for relative protein quantiation by mass spectrometry (Figs. 3 and 4) (*Wu CC, et al. 2004; Filiou MD, et al. 2011; Zhang Y, et al. 2011*). The labeled tissue specimens (adrenal gland, brain sections, heart, kidney, liver, lung, muscle, pancreas, plasma, red blood cells, spleen, thymus) can not only be used for comparing 2 states of the same type of tissue from the same species. As was recently shown, ^{15}N-labeled tissue can also serve as reference material for primary cells in culture (*Liao L, et al. 2011*).

- Partially labeled mouse specimens for global protein turnover analysis by mass spectrometry (Figs. 5 and 6) (*Zhang YY, et al. 2011*). *ProTurnyzer* software for the analysis of individual protein turnover by mass spectrometry has been developed in Prof. Turck's laboratory and is available upon request.

Metabolomics:

- Labeled metabolite standards from different tissues (adrenal gland, brain sections, heart, kidney, liver, lung, muscle, pancreas, plasma, red blood cells, spleen, thymus) for molecular structure confirmation.

- Biomarker discovery and verification analogous to proteomics (see above).

Genomics:

- Utility not yet explored.

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Fig. 3

Stable Isotope Metabolic Labeling in Mammals (SILAM)

- Relative protein quantitation by mass spectrometry -

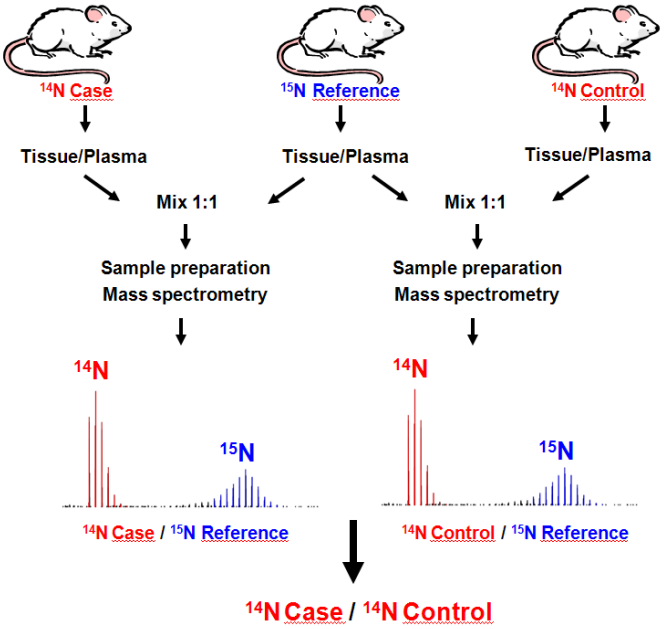

Fig. 4

Stable Isotope Metabolic Labeling in Mammals (SILAM)

- Relative protein quantitation by mass spectrometry -

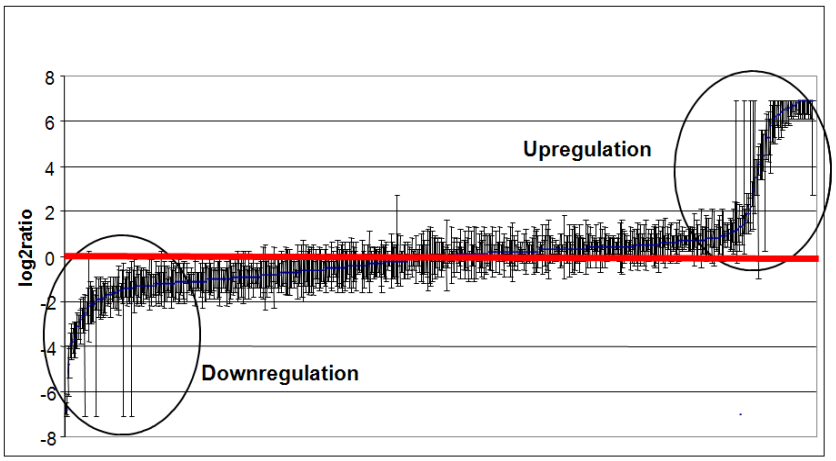

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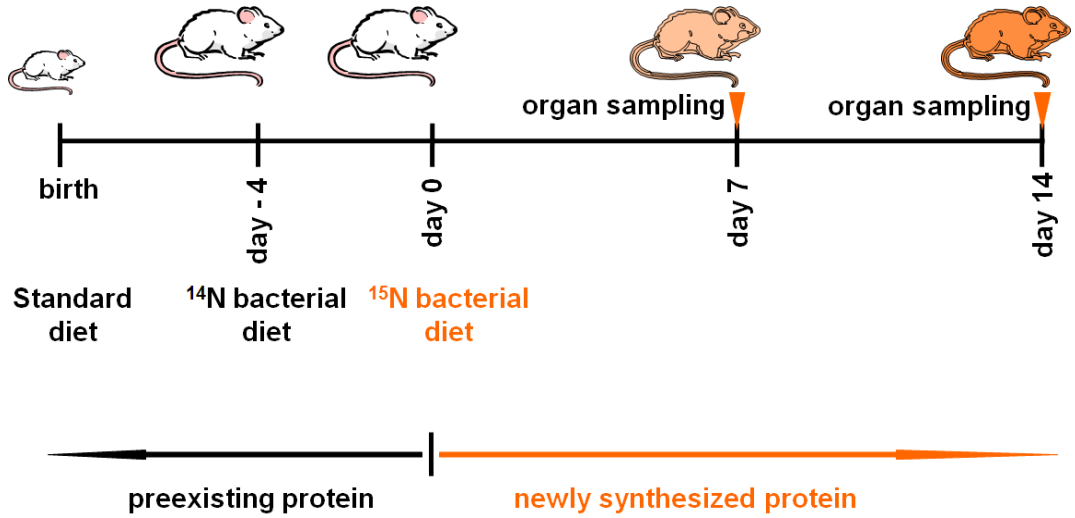
Fig. 5

Stable Isotope Metabolic Labeling in Mammals (SILAM)

- Partial labeling for global protein tunover analysis by mass spectrometry -

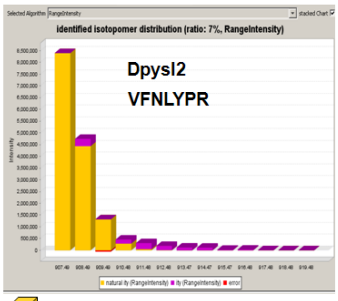


adrenal gland, brain sections, heart, kidney, liver, lung, muscle, pancreas, plasma, red blood cells, spleen, thymus

Fig. 6

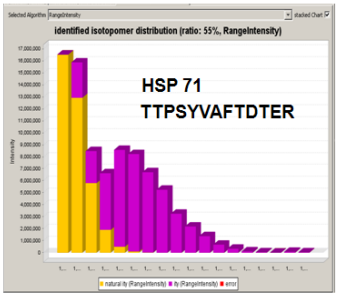
Stable Isotope Metabolic Labeling in Mammals (SILAM)

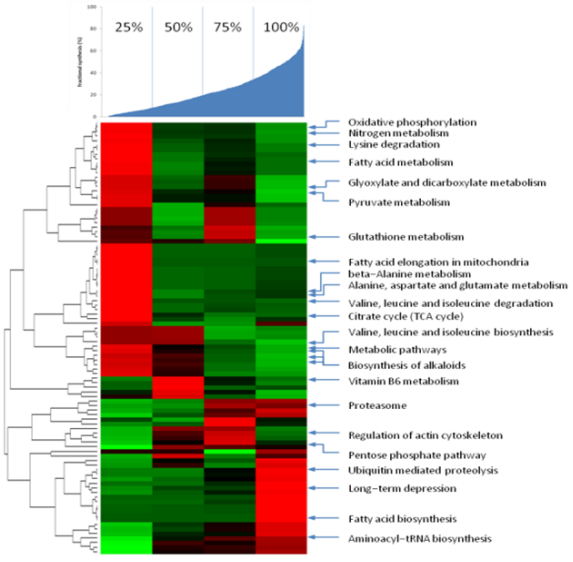
- Global protein tunover analysis with *ProTurnyzer* software -



Existing Protein

Newly Synthesized Protein





References

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Filiou MD, Zhang Y, Teplytska L, Reckow S, Gormanns P, Maccarrone G, Frank E, Kessler MS, Hambsch B, Nussbaumer M, Bunck M, Ludwig T, Yassouridis A, Holsboer F, Landgraf R, Turck CW. (2011) Proteomics and metabolomics analysis of a trait anxiety mouse model reveals divergent mitochondrial pathways. Biol Psychiatry 70(11):1074-1082.

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