







The mouse is the most commonly used animal model in biological and biomedical research. A new and promising labeling technique for increasing the multiplexing potential of traditional SILAC quantitative experiments involves neutron encoding (NeuCode™).¹ NeuCode uses different isotopologues of lysine (Lys) for multiplexed relative quantification of proteins by high-resolution MS. The ability to incorporate NeuCode labeled amino acids into the proteomes of actively growing mouse cells is beneficial for molecular phenotyping and screening studies.

Cambridge Isotope Laboratories, Inc. (CIL) is pleased to offer Mouse Express® L-Lysine NeuCode™ mouse feed for 2-plex MS proteomic studies.

The 2-plex kit contains:

- mouse feed with different combinations of labeled Lys isotopologues (see table for options)
- 1- or 3-week supply for 3 mice. Note: Supply is based on daily food intake of 4 g/mouse.²

Table. Mouse Express NeuCode mouse feed plex options. The pellets are color coded for ease of use. Please inquire for pricing and delivery.

Catalog No.	MF-LYS-NEU2-1WK or MF-LYS-NEU2-3WK		
NeuCode Lys*	080	or	202
	602		040

^{*}Nomenclature refers to the number of ¹³C, D, and ¹⁵N.

Potential benefits compared to traditional SILAC¹ and/or SILAM:

- Enhanced multiplexing
- Reduced labeling time
- Increased peptide/protein identification and quantification
- Increased sampling depth



Mouse Express NeuCode Mouse Feed: for identification, characterization, or quantification

The kits contain feed supplemented with heavy Lys isotopologues for *in vivo* labeling of mouse proteomes. The time required for isotopic incorporation is dependent on the intended sample of analysis (i.e., proteins with slower turnover rates require longer labeling periods),³ while the MS resolution required for analysis is directly correlated to the degree of plexing. The utility of NeuCode has been demonstrated in bottom-up and top-down proteomic studies using different high-resolution mass spectrometers (e.g., Q Exactive and LTQ Orbitrap Elite), acquisition modes (i.e., DDA, MRM, PRM, and SWATH), and fragmentation mechanisms (e.g., CID and ETD).⁴⁻⁶ NeuCode MS data can be analyzed with MaxQuant quantitative proteomics software.⁷ Use of these kits enables the qualitative and quantitative MS analyses of a variety of sample types (including cells, tissues, and fluids) at either the protein or peptide level.⁸

NeuCode[™] is a trademark of WARF.

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References

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