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RESEARCH PRODUCTS

Mouse Express® NeuCode™ Mouse Feed

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® NeuCode™ mouse feed with various combinations of labeled Lys isotopologues for MS proteomic studies.

The kits contain material for:

- 2-, 3-, or 4-plex analysis (see table below for details)
- 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		MF-LYS-NEU3	MF-LYS-NEU4
NeuCode Lys*	**2-Plex**		**3-Plex**	**4-Plex**
080	✓		✓	✓
341			✓	
602	✓		✓	✓
521				✓
440				✓
202		✓		
040		✓		

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

Potential benefits compared to traditional SILAC[1] 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.

NeuCode™ is a trademark of WARF.

Mouse Express is a registered trademark of Cambridge Isotope Laboratories, Inc.

References

1. Coon, J.J., et al. **2013**. Neutron-encoded mass signatures for multiplexed proteome quantification. *Nat Methods, 10(4),* 332-334.
2. Bachmanov, A.A., et al. **2002**. Food intake, water intake, and drinking spout side preference of 28 mouse strains. *Behav Genet, 32(6),* 435-443.
3. Dey, A., et al. **2016**. NeuCode Proteomics Reveals Bap1 Regulation of Metabolism. *Cell Rep, 16(2),* 583-595.
4. Coon, J.J., et al. **2016**. Neucode labels for multiplexed, absolute protein quantification. *Anal Chem, 88(6),* 3295-3203.
5. Coon, J.J., et al. **2015**. Multiplexed quantification for data-independent acquisition. *Anal Chem, 87(5),* 2570-2575.
6. Coon, J.J., et al. **2014**. Neutron-encoded mass signatures for quantitative top-down proteomics. *Anal Chem, 86(5),* 2314-2319.
7. http://www.coxdocs.org/doku.php?id=maxquant:start