



CIL

Cambridge Isotope Laboratories, Inc.  
isotope.com

Product Data Sheet

## Heavy-Labeled MS Protein Standard

Human ApoA-1 (U-<sup>15</sup>N, 98%)

Catalog No. NLM-9539

### Significance

Apolipoprotein A-1 (ApoA-1) is the primary protein component of high-density lipoprotein (HDL) in plasma and has a specific role in lipid metabolism. It is a structural and functional protein that promotes cholesterol efflux from tissues to the liver. Testing for ApoA-1 is used to approximate HDL levels in a subject, which can be used to help determine a person's risk for developing cardiovascular disease. By combining the power of LC/MS and a heavy-labeled ApoA-1 internal standard, accurate quantitation of this protein in a biological sample is achievable using a bottom-up proteomic workflow.<sup>1</sup>

### Product Description

Human ApoA-1, uniformly labeled <sup>15</sup>N enriched, dissolved in phosphate-buffered saline at a nominal concentration of 2 mg/mL.

### Product Specifications

Analytical Test	Specification
LC/MS for isotopic enrichment*	>98% <sup>15</sup> N
SDS-PAGE for purity	>90%
BCA for concentration	~2 mg/mL**

\*LC/MS of tryptic peptides

\*\*actual result reported on CoA

### Additional Information

pH = 7.4

Storage: Store at -80°C; avoid freeze-thaw cycles

Stability: 1 year if stored in recommended conditions

Molecular weight (calculated):

ApoA-1 (unlabeled) = 29.8 kDa

ApoA-1 (U-<sup>15</sup>N) = 30.2 kDa

Offered in partnership with:



### Protein Sequence

**MHHHHHHHGLVPRGSI**DEPPQSPWDRVKDLATVYVDVLKDS  
GRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLRQLGPVT  
QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQ  
EEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRA  
RAHVDALRTHLAPYSDELQRQLAARLEALKENGGARLAHEYHAK  
ATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSA

Note: The underlined residues are different from wild-type ApoA-1. The bold text is indicative of a polyhistidine tag. Because ApoA-1 has an inherent pre-pro sequence, the presence of this element on the mature protein is well tolerated.

### Reference

1. Hoofnagle, A.N.; Becker, J.O.; Oda, M.N.; Cavigiolio, G.; Mayer, P.; Vaisar, T. **2012**. Multiple-reaction monitoring-mass spectrometric assays can accurately measure the relative protein abundance in complex mixtures. *Clin Chem*, 58(4):777-81.

