

## **Antibody Validation Report**

aVR.APOA1.P02647.AB\_1238779.v1.0 (January 4\_2021)



### **A. Basic Target Information**

#### **Target Information**

**UniProt Accession Number:** P02647

**Target Name:** Apolipoprotein A-I

#### **Antibody Information**

**RRID:** AB\_1238779

**Antibody Name:** [A03] GOAT ANTI-HUMAN APOLIPOPROTEIN AI POLYCLONAL ANTI

**Host Organism:** Goat

**Clonality:** Polyclonal

**Vendor:** Academy Bio-Medical Company, Inc.

**Catalog Number:** 11A-G2

**Lot Number:** 012075

**Recombinant (Y/N):** No

**Organ/Tissue used for validation:** Serum

**HuBMAP Platform Used:** IP-MS

**Protocols.io doi for Validation Protocol:** 10.17504/protocols.io.brp9m5r6

**ORCID ID of submitter:** 0000-0002-4549-2585

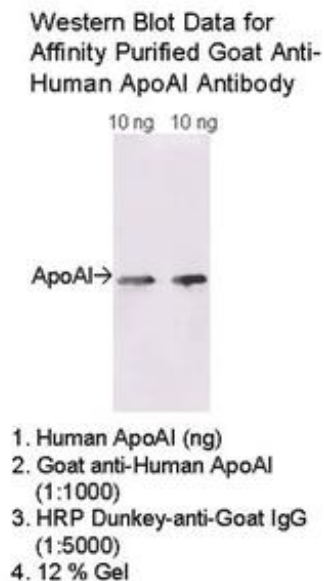
### **B. Validation Data**

#### **B.1. Vendor Validation: IP, WB**

Date Accessed: 01/07/21

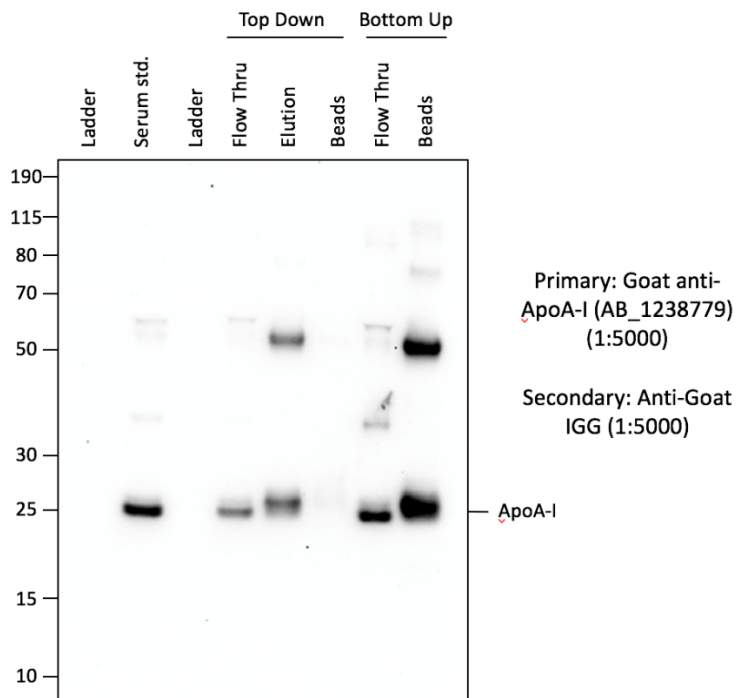
URL: <https://www.academybiomed.com/products/a03-goat-anti-human-apolipoprotein-ai-polyclonal-antibody>

#### *Western blotting*

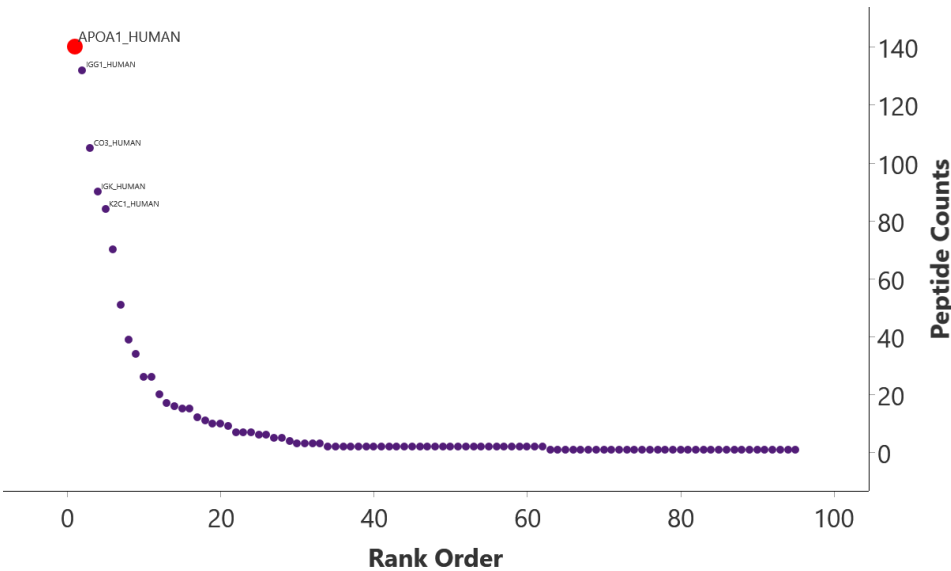


**B.2. Laboratory Validation:**  
**Immunoprecipitation/Western Blot**

Western Blot of ApoA-I  
Immunoprecipitation from  
Commercial Serum



**Immunoprecipitation/Bottom-Up MS**



## **Immunoprecipitation/Top-Down MS**

Proteoforms Identified:

1: PFR00000053599, ApoA1 (25-267), 28,062.482

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQE  
KLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPA  
LEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

2: PFR00000056138, ProApoA1 (19-267), 28,944.906,

RHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQ  
LG PVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQ  
KLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLSTL  
SEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

3: PFR00000073908, Truncated ApoA1 (25-266), 27,934.423,

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHELQE  
KLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLSTLSEKAKPA  
LEDLRQG LLPVLESFKVSFLSALEEYTKKLNT

4: PFR00000216392, ApoA1 (25-267) Mono-oxidation, 28,078.476,

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEM[MOD:00425]SKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGA  
RQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLS  
TLSEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

5: PFR00005052085, ApoA1 (25-267) Mono-oxidation, 28,078.476,

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEM[MOD:00425]ELYRQKVEPLRAELQEGA  
RQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLS  
TLSEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

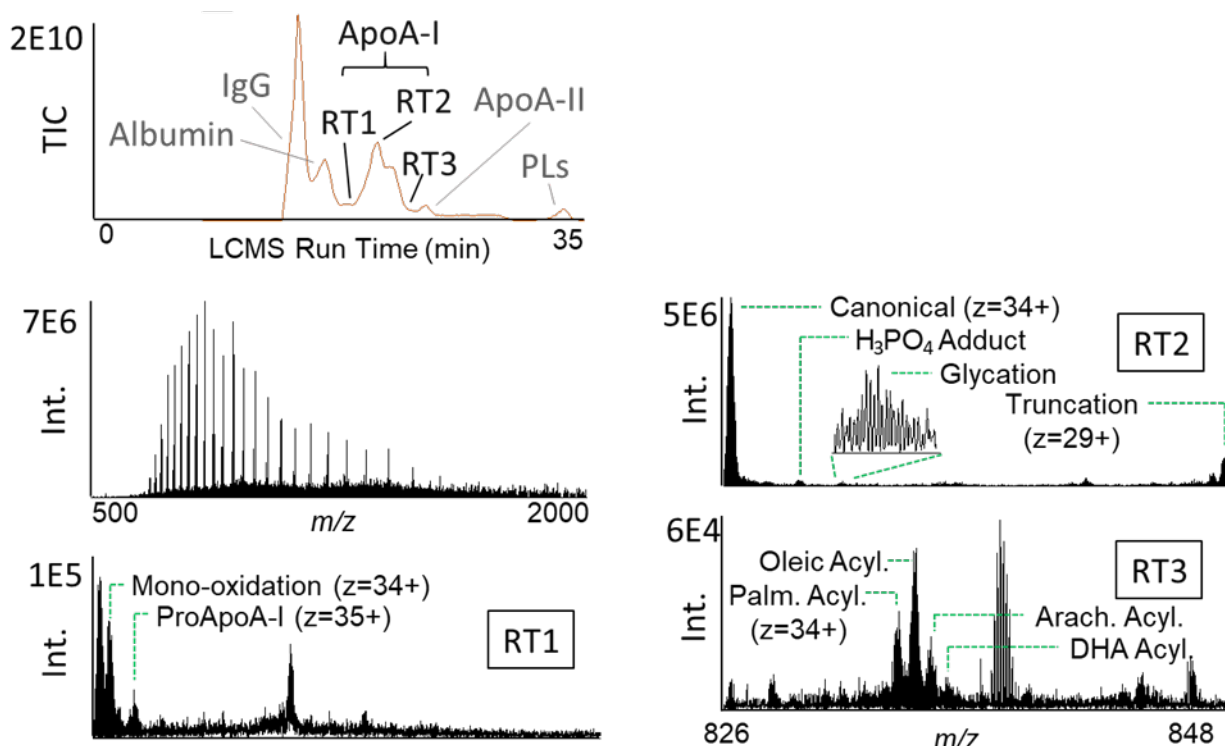
6: PFR00000216398, ApoA1 (25-267) Palmitoylated, 28,299.70,

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEMSK[MOD:00440]DLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGA  
RQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLS  
TLSEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

7: PFR00000216399, ApoA1 (25-267) Oleoylated, 28,325.72

DEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQE  
FWDNLEKETEGLRQEMSK[MOD:02012]DLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGA  
RQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL RQRLAARLEALKENG GARLA EYHAKATEHLS  
TLSEKAKPALEDLRQG LLPVLESFKVSFLSALEEYTKKLNTQ

## Intact Mass Profile



LC-TDMS results on Fusion Lumos. Different peaks correspond to elution times of different proteins and molecules (e.g. immunoglobulin G, IgG; phospholipids, PL). Proteoforms of ApoA-I elute at three different retention times. At the middle, the Full MS scan at the main retention time of ApoA-I proteoforms (RT2). At the bottom, SIM scans set between two charge states of canonical ApoA-I, at the different retention times. Notably, a different profile of proteoforms of ApoA-I is observable at the different retention times. At RT3, ApoA-I modified by different fatty acids (from left to right: palmitic, oleic, arachidonic and docohexaenoic acylations), can be observed.

Protter (Omasits et al., Bioinformatics. 2013 Nov 21)

