



# Human alanyl (membrane) aminopeptidase (ANPEP)ELISA kit

<b>Product Code</b>	CSB-EL001827HU
<b>Abbreviation</b>	ANPEP
<b>Protein Biological Process 1</b>	Angiogenesis
<b>Target Name</b>	alanyl (membrane) aminopeptidase
<b>Uniprot No.</b>	P15144
<b>Alias</b>	APN, CD13, GP150, LAP1, P150, PEPN, aminopeptidase M aminopeptidase N membrane alanine aminopeptidase microsomal aminopeptidase myeloid plasma membrane glycoprotein CD13
<b>Product Type</b>	ELISA Kit
<b>Immunogen Species</b>	Homo sapiens (Human)
<b>Protein Biological Process 3</b>	Angiogenesis
<b>Sample Types</b>	serum, plasma, tissue homogenates
<b>Detection Range</b>	31.25 pg/mL-2000 pg/mL
<b>Sensitivity</b>	7.81 pg/mL
<b>Assay Time</b>	1-5h
<b>Sample Volume</b>	50-100ul
<b>Detection Wavelength</b>	450 nm
<b>Lead Time</b>	3-5 working days after you place the order, and it takes another 3-5 days for delivery via DHL or FedEx.
<b>Research Area</b>	Cardiovascular
<b>Gene Names</b>	ANPEP
<b>Tag Info</b>	quantitative
<b>Protein Description</b>	Sandwich

## Description

The Human alanyl (membrane) aminopeptidase (ANPEP) ELISA kit is a reliable and efficient tool for the quantitative detection of Aminopeptidase N (AP-N), also known as hAPN or CD13, in serum, plasma, and tissue homogenates from Homo sapiens (Human) samples.

The ANPEP ELISA kit offers a broad detection range of 31.25 pg/mL to 2000 pg/mL and an impressive sensitivity of 7.81 pg/mL, enabling accurate and precise quantification of AP-N levels in your samples. The assay time is short, ranging from 1 to 5 hours, and requires only a small sample volume of 50-100ul.



The assay principle is a sandwich method, where the AP-N in the sample is captured by a coated antibody and detected by a biotinylated detection antibody, followed by a streptavidin-HRP conjugate, and finally, substrate solution. The signal is detected at a wavelength of 450 nm.

### Target Details

Aminopeptidase N is located in the small-intestinal and renal microvillar membrane, and also in other plasma membranes. In the small intestine aminopeptidase N plays a role in the final digestion of peptides generated from hydrolysis of proteins by gastric and pancreatic proteases. Its function in proximal tubular epithelial cells and other cell types is less clear. The large extracellular carboxyterminal domain contains a pentapeptide consensus sequence characteristic of members of the zinc-binding metalloproteinase superfamily. Sequence comparisons with known enzymes of this class showed that CD13 and aminopeptidase N are identical. The latter enzyme was thought to be involved in the metabolism of regulatory peptides by diverse cell types, including small intestinal and renal tubular epithelial cells, macrophages, granulocytes, and synaptic membranes from the CNS. Human aminopeptidase N is a receptor for one strain of human coronavirus that is an important cause of upper respiratory tract infections. Defects in this gene appear to be a cause of various types of leukemia or lymphoma.

### Product Precision

Intra-assay Precision (Precision within an assay): CV%<8%

Three samples of known concentration were tested twenty times on one plate to assess.

Inter-assay Precision (Precision between assays): CV%<10%

Three samples of known concentration were tested in twenty assays to assess.

### Linearity

To assess the linearity of the assay, samples were spiked with high concentrations of human ANPEP in various matrices and diluted with the Sample Diluent to produce samples with values within the dynamic range of the assay.

?	Sample	Serum(n=4)
1:20	Average %	91
	Range %	84-99
1:40	Average %	91
	Range %	85-96
1:80	Average %	96
	Range %	92-103
1:160	Average %	103
	Range %	96-109

### Recovery

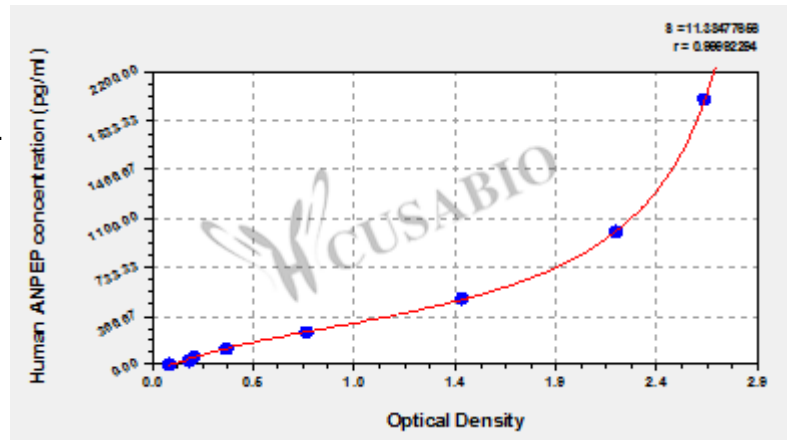
The recovery of human ANPEP spiked to levels throughout the range of the assay in various matrices was evaluated. Samples were diluted prior to assay as directed in the Sample Preparation section.

Sample Type	Average % Recovery	Range
Serum (n=5)	92	88-97
EDTA plasma (n=4)	96	90-102



**Typical**

These standard curves are provided for demonstration only. A standard curve should be generated for each set of samples assayed.



pg/ml	OD1	OD2	Average	Corrected
2000	2.627	2.645	2.636	2.545
1000	2.131	2.298	2.215	2.124
500	1.458	1.502	1.480	1.389
250	0.731	0.755	0.743	0.652
125	0.377	0.352	0.365	0.274
62.5	0.201	0.212	0.207	0.116
31.25	0.189	0.188	0.189	0.098
0	0.087	0.094	0.091	?

**MsdS**

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