

Macroglobulin α -2 Polyclonal Antibody
Catalog # AP73551**Specification**

Macroglobulin α -2 Polyclonal Antibody - Product Information

Application	WB
Primary Accession	P01023
Reactivity	Human
Host	Rabbit
Clonality	Polyclonal

Macroglobulin α -2 Polyclonal Antibody - Additional Information**Gene ID 2****Other Names**

A2M; CPAMD5; FWP007; Alpha-2-macroglobulin; Alpha-2-M; C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5

Dilution

WB~~Western Blot: 1/500 - 1/2000. IHC-p: 1/100-1/300. ELISA: 1/20000. Not yet tested in other applications.

Format

Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.09% (W/V) sodium azide.

Storage Conditions

-20°C

Macroglobulin α -2 Polyclonal Antibody - Protein Information**Name A2M****Synonyms CPAMD5****Function**

Is able to inhibit all four classes of proteinases by a unique 'trapping' mechanism. This protein has a peptide stretch, called the 'bait region' which contains specific cleavage sites for different proteinases. When a proteinase cleaves the bait region, a conformational change is induced in the protein which traps the proteinase. The entrapped enzyme remains active against low molecular weight substrates (activity against high molecular weight substrates is greatly reduced). Following cleavage in the bait region, a thioester bond is hydrolyzed and mediates the covalent binding of the protein to the proteinase.

Cellular Location

Secreted.

Tissue Location

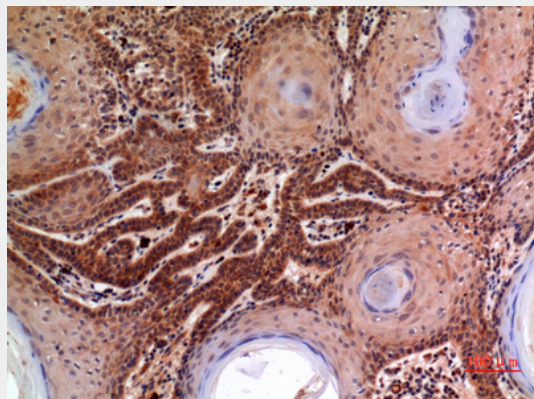
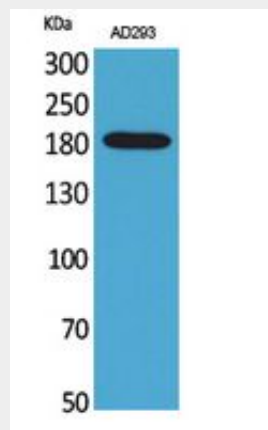
Secreted in plasma..

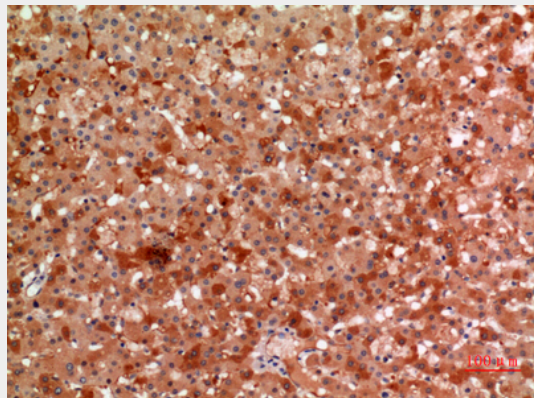
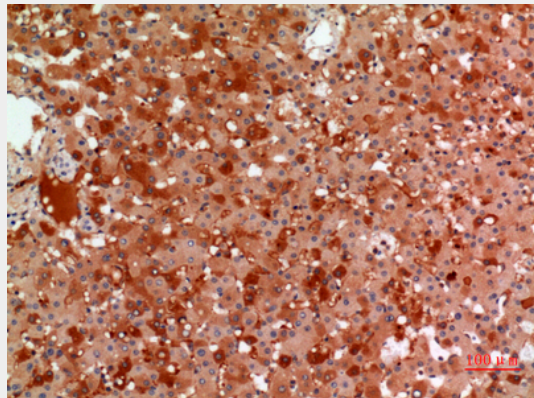
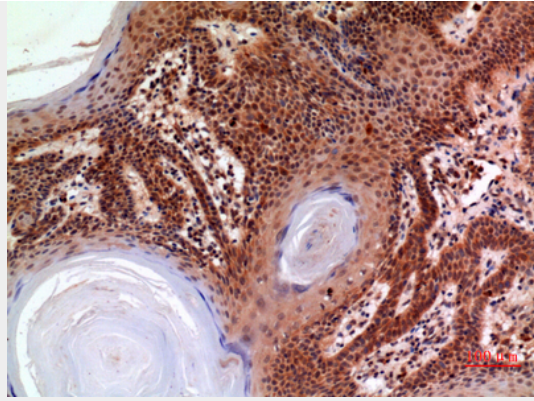
Macroglobulin α -2 Polyclonal Antibody - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

Macroglobulin α -2 Polyclonal Antibody - Images





Macroglobulin α -2 Polyclonal Antibody - Background

Is able to inhibit all four classes of proteinases by a unique 'trapping' mechanism. This protein has a peptide stretch, called the 'bait region' which contains specific cleavage sites for different proteinases. When a proteinase cleaves the bait region, a conformational change is induced in the protein which traps the proteinase. The entrapped enzyme remains active against low molecular weight substrates (activity against high molecular weight substrates is greatly reduced). Following cleavage in the bait region, a thioester bond is hydrolyzed and mediates the covalent binding of the protein to the proteinase.