

DESCRIPTION

Species Reactivity	Human
Specificity	Detects human α_2 -Macroglobulin in direct ELISAs and Western blots. In direct ELISAs, less than 2% cross-reactivity with recombinant human α_2 -Macroglobulin-like 1 is observed.
Source	Polyclonal Goat IgG
Purification	Antigen Affinity-purified
Immunogen	Human plasma-derived α_2 -Macroglobulin
Conjugate	Alexa Fluor 405 Excitation Wavelength: 405 nm Emission Wavelength: 421 nm
Formulation	Supplied 0.2mg/ml in 1X PBS with RDF1 and 0.09% Sodium Azide
*Contains <0.1% Sodium Azide, which is not hazardous at this concentration according to GHS classifications. Refer to the Safety Data Sheet (SDS) for additional information and handling instructions.	

APPLICATIONS

Please Note: Optimal dilutions should be determined by each laboratory for each application. General Protocols are available in the Technical Information section on our website.

Western Blot	Optimal dilution of this antibody should be experimentally determined.
Immunocytochemistry	Optimal dilution of this antibody should be experimentally determined.
Immunoprecipitation	Optimal dilution of this antibody should be experimentally determined.

PREPARATION AND STORAGE

Shipping	The product is shipped with polar packs. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	Protect from light. Do not freeze. 12 months from date of receipt, 2 to 8 °C as supplied

BACKGROUND

Human α_2 -macroglobulin (h α_2 M) is a serum glycoprotein that has sequence similarity to other members of the α_2 M family including complement components C3, C4 and C5 (1). α_2 M is synthesized as a polypeptide of 1474 amino acids with a signal peptide (23 residues) (2). The mature protein is a tetramer (720 kDa) of 4 identical subunits (180 kDa), which form two disulfide bond-linked dimers. As a general and irreversible protease inhibitor implicated in many processes, α_2 M is able to inhibit all four classes of proteases by a unique trapping mechanism. The bait region of h α_2 M (residues 690-728) contains specific cleavage sites for different proteases. The cleavage of the bait region by a protease induces a conformation change in α_2 M, which then traps and forms a covalent bond with the protease. The trapped protease remains active against small peptide substrates but loses its ability to interact with large protein substrates or inhibitors.

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