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ADAM32 Rabbit pAb

Catalog Number: bs-5855R

Target Protein: ADAM32 Concentration: 1mg/ml

Form: Liquid

Host: Rabbit

Clonality: Polyclonal

Isotype: IgG

Applications: WB (1:500-2000)

Reactivity: Human, Mouse (predicted:Rat, Cow, Dog, GuineaPig, Horse)

Predicted MW: 88 kDa Entrez Gene: 203102

Swiss Prot: Q8TC27

Source: KLH conjugated synthetic peptide derived from human ADAM32: 181-280/787.

Purification: affinity purified by Protein A

Storage: 0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.

Shipped at 4°C. Store at -20°C for one year. Avoid repeated freeze/thaw cycles.

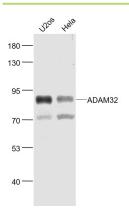
Background: ADAM32 was first discovered in a search for testis-specific proteinases. ADAM32 was

identified in human, rat, mouse, macaque and chimp, and thus far has been found only in

testis. In mice, ADAM32 is found on the sperm surface, where it may play a role in fertilization. ADAM32 is a member of the ADAMs family (A Disintegrin And Metalloproteinase), but does not contain the canonical HExxHxxxxH zinc-binding metalloproteinase catalytic site. The domain structure of the full length ADAM32 includes a signal sequence, propeptide domain, metalloproteinase-like domain, disintegrin-like domain, cys-rich domain, EGF-like domain, a short spacer region, then the transmembrane domain and a cytoplasmic domain. Like many of the reproductive-specific ADAMS, ADAM32 plays a non-enzymatic role, or (as is the case for ADAMs 1 & 2 (fertilin alpha and beta)), the protein acts in concert with a proteolytically active ADAM to process proteins. Little is known about interactions between ADAM32 and other ADAMs. Several different sequences for human ADAM32 are published; 787, 688, 649, 629, and 279 amino acids in length. The 688 amino acid form is identical to the 787 AA form until the EGF-like domain, and lacks the TM and cytoplasmic domains. The 649 AA form is likewise identical to the longer form, just to the start of the TM domain, and also lacks the TM and cytoplasmic domains. The 629 AA form has a deletion of 107 residues midway into the MP-like domain, and lacks the amino end of the disintegrin domain, but

contains the rest of the domains found in the full-length ADAM32. The predicted masses for the different versions are 87.8, 76.9, 72.9, 70.9 and 32.1, respectively, for the 786, 688, 649, 629 and 279 AA forms.

VALIDATION IMAGES



Sample: U2os (Human) Cell Lysate at 30 ug Hela(Human) Cell Lysate at 30 ug Primary: Anti- ADAM32 (bs-5855R) at 1/1000 dilution Secondary: IRDye800CW Goat Anti-Rabbit IgG at 1/20000 dilution Predicted band size: 88 kD Observed band size: 88 kD