

## HYOU1 rabbit pAb

Catalog_no :	AT7197
Applications :	WB
Reactivity :	Human, Mouse,Rat
Category :	抗原抗体
Size :	100µg/50µg/20µg
Gene_name :	HYOU1 GRP170 ORP150
Protein_name :	HYOU1
Humangene_id :	<u>10525</u>
Humanswissprot _no :	t <u>Q9Y4L1</u>
Mousegene_id :	12282
Mouseswissprot _no:	<u>Q9jKR6</u>
Ratgene_id :	<u>192235</u>
Ratswissprot_no :	<u>Q63617</u>
Immunogen :	Synthesized peptide derived from human HYOU1
Specificity :	This antibody detects endogenous levels of HYOU1 at Human/Mouse/Rat
Formulation :	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Source :	Rabbit
Dilution :	WB 1 : 500-2000
Purification :	The antibody was affinity-purified from rabbit serum by affinity-chromatography using specific immunogen.
Concentration :	1 mg/ml
Storage_stability :	-20°C/1 year
Background :	The protein encoded by this gene belongs to the heat shock protein 70 family. This gene uses alternative transcription start sites. A cis-acting segment found in the 5' UTR is involved in stress-dependent induction, resulting in the accumulation of this protein



in the endoplasmic reticulum (ER) under hypoxic conditions. The protein encoded by this gene is thought to play an important role in protein folding and secretion in the ER. Since suppression of the protein is associated with accelerated apoptosis, it is also suggested to have an important cytoprotective role in hypoxia-induced cellular perturbation. This protein has been shown to be up-regulated in tumors, especially in breast tumors, and thus it is associated with tumor invasiveness. This gene also has an alternative translation initiation site, resulting in a protein that lacks the N-terminal signal peptide. This signal peptide-lacking protein, which is only 3 amino acids shorter than the mature protein in the ER, is thought to have a housekeeping function in the cytosol. In rat, this protein localizes to both the ER by a carboxy-terminal peptide sequence and to mitochondria by an amino-terminal targeting signal. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2014],