

# RBM10 Rabbit pAb

CatalogNo: YN3020

# Key Features

Host Species

Rabbit

Reactivity

Human,Mouse,Rat

ApplicationsWB,ELISA

MW • 102kD (Observed) Isotype • IgG

# Recommended Dilution Ratios

WB 1:500-2000 ELISA 1:5000-20000

### **Storage**

Storage*	-15°C to -25°C/1 year(Do not lower than -25°C)
Formulation	Liquid in PBS containing 50% glycerol,0.5% BSA and 0.02% sodium azide.

### **Basic Information**

Clonality Polyclonal

#### Immunogen Information

Immunogen Synthesized peptide derived from part region of human protein

**Specificity** RBM10 Polyclonal Antibody detects endogenous levels of protein.

### **Target Information**

Gene name RBM10 DXS8237E GPATC9 GPATCH9 KIAA0122

Protein Name	RNA-binding protein 10 (G patch domain-containing protein 9) (RNA-binding motif protein
	10) (RNA-binding protein S1-1) (S1-1)

Organism	Gene ID	UniProt ID	
Human	<u>8241;</u>	<u>P98175;</u>	
Mouse		<u>Q99KG3;</u>	
Rat		<u>P70501;</u>	

CellularNucleus . In the extranucleolar nucleoplasm constitutes hundreds of nuclear domains, which<br/>dynamically change their structures in a reversible manner. Upon globally reducing RNA<br/>polymerase II transcription, the nuclear bodies enlarge and decrease in number. They occur<br/>closely adjacent to nuclear speckles or IGCs (interchromatin granule clusters) but coincide<br/>with TIDRs (transcription-inactivation-dependent RNA domains).

Tissue specificity Bone marrow, Brain, Colon, Epithelium, Fetal brain, Human endometrium, Liver, Lung

Function Function:May be involved in post-transcriptional processing, most probably in mRNA splicing. Binds to RNA homopolymers, with a preference for poly(G) and poly(U) and little for poly(A).,PTM:Phosphorylated upon DNA damage, probably by ATM or ATR.,sequence Caution:Translation N-terminally extended.,similarity:Contains 1 C2H2-type zinc finger.,similarity:Contains 1 G-patch domain.,similarity:Contains 1 RanBP2-type zinc finger.,similarity:Contains 2 RRM (RNA recognition motif) domains.,subcellular location:In the extranucleolar nucleoplasm constitutes hundreds of nuclear domains, which dynamically change their structures in a reversible manner. Upon globally reducing RNA polymerase II transcription, the nuclear bodies enlarge and decrease in number. They occur closely adjacent to nuclear speckles or IGCs (interchromatin granule clusters) but coincide with TIDRs (transcription-inactivation-dependent RNA domains).,subunit:Associates with the spliceosome. Component of a large chromatin remodeling complex, at least composed of MYSM1, PCAF, RBM10 and KIF11/TRIP5.,

# Validation Data

### **Contact information**

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