

Anti-SETMAR antibody



Description	Rabbit polyclonal to SETMAR.
Model	STJ95625
Host	Rabbit
Reactivity	Human
Applications	ELISA, IHC
Immunogen	Synthesized peptide derived from human SETMAR.
Immunogen Region	Internal
Gene ID	6419
Gene Symbol	SETMAR
Dilution range	IHC 1:100-1:300ELISA 1:40000
Specificity	SETMAR Polyclonal Antibody detects endogenous levels of SETMAR protein.
Tissue Specificity	Widely expressed, with highest expression in placenta and ovary and lowest expression in skeletal muscle.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Note	For Research Use Only (RUO).
Protein Name	Histone-lysine N-methyltransferase SETMAR SET domain and mariner transposase fusion protein Metnase Includes: Histone-lysine N-methyltransferase Transposon Hsmar1 transposase

Molecular Weight	76.669 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:10762OMIM:609834
Alternative Names	Histone-lysine N-methyltransferase SETMAR SET domain and mariner transposase fusion protein Metnase Includes: Histone-lysine N-methyltransferase Transposon Hsmar1 transposase
Function	Protein derived from the fusion of a methylase with the transposase of an Hsmar1 transposon that plays a role in DNA double-strand break repair, stalled replication fork restart and DNA integration. DNA-binding protein, it is indirectly recruited to sites of DNA damage through protein-protein interactions. Has also kept a sequence-specific DNA-binding activity recognizing the 19-mer core of the 5'-terminal inverted repeats (TIRs) of the Hsmar1 element and displays a DNA nicking and end joining activity . In parallel, has a histone methyltransferase activity and methylates 'Lys-4' and 'Lys-36' of histone H3. Specifically mediates dimethylation of H3 'Lys-36' at sites of DNA double-strand break and may recruit proteins required for efficient DSB repair through non-homologous end-joining . Also regulates replication fork processing, promoting replication fork restart and regulating DNA decatenation through stimulation of the topoisomerase activity of TOP2A .
Sequence and Domain Family	The mariner transposase Hsmar1 region mediates DNA-binding. It has retained some of the nucleases activity but has lost its transposase activity because the active site contains an Asn in position 610 instead of an Asp residue. In the pre-SET domain, Cys residues bind 3 zinc ions that are arranged in a triangular cluster; some of these Cys residues contribute to the binding of two zinc ions within the cluster.
Cellular Localization	Nucleus Chromosome. Recruited on damaged DNA at sites of double-strand breaks.
Post-translational Modifications	Methylated. Methylation regulates activity in DNA decatenation. Phosphorylated at Ser-508 by CHEK1 and dephosphorylated by protein phosphatase 2A/PP2A. Phosphorylation at Ser-508 is enhanced by DNA damage and promotes recruitment to damaged DNA. It stimulates DNA repair and impairs replication fork restart.