SETMAR Antibody – Rabbit Polyclonal

PRODUCT OVERVIEW

Product Name	SETMAR, Polyclonal Antibody
Full Product Name	SETMAR Antibody
Product Gene Name	anti-SETMAR antibody
Product Synonym Names	Histone-lysine N-methyltransferase SETMAR; SET domain and mariner transposase fusion gene-containing protein; Metnase; Hsmar1; SETMAR
Clonality	Polyclonal
Host	Rabbit
Species Reactivity	Human
Form/Format	Rabbit IgG in phosphate buffered saline (without Mg2+ and Ca2+), pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Purity/Purification	Purified from rabbit antiserum by affinity-chromatography using immunogen.
Concentration	1 mg/ml (lot specific)
Specificity	SETMAR Antibody detects endogenous levels of SETMAR.
Preparation and Storage	Stable at -20 degree C for at least 1 year.
Molecular Weight	76 kDa
OMIM	AK222734 mRNA
3D Structure	ModBase 3D Structure for Q53H47
Target Modification	Unmodified/Total
Immunogen	The antiserum was produced against synthesized peptide derived from human SETMAR.
Immunogen Range	350-400
Applications Tested/Suitable for anti-SETMAR antibody	Immunohistochemistry (IHC), ELISA (EIA)
Application Notes for anti-SETMAR antibody	IHC: 1:50~1:100 ELISA: 1:10000
Related Product Information for anti-SETMAR antibody	MBS9507192 is an antibody targeting SETMAR. Also known as SETMAR Antibody. Reactive in Human. Host: Rabbit.
Other Notes	Small volumes of anti-SETMAR antibody vial(s) may occasionally become entrapped in the seal of the product vial during shipment and storage. If necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container`s cap. Certain products may require to ship with dry ice and additional dry ice fee may apply.

ADDITIONAL DETAILS

NCBI/Uniprot data below describe general gene information for SETMAR. It may not necessarily be applicable to this product.

NCBI GI #	344030209
NCBI GeneID	6419
NCBI Accession #	NP_001230652.1

UniProt Primary Accession #	Q53H47
UniProt Secondary Accession #	Q13579; Q1G668; Q96F41; B4DY74; E7EN68
UniProt Related Accession #	Q53H47
GenBank Nucleotide #	NM_001243723.1
NCBI Official Full Name	histone-lysine N-methyltransferase SETMAR isoform 2
NCBI Official Synonym Full Names	SET domain and mariner transposase fusion gene
NCBI Official Symbol	SETMAR
NCBI Official Synonym Symbols	Mar1; METNASE
UniProt Protein Name	Histone-lysine N-methyltransferase SETMAR
UniProt Synonym Protein Names	SET domain and mariner transposase fusion protein
Protein Family	Histone-lysine N-methyltransferase
UniProt Gene Name	SETMAR
UniProt Synonym Gene Names	Metnase
NCBI Protein Information	histone-lysine N-methyltransferase SETMAR
NCBI Summary for SETMAR	This gene encodes a fusion protein that contains an N-terminal histone-lysine N-methyltransferase domain and a C-terminal mariner transposase domain. The encoded protein binds DNA and functions in DNA repair activities including non-homologous end joining and double strand break repair. The SET domain portion of this protein specifically methylates histone H3 lysines 4 and 36. This gene exists as a fusion gene only in anthropoid primates, other organisms lack mariner transposase domain. Alternate splicing results in multiple transcript variants. [provided by RefSeq, Jan 2013]
UniProt Comments for SETMAR	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 (PubMed:16332963, PubMed:16672366, PubMed:17877369, PubMed:17403897, PubMed:18263876, PubMed:22231448, PubMed:24573677, PubMed:20521842). 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 (PubMed:16332963, PubMed:21187428, PubMed:22231448). Also regulates replication fork processing, promoting replication fork restart and regulating DNA decatenation through stimulation of the topoisomerase activity of TOP2A (PubMed:18790802, PubMed:20457750).
Research Articles on SETMAR	**1.** These results suggest that Metnase enhances Exo1-mediated exonuclease activity on the lagging strand DNA by facilitating Exo1 loading onto a single strand gap at the stalled replication fork.
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