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Anti-MMP9 Rabbit Monoclonal Antibody

Catalog Number: M00139

Overview

Product Name	Anti-MMP9 Rabbit Monoclonal Antibody
Reactive Species	Human, Rat
Description	Boster Bio Anti-MMP9 Rabbit Monoclonal Antibody catalog # M00139. Tested in WB, IHC, ICC/IF, Flow Cytometry applications. This antibody reacts with Human, Rat.
Application	Flow Cytometry, IF, IHC, ICC, WB
Clonality	Monoclonal BCD-13
Formulation	Rabbit IgG in stabilizing components, phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol. *This antibody is supplied in a stabilized formulation. Compatibility with conjugation reactions depends on the chemistry of the conjugation method used. For conjugation methods that are not compatible with the stabilizing components present in this formulation, a carrier-free antibody format is required.
Storage Instructions	Store at -20°C for one year. For short term storage and frequent use, store at 4°C for up to one month. Avoid repeated freeze-thaw cycles.
Host	Rabbit
Uniprot ID	P14780

Technical Details

Immunogen	A synthesized peptide derived from human MMP9
Isotype	Rabbit IgG
Form	Liquid
Concentration	0.5mg/ml
Purification	Affinity-chromatography
Suggested Dilutions	WB 1:500-2000 IHC 1:50-200 ICC/IF 1:50-200 FC 1:50

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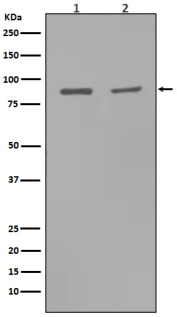
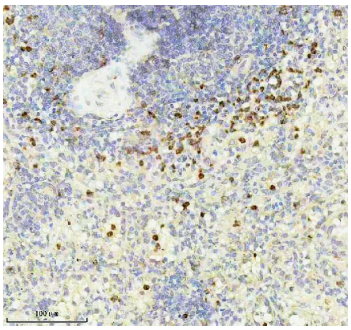
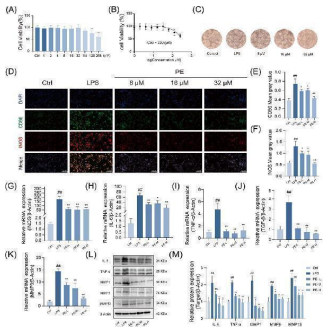
Anti-MMP9 Rabbit Monoclonal Antibody (M00139) Images



Western blot analysis of MMP9 expression in (1)Rat kidney tissue lysate;(2)Rat lung tissue lysate.



IHC analysis of MMP9 using anti-MMP9 antibody (M00139). MMP9 was detected in a paraffin-embedded section of human spleen tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 1:50 rabbit anti-MMP9 Antibody (M00139) overnight at 4°C. Peroxidase Conjugated Goat Anti-rabbit IgG was used as secondary antibody and incubated for 30 minutes at 37°C. The tissue section was developed using HRP Conjugated Rabbit IgG Super Vision Assay Kit (Catalog # SV0002) with DAB as the chromogen.



Nti-inflammatory activity of PE against LPS-Induced M1 polarization in RAW264.7 macrophages. (A) Assessment of RAW264.7 cell viability after PE treatment; (B) Determination of the half-inhibitory concentration of PE on RAW264.7 cells (>200 uM) (n = 6); (C) Changes in cell morphology of RAW264.7 cells stimulated with LPS and treated with PE at concentrations of 8, 16, and 32 uM; (D) Measurement of fluorescence intensity of CD86 and INOS in RAW264.7 cells via immunofluorescence staining; (E,F) Quantification of fluorescence intensity from images (D) ; (G–K) Analysis of gene expression of INOS, IL-6, TNF-alpha, TGF-beta, and MMP3 in RAW264.7 cells after modeling and PE treatment by RT-PCR; (L) Evaluation of protein expression of TNF-alpha, IL-6, MMP1, MMP9, and MMP13 in RAW264.7 cells after modeling and PE treatment; (M) Densitometric analysis of the protein expression shown in image (L) . Data are the mean ± SD of 3 independent experiments. # P < 0.05, ## P < 0.01, vs. Ctrl group; * P < 0.05, ** P < 0.01, vs. LPS group; ns, not significant.Index in PubMed under a CC BY license. PMID: 41230092

IHC analysis of MMP9 using anti-MMP9 antibody (M00139). MMP9 was detected in a paraffin-embedded section of human tonsil tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 1:50 rabbit anti-MMP9 Antibody (M00139) overnight at 4°C.

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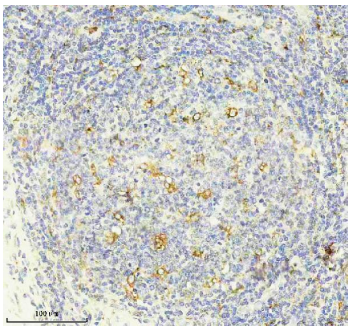
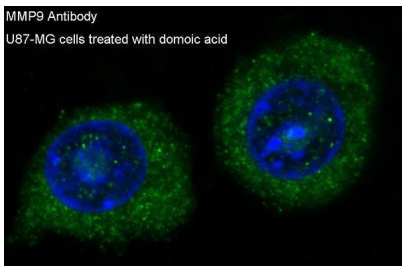
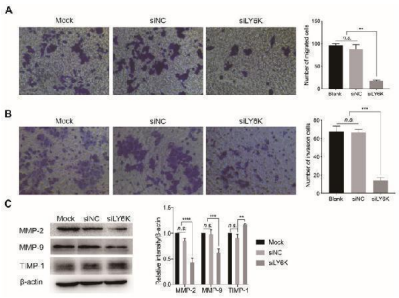


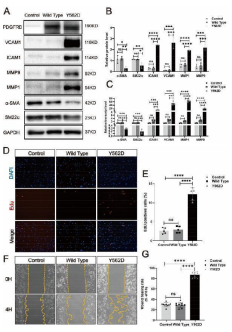
Peroxidase Conjugated Goat Anti-rabbit IgG was used as secondary antibody and incubated for 30 minutes at 37°C. The tissue section was developed using HRP Conjugated Rabbit IgG Super Vision Assay Kit (Catalog # SV0002) with DAB as the chromogen.



Immunofluorescent analysis of U87-MG cells, using MMP9 Antibody.



Knockdown of LY6K inhibits migration and invasion of CCSCs in vitro. Optical micrographs and the number of migrated (A) and invaded (B) CCSCs following siLY6K or siNC transfection for 48 h according to Transwell migration and invasion assay. n = 3. (C) Western blot analyses showing the protein levels of MMP-2, MMP-9, and TIMP-1 in CCSCs after treatment with siLY6K or siNC for 48 h. Values are the mean ± SE (n = 3). ** p < 0.01, *** p < 0.001, or **** p < 0.0001 indicates significant differences from the Mock and siNC group as assessed by one-way ANOVA with Tukey–Kramer multiple comparisons tests. LY6K, lymphocyte antigen 6, locus K; CCSC, colon cancer stem cells; MMP, matrix metalloproteinase; TIMP-1, tissue inhibitor of MMP-1; n.s., not significant. Index in PubMed under a CC BY license. PMID: 39727968



PDGFRB somatic mutation induce phenotypic modulation in SMCs. Immunostaining reveals the expression levels of smooth muscle markers (a-SMA and SM22a) and inflammatory markers (VCAM1, ICAM1, MMP1 and MMP9) in HBVSMCs transfected with different viruses (Control: vector; Wild Type: PDGFRB; Y562D: PDGFRB Y562D) (a). The relative density of immunoblot bands about markers shown in (A) were display (B) (normalized to those in cells transfected with vector viruses). RT-qPCR (C) of SMCs markers (alpha-SMA and SM22alpha) and inflammatory markers (VCAM-1, ICAM1, MMP-9 and MMP-1) in HBVSMCs underwent different treatments. Student's t-test and Benjamini–Hochberg correction are employed to assess the statistical significance. Edu assay exhibit the proliferation ability of HBVSMCs under different treatment conditions (D). Statistical analysis of the proportion of Edu-positive cells in the different groups from 5 different fields of each group at × 200 magnification. Tukey's multiple comparisons test is used for statistical differences (E). Scratch assay displays migratory ability of HBVSMCs underwent different treatment

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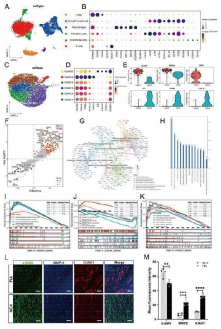
(F). Statistical analysis of the rate of wound healing (reduced area at 4H /area at 0H) in the different groups from 9 different fields of each group at × 200 magnification. Tukey's multiple comparisons test is utilized to evaluate the statistical significance. * p adj<0.05, ** p adj<0.01, *** p adj<0.001, **** p adj<0.0001 (G). The above experiments are all repeated three times Index in PubMed under a CC BY license. PMID: 38741091



Single-cell transcriptional profiling of intracranial fusiform aneurysmal cells (A - K) and multi-color immunofluorescence (mIF) of smooth muscle cells (SMCs) markers and inflammatory markers between intracranial fusiform aneurysms (IFAs) and normal cerebral arteries (NCAs) (L - M). T-SNE visualization of intracranial fusiform aneurysmal cells type. Colored according to cell type (A). Visualization of specific gene expression patterns related to cell subsets identified in (A) using a bubble plot (B). T-SNE visualization of VSMC cell clusters. Colored according to clusters (C). Visualization of structural protein and inflammation-related genes expression patterns within the subsets of smooth muscle cells identified in (C) using a bubble plot (D). The violin plots show the expression differences of structural protein genes and inflammatory genes between the contraction subgroup (VSMC5) and the inflammatory subgroup (VSMC6) (E). The volcano plot specifically shows the gene expression differences between the two cell groups (F). The petal plot displays the GO enrichment analysis results of differential genes between the VSMC5 and VSMC6 (G). The bar graph shows the KEGG enrichment analysis results of differential genes between these two cell subsets (H). The GSEA enrichment analysis results of differential genes between the two groups. The enrichment results of differential genes related to signaling pathways (I). The enrichment results of differential genes related to structural protein genes (J). The enrichment results of differential genes related to the process of inflammatory factor secretion (K). alpha-SMA (green, SMCs marker), MMP-9 (blue, inflammatory marker) and ICAM-1 (red, inflammatory marker) in FIAs and NCAs are detected using mIF. Scale bar, 100 um (L). Statistical analysis of mean fluorescence intensity about SMCs marker (alpha-SMA) and inflammatory markers (ICAM-1 and MMP-9) between NCAs (n = 4) and FIAs (n = 5). 'n' represented the number of samples. Three random fields were selected for statistical analysis in each sample, and the average value represented the detection value of this marker in this sample. The Student's t-test is utilized to examine the statistical differences among each marker. ns, no significant; ** p

31 Publications Citing This Product

1. PubMed ID: 32974191, Gao X,Qiao X,Xing X,Huang J,Qian J,Wang Y,Zhang Y,Zhang X,Li M,Cui J,Yang Y.Matrix Stiffness-Upregulated MicroRNA-17-5p Attenuates the Intervention Effects of Metformin on HCC Invasion and Metastasis by Targeting the PTEN/PI3K/Akt Pathway.Front Oncol.2020 Aug 19;10:1563.doi:10.3389/fonc.2020.01563.PMID:32974191;PMCID:PMC7466473.

2. PubMed ID: 32974191, Gao X,Qiao X,Xing X,Huang J,Qian J,Wang Y,Zhang Y,Zhang X,Li M,Cui J,Yang Y.Matrix Stiffness-Upregulated

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MicroRNA-17-5p Attenuates the Intervention Effects of Metformin on HCC Invasion and Metastasis by Targeting the PTEN/PI3K/Akt Pathway.Front Oncol.2020

3. PubMed ID: 32777528, Li CH,Liu M,Pan LH,Sun Y.ANP reduced Hedgehog signaling-mediated activation of matrix metalloproteinase-9 in gastric cancer cell line MGC-803.Gene.2020 Dec 15;762:145044.doi:10.1016/j.gene.2020.145044.Epub 2020 Aug 7.PMID:32777528.

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