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Anti-Myeloperoxidase/MPO Antibody Picoband®

Catalog Number: PA1054

About MPO

Myeloperoxidase (MPO) is a mammalian phagocyte hemoprotein though to primarily mediate host defense reactions. It is abundantly expressed in neutrophils and secreted during their activation. Myeloperoxidase is part of the host defense system of human polymorphonuclear leukocytes, responsible for microbicidal activity against a wide range of organisms. It is located in the nucleus as well as in the cytoplasm. Intranuclear MPO may help to protect DNA against damage resulting from oxygen radicals produced during myeloid cell maturation and function.

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Overview

Product Name	Anti-Myeloperoxidase/MPO Antibody Picoband®
Reactive Species	Human, Mouse, Rat
Description	Boster Bio Anti-Myeloperoxidase/MPO Antibody catalog # PA1054. Tested in Flow Cytometry, IF, IHC, WB applications. This antibody reacts with Human, Mouse, Rat. The brand Picoband indicates this is a premium antibody that guarantees superior quality, high affinity, and strong signals with minimal background in Western blot applications. Only our best-performing antibodies are designated as Picoband, ensuring unmatched performance.
Application	Flow Cytometry, IF, IHC, WB
Clonality	Polyclonal
Formulation	Each vial contains antibody formulated with stabilizing components, 0.9mg NaCl, 0.2mg Na2HPO4, 0.05mg Thimerosal, 0.05mg NaN3. *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 from date of receipt. After reconstitution, at 4˚C for one month. It can also be aliquotted and stored frozen at -20˚C for six months. Avoid repeated freeze-thaw cycles.
Host	Rabbit
Uniprot ID	P05164

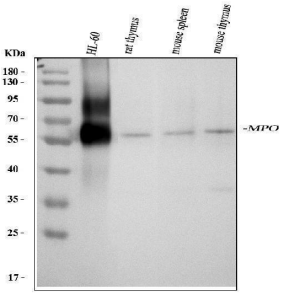
Technical Details

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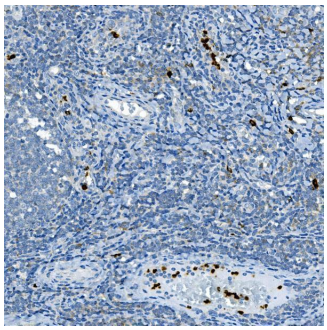
Immunogen	A synthetic peptide corresponding to a sequence at the C-terminus of human MPO, different from the related mouse and rat sequences by one amino acid.
Recommended Detection Systems	Boster recommends Enhanced Chemiluminescent Kit with anti-Rabbit IgG (EK1002) for Western blot, and HRP Conjugated anti-Rabbit IgG Super Vision Assay Kit (SV0002-1) for IHC(P).
Cross Reactivity	No cross-reactivity with other proteins
Isotype	Rabbit IgG
Form	Lyophilized
Concentration	Adding 0.2 ml of distilled water will yield a concentration of 500 μg/ml.
Purification	Immunogen affinity purified.
Suggested Dilutions	Western blot, 0.1-0.5ug/ml, Human, Mouse, Rat Immunohistochemistry (Paraffin-embedded Section), 2-5ug/ml, Human, Mouse, Rat Immunofluorescence, 5 ug/ml, Human Flow Cytometry (Fixed), 1-3 ug/1x10^6 cells, Human Note: For flow cytometry (FCM), suitable for fixed cells only. Not suitable for FACS or surface flow cytometry using live cells.

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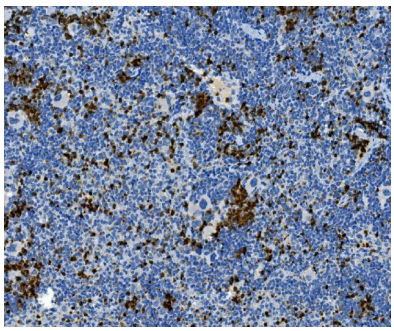
Anti-Myeloperoxidase/MPO Antibody Picoband® (PA1054) Images



Western blot analysis of MPO using anti-MPO antibody (PA1054). Electrophoresis was performed on a 5-20% SDS-PAGE gel at 70V (Stacking gel) / 90V (Resolving gel) for 2-3 hours. The sample well of each lane was loaded with 30 ug of sample under reducing conditions. Lane 1: human HL-60 whole cell lysates, Lane 2: rat thymus tissue lysates, Lane 3: mouse spleen tissue lysates, Lane 4: mouse thymus tissue lysates. After electrophoresis, proteins were transferred to a nitrocellulose membrane at 150 mA for 50-90 minutes. Blocked the membrane with 5% non-fat milk/TBS for 1.5 hour at RT. The membrane was incubated with rabbit anti-MPO antigen affinity purified polyclonal antibody (Catalog # PA1054) at 0.5 ug/mL overnight at 4°C, then washed with TBS-0.1%Tween 3 times with 5 minutes each and probed with a goat anti-rabbit IgG-HRP secondary antibody at a dilution of 1:5000 for 1.5 hour at RT. The signal is developed using an Enhanced Chemiluminescent detection (ECL) kit (Catalog # EK1002) with Tanon 5200 system. A specific band was detected for MPO at approximately 60 kDa. The expected band size for MPO is at 84 kDa.



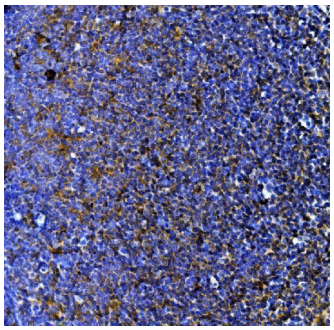
IHC analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of human tonsil tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 2 ug/ml rabbit anti-MPO Antibody (PA1054) 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.



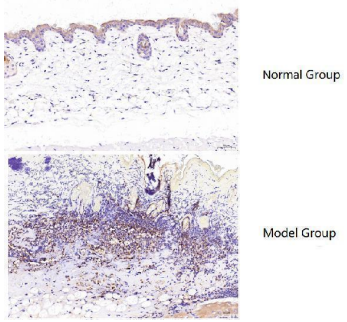
IHC analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of mouse spleen tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 2 ug/ml rabbit anti-MPO Antibody (PA1054) 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.

IHC analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of rat lymphaden tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat

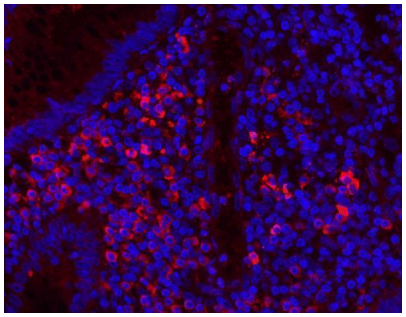
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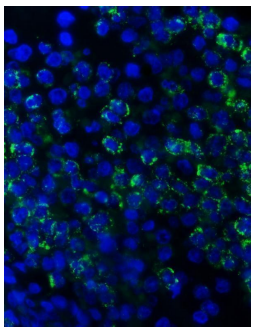
serum. The tissue section was then incubated with 2 ug/ml rabbit anti-MPO Antibody (PA1054) overnight at 4°C. Peroxidase Conjugated Goat Anti-rabbit IgG was used as secondary antibody and incubated for 30 minutes at 37°C. The tissue section was developed using HRP Conjugated Rabbit IgG Super Vision Assay Kit (Catalog # SV0002) with DAB as the chromogen.



IHC analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of mouse dorsal skin (normal group) and burned skin (model group) tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 9.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 1:100 rabbit anti-MPO Antibody (PA1054) overnight at 4°C. Polymer Anti-Rabbit IgG–HRP IHC Kit 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.



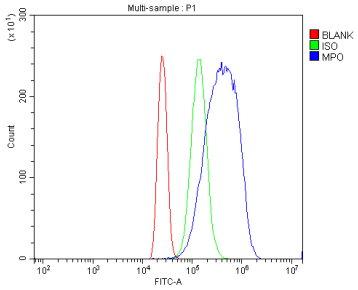
IF analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of human appendicitis tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 5 ug/mL rabbit anti-MPO Antibody (PA1054) overnight at 4°C. Cy3 Conjugated Goat Anti-Rabbit IgG (BA1032) was used as secondary antibody at 1:500 dilution and incubated for 30 minutes at 37°C. The section was counterstained with DAPI. Visualize using a fluorescence microscope and filter sets appropriate for the label used.



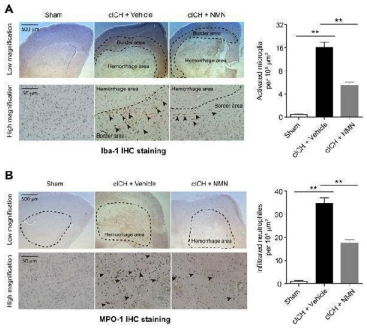
IF analysis of MPO using anti-MPO antibody (PA1054). MPO was detected in a paraffin-embedded section of human spleen tissue. Heat mediated antigen retrieval was performed in EDTA buffer (pH 8.0, epitope retrieval solution). The tissue section was blocked with 10% goat serum. The tissue section was then incubated with 5 ug/mL rabbit anti-MPO Antibody (PA1054) overnight at 4°C. DyLight488 Conjugated Goat Anti-Rabbit IgG (BA1127) was used as secondary antibody at 1:500 dilution and incubated for 30 minutes at 37°C. The section was counterstained with DAPI. Visualize using a fluorescence microscope and filter sets appropriate for the label used.

Flow Cytometry analysis of HL-60 cells using anti-MPO antibody (PA1054). Overlay histogram showing HL-60 cells stained with PA1054 (Blue line). To facilitate intracellular staining, cells were fixed with 4% paraformaldehyde and permeabilized with permeabilization buffer. The cells were

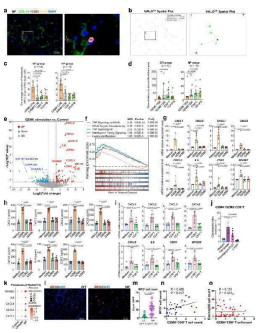
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blocked with 10% normal goat serum. And then incubated with rabbit anti-MPO Antibody (PA1054, 1 ug/1x106 cells) for 30 min at 20°C. DyLight®488 conjugated goat anti-rabbit IgG (BA1127, 5-10 ug/1x106 cells) was used as secondary antibody for 30 minutes at 20°C. Isotype control antibody (Green line) was rabbit IgG (1 ug/1x106) used under the same conditions. Unlabelled sample without incubation with primary antibody and secondary antibody (Red line) was used as a blank control.



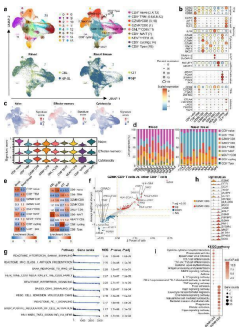
Effects of NMN on microglia activation and neutrophil infiltration in cICH model. (A) Representative images and quantitative analysis of Iba-1 (microglia marker) immunohistochemistry staining at 24 hours post cICH. ** P < 0.01, n = 5 per group. (B) Representative images and quantitative analysis of MPO-1 (neutrophil marker) immunohistochemistry staining at 24 hours post cICH. ** P < 0.01, n = 5 per group. Index in PubMed under a CC BY license. PMID: 28386082



Interaction between GZMK + CD8 + T cells and fibroblasts contributes to neutrophilic inflammation in nasal polyps. a Representative immunofluorescence staining of collagen I (COL1A1, green), CD8 (red), and GZMK (yellow) in NPs. The right image shows a greater magnification of the outlined area. b Spatial distribution analysis of GZMK + CD8 + T and COL1A1 + cells in the same tissue field demonstrated in (a) using HALO software. c–d The number of COL1A1 + fibroblasts within a radius of 25 um from the nuclear center of GZMK + CD8 + T, GZMB + CD8 + T, CD4 + T, or CD19 + B cells in CIT group (left, n = 10 samples) and NP group (right, n = 10 samples) (c). Average distance from the indicated cell types to the closest COL1A1 + fibroblasts in CIT group (left, n = 10 samples) and NP group (right, n = 10 samples) (d). e DEGs between NP-derived primary fibroblasts (NPDF) treated with and without recombinant human GZMK (n = 4). Two-sided Wald test (default for DESeq2 r-package) was used for differential expression analysis utilizing standard cutoffs of |log2(fold change) | >1 and P value < 0.05. f GSEA plots showing signaling pathways enriched in the GZMK stimulated NPDF. Two-sided permutation test with Benjamini-Hochberg adjustments was used for GSEA analysis. Normalized enrichment score (NES) > 1 and adjusted P < 0.05 was considered significant. g Expression levels of selected genes in NPDF stimulated with GZMK, GZMA or GZMB (n = 7 biological replicates). h Protein levels of chemokines and cytokines secreted by NPDF stimulated with GZMK, GZMA, or GZMB (n = 10 biological replicates). i Gene expression levels in NPDF cultured with supernatants of NP-derived and activated CD4 + T or CD8 + T cells (n = 8 biological replicates). j Migration of GZMK + CD8 + T cells towards NPDF in the presence or absence of CXCL12 neutraligand LIT-927 (n = 7 biological replicates). Data are presented as mean with standard deviation; two-sided paired t test. k Expression of neutrophil chemokines and inflammatory marker in fibroblasts from the indicated group (5 controls, 5 CRSsNP, and 11 NP samples)

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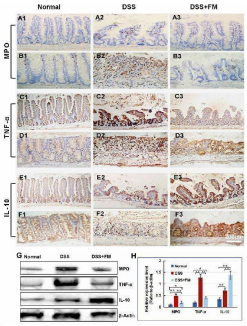
in a public dataset (HRA000772). l Representative immunofluorescence staining of myeloperoxidase (MPO, red) positive cells in CIT and NP. Scale bar: 40 um. m Quantification of MPO + cells in the indicated group (17 CIT and 34 NP samples). Data are presented as median with interquartile ranges; Two-sided unpaired Wilcoxon test. Spearman correlation between GZMK + CD8 + T cells and MPO + neutrophil counts (n = 34 samples) (n) or eosinophil counts in NP (n = 57 samples) (o). Two-sided Spearman's rank correlations test. For (c , d), and (g–i), data are presented as median with interquartile ranges; Two-sided Friedman test with Dunn's multiple comparisons test. CIT control inferior turbinate sample, NP nasal polyp. Source data are provided as a Source Data file. Index in PubMed under a CC BY license. PMID: 39614076



GZMK + CD8 + T cells are preferentially increased in NPs with a distinct transcriptional program. a UMAP plots showing that 81,202 CD8 + T cells from 25 samples (5 CBL, 8 NP-BL, 4 CIT, and 8 NP samples) are separated into 16 clusters (upper left). Clusters are annotated into nine major cell types by canonical markers (upper right) and colored by different sampling locations (lower left and right). b Dot plots showing the scaled expression of selected canonical marker genes in the indicated cell types. c Feature plots and violin plots illustrating expression of naive, effector memory and cytotoxicity curated gene signatures across CD8 + T cell clusters. d Bar plots showing the compositions of major cell types in each sample across different sampling locations in control participants and patients with CRSwNP. e Tissue prevalence of major cell types in the indicated group (13 blood samples (including 5 CBL and 8 NP-BL samples) and 12 nasal tissue samples (including 4 CIT and 8 NP samples)) is estimated by Ro/e score. f Scatter-plot shows differentially expressed genes (DEGs) between GZMK + CD8 + T cells and other CD8 + T cells. Two-sided Wilcoxon rank-sum tests with Bonferroni correction. Genes with |log2(fold change)| > 0.5 and adjusted P < 0.05 were considered significant. NS, no significant difference; P adj, adjusted P value; Δ percent of cells, the difference in the percentage of cells expressing the gene comparing GZMK + CD8 + T versus all other CD8 + T cells. g Gene set enrichment analysis (GSEA) showing significantly differentially upregulated pathways in GZMK + CD8 + T cells compared to other CD8 + T cells. Two-sided permutation test with Benjamini-Hochberg adjustments was used for GSEA analysis. Normalized enrichment score (NES) > 1 and adjusted P < 0.05 was considered significant. h Violin plots displaying top10 differentially expressed genes (DEGs) among GZMK + CD8 + T and GZMB + CD8 + T cells in NPs. Two-sided Wilcoxon rank-sum tests with Bonferroni correction. Genes with |log2(fold change)| > 0.5 and adjusted P < 0.05 were considered significant. i , Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of DEGs that enriched in indicated CD8 + T clusters. Two-sided Fisher's Exact test with Benjamini-Hochberg adjustments was used for KEGG analysis. Adjusted P < 0.05 was considered significant. CBL control blood sample, CD8 + Tpex, CD8 + progenitor exhausted cells, CIT control inferior turbinate sample, MAIT mucosal associated invariant T cell, NP nasal polyp, NP-BL blood sample from CRSwNP patient,

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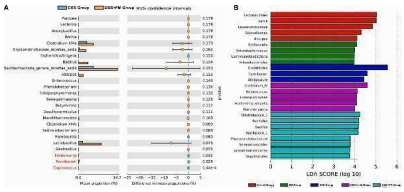
TRM tissue-resident memory T cell. Source data are provided as a Source Data file. Index in PubMed under a CC BY license. PMID: 39614076



The infiltration of MPO + neutrophils, and the cellular distribution and relative expression level detection of the TNF and IL-10 in the small intestinal and colonic mucosa at 7 days after the termination of DSS administration. (A) The MPO immunohistochemistry staining of the small intestinal mucosa: (A1) the normal group: few neutrophils were observed in the small intestinal mucosa; (A2) the DSS group: a number of accumulative MPO + neutrophils (brown) infiltrated into the mucosa epithelium; (A3) the DSS + B. subtilis- fermented milk group: only limited neutrophil infiltration could be observed in the small intestinal mucosa. (B) The MPO immunohistochemistry staining of the colonic mucosa: (B1) the normal group: few neutrophils were observed in the colonic mucosa; (B2) the DSS group: colonic epithelium and the glands disappeared, and the ulcer was locally replaced by scars and a number of accumulative MPO + neutrophils (brown) were observed in the scars; (B3) the DSS + B. subtilis -fermented milk group: only limited MPO + neutrophils observed in the colonic mucosa. (C) The TNF immunohistochemistry staining of the small intestinal mucosa: (C1) the normal group: the epithelium was integrated with faint yellow staining, suggesting low expression of TNF; (C2) the DSS group: the villus structure is not integrated, and the epithelial cells showed black brown, suggesting overexpression of TNF; (C3) the DSS + B. subtilis -fermented milk group: the villus and the glands were almost integrated, and the staining of epithelial cells was similar to that of the normal group (C1) , suggesting low expression of TNF. (D) The TNF immunohistochemistry staining of the colonic mucosa: (D1) the normal colonic mucosa: the epithelium was integrated with low TNF expression (faint yellow); (D2) the DSS group: the epithelium structure and the glands were destroyed and replaced by a scar, and there were a number of TNF + inflammatory cells (black brown) in the scar; (D3) the DSS + B. subtilis -fermented milk group: the recovered epithelium showed faint yellow, suggesting low TNF expression. (E) The IL-10 immunohistochemistry staining of the small intestinal mucosa: (E1) the normal small intestinal mucosa: the IL-10 staining dispersed in the villi and the crypts with faint yellow, suggesting low-level expression of IL-10; (E2) the DSS group, the residual epithelium and the crypts were light brown, suggesting mid-level of IL-10 expression; (E3) the DSS + B. subtilis -fermented milk group: the dark brown staining of the regenerative epithelium represented high-level expression of IL-10. (F) The IL-10 immunohistochemistry staining of the colonic mucosa: (F1) the normal group: the IL-10 staining dispersed in the glands with bright yellow, suggesting low-level expression of IL-10; (F2) the DSS group: there were few IL-10 + cells in the scars; (F3) the DSS + B. subtilis -fermented milk group, the dark brown staining of the epithelial cells represented high-level expression of IL-10. (G,H) Western blotting analysis for the expression of MPO, TNF, and IL-10 in the samples containing equivalent ileum and colon. The expression level of MPO, TNF, and IL-10 in the DSS group was significantly higher

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than that of the normal (control) group. The expression level of MPO and TNF in the DSS + B. subtilis -fermented milk (FM) group was significantly lower than that of the DSS group, while the expression level of IL-10 in the DSS + B. subtilis -fermented milk (FM) group was significantly higher than that of the DSS group (n = 5, * represents p < 0.05, ** represents p < 0.01).Index in PubMed under a CC BY license. PMID: 33519783



Difference in the mean proportions of the major composition of the intestinal flora. (A) Mean proportions of the top 25 genus in the intestinal flora at 7 days after termination of DSS intake and the statistical difference between group 3 (DSS group) and group 5 (DSS + B. subtilis -fermented milk group) (n = 5). (B) Significantly different taxa as measured by LEfSe analysis (threshold > 3.5).Index in PubMed under a CC BY license. PMID: 33519783

7 Publications Citing This Product

1. PubMed ID: -, Wei Gao,Qiushi Huang,Ting Qin et al.HSP60 regulates monosodium urate crystal-induced inflammation by activating the TLR4-NF-kappa B-MyD88 signaling pathway and disrupting mitochondrial function,30 April 2020, PREPRINT(Version 1) available at Research Square

2. PubMed ID: 28386082, Wei CC, Kong YY, Li GQ, Guan YF, Wang P, Miao CY. Sci Rep. 2017 Apr 6;7(1):717. doi: 10.1038/s41598-017-00851-z. Nicotinamide mononucleotide attenuates brain injury after intracerebral hemorrhage by activating Nrf2/HO-1 signaling pathway.

3. PubMed ID: 28386082, Wei CC, Kong YY, Li GQ, Guan YF, Wang P, Miao CY. Sci Rep. 2017 Apr 6;7(1):717. doi: 10.1038/s41598-017-00851-z. Nicotinamide mononucleotide attenuates brain injury after intracerebral hemorrhage by activating Nrf2/HO-1 signaling pathway.

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