Product Datasheet

TAF10 Antibody - BSA Free
NBP1-80706

Unit Size: 0.1 ml

Store at 4C short term. Aliquot and store at -20C long term. Avoid freeze-thaw cycles.

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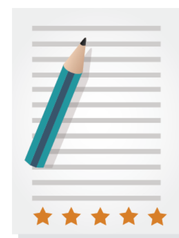


NBP1-80706

TAF10 Antibody - BSA Free

Product Information

Unit Size	0.1 ml
Concentration	Concentrations vary lot to lot. See vial label for concentration. If unlisted please contact technical services.
Storage	Store at 4C short term. Aliquot and store at -20C long term. Avoid freeze-thaw cycles.
Clonality	Polyclonal
Preservative	0.02% Sodium Azide
Isotype	IgG
Purity	Affinity purified
Buffer	PBS (pH 7.2) and 40% Glycerol

Product Description

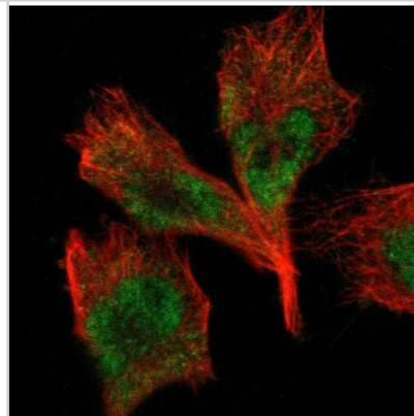
Description	Novus Biologicals Rabbit TAF10 Antibody - BSA Free (NBP1-80706) is a polyclonal antibody validated for use in IHC, WB and ICC/IF. Anti-TAF10 Antibody: Cited in 3 publications. All Novus Biologicals antibodies are covered by our 100% guarantee.
Host	Rabbit
Gene ID	6881
Gene Symbol	TAF10
Species	Human
Immunogen	This antibody was developed against Recombinant Protein corresponding to amino acids: SNGVYVLPSAANGDVKPVVSSTPLVDFLMQLEDYTPTIPDAVTGYYLNRAGFE ASDPRIIRLISLAAQKFISDIANDALQHCKMKGTASGSSRSKSKDRKYTLTMEDL TPALSEYGINVKKP

Product Application Details

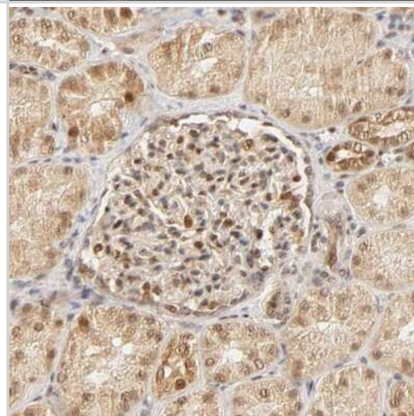
Applications	Immunohistochemistry-Paraffin, Immunocytochemistry/ Immunofluorescence, Immunohistochemistry, Chromatin Immunoprecipitation-exo-Seq
Recommended Dilutions	Immunohistochemistry 1:20 - 1:50, Immunocytochemistry/ Immunofluorescence 0.25-2 ug/ml, Immunohistochemistry-Paraffin 1:20 - 1:50, Chromatin Immunoprecipitation-exo-Seq 1-10ug per reaction
Application Notes	For IHC-Paraffin, HIER pH 6 retrieval is recommended. ICC/IF Fixation Permeabilization: Use PFA/Triton X-100.

Images

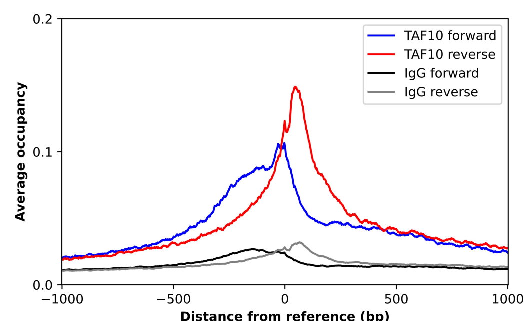
Immunocytochemistry/Immunofluorescence: TAF10 Antibody [NBP1-80706] - Staining of human cell line U-251 MG shows localization to nucleoplasm. Antibody staining is shown in green.



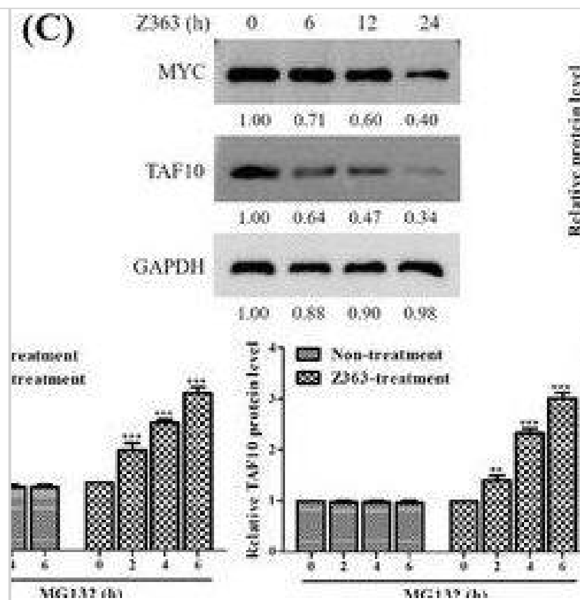
Immunohistochemistry-Paraffin: TAF10 Antibody [NBP1-80706] - Staining of human kidney shows distinct nuclear positivity in glomeruli.



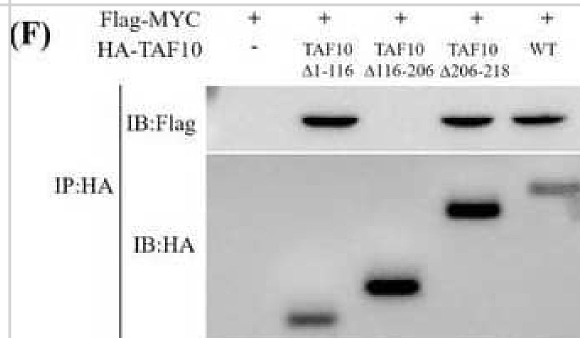
ChIP-Exo-Seq composite graph for Anti-TAF10 (NBP1-80706) tested in K562 cells. Strand-specific reads (blue: forward, red: reverse) and IgG controls (black: forward, grey: reverse) are plotted against the distance from a composite set of reference binding sites. The antibody exhibits robust target enrichment compared to a non-specific IgG control and precisely reveals its structural organization around the binding site. Data generated by Prof. B. F. Pugh´s Lab at Cornell University.



Z363 promotes MYC and TAF10 degradation. (A) Identification of small inhibitory molecules for MYC. (B) MCF7 cells were treated with Z363 (0, 2.5, 7.5 and 15 μg/ml) for 24 h. The protein levels of MYC and TAF10 were analysed by Western blotting. (C) MCF7 cells were treated with Z363 (7.5 μg/ml) for 0, 6, 12 and 24 h. Furthermore, the protein levels of MYC and TAF10 were analysed by Western blotting. (D) MCF7 cells were treated with 25 μM MG132 at the indicated time points, followed by treatment with or without Z363 (7.5 μg/ml) for 24 h, and MYC and TAF10 expressions were analysed by Western blotting. (E) Western blots for MYC, phosphorylated MYC T58 and S62 in MCF7 cells treated with Z363 at the times indicated. (F) Ratios of pT58 or pS62 to total MYC protein levels from the experiment (E). (G) IF staining for Ki67 and pT58 in Z363□treated MCF7 cells, scale bar, 10 μm. (H) MCF7 cells were treated with 25 μM MG132 for 2 h, followed by Z363 treatment (7.5 μg/ml) for 24 h. Expressions of MYC and TAF10 were assessed using Western blot analysis. Data shown in F were analysed by two□way ANOVA. Fluorescence images and blots were representative of three independent experiments. All data are presented as the mean +/- SEM of n = 3. ***p < .001, ns, no significance Image collected and cropped by CiteAb from the following open publication (https://pubmed.ncbi.nlm.nih.gov/36639831), licensed under a CC-BY license. Not internally tested by Novus Biologicals.



TAF10 promotes cancer cell proliferation and migration. (A and B) MCF7 cells were transfected with Flag□labelled MYC and HA□labelled TAF10, and the interaction between MYC and TAF10 was detected by Co□IP. (C) Endogenous interaction of MYC and TAF10 was tested in MCF7 cells. (D) Schematic representation of MYC mutants. (E) Schematic representation of TAF10 mutants. Co□IP was used to detect the interaction between the TAF10 mutants and MYC in MCF7 cells. Co□IP was used to detect the interaction. (G) Interaction between the MYC mutants and TAF10 in MCF7 cells was detected using Co□IP. (H) MCF7 cells were co□transfected with empty vector (Vec) and HA□labelled TAF10 wild□type (HA□TAF10 WT) or mutants (HA□TAF10 Δ1□116, HA□TAF10 Δ116□206, HA□TAF10 Δ206□218). The MYC promoter activity was analysed using the dual luciferase reporter assay 24 h later. (I) Overexpression of TAF10 assessed the capacity for colony formation. MCF7 cells were transfected with either Control□vec or HA□TAF10. The ability of cells to form colonies was measured using crystal violet staining. (J) Overexpression of TAF10 measured the migration capacity of cells. MCF7 cells were transfected with either Control□vec or HA□TAF10. Transwell assays were used to assess the migration capacity of cells. Scale bar, 20 μm. Data shown in H were analysed by one□way ANOVA. Data shown in I and J were analysed by t□test. The blots represented three independent experiments. All data are presented as the mean +/- SEM of n = 3. ***p < .001, **p < .01, ns, no significance Image collected and cropped by CiteAb from the following open publication (https://pubmed.ncbi.nlm.nih.gov/36639831), licensed under a CC-BY license. Not internally tested by Novus Biologicals.



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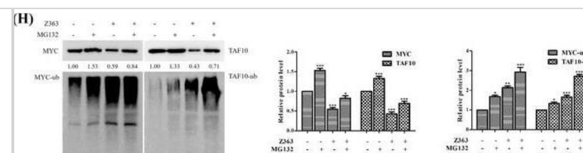
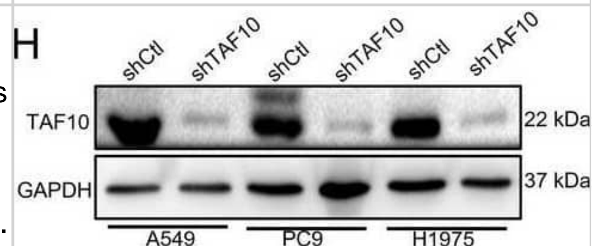


TAF10 plays oncogenic role in LUAD. A mRNA expression levels of the corresponding gene in human normal bronchial epithelial cells (16HBE) and LUAD cell lines. B TAF10 mRNA expression levels in various tumors and matched normal tissues from the TCGA and GTEx databases, analyzed using SangerBox platform. C The stemness features (RNA expression-based stemness scores) analyses of TAF10 across different types of tumors in the TCGA database, analyzed by SangerBox platform. (D-E) Disease-free survival (D) and overall survival (E) analyses of TAF10 in LUAD samples from the TCGA database, performed using the GEPIA2 platform. (F) Protein expression levels of TAF10 in 16HBE and LUAD cell lines. G Representative IHC analysis of TAF10 expression in paired adjacent and tumorous tissues from LUAD patients (n = 5 pairs, 10 tissues in total). Black scale bar: 50 µm; red scale bar: 20 µm. H TAF10 knockdown in LUAD cells was confirmed by Western blot analysis. I LUAD cell lines were stably transfected with either shCtl or shTAF10 for 24, 48, and 72 h, and cell viability was measured using a CCK-8 assay. (J) The effect of TAF10 knockdown on colony formation in LUAD cells was assessed using a colony formation assay. (K) Representative micrographs and quantification of tumor sphere formation by TAF10-silenced cells (shTAF10) or vector control cells (shCtl). Scale bar, 100 µm. L–N GSEA plot of KEGG (L), GOBP (M), and Hallmark pathways (N), grouped by TAF10 expression into TAF10-high and TAF10-low subgroups. NES represents the normalized enrichment score, and FDR represents the adjusted p-value Image collected and cropped by CiteAb from the following open publication (https://pubmed.ncbi.nlm.nih.gov/39987127), licensed under a CC-BY license. Not internally tested by Novus Biologicals.



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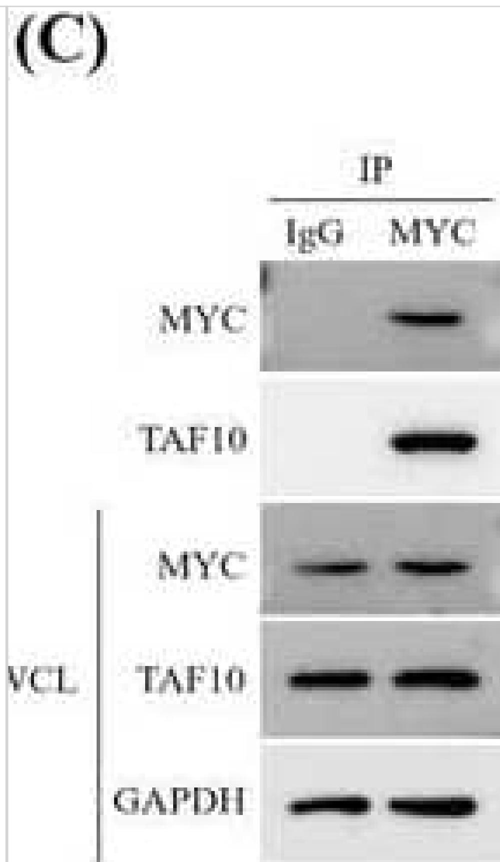

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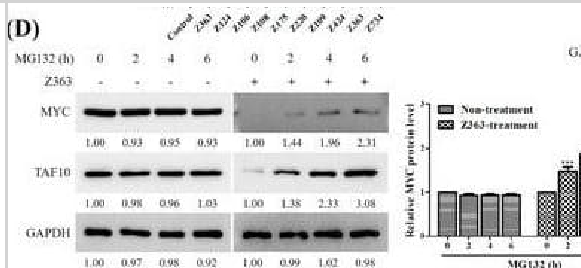
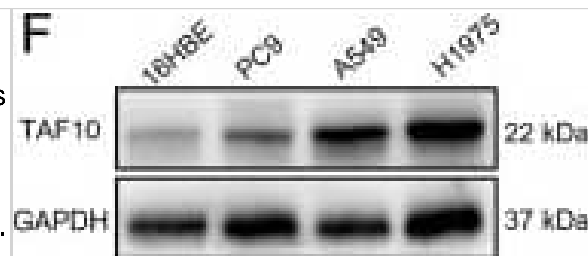
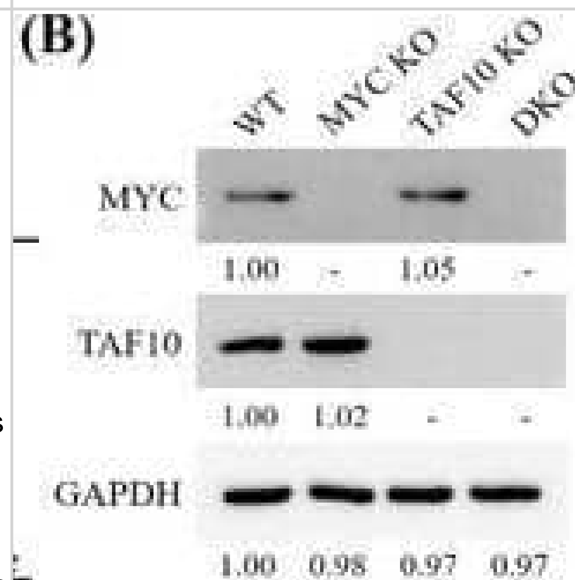


TAF10 plays oncogenic role in LUAD. A mRNA expression levels of the corresponding gene in human normal bronchial epithelial cells (16HBE) and LUAD cell lines. B TAF10 mRNA expression levels in various tumors and matched normal tissues from the TCGA and GTEx databases, analyzed using SangerBox platform. C The stemness features (RNA expression-based stemness scores) analyses of TAF10 across different types of tumors in the TCGA database, analyzed by SangerBox platform. (D-E) Disease-free survival (D) and overall survival (E) analyses of TAF10 in LUAD samples from the TCGA database, performed using the GEPIA2 platform. (F) Protein expression levels of TAF10 in 16HBE and LUAD cell lines. G Representative IHC analysis of TAF10 expression in paired adjacent and tumorous tissues from LUAD patients (n = 5 pairs, 10 tissues in total). Black scale bar: 50 μm; red scale bar: 20 μm. H TAF10 knockdown in LUAD cells was confirmed by Western blot analysis. I LUAD cell lines were stably transfected with either shCtl or shTAF10 for 24, 48, and 72 h, and cell viability was measured using a CCK-8 assay. (J) The effect of TAF10 knockdown on colony formation in LUAD cells was assessed using a colony formation assay. (K) Representative micrographs and quantification of tumor sphere formation by TAF10-silenced cells (shTAF10) or vector control cells (shCtl). Scale bar, 100 μm. L–N GSEA plot of KEGG (L), GOBP (M), and Hallmark pathways (N), grouped by TAF10 expression into TAF10-high and TAF10-low subgroups. NES represents the normalized enrichment score, and FDR represents the adjusted p-value Image collected and cropped by CiteAb from the following open publication (https://pubmed.ncbi.nlm.nih.gov/39987127), licensed under a CC-BY license. Not internally tested by Novus Biologicals.	
Coinhibition of MYC and TAF10 causes synergistic reduction of cell proliferation and tumour growth. (A) Cells (WT, TAF10 KO) were treated with different doses of Z363 for 24 h. Cell proliferation was determined by the CCK8 assay. (B) Knockout reliability was detected by Western blotting. (C) The proliferation of wildtype cells (WT), single and double KO cells (MYC KO, TAF10 KO, DKO) and Z363treated cells were detected by Ki67 ELISA kit. (D) The apoptosis of wildtype cells (WT), single and double KO cells (MYC KO, TAF10 KO, DKO) and Z363treated cells were detected by flow cytometry. (E) Cell apoptosisrelated proteins levels were detected by Western blotting. (F) The migration of wildtype cells (WT), single and double KO cells (MYC KO, TAF10 KO, DKO), and Z363treated cells were detected by a Transwell migration assay. Scale bar, 20 μm. (G) Representative images showing xenograft tumours at day 28 postsubcutaneous injection (n = 5). (H and I) Tumours were measured and depicted as tumour volume (H) or tumour weight (I). Data shown in A were analysed by twoway ANOVA. Data shown in C, D, F, H and I were analysed by oneway ANOVA. Flow cytometry, transwell and blots were representative of three independent experiments. All data are presented as the mean +/- SEM of n = 3. ***p < .001, **p < .01, *p < .05 Image collected and cropped by CiteAb from the following open publication (https://pubmed.ncbi.nlm.nih.gov/36639831), licensed under a CC-BY license. Not internally tested by Novus Biologicals.	

Publications

Xiong Y, Wang L, Xu S et al. Small molecule Z363 co-regulates TAF10 and MYC via the E3 ligase TRIP12 to suppress tumour growth Clinical and Translational Medicine 2023-01-13 [PMID: 36639831] (Western Blot, Mouse)

Choi SW, Oh H, Park SY et al. Netrin-1 attenuates hepatic steatosis via UNC5b/PPARγ-mediated suppression of inflammation and ER stress Life sciences 2022-12-15 [PMID: 36400204] (WB, Mouse)

Details:
Dilution used in WB 1:1000

Seth A, Bournat JC, Medina-Martinez O et al. Loss of WNT4 in the gubernaculum causes unilateral cryptorchidism and fertility defects Development (Cambridge, England) 2022-12-01 [PMID: 36448532] (IHC-P)

Details:
Dilution used 1:500

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NBP1-80706PEP	TAF10 Recombinant Protein Antigen
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NB7160	Goat anti-Rabbit IgG (H+L) Secondary Antibody [HRP]
NBP2-24891	Rabbit IgG Isotype Control

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