

RUNX3 Polyclonal Antibody
Catalog # AP72377**Specification****RUNX3 Polyclonal Antibody - Product Information**

Application	WB
Primary Accession	Q13761
Reactivity	Human, Mouse
Host	Rabbit
Clonality	Polyclonal

RUNX3 Polyclonal Antibody - Additional Information**Gene ID** 864**Other Names**

RUNX3; AML2; CBFA3; PEBP2A3; Runt-related transcription factor 3; Acute myeloid leukemia 2 protein; Core-binding factor subunit alpha-3; CBF-alpha-3; Oncogene AML-2; Polyomavirus enhancer-binding protein 2 alpha C subunit; PEA2-alpha C; PEB

Dilution

WB~~Western Blot: 1/500 - 1/2000. ELISA: 1/40000. Not yet tested in other applications.

Format

Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.09% (W/V) sodium azide.

Storage Conditions

-20°C

RUNX3 Polyclonal Antibody - Protein Information**Name** RUNX3**Synonyms** AML2, CBFA3, PEBP2A3**Function**

Forms the heterodimeric complex core-binding factor (CBF) with CBFB. RUNX members modulate the transcription of their target genes through recognizing the core consensus binding sequence 5'- TGTGGT-3', or very rarely, 5'-TGCGGT-3', within their regulatory regions via their runt domain, while CBFB is a non-DNA-binding regulatory subunit that allosterically enhances the sequence-specific DNA-binding capacity of RUNX. The heterodimers bind to the core site of a number of enhancers and promoters, including murine leukemia virus, polyomavirus enhancer, T-cell receptor enhancers, LCK, IL3 and GM-CSF promoters (By similarity). May be involved in the control of cellular proliferation and/or differentiation. In association with ZFH3, up- regulates CDKN1A promoter activity following TGF-beta stimulation (PubMed:20599712). CBF complexes repress ZBTB7B transcription factor during cytotoxic (CD8+) T cell development. They bind to RUNX-binding sequence within the ZBTB7B locus acting as transcriptional silencer and

allowing for cytotoxic T cell differentiation. CBF complexes binding to the transcriptional silencer is essential for recruitment of nuclear protein complexes that catalyze epigenetic modifications to establish epigenetic ZBTB7B silencing (By similarity).

Cellular Location

Nucleus {ECO:0000255|PROSITE-ProRule:PRU00399, ECO:0000269|PubMed:20100835, ECO:0000269|PubMed:20599712}. Cytoplasm. Note=The tyrosine phosphorylated form localizes to the cytoplasm. Translocates from the cytoplasm to the nucleus following TGF-beta stimulation

Tissue Location

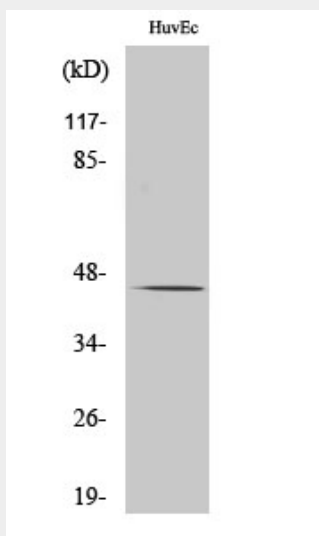
Expressed in gastric cancer tissues (at protein level).

RUNX3 Polyclonal Antibody - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

RUNX3 Polyclonal Antibody - Images



RUNX3 Polyclonal Antibody - Background

Forms the heterodimeric complex core-binding factor (CBF) with CBFβ. RUNX members modulate the transcription of their target genes through recognizing the core consensus binding sequence 5'-TGTGGT-3', or very rarely, 5'-TGCGGT-3', within their regulatory regions via their runt domain, while CBFβ is a non-DNA-binding regulatory subunit that allosterically enhances the sequence-specific DNA-binding capacity of RUNX. The heterodimers bind to the core site of a number of enhancers and promoters, including murine leukemia virus, polyomavirus enhancer,

T-cell receptor enhancers, LCK, IL3 and GM-CSF promoters (By similarity). May be involved in the control of cellular proliferation and/or differentiation. In association with ZFH3, upregulates CDKN1A promoter activity following TGF-beta stimulation (PubMed:20599712). CBF complexes repress ZBTB7B transcription factor during cytotoxic (CD8+) T cell development. They bind to RUNX-binding sequence within the ZBTB7B locus acting as transcriptional silencer and allowing for cytotoxic T cell differentiation. CBF complexes binding to the transcriptional silencer is essential for recruitment of nuclear protein complexes that catalyze epigenetic modifications to establish epigenetic ZBTB7B silencing (By similarity).