Datasheet for ABIN6147309

anti-RUNX1 antibody (AA 221-480)

9 Images

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Overview

Quantity:	100 µL
Target:	RUNX1
Binding Specificity:	AA 221-480
Reactivity:	Human
Host:	Rabbit
Clonality:	Polyclonal
Conjugate:	This RUNX1 antibody is un-conjugated
Application:	Western Blotting (WB)

Product Details

Immunogen:	Recombinant fusion protein containing a sequence corresponding to amino acids 221-480 of human RUNX1 (NP_001745.2).
Sequence:	FSERLSELEQ LRRTAMRVSP HHPAPTPNPR ASLNHSTAFN PQPQSQMQDT RQIQPSPPWS YDQSYQYLGS IASPSVHPAT PISPGRASGM TTLSAELSSR LSTAPDLTAF SDPRQFPALP SISDPRMHYP GAFTYSPTPV TSGIGIGMSA MGSATRYHTY LPPPYPGSSQ AQGGPFQASS PSYHLYYGAS AGSYQFSMVG GERSPPRILP PCTNASTGSA LLNPSLPNQS DVVEAEGSHS NSPTNMAPSA RLEEAVWRPY
Isotype:	IgG
Cross-Reactivity:	Human, Mouse, Rat
Characteristics:	Polyclonal Antibodies

Target Details

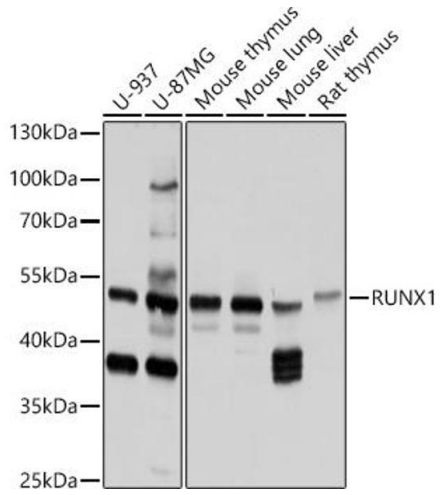
Target:	RUNX1
Alternative Name:	RUNX1 (RUNX1 Products)
Background:	Core binding factor (CBF) is a heterodimeric transcription factor that binds to the core element of many enhancers and promoters. The protein encoded by this gene represents the alpha subunit of CBF and is thought to be involved in the development of normal hematopoiesis. Chromosomal translocations involving this gene are well-documented and have been associated with several types of leukemia. Three transcript variants encoding different isoforms have been found for this gene.,RUNX1,AML1,AML1-EVI-1,AMLCR1,CBF2alpha,CBFA2,EVI-1,PEBP2aB,PEBP2alpha,Epigenetics & Nuclear Signaling,Transcription Factors,Cancer,Cell Biology & Developmental Biology,Hippo Signaling Pathway,Neuroscience,Stem Cells,Hematopoietic Progenitors,Cardiovascular,Angiogenesis,RUNX1
Molecular Weight:	20-28 kDa/37 kDa/48-51 kDa
Gene ID:	861
UniProt:	Q01196

Application Details

Application Notes:	WB,1:500 - 1:2000
Restrictions:	For Research Use only

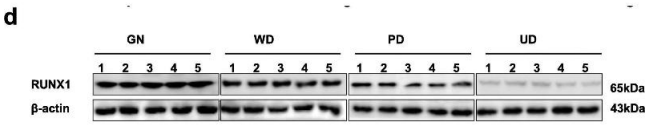
Handling

Format:	Liquid
Buffer:	PBS with 0.02 % sodium azide,50 % glycerol, pH 7.3.
Preservative:	Sodium azide
Precaution of Use:	This product contains Sodium azide: a POISONOUS AND HAZARDOUS SUBSTANCE which should be handled by trained staff only.
Storage:	-20 °C
Storage Comment:	Store at -20°C. Avoid freeze / thaw cycles.



Western Blotting

Image 1. Western blot analysis of extracts of various cell lines, using RUNX1 antibody (ABIN6129946, ABIN6147309, ABIN6147311 and ABIN6213835) at 1:1000 dilution.Secondary antibody: HRP Goat Anti-Rabbit IgG (H+L) (ABIN1684268 and ABIN3020597) at 1:10000 dilution.Lysates/proteins: 25 µg per lane.Blocking buffer: 3 % nonfat dry milk in TBST.Detection: ECL Basic Kit (RM00020).Exposure time: 15s.



Western Blotting

Image 2. Identification of RUNX1 as an apoptosis transcription factor and an independent prognostic factor in NB tissue and cell lines. a Cluster analysis of apoptosis genes in the KEGG and ChIP-X databases. We selected the top ten transcription factors (TFs), as shown. b Kaplan-Meier curves indicating the survival of 498 (GES49710, cutoff value=292.04) NB patients with high or low HNF4A and RUNX1 expression, respectively (Log-rank test, p=0.053, p=0019, respectively). c Mining of public microarray datasets (GSE49710) revealing the RUNX1 expression levels in tumors with various MYCN amplification levels, progression and INSS stages. (unpaired t-test, p<0.0001, p<0.0001, P=0.0014.) d and e Western blot and immunohistochemical staining images indicated protein levels of RUNX1 in g ganglioneuroma (GN, control), well differentiated (WD) NB, poor differentiated (PD) NB, and undifferentiated NB tissues (n=5 per group). Scale bar: 100µm. ***P<0.001 versus GN. f Western blot assay indicating the levels of RUNX1 in NB cell lines (SH-SY5Y, SK-N-SH, SK-N-AS, IMR-32, TN-2). Data are shown as mean±SEM and representative of three independent experiments in panels (d)-(f). Exact P values are specified in Additional file 2: Table S3 - figure provided by CiteAb. Source: PMID32197643

Western Blotting

Image 3. Identification of RUNX1 as an apoptosis transcription factor and an independent prognostic factor in NB tissue and cell lines. a Cluster analysis of apoptosis genes in the KEGG and ChIP-X databases. We selected the top ten transcription factors (TFs), as shown. b Kaplan-Meier curves indicating the survival of 498 (GES49710, cutoff value=292.04) NB patients with high or low HNF4A and RUNX1 expression, respectively (Log-rank test, p=0.053, p=0019, respectively). c Mining of public microarray datasets (GSE49710) revealing the RUNX1 expression levels in tumors with various MYCN amplification levels, progression and INSS stages. (unpaired t-test, p<0.0001, p<0.0001, P=0.0014.) d and e Western blot and immunohistochemical staining images indicated protein levels of RUNX1 in g ganglioneuroma (GN, control), well differentiated (WD) NB, poor differentiated (PD) NB, and undifferentiated NB tissues (n=5 per group). Scale bar: 100μm. ***P<0.001 versus GN. f Western blot assay indicating the levels of RUNX1 in NB cell lines (SH-SY5Y, SK-N-SH, SK-N-AS, IMR-32, TN-2). Data are shown as mean±SEM and representative of three independent experiments in panels (d)-(f). Exact P values are specified in Additional file 2: Table S3 - figure provided by CiteAb. Source: PMID32197643

Please check the product details page for more images. Overall 9 images are available for ABIN6147309.