

<b>Product name:</b>	Max (phospho Ser2) Rabbit Polyclonal Antibody
<b>Cat number:</b>	ABN04979
<b>Conjugate:</b>	Unconjugated
<b>Size:</b>	100µL
<b>Clone:</b>	Polyclonal
<b>Concentration:</b>	1mg/ml
<b>Host:</b>	Rabbit
<b>Isotype:</b>	IgG
<b>Immunogen:</b>	The antiserum was produced against synthesized peptide derived from human MAX around the phosphorylation site of Ser2. AA range:1-50
<b>Reactivity:</b>	Human,Mouse,Rat
<b>Applications:</b>	IHC 1:100-1:300,ICC/IF 1:50-1:200,ELISA 1:5000-1:10000
<b>Purification:</b>	Affinity purification
<b>Form:</b>	Liquid
<b>Buffer:</b>	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% New type preservative N.
<b>Storage:</b>	Store at 4°C short term. Aliquot and store at -20°C for 12 months. Avoid freeze/thaw cycles.

**Background:**

The protein encoded by this gene is a member of the basic helix-loop-helix leucine zipper (bHLHZ) family of transcription factors. It is able to form homodimers and heterodimers with other family members, which include Mad, Mxi1 and Myc. Myc is an oncoprotein implicated in cell proliferation, differentiation and apoptosis. The homodimers and heterodimers compete for a common DNA target site (the E box) and rearrangement among these dimer forms provides a complex system of transcriptional regulation. Mutations of this gene have been reported to be associated with hereditary pheochromocytoma. A pseudogene of this gene is located on the long arm of chromosome 7. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2012], alternative products: Additional isoforms seem to exist, caution: The sequence shown here is derived from an Ensembl automatic analysis pipeline and should be considered as preliminary data., function: Transcription regulator. Forms a sequence-specific DNA-binding protein complex with MYC or MAD which recognizes the core sequence 5'-CAC[GA]TG-3'. The MYC-MAX complex is a transcriptional activator, whereas the MAD-MAX complex is a repressor. May repress transcription via the recruitment of a chromatin remodeling complex containing H3-K9 histone methyltransferase activity., PTM: Reversible lysine acetylation might regulate the nuclear-cytoplasmic shuttling of specific Max complexes., similarity: Contains 1 basic helix-loop-helix (bHLH) domain., subunit: Efficient DNA binding requires dimerization with another bHLH protein. Binds DNA as a heterodimer with MYC or MAD. Part of the E2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, L3MBTL2 and YAF2. Interacts with SPAG9., tissue specificity: High levels found in the brain, heart and lung while lower levels are seen in the liver, kidney and skeletal muscle.,