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# Phospho-MYC-T58

**Reactivity:**Human

**Tested applications:**WB IF

**Recommended Dilution:**WB 1:500 - 1:2000 IF 1:50 - 1:100

**Observed MW:**Refer to Figures

**Immunogen:**

A phospho specific peptide corresponding to residues surrounding T58 of human MYC

**Storage Buffer:**

Store at -20. Avoid freeze / thaw cycles. Buffer: PBS with 0.02% sodium azide, 50% glycerol, pH7.3.

**Concentration:**

bkmoq

**Synonym:**

MRTL; c-Myc; bHLHe39;

**Catalog #:**AP0080

**Antibody Type:**

Polyclonal Antibody

**Species:**Rabbit

**Gene ID:**4609

**Isotype:**IgG

**Swiss Prot:**P01106

**Purity:**Affinity purification

For research use only.

**Background:**

Members of the Myc/Max/Mad network function as transcriptional regulators with roles in various aspects of cell behavior including proliferation, differentiation and apoptosis (1). These proteins share a common basic-helix-loop-helix leucine zipper (bHLH-ZIP) motif required for dimerization and DNA-binding. Max was originally discovered based on its ability to associate with c-Myc and found to be required for the ability of Myc to bind DNA and activate transcription (2). Subsequently, Max has been viewed as a central component of the transcriptional network, forming homodimers as well as heterodimers with other members of the Myc and Mad families (1). The association between Max and either Myc or Mad can have opposing effects on transcriptional regulation and cell behavior (1). The Mad family consists of four related proteins; Mad1, Mad2 (Mxi1), Mad3 and Mad4, and the more distantly related members of the bHLH-ZIP family, Mnt and Mga. Like Myc, the Mad proteins are tightly regulated with short half-lives. In general, Mad family members interfere with Myc-mediated processes such as proliferation, transformation and prevention of apoptosis by inhibiting transcription (3,4).

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