

ERG (AB2444) mouse mAb

W0160

Key Features

Host Species

- Mouse

Reactivity

- Human;

Applications

- WB; IF; ELISA

MW

- 55 kDa (calculated)
- 68 kDa (observed)

Isotype

- IgG3, kappa

Recommended Dilution Ratios

Application

WB; IF; ELISA

Dilution

WB, 1:500-1:2000 | IF, 1:100-1:500 | ELISA, Recommended starting concentration is 1 µg/mL.

Please optimize the concentration based on your specific assay requirements.

Storage

Storage Conditions

Store at -20°C. Avoid freeze / thaw cycles.

Storage buffer

The antibody is provided in liquid form in phosphate - buffered saline with 50% glycerol, 0.05% BSA, and 0.05% Proclin 300.

Basic Information

Clonality Monoclonal

Clone Number AB2444

Immunogen A synthetic peptide corresponding to the amino acid region 200 - 300 of the human ERG protein.

Specificity This antibody detects endogenous levels of ERG protein.

Purification Affinity purification Protein A

Concentration Product concentration may vary by batch. Please refer to the product COA for details.

Target Information

Gene name ERG

Protein Name ERG

Database Link	Organism	Swiss Prot.	Gene ID
	Human	P11308	2078

Background

This gene encodes a member of the erythroblast transformation-specific (ETS) family of transcription factors. All members of this family are key regulators of embryonic development, cell proliferation, differentiation, angiogenesis, inflammation, and apoptosis. The protein encoded by this gene is mainly expressed in the nucleus. It contains an ETS DNA-binding domain and a PNT (pointed) domain which is implicated in the self-association of chimeric oncoproteins. This protein is required for platelet adhesion to the subendothelium, inducing vascular cell remodeling. It also regulates hematopoiesis, and the differentiation and maturation of megakaryocytic cells. This gene is involved in chromosomal translocations, resulting in different fusion gene products, such as TMPSSR2-ERG and NDRG1-ERG in prostate cancer, EWS-ERG in Ewing's sarcoma and FUS-ERG in acute myeloid leukemia. More than two

W0160-V.2-EN

dozens of transcript variants generated from combinatorial usage of three alternative promoters and multiple alternative splicing events have been reported, but the full-length nature of many of these variants has not been determined. [provided by RefSeq, Apr 2014]