

CREB3 Polyclonal Antibody

catalog number: E-AB-61218

Note: Centrifuge before opening to ensure complete recovery of vial contents.

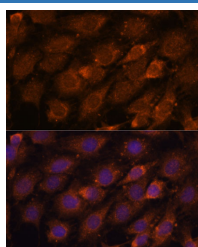
Description

| | |
|---------------------|--|
| Reactivity | Human;Mouse;Rat |
| Immunogen | Recombinant fusion protein of human CREB3 (NP_006359.3). |
| Host | Rabbit |
| Isotype | IgG |
| Purification | Affinity purification |
| Buffer | Phosphate buffered solution, pH 7.4, containing 0.05% stabilizer and 50% glycerol. |

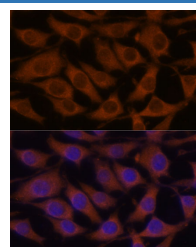
Applications

| Applications | Recommended Dilution |
|--------------|----------------------|
| IF | 1:10-1:100 |

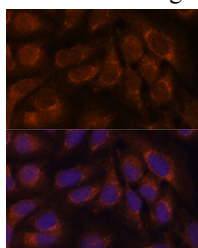
Data



Immunofluorescence analysis of C6 cells using CREB3 Polyclonal Antibody at dilution of 1:100. Blue: DAPI for nuclear staining.



Immunofluorescence analysis of L929 cells using CREB3 Polyclonal Antibody at dilution of 1:100. Blue: DAPI for nuclear staining.



Immunofluorescence analysis of U-2 OS cells using CREB3 Polyclonal Antibody at dilution of 1:100. Blue: DAPI for nuclear staining.

Preparation & Storage

| | |
|-----------------|--|
| Storage | Store at -20°C Valid for 12 months. Avoid freeze / thaw cycles. |
| Shipping | The product is shipped with ice pack, upon receipt, store it immediately at the temperature recommended. |

Background

For Research Use Only

This gene encodes a transcription factor that is a member of the leucine zipper family of DNA binding proteins. This protein binds to the cAMP-response element and regulates cell proliferation. The protein interacts with host cell factor C1, which also associates with the herpes simplex virus (HSV) protein VP16 that induces transcription of HSV immediate-early genes. This protein and VP16 both bind to the same site on host cell factor C1. It is thought that the interaction between this protein and host cell factor C1 plays a role in the establishment of latency during HSV infection. This protein also plays a role in leukocyte migration, tumor suppression, and endoplasmic reticulum stress-associated protein degradation. Additional transcript variants have been identified, but their biological validity has not been determined.

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