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E2F6 Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP51174

Product Information

Application	WB, IP, IHC-P
Primary Accession	O75461
Reactivity	Human, Mouse, Rat
Host	Rabbit
Clonality	Polyclonal
Calculated MW	31844

Additional Information

Gene ID	1876
Other Names	Transcription factor E2F6, E2F-6, E2F6
Dilution	WB~~1:1000 IP~~N/A IHC-P~~N/A
Format	0.01M PBS, pH 7.2, 0.09% (W/V) Sodium azide, Glycerol 50%
Storage	Store at -20 °C.Stable for 12 months from date of receipt

Protein Information

Name	E2F6 {ECO:0000303|PubMed:9689056, ECO:0000312|HGNC:HGNC:3120}
Function	Inhibitor of E2F-dependent transcription (PubMed: 9501179, PubMed:9689056, PubMed:9704927). Binds DNA cooperatively with DP proteins through the E2 recognition site, 5'-TTTC[CG]CGC-3' (PubMed:9501179). Has a preference for the 5'-TTTCCCGC-3' E2F recognition site (PubMed:9501179). E2F6 lacks the transcriptional activation and pocket protein binding domains (PubMed:9501179, PubMed:9704927). Appears to regulate a subset of E2F-dependent genes whose products are required for entry into the cell cycle but not for normal cell cycle progression (PubMed:9501179, PubMed:9689056). Represses expression of some meiosis-specific genes, including SLC25A31/ANT4 (By similarity). May silence expression via the recruitment of a chromatin remodeling complex containing histone H3-K9 methyltransferase activity. Overexpression delays the exit of cells from the S-phase (PubMed:9501179).
Cellular Location	Nucleus
Tissue Location	Expressed in all tissues examined. Highest levels in placenta, skeletal muscle, heart, ovary, kidney, small intestine and spleen.

Background

Inhibitor of E2F-dependent transcription. Binds DNA cooperatively with DP proteins through the E2 recognition site, 5'-TTTC[CG]CGC-3'. Has a preference for the 5'-TTTCCCGC-3' E2F recognition site. E2F6 lacks the transcriptional activation and pocket protein binding domains. Appears to regulate a subset of E2F-dependent genes whose products are required for entry into the cell cycle but not for normal cell cycle progression. May silence expression via the recruitment of a chromatin remodeling complex containing histone H3-K9 methyltransferase activity. Overexpression delays the exit of cells from the S-phase.

References

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