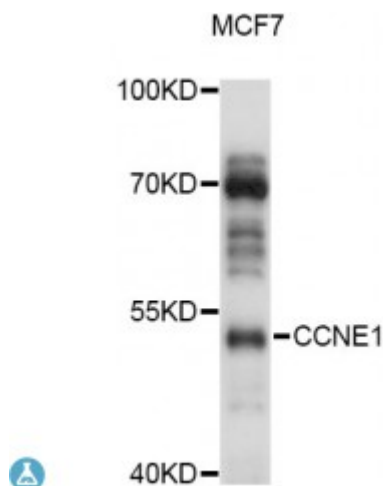


Anti-CCNE1 Antibody



Description

The protein encoded by this gene belongs to the highly conserved cyclin family, whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle. Cyclins function as regulators of CDK kinases. Different cyclins exhibit distinct expression and degradation patterns which contribute to the temporal coordination of each mitotic event. This cyclin forms a complex with and functions as a regulatory subunit of CDK2, whose activity is required for cell cycle G1/S transition. This protein accumulates at the G1-S phase boundary and is degraded as cells progress through S phase. Overexpression of this gene has been observed in many tumors, which results in chromosome instability, and thus may contribute to tumorigenesis. This protein was found to associate with, and be involved in, the phosphorylation of NPAT protein (nuclear protein mapped to the ATM locus), which participates in cell-cycle regulated histone gene expression and plays a critical role in promoting cell-cycle progression in the absence of pRB.

Model	STJ116441
Host	Rabbit
Reactivity	Human, Mouse
Applications	WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 300-410 of human CCNE1 (NP_001229.1).
Gene ID	898
Gene Symbol	CCNE1
Dilution range	WB 1:500 - 1:2000

Tissue Specificity	Highly expressed in testis and placenta, Low levels in bronchial epithelial cells
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	G1/S-specific cyclin-E1
Molecular Weight	47.077 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	PBS with 0.02% sodium azide, 50% glycerol, pH7.3.
Storage Instruction	Store at -20C. Avoid freeze / thaw cycles.
Database Links	HGNC:15890MIM:123837Reactome:R-HSA-1538133
Alternative Names	G1/S-specific cyclin-E1
Function	Essential for the control of the cell cycle at the G1/S (start) transition,
Cellular Localization	Nucleus
Post-translational Modifications	Phosphorylation of both Thr-395 by GSK3 and Ser-399 by CDK2 creates a high affinity degron recognized by FBXW7, and accelerates degradation via the ubiquitin proteasome pathway, Phosphorylation at Thr-77 creates a low affinity degron also recognized by FBXW7,

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