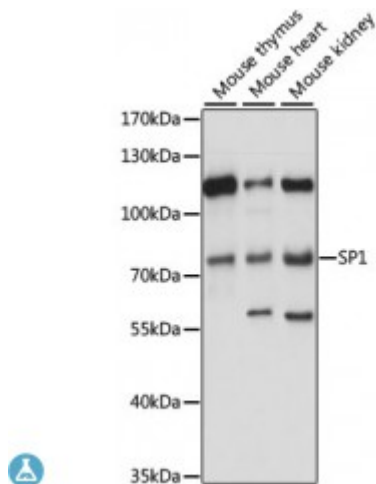


Anti-SP1 Antibody



Description

The protein encoded by this gene is a zinc finger transcription factor that binds to GC-rich motifs of many promoters. The encoded protein is involved in many cellular processes, including cell differentiation, cell growth, apoptosis, immune responses, response to DNA damage, and chromatin remodeling. Post-translational modifications such as phosphorylation, acetylation, glycosylation, and proteolytic processing significantly affect the activity of this protein, which can be an activator or a repressor. Three transcript variants encoding different isoforms have been found for this gene.

Model	STJ116866
Host	Rabbit
Reactivity	Human, Mouse
Applications	WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 420-620aa of human SP1 (NP_612482.2).
Gene ID	6667
Gene Symbol	SP1
Dilution range	WB 1:500 - 1:2000
Tissue Specificity	Up-regulated in adenocarcinomas of the stomach (at protein level), Isoform 3 is ubiquitously expressed at low levels
Purification	Affinity purification
Note	For Research Use Only (RUO).

Protein Name	Transcription factor Sp1
Molecular Weight	80.693 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:11205OMIM:189906Reactome:R-HSA-1989781
Alternative Names	Transcription factor Sp1
Function	Transcription factor that can activate or repress transcription in response to physiological and pathological stimuli, Binds with high affinity to GC-rich motifs and regulates the expression of a large number of genes involved in a variety of processes such as cell growth, apoptosis, differentiation and immune responses, Highly regulated by post-translational modifications (phosphorylations, sumoylation, proteolytic cleavage, glycosylation and acetylation), Binds also the PDGFR-alpha G-box promoter, May have a role in modulating the cellular response to DNA damage, Implicated in chromatin remodeling, Plays a role in the recruitment of SMARCA4/BRG1 on the c-FOS promoter, Plays an essential role in the regulation of FE65 gene expression, In complex with ATF7IP, maintains telomerase activity in cancer cells by inducing TERT and TERC gene expression, Isoform 3 is a stronger activator of transcription than isoform 1, Positively regulates the transcription of the core clock component ARNTL/BMAL1,
Cellular Localization	Nucleus, Cytoplasm,
Post-translational Modifications	Phosphorylated on multiple serine and threonine residues, Phosphorylation is coupled to ubiquitination, sumoylation and proteolytic processing, Phosphorylation on Ser-59 enhances proteolytic cleavage, Phosphorylation on Ser-7 enhances ubiquitination and protein degradation, Hyperphosphorylation on Ser-101 in response to DNA damage has no effect on transcriptional activity, MAPK1/MAPK3-mediated phosphorylation on Thr-453 and Thr-739 enhances VEGF transcription but, represses FGF2-triggered PDGFR-alpha transcription, Also implicated in the repression of RECK by ERBB2, Hyperphosphorylated on Thr-278 and Thr-739 during mitosis by MAPK8 shielding SP1 from degradation by the ubiquitin-dependent pathway, Phosphorylated in the zinc-finger domain by calmodulin-activated PKCzeta, Phosphorylation on Ser-641 by PKCzeta is critical for TSA-activated LHR gene expression through release of its repressor, p107, Phosphorylation on Thr-668, Ser-670 and Thr-681 is stimulated by angiotensin II via the AT1 receptor inducing increased binding to the PDGF-D promoter, This phosphorylation is increased in injured artery wall, Ser-59 and Thr-681 can both be dephosphorylated by PP2A during cell-cycle interphase, Dephosphorylation on Ser-59 leads to increased chromatin association during interphase and increases the transcriptional activity, On insulin stimulation, sequentially glycosylated and phosphorylated on several C-terminal serine and threonine residues,

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