

Rabbit Anti-phospho-SP1 (Thr453) antibody

SL12412R

Product Name:	phospho-SP1 (Thr453)
Chinese Name:	₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩
Alias:	SP1 (phospho T453); p-SP1 (phospho T453); SP1 (phospho-Thr453); SP1 (phospho- T453); p-SP1 (phospho T453); p-TSFP1 (phospho T453); Sp1 transcription factor isoform a; TSFP1; TSFP 1; Specificity protein 1; Transcription factor Sp1; SP 1; SP1; Sp1 transcription factor; SP1 HUMAN.
Organism Species:	Rabbit
Clonality:	Polyclonal
React Species:	Human,Mouse,Rat,
Applications:	WB=1:500-2000ELISA=1:500-1000IHC-P=1:400-800IHC-F=1:400-800ICC=1:100- 500IF=1:100-500 (Paraffin sections need antigen repair) not yet tested in other applications.
Molecular weight•	81kDa
Cellular localization	The nucleuscytonlasmic
Form:	Lyophilized or Liquid
Concentration:	1mg/ml
immunogen:	KLH conjugated synthesised phosphopeptide derived from human TSFP1 around the phosphorylation site of Thr453:IR(p-T)PT
Lsotype:	IgG
Purification:	affinity purified by Protein A
Storage Buffer:	0.01M TBS(pH7.4) with 1% BSA, 0.03% Proclin300 and 50% Glycerol.
Storage:	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.
PubMed:	PubMed
Product Detail:	Sp1 is a sequence-specific transcription factor that recognizes GGGGCGGGGC and closely related sequences, which are often referred to as GC boxes. Sp1 was initially

identified as a HeLa cell-derived factor that selectively activates in vitro transcription from the SV40 promoter and binds to the multiple GC boxes in the 21-bp repeated elements in SV40. The sequence specificity of DNA binding is conferred by Zn (II) fingers, whereas a different region of Sp1 appears to regulate the affinity of DNA binding. Sp1 belongs to a subgroup of transcription factors that are phosphorylated upon binding to promoter sequences. Evidence suggests that the early growth response gene, Erg-1 (also known as Zif268 or NGF1-A) (7), may downregulate certain mammalian gene promoters by competing with Sp1 for binding to an overlapping binding motif. The gene encoding human Sp1 maps to chromosome 12q13.1.

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.

Subunit:

Interacts with ATF7IP, ATF7IP2, BAHD1, POGZ, HCFC1, AATF and PHC2. Interacts with varicella-zoster virus IE62 protein. Interacts with HIV-1 Vpr; the interaction is inhibited by SP1 O-glycosylation. Interacts with SV40 VP2/3 proteins. Interacts with SV40 major capsid protein VP1; this interaction leads to a cooperativity between the 2 proteins in DNA binding. Interacts with HLTF; the interaction may be required for basal transcriptional activity of HLTF. Interacts (deacetylated form) with EP300; the interaction enhances gene expression. Interacts with HDAC1 and JUN. Interacts with ELF1; the interaction is inhibited by glycosylation of SP1. Interacts with SMARCA4/BRG1. Interacts with ATF7IP and TBP. Interacts with MEIS2 isoform 4 and PBX1 isoform PBX1a.

Subcellular Location:

Nucleus. Cytoplasm. Nuclear location is governed by glycosylated/phosphorylated states. Insulin promotes nuclear location, while glucagon favors cytoplasmic location.

Tissue Specificity:

Up-regulated in adenocarcinomas of the stomach (at protein level).

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 MAPK 1/MAPK 3-mediated phosphorylation on
Thr_453 and Thr_739 enhances VEGE transcription but represses EGE2-triggered
DCED alpha transpirition. Also implicated in the representation of DECK by EDDD2
PDGFR-alpha transcription. Also implicated in the repression of RECK by ERBB2.
Hyperphosphorylated on 1 hr-2/8 and 1 hr-/39 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
nhosphorylation is increased in injured artey wall Ser-59 and Thr-681 can both be
dephosphorylated by DD2A during call evals interphase. Dephosphorylation on Ser 50
leads to increased charactin association during interplase. Dephospholylation on Sel-39
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.
Acetylated. Acetylation/deacetylation events affect transcriptional activity.
Deacetylation leads to an increase in the expression the 12(s)-lipooxygenase gene
though recruitment of p300 to the promoter.
Ubiquitinated. Ubiquitination occurs on the C-terminal proteolytically-cleaved peptide
and is triggered by phosphorylation.
Sumovlated by SUMO1 Sumovlation modulates proteolytic cleavage of the N-terminal
repressor domain Sumovlation levels are attenuated during tumorigenesis
Dhoghogylation modiates SD1 dogumoylation
Protoclytic closure of the N terminal represent demain is prevented by sum explotion
Proteorytic cleavage in the N-terminal repressor domain is prevented by sumoyilation.
The C-terminal cleaved product is susceptible to degradation. O-glycosylated; contains
at least 8 N-acetylglucosamine
side chains. Levels are controlled by insulin and the SP1 phosphorylation states.
Insulin-mediated O-glycosylation locates SP1 to the nucleus, where it is sequentially
deglycosylated and phosphorylated. O-glycosylation affects transcriptional activity
through disrupting the interaction with a number of transcription factors including
ELF1 and NFYA. Also inhibits interaction with the HIV1 promoter. Inhibited by
neroxisomome proliferator receptor gamma (PPARgamma)
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Similarity
Dalangs to the Sn1 C2U2 tune zine finger protein family
Gentaine 2 COLO tema aine fina en
Contains 3 C2H2-type zinc fingers.
SWISS:
P08047
Gene ID:
6667
Database links:

Entrez Gene: 6667 Human
Entrez Gene: 20683 Mouse
Entrez Gene: 24790 Rat
<u>Omim: 189906</u> Human
<u>SwissProt: P08047</u> Human
SwissProt: 089090 Mouse
SwissProt: Q01714 Rat
Unigene: 620754 Human
Unigene: 649191 Human
Unigene: 4618 Mouse
Unigene: 44609 Rat
Important Note:
This product as supplied is intended for research use only, not for use in human,
therapeutic or diagnostic applications.
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