

Product datasheet for **TP510883**

Trim28 (NM_011588) Mouse Recombinant Protein

Product data:

Product Type:	Recombinant Proteins
Description:	Purified recombinant protein of Mouse tripartite motif-containing 28 (Trim28), with C-terminal MYC/DDK tag, expressed in HEK293T cells, 20ug
Species:	Mouse
Expression Host:	HEK293T
Expression cDNA Clone or AA Sequence:	>MR210883 representing NM_011588 Red=Cloning site Green=Tags(s)

MAASAAATAAASAATAASAASGSPGSGEGSAGGEKRPAASSAAAAAASSPAGGGGGEAQELLEHCGVCR
ERLRPERDPRLLPCLHSACSACLGPATPAAANNNSGDGGSAGDGAMVDCPVCKQQCYSKDIVENYFMRDSG
SKASSDSQDANQCCTSCEDNAPATSYCVECEPLCETCVEAHQRVKYTKDHTVRSTGPAKTRDGERTVYC
NVHKHEPLVLFCECDTLTCRDCQLNAHKDHQYQFLEDAVRNQRKLLASLVKRLGDKHATLQKNTKEVRS
SIRQVSDVQKRVQVDVKMAILQIMKELNKRGRVLVNDAAQKVTEGQQRERLERQHWTMTKIQKHQEHILRFA
SWALESNNTALLSKKLIYFQLHRALKMIVDPVEPHGEMKFQWDLNAWTKSAEAFGKIVAERP GTNSTG
PGPMAPPRAPGPLSKQSGSSQPMEVQEGYGFSGDDPYSSAEPHVSGMKRSRSGEGEVSGLLRKVPRVSL
ERLDLDTSDSQPPVFKVFPGSTTEDYNLIVIERGAAAAAAGQAGTVPPGAPGAPPLPGMAIVKEEETA
AIGAPPAPEGPETKPVLMPLTEGPGAEGPRLASPSGSTSSGLEVVAPEVTSAPVSGPGILDDSATICRV
CQKPGDLVMCNQCEFCFHLDCPLALQDVPGEWSCSLCHVLPDLKEEDGSLSLDGADSTGVVAKLSPAN
QRKCEVLLALFCHPCRPPLHLQATDSTFSMEQPGGTLDLTLIRARLQEKLSPPYSSPQFAQDVG RMFK
QFNKLTEDKADVQSIIGLQRFETRMNDAFGDTKFSAVLVEPPPLNLPSAGLSSQELSGPGDGP

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Tag:	C-MYC/DDK
Predicted MW:	89.3 kDa
Concentration:	>0.05 µg/µL as determined by microplate BCA method
Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
Buffer:	25 mM Tris-HCl, 100 mM glycine, pH 7.3, 10% glycerol
Note:	For testing in cell culture applications, please filter before use. Note that you may experience some loss of protein during the filtration process.
Storage:	Store at -80°C after receiving vials.



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Stability:	Stable for 12 months from the date of receipt of the product under proper storage and handling conditions. Avoid repeated freeze-thaw cycles.
RefSeq:	NP_035718
Locus ID:	21849
UniProt ID:	Q62318 , Q5EBP9
RefSeq Size:	3255
Cytogenetics:	7 A1
RefSeq ORF:	2502
Synonyms:	AA408787; KAP-1; KRIP-1; MommeD9; Tif1b; Tif1beta
Summary:	<p>Nuclear corepressor for KRAB domain-containing zinc finger proteins (KRAB-ZFPs). Mediates gene silencing by recruiting CHD3, a subunit of the nucleosome remodeling and deacetylation (NuRD) complex, and SETDB1 (which specifically methylates histone H3 at 'Lys-9' (H3K9me)) to the promoter regions of KRAB target genes. Enhances transcriptional repression by coordinating the increase in H3K9me, the decrease in histone H3 'Lys-9 and 'Lys-14' acetylation (H3K9ac and H3K14ac, respectively) and the disposition of HP1 proteins to silence gene expression. Recruitment of SETDB1 induces heterochromatinization. May play a role as a coactivator for CEBPB and NR3C1 in the transcriptional activation of ORM1. Also corepressor for ERBB4. Inhibits E2F1 activity by stimulating E2F1-HDAC1 complex formation and inhibiting E2F1 acetylation. May serve as a partial backup to prevent E2F1-mediated apoptosis in the absence of RB1. Important regulator of CDKN1A/p21(CIP1). Has E3 SUMO-protein ligase activity toward itself via its PHD-type zinc finger. Specifically sumoylates IRF7, thereby inhibiting its transactivation activity. Ubiquitinates p53/TP53 leading to its proteosomal degradation; the function is enhanced by MAGEC2 and MAGEA2, and possibly MAGEA3 and MAGEA6. Mediates the nuclear localization of KOX1, ZNF268 and ZNF300 transcription factors. Probably forms a corepressor complex required for activated KRAS-mediated promoter hypermethylation and transcriptional silencing of tumor suppressor genes (TSGs) or other tumor-related genes in colorectal cancer (CRC) cells. Required to maintain a transcriptionally repressive state of genes in undifferentiated embryonic stem cells (ESCs). In ESCs, in collaboration with SETDB1, is also required for H3K9me3 and silencing of endogenous and introduced retroviruses in a DNA-methylation independent-pathway (PubMed:20164836). Associates at promoter regions of tumor suppressor genes (TSGs) leading to their gene silencing. The SETDB1-TRIM28-ZNF274 complex may play a role in recruiting ATRX to the 3'-exons of zinc-finger coding genes with atypical chromatin signatures to establish or maintain/protect H3K9me3 at these transcriptionally active regions (By similarity). Acts as a corepressor for ZFP568 (PubMed:22110054, PubMed:27658112).[UniProtKB/Swiss-Prot Function]</p>