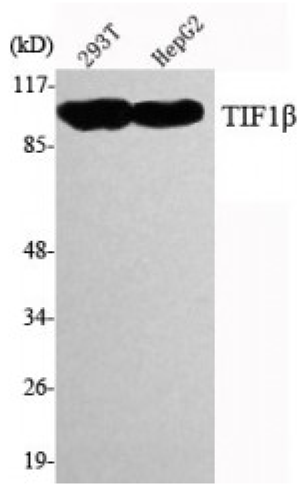
St John's Laboratory

Anti-TIF beta antibody



Description	Mouse monoclonal to TIF1beta.

Model	STJ98563
Host	Mouse
Reactivity	Canine, Human, Mouse, Rabbit, Rat
Applications	WB
Immunogen	Purified recombinant human TIF1beta (C-terminal) protein fragments expressed in E.coli.
Immunogen Region	C-terminal
Gene ID	10155
Gene Symbol	TRIM28
Dilution range	WB 1:1000-1:2000
Specificity	TIF1beta Monoclonal Antibody detects endogenous levels of TIF1beta protein.
Tissue Specificity	Expressed in all tissues tested including spleen, thymus, prostate, testis, ovary, small intestine, colon and peripheral blood leukocytes.
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Transcription intermediary factor 1-beta TIF1-beta E3 SUMO-protein ligase TRIM28 KRAB-associated protein 1 KAP-1 KRAB-interacting protein 1 KRIP-1 Nuclear corepressor KAP-1 RING finger protein 96 RING-

Clonality	Monoclonal
Conjugation	Unconjugated
Formulation	Purified mouse monoclonal in buffer containing 0.1M Tris-Glycine (pH 7.4, 150 mM NaCl) with 0.2% sodium azide, 50% glycerol.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:16384OMIM:601742
Alternative Names	Transcription intermediary factor 1-beta TIF1-beta E3 SUMO-protein ligase TRIM28 KRAB-associated protein 1 KAP-1 KRAB-interacting protein 1 KRIP-1 Nuclear corepressor KAP-1 RING finger protein 96 RING-
Function	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. Also 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. In association with isoform 2 of ZFP90, is required for the transcriptional repressor activity of FOXP3 and the suppressive function of regulatory T-cells (Treg) . 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 . Also required to maintain a transcriptionally repressive state of genes in undifferentiated embryonic stem cells (ESCs) . 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 . Acts as a corepressor for ZFP568 .
Sequence and Domain Family	The HP1 box is both necessary and sufficient for HP1 binding. The PHD-type zinc finger enhances CEBPB transcriptional activity. The PHD-type zinc finger, the HP1 box and the bromo domain, function together to assemble the machinery required for repression of KRAB domain-containing proteins. Acts as an intramolecular SUMO E3 ligase for autosumoylation of bromodomain. The RING-finger-B Box-coiled-coil/tripartite motif (RBCC/TRIM motif) is required for interaction with the KRAB domain of KRAB-zinc finger proteins.

	Binds four zinc ions per molecule. The RING finger and the N-terminal of the leucine zipper alpha helical coiled-coil region of RBCC are required for oligomerization. Contains one Pro-Xaa-Val-Xaa-Leu (PxVxL) motif, which is required for interaction with chromoshadow domains. This motif requires additional residues -7, -6, +4 and +5 of the central Val which contact the chromoshadow domain.
Cellular Localization	Nucleus. Associated with centromeric heterochromatin during cell differentiation through CBX1.
Post-translational Modifications	ATM-induced phosphorylation on Ser-824 represses sumoylation leading to the de-repression of expression of a subset of genes involved in cell cycle control and apoptosis in response to genotoxic stress. Dephosphorylation by the phosphatases, PPP1CA and PP1CB forms, allows sumoylation and expression of TRIM28 target genes. Sumoylation/desumoylation events regulate TRIM28-mediated transcriptional repression. Sumoylation is required for interaction with CHD3 and SETDB1 and the corepressor activity. Represses and is repressed by Ser-824 phosphorylation. Enhances the TRIM28 corepressor activity, inhibiting transcriptional activity of a number of genes including GADD45A and CDKN1A/p21. Lys-554, Lys-779 and Lys-804 are the major sites of sumoylation. In response to Dox-induced DNA damage, enhanced phosphorylation on Ser-824 prevents sumoylation and allows de-repression of CDKN1A/p21. Auto-ubiquitinated; enhanced by MAGEA2 and MAGEC2. Citrullinated by PADI4.