## 32-5128: Recombinant Human Tripartite Motif Containing 28

> Alternative 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 ,Tripartite motif-containing protein 28 ,TRIM2

## Description

Source : E.coli. TRIM28 Human Recombinant produced in E. coli is a single polypeptide chain containing 460 amino acids (366-802) and having a molecular mass of 48.7 kDa .TRIM28 is fused to a 23 amino acid His-tag at N-terminus \& purified by proprietary chromatographic techniques. Tripartite Motif Containing 28 (TRIM28) which is a member of the tripartite motif family includes 3 zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. TRIM28 mediates transcriptional control by interaction with the Kruppel-associated box repression domain found in many transcription factors. TRIM28 is restricted to the nucleus and connected with particular chromatin regions.

## Product Info

| Amount : | $20 \mu \mathrm{~g}$ |
| :---: | :---: |
| Purification : | Greater than $90 \%$ as determined by SDS-PAGE. |
| Content : | The TRIM28 solution ( $1 \mathrm{mg} / 1 \mathrm{ml}$ ) contains 20 mM Tris- HCl buffer ( pH 8.0 ), $10 \%$ glycerol and 0.4 M Urea. |
| Storage condition : | Store at $4^{\circ} \mathrm{C}$ if entire vial will be used within $2-4$ weeks. Store, frozen at $-20^{\circ} \mathrm{C}$ for longer periods of time. For long term storage it is recommended to add a carrier protein ( $0.1 \%$ HSA or BSA).Avoid multiple freeze-thaw cycles. |
| Amino Acid : | MGSSHHHHHH SSGLVPRGSH MGSKLIYFQL HRALKMIVDP VEPHGEMKFQ WDLNAWTKSA |
|  | EAFGKIVAER PGTNSTGPAP MAPPRAPGPL SKQGSGSSQP MEVQEGYGFG SGDDPYSSAE |
|  | PHVSGVKRSR SGEGEVSGLM RKVPRVSLER LDLDLTADSQ PPVFKVFPGS TTEDYNLIVI |
|  | ERGAAAAATG QPGTAPAGTP GAPPLAGMAI VKEEETEAAI GAPPTATEGP ETKPVLMALA |
|  | EGPGAEGPRL ASPSGSTSSG LEVVAPEGTS APGGGPGTLD DSATICRVCQ KPGDLVMCNQ |
|  | CEFCFHLDCH LPALQDVPGE EWSCSLCHVL PDLKEEDGSL SLDGADSTGV VAKLSPANQR |
|  | KCERVLLALF CHEPCRPLHQ LATDSTFSLD QPGGTLDLTL IRARLQEKLS PPYSSPQEFA |
|  | QDVGRMFKQF NKLTEDKADV QSIIGLQRFF ETRMNEAFGD. |



