

## Product datasheet for **RC222759L1V**

### **Pokemon (ZBTB7A) (NM\_015898) Human Tagged ORF Clone Lentiviral Particle**

#### **Product data:**

Product Type:	Lentiviral Particles
Product Name:	Pokemon (ZBTB7A) (NM_015898) Human Tagged ORF Clone Lentiviral Particle
Symbol:	Pokemon
Synonyms:	FBI-1; FBI1; LRF; pokemon; TIP21; ZBTB7; ZNF857A
Mammalian Cell Selection:	None
Vector:	pLenti-C-Myc-DDK (PS100064)
Tag:	Myc-DDK
ACCN:	NM_015898
ORF Size:	1752 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC222759).
OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. <a href="#">More info</a>
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	<a href="#">NM_015898.2</a>
RefSeq Size:	4456 bp
RefSeq ORF:	1755 bp
Locus ID:	51341
UniProt ID:	<a href="#">O95365</a>
Cytogenetics:	19p13.3
Domains:	BTB, zf-C2H2
Protein Families:	Transcription Factors



[View online »](#)

MW: 61.3 kDa

**Gene Summary:** Transcription factor that represses the transcription of a wide range of genes involved in cell proliferation and differentiation (PubMed:14701838, PubMed:17595526, PubMed:20812024, PubMed:25514493, PubMed:26455326, PubMed:26816381). Directly and specifically binds to the consensus sequence 5'-[GA][CA]GACCCCCCCC-3' and represses transcription both by regulating the organization of chromatin and through the direct recruitment of transcription factors to gene regulatory regions (PubMed:12004059, PubMed:17595526, PubMed:20812024, PubMed:25514493, PubMed:26816381). Negatively regulates SMAD4 transcriptional activity in the TGF-beta signaling pathway through these two mechanisms (PubMed:25514493). That is, recruits the chromatin regulator HDAC1 to the SMAD4-DNA complex and in parallel prevents the recruitment of the transcriptional activators CREBBP and EP300 (PubMed:25514493). Collaborates with transcription factors like RELA to modify the accessibility of gene transcription regulatory regions to secondary transcription factors (By similarity). Also directly interacts with transcription factors like SP1 to prevent their binding to DNA (PubMed:12004059). Functions as an androgen receptor/AR transcriptional corepressor by recruiting NCOR1 and NCOR2 to the androgen response elements/ARE on target genes (PubMed:20812024). Thereby, negatively regulates androgen receptor signaling and androgen-induced cell proliferation (PubMed:20812024). Involved in the switch between fetal and adult globin expression during erythroid cells maturation (PubMed:26816381). Through its interaction with the NuRD complex regulates chromatin at the fetal globin genes to repress their transcription (PubMed:26816381). Specifically represses the transcription of the tumor suppressor ARF isoform from the CDKN2A gene (By similarity). Efficiently abrogates E2F1-dependent CDKN2A transactivation (By similarity). Regulates chondrogenesis through the transcriptional repression of specific genes via a mechanism that also requires histone deacetylation (By similarity). Regulates cell proliferation through the transcriptional regulation of genes involved in glycolysis (PubMed:26455326). Involved in adipogenesis through the regulation of genes involved in adipocyte differentiation (PubMed:14701838). Plays a key role in the differentiation of lymphoid progenitors into B and T lineages (By similarity). Promotes differentiation towards the B lineage by inhibiting the T-cell instructive Notch signaling pathway through the specific transcriptional repression of Notch downstream target genes (By similarity). Also regulates osteoclast differentiation (By similarity). May also play a role, independently of its transcriptional activity, in double-strand break repair via classical non-homologous end joining/cNHEJ (By similarity). Recruited to double-strand break sites on damage DNA, interacts with the DNA-dependent protein kinase complex and directly regulates its stability and activity in DNA repair (By similarity). May also modulate the splicing activity of KHDRBS1 toward BCL2L1 in a mechanism which is histone deacetylase-dependent and thereby negatively regulates the pro-apoptotic effect of KHDRBS1 (PubMed:24514149). [UniProtKB/Swiss-Prot Function]