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Product datasheet for RC203007L3V

KAZALD1 (NM_030929) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	KAZALD1 (NM_030929) Human Tagged ORF Clone Lentiviral Particle
Symbol:	KAZALD1
Synonyms:	BONO1; FKSG28; FKSG40; IGFBP-rP10
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_030929
ORF Size:	912 bp
ORF Nucleotide Sequence:	`The ORF insert of this clone is exactly the same as(RC203007).`
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. More info
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:	NM_030929.3
RefSeq Size:	2514 bp
RefSeq ORF:	915 bp
Locus ID:	81621
UniProt ID:	Q96I82
Cytogenetics:	10q24.31
Domains:	kazal, ig, IGc2, IG
Protein Families:	Secreted Protein

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MW: 32.9 kDa

Gene Summary: This gene encodes a secreted member of the insulin growth factor-binding protein (IGFBP) superfamily. The protein contains an insulin growth factor-binding domain in its N-terminal region, a Kazal-type serine protease inhibitor and follistatin-like domain in its central region, and an immunoglobulin-like domain in its C-terminal region. Studies of the mouse ortholog suggest that this protein may function in bone development and bone regeneration. This gene is hypomethylated and over-expressed in high-grade glioma compared to low-grade glioma, and thus the hypomethylated gene may be associated with cell proliferation and the shorter survival of patients with high-grade glioma. It is also one of numerous genes found to be deleted in a novel 5.54 Mb interstitial deletion, which is associated with multiple congenital anomalies. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2016]