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Product datasheet for RC223780L1V

FADS2 (NM_004265) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	FADS2 (NM_004265) Human Tagged ORF Clone Lentiviral Particle
Symbol:	FADS2
Synonyms:	D6D; DES6; FADSD6; LLCDL2; SLL0262; TU13
Mammalian Cell Selection:	None
Vector:	pLenti-C-Myc-DDK (PS100064)
Tag:	Myc-DDK
ACCN:	NM_004265
ORF Size:	1332 bp
ORF Nucleotide Sequence:	`The ORF insert of this clone is exactly the same as(RC223780).`
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_004265.2
RefSeq Size:	3149 bp
RefSeq ORF:	1335 bp
Locus ID:	9415
UniProt ID:	O95864
Cytogenetics:	11q12.2
Domains:	heme_1, FA_desaturase
Protein Families:	Transmembrane

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Protein Pathways:	alpha-Linolenic acid metabolism, Biosynthesis of unsaturated fatty acids, PPAR signaling pathway
MW:	52.1 kDa
Gene Summary:	The protein encoded by this gene is a member of the fatty acid desaturase (FADS) gene family. Desaturase enzymes regulate unsaturation of fatty acids through the introduction of double bonds between defined carbons of the fatty acyl chain. FADS family members are considered fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both of which are characterized by conserved histidine motifs. This gene is clustered with family members at 11q12-q13.1; this cluster is thought to have arisen evolutionarily from gene duplication based on its similar exon/intron organization. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2013]