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Product datasheet for MC208425

Efna5 (NM_010109) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Efna5 (NM_010109) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Efna5
Synonyms:	AL-1; AV158822; EFL-5; Ephrin-A5; Epl7; LERK-7; RAGS
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC208425 representing NM_010109 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGTTGCACGTGGAGATGTTGACGCTGCTCTTTCTGGTGCTCTGGATGTGTGTGTTCAGCCAGGACCCGG GCTCCAAAGTCGTCGCCGACCGCTACGCCGTCTACTGGAACAGCAGCAACCCCAGATTCCAGAGGGGTGA CTACCACATTGATGTCTGTATCAATGACTACCTGGATGTTTTCTGCCCTCACTATGAGGACTCTGTCCCA GAAGACAAGACTGAGCGCTACGTCCTGTACATGGTGAATTTTGATGGGTACAGTGCCTGCGACCACACGT CCAAAGGGTTCAAGAGATGGGAATGTAACCGGCCTCACTCCCCAAACGGACCGCTGAAGTTCTCGGAAAA ATTCCAGCTCTTCACTCCCTTTTCTTTAGGATTTGAATTCAGGCCAGGCCGAGAGTATTTCTACATCTCC TCTGCAATCCCAGACAACGGAAGAAGGTCCTGTCTAAAGCTCAAAGTCTTTGTGAGACCAACAAATGACA CCGTACATGAGTCAGCCGAGCCATCCCGCGGTGAGAACGCGGCGCAGACACCAAGGATACCCAGCCGCCT TTTGGCAATCCTACTGTTCCTCCTGGCGATGCTTTTGACATTATAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_010109
Insert Size:	606 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

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Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_010109.3, NP_034239.1
RefSeq Size:	5178 bp
RefSeq ORF:	606 bp
Locus ID:	13640
UniProt ID:	O08543
Cytogenetics:	17 32.57 cM
Gene Summary:	Cell surface GPI-bound ligand for Eph receptors, a family of receptor tyrosine kinases which are crucial for migration, repulsion and adhesion during neuronal, vascular and epithelial development. Binds promiscuously Eph receptors residing on adjacent cells, leading to contact-dependent bidirectional signaling into neighboring cells. The signaling pathway downstream of the receptor is referred to as forward signaling while the signaling pathway downstream of the ephrin ligand is referred to as reverse signaling. Induces compartmentalized signaling within a caveolae-like membrane microdomain when bound to the extracellular domain of its cognate receptor. This signaling event requires the activity of the Fyn tyrosine kinase. Activates the EPHA3 receptor to regulate cell-cell adhesion and cytoskeletal organization. With the receptor EPHA2 may regulate lens fiber cells shape and interactions and be important for lens transparency maintenance. May function actively to stimulate axon fasciculation. The interaction of EFNA5 with EPHA5 also mediates communication between pancreatic islet cells to regulate glucose-stimulated insulin secretion. Cognate/functional ligand for EPHA7, their interaction regulates brain development modulating cell-cell adhesion and repulsion.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) lacks an alternate in-frame exon compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.