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Product datasheet for SC331529

LIMPII (SCARB2) (NM_001204255) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: LIMPII (SCARB2) (NM_001204255) Human Untagged Clone

Tag: Tag Free

Symbol: LIMPII

Synonyms: AMRF; CD36L2; EPM4; HLGP85; LGP85; LIMP-2; LIMPII; SR-BII

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF:

>SC331529 representing NM_001204255.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGGCCGATGCTGCTTCTACACGGCGGGGACGTTGTCCCTGCTCCTGCTGGTGACCAGCGTCACGCTG
CTGGTGGCCCGGGTCTTCCAGAAGGCTGTAGACCAGAGTATCGAGAAGAAAATTGTGTTAAGGAATGGT
ACTGAGGCATTTGACTCCTGGGAGAAGCCCCCTCTGCCTGTGTATACTCAGTTCTATTTCTTCAATGTC
ACCAATCCAGAGGAGATCCTCAGAGGGGAGACCCCTCGGGTGGAAGAAGTGGGGCCATACACCTACAGG
TCACTTGACTGGTGGATAACAGACAAGTGCAATATGATTAATGGAACAGATGGAGATTCTTTTCACCCA
CTAATAACCAAAGATGAGGTCCTTTATGTCTTCCCATCTGACTTTTGCAGGTCAGTGTATATTACTTTC
AGTGACTATGAGAGTGTACAGGGACTGCCTGCCTTTCGGTATAAAGTTCCTGCAGAAATATTAGCCAAT
ACGTCAGACAATGCCGGCTTCTGTATACCTGAGGGAAACTGCCTGGGCTCAGGAGTTCTGAATGTCAGC
ATCTGCAAGAATGGTGCACCCATCATTATGTCTTTCCCACACTTTTACCAAGCAGATGAGAGGTTTGTT
TCTGCCATAGAAGGCATGCACCCAAATCAGGAAGACCATGAGACATTTGTGGACATTAATCCTTTGACT
GGAATAATCCTAAAAGCAGCCAAGAGGTTCCAAATCAACATTTATGTCAAAAAATTAGATGACTTTGTT
GAAACGGGAGACATTAGAACCATGGTTTTCCCAGTGATGTACCTCAATGAGAGTGTTCACATTGATAAA
GAGACGGCGAGTCGACTGAAGTCTATGATTAACACTACTTTGATCATCACCAACATACCCTACATCATC
ATGGCGCTGGGTGTGTTCTTTGGTTTGGTTTTTACCTGGCTTGCATGCAAAGGACAGGGATCCATGGAT
GAGGGAACAGCGGATGAAAGAGCACCCCTCATTCGAACCTAA

Restriction Sites: SgfI-MluI

ACCN: NM_001204255

Insert Size: 1008 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).

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).

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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_001204255.1
RefSeq Size:	4340 bp
RefSeq ORF:	1008 bp
Locus ID:	950
UniProt ID:	Q14108
Cytogenetics:	4q21.1
Protein Families:	Druggable Genome, Transmembrane
Protein Pathways:	Lysosome
MW:	37.8 kDa
Gene Summary:	The protein encoded by this gene is a type III glycoprotein that is located primarily in limiting membranes of lysosomes and endosomes. Earlier studies in mice and rat suggested that this protein may participate in membrane transportation and the reorganization of endosomal/lysosomal compartment. The protein deficiency in mice was reported to impair cell membrane transport processes and cause pelvic junction obstruction, deafness, and peripheral neuropathy. Further studies in human showed that this protein is a ubiquitously expressed protein and that it is involved in the pathogenesis of HFMD (hand, foot, and mouth disease) caused by enterovirus-71 and possibly by coxsackievirus A16. Mutations in this gene caused an autosomal recessive progressive myoclonic epilepsy-4 (EPM4), also known as action myoclonus-renal failure syndrome (AMRF). Alternatively spliced transcript variants encoding different isoforms have been found for this gene.[provided by RefSeq, Feb 2011] Transcript Variant: This variant (2) lacks three consecutive exons in the CDS, as compared to variant 1. The reading frame is not affected and the resulting isoform (2) lacks an internal segment, as 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.