

## **Product datasheet for SC330260**

LUZP2 (NM 001252010) Human Untagged Clone

## **Product data:**

**Product Type:** Expression Plasmids

**Product Name:** LUZP2 (NM\_001252010) Human Untagged Clone

Tag: Tag Free Symbol: LUZP2

Synonyms: KFSP2566; PRO6246

**Vector:** pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC330260 representing NM\_001252010.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GAAGAAAAAATACTG<mark>TAA</mark>

Restriction Sites: Sgfl-Mlul

ACCN: NM 001252010

**Insert Size:** 915 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: <u>NM 001252010.1</u>

 RefSeq Size:
 5185 bp

 RefSeq ORF:
 915 bp

 Locus ID:
 338645

 UniProt ID:
 Q86TE4

 Cytogenetics:
 11p14.3

 MW:
 34.2 kDa

**Gene Summary:** This gene encodes a leucine zipper protein. This protein is deleted in some patients with

Wilms tumor-Aniridia-Genitourinary anomalies-mental Retardation (WAGR) syndrome. Alternate splicing results in multiple transcript variants. [provided by RefSeq, Oct 2011] Transcript Variant: This variant (3) lacks two in-frame exons in the coding region, compared to

variant 1. This results in a shorter protein (isoform 3), 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.