

## Product datasheet for **SC337418**

### **KIRREL 3 (KIRREL3) (NM\_001301097) Human Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	KIRREL 3 (KIRREL3) (NM_001301097) Human Untagged Clone
Tag:	Tag Free
Symbol:	KIRREL3
Synonyms:	KIRRE; MRD4; NEPH2; PRO4502
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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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\\_001301097.1](#), [NP\\_001288026.1](#)

**RefSeq Size:** 3758 bp

**RefSeq ORF:** 2301 bp

**Locus ID:** 84623

**Cytogenetics:** 11q24.2

**Protein Families:** Transmembrane

**Gene Summary:** The protein encoded by this gene is a member of the nephrin-like protein family. These proteins are expressed in fetal and adult brain, and also in podocytes of kidney glomeruli. The cytoplasmic domains of these proteins interact with the C-terminus of podocin, also expressed in the podocytes, cells involved in ensuring size- and charge-selective ultrafiltration. The protein encoded by this gene is a synaptic cell adhesion molecule with multiple extracellular immunoglobulin-like domains and a cytoplasmic PDZ domain-binding motif. Mutations in this gene are associated with several neurological and cognitive disorders. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2017]

Transcript Variant: This variant (3) lacks an alternate in-frame exon compared to variant 1. The resulting isoform (3) 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.