

## Product datasheet for **SC326771**

### FLJ14213 (PRR5L) (NM\_001160169) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Tag:	Tag Free
Symbol:	FLJ14213
Synonyms:	PROTOR2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC326771 representing NM_001160169. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGACCCGCGGCTTCGCTCCCATCTGCCCCTCGAGTTCCACAAGATGGGCTCCTTCCGAGGCCTAGA
CCGCGCTTCATGAGCTCCCCGTGCTCAGCGACCTTCCCCGATTCCAAGCAGCTCGGCAGGCTCTGCAG
CTGAGCTCCAGCTCAGCTGGAACAGCGTTTCAGACTGCTGTGATCAACGTTTTCAAAGGGGGTGGCTTG
CAAAGCAACGAGCTCTATGCCCTGAACGAAACATCAGGCGGCTGTTGAAGAGTGAACCTGGATCATTC
ATTACAGACTATTTTCAAGACAGCTTCTTGCAAAGGACTGTTCTTTGTGGAGGAGAAGATCAAGCTG
TGTGAAGGTGAAAATCGCATTGAGGTTCTGGCTGAAGTCTGGGACCACTTCTTCACTGAGACTCTCCCT
ACCCTGCAGGCAATATTTATCCAGTTTCAGGGCCAGGAGCTGACTATCCGCCAGATCTCCCTGCTGGGC
TTCCGAGACCTAGTCTTGCTGAAGGTGAAGCTGGGTGACCTGCTGCTGCTGGCCAGTCCAAGCTGCC
TCGTCCATTGTCCAGATGTTGCTCATCTGCAGCCAGGCGGCACTCCAGGGTCCGGCCCAAGGTGA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGCCCGGC
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Restriction Sites:	SgfI-MluI
ACCN:	NM_001160169
Insert Size:	618 bp



<b>OTI Disclaimer:</b>	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).
<b>OTI Annotation:</b>	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<a href="#">NM_001160169.1</a>
<b>RefSeq Size:</b>	3588 bp
<b>RefSeq ORF:</b>	618 bp
<b>Locus ID:</b>	79899
<b>UniProt ID:</b>	<a href="#">Q6MZO0</a>
<b>Cytogenetics:</b>	11p13-p12
<b>MW:</b>	23 kDa

**Gene Summary:**

Associates with the mTORC2 complex that regulates cellular processes including survival and organization of the cytoskeleton (PubMed:17461779). Regulates the activity of the mTORC2 complex in a substrate-specific manner preventing for instance the specific phosphorylation of PKCs and thereby controlling cell migration (PubMed:22609986). Plays a role in the stimulation of ZFP36-mediated mRNA decay of several ZFP36-associated mRNAs, such as TNF-alpha and GM-CSF, in response to stress (PubMed:21964062). Required for ZFP36 localization to cytoplasmic stress granule (SG) and P-body (PB) in response to stress (PubMed:21964062).

[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (4) differs in the 5' UTR and lacks an exon in the 3' coding region, which results in a frameshift and an early stop codon, compared to variant 1. The encoded isoform (c) has a shorter and distinct C-terminus compared to isoform a. 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.