

## Product datasheet for **SC326171**

### **GIT2 (NM\_001135213) Human Untagged Clone**

#### **Product data:**

Product Type:	Expression Plasmids
Product Name:	GIT2 (NM_001135213) Human Untagged Clone
Tag:	Tag Free
Symbol:	GIT2
Synonyms:	CAT-2; CAT2; PKL
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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**Fully Sequenced ORF:** >SC326171 representing NM\_001135213.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGCATCGCC
ATGTCGAAACGGCTCCGGAGCAGCGAGGTGTGCGCTGACTGCAGCGGGCCGGATCCTTCCTGGGCATCA
GTAATAGGGGAACGTTTTTATGTGATGAGTGTGCAGTGTCCATCGGAGTCTAGGGGCCATATCTCC
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GACAGACGGCTCAGCCTGGATTTGTCTGAATTGGCAAAAGCTGCTAAGAAGAAAATTCAATCTCTAAGT
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AACAGCACACCTGAGAGTACTACGACAACACTCCCAACGACATGGAGCCAGATGGCATGGGGTCAAGC
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ATACAGGAGCTCTTAAGAGCAGCCAAGAAAATAAACATGACAGTTATATTCCCTGCTCAGAGAGGATA
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CTTCGTTTACTGACGTCCAGTGCCTACCGACTGCAGTGCAGTGCAGAGTGAAGAAGACCCCTCCAGGGGACCCC
GGCTCACCCACAGACGTTTCCAGCTGGTACGCAGCAGGTCATCCAGTGTGCGTACGACATCGCCAAGGCT
GCCAAGCAGCTGGTTACCATCACCAAAAGAGAACAACAACTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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**Restriction Sites:** Sgfl-Mlul

**ACCN:** NM\_001135213

**Insert Size:** 2046 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).

**OTI Annotation:** 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>RefSeq:</b>	<a href="#">NM_001135213.1</a>
<b>RefSeq Size:</b>	5409 bp
<b>RefSeq ORF:</b>	2046 bp
<b>Locus ID:</b>	9815
<b>UniProt ID:</b>	<a href="#">Q14161</a>
<b>Cytogenetics:</b>	12q24.11
<b>Protein Families:</b>	Druggable Genome
<b>Protein Pathways:</b>	Endocytosis
<b>MW:</b>	76.1 kDa
<b>Gene Summary:</b>	<p>This gene encodes a member of the GIT protein family, which interact with G protein-coupled receptor kinases and possess ADP-ribosylation factor (ARF) GTPase-activating protein (GAP) activity. GIT proteins traffic between cytoplasmic complexes, focal adhesions, and the cell periphery, and interact with Pak interacting exchange factor beta (PIX) to form large oligomeric complexes that transiently recruit other proteins. GIT proteins regulate cytoskeletal dynamics and participate in receptor internalization and membrane trafficking. This gene has been shown to repress lamellipodial extension and focal adhesion turnover, and is thought to regulate cell motility. This gene undergoes extensive alternative splicing to generate multiple isoforms, but the full-length nature of some of these variants has not been determined. The various isoforms have functional differences, with respect to ARF GAP activity and to G protein-coupled receptor kinase 2 binding. [provided by RefSeq, Sep 2008]</p> <p>Transcript Variant: This variant (6) lacks two in-frame exons in the 3' coding region and includes an additional short in-frame exon in the central coding region, compared to isoform 1. The resulting isoform (6) is missing two internal fragments and includes a 2 residue insertion, compared to isoform 1.</p>