

Product datasheet for **SC335588**

GANC (NM_001301409) Human Untagged Clone

Product data:

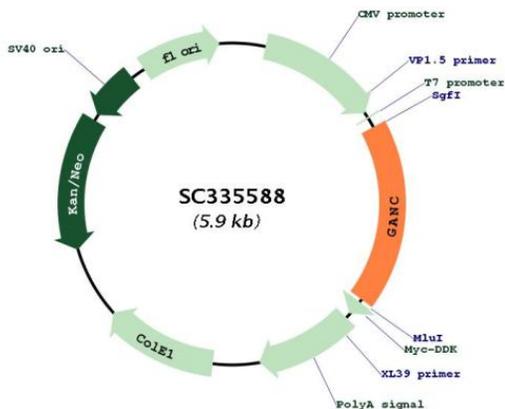
Product Type:	Expression Plasmids
Product Name:	GANC (NM_001301409) Human Untagged Clone
Tag:	Tag Free
Symbol:	GANC
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335588 representing NM_001301409. Blue=Insert sequence Red=Cloning site Green=Tag(s)

```
GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGAAGCAGCAGTGAAGAGGAAATAAGTCTTGAAGTGAAGCTGTAGATAAAAAACATTTTCAGAGAC
TGTAACAAGATCGCATTTTACAGGCGTCAGAAACAGTGGCTTTCCAAGAAGTCCACCTATCAGGCATTA
TTGGATTCACTCACAACAGATGAAGACAGCACCAGGTTCCAAATCATCAATGAAGCAAGTAAGGTTCCCT
CTCCTGGCTGAAATTTATGGTATAGAAGGAAACATTTTCAGGCTTAAAAATTAATGAAGAGACTCCTCTA
AAACCCAGATTTGAAGTCCGGATGTCCTCACAAGCAAGCAAGCACTGAAGGCTGATTTTCATGCTCTT
GGGGACACAGGCAGTCTGATATTGGCAGATGGAAAAGGAGACCTGAAGTGCCATATCACAGCAAACCCA
TTCAAGGTAGACTTGGTGTCTGAAGAAGAGGTTGTGATTAGCATAAATCCCTGGGCCAATTATACTTT
GAGCATCTACAGATTCTCACAACAAAGAGCTGCTAAAGAAAATGAGGAGGAGACATCAGTGGACACC
TCTCAGGAAAATCAAGAAGATCTGGCCTGTGGGAAGAGAAAATTTGAAAATTTGTGGATATCAAAGCT
AATGGCCCTTCTTCTATTGGTTTGGATTCTCCTTGCATGGATTTGAGCATCTTTATGGGATCCACAA
CATGCAGAATCACACCAACTTAAAAATACTGGTGATGGAGATGCTTACCGTCTTTATAACCTGGATGTC
TATGGATACCAAATATATGATAAAATGGGCATTTATGGTTCAGTACCTTATCTCCTGGCCCAAACTG
GGCAGAACTATAGGTATTTCTGGCTGAATGCCTCGGAAACACTGGTGGAGATCAATACAGAGCCTGCA
GTAGAGTACACACTGACCCAGATGGGCCAGTTGCTGCTAAACAAAAGGTCAGATCTCGCACTCATGTG
CACTGGATGTCAGAGAGTGGCATATTGATGTTTTCTGCTGACAGGACCTACACCTTCTGATGTCTTC
AAACAGTACTCACACCTTACAGACATTGGAGAAAAATAG
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
```

Restriction Sites: Sgfl-Mlul



[View online »](#)

Plasmid Map:


ACCN: NM_001301409

Insert Size: 1074 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).

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_001301409.1](#)

RefSeq Size: 2533 bp

RefSeq ORF: 1074 bp

Locus ID: 2595

Cytogenetics: 15q15.1

Protein Families: Druggable Genome

Protein Pathways:	Galactose metabolism, Metabolic pathways, Starch and sucrose metabolism
MW:	40.3 kDa
Gene Summary:	<p>Glycosyl hydrolase enzymes hydrolyse the glycosidic bond between two or more carbohydrates, or between a carbohydrate and a non-carbohydrate moiety. This gene encodes a member of glycosyl hydrolases family 31. This enzyme hydrolyses terminal, non-reducing 1,4-linked alpha-D-glucose residues and releases alpha-D-glucose. This is a key enzyme in glycogen metabolism and its gene localizes to a chromosomal region (15q15) that is associated with susceptibility to diabetes. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Aug 2014]</p> <p>Transcript Variant: This variant (2) lacks several exons in the 3' coding region, and contains an alternate 3' terminal exon, compared to variant 1. It encodes isoform 2 which is shorter, and has a distinct C-terminus, 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.</p>