

Product datasheet for **SC308933**

NRG2 (NM_013981) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NRG2 (NM_013981) Human Untagged Clone
Tag:	Tag Free
Symbol:	NRG2
Synonyms:	DON1; HRG2; NTAK
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)



[View online »](#)

Fully Sequenced ORF: >SC308933 representing NM_013981.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

[illegible]

Restriction Sites:	Sgfl-Mlul
ACCN:	NM_013981
Insert Size:	2535 bp

OTI Disclaimer: Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. [More info](#)

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.

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.

Note: Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.

RefSeq: [NM_013981.1](#)

RefSeq Size: 3002 bp

RefSeq ORF: 2535 bp

Locus ID: 9542

UniProt ID: [O14511](#)

Cytogenetics: 5q31.2

Protein Families: Druggable Genome, Transmembrane

Protein Pathways: ErbB signaling pathway

MW: 90.9 kDa

Gene Summary:

This gene encodes a novel member of the neuregulin family of growth and differentiation factors. Through interaction with the ERBB family of receptors, this protein induces the growth and differentiation of epithelial, neuronal, glial, and other types of cells. The gene consists of 12 exons and the genomic structure is similar to that of neuregulin 1, another member of the neuregulin family of ligands. The products of these genes mediate distinct biological processes by acting at different sites in tissues and eliciting different biological responses in cells. This gene is located close to the region for demyelinating Charcot-Marie-Tooth disease locus, but is not responsible for this disease. Alternative transcript variants encoding distinct isoforms have been described. [provided by RefSeq, May 2010]

Transcript Variant: This variant (2) lacks an alternate in-frame exon but includes a different in-frame exon in the central coding region, compared to variant 1. The encoded isoform (2, also known as beta or beta1) is shorter than isoform 1. This variant is supported by data in PMID:10369162. 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.