

Product datasheet for SC308934

NRG2 (NM_013982) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NRG2 (NM_013982) Human Untagged Clone
Tag:	Tag Free
Symbol:	NRG2
Synonyms:	DON1; HRG2; NTAK
Mammalian Cell	Neomycin
Selection:	
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

OriGene Technologies, Inc.

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Fully Sequenced ORF:	<pre>ced ORF: >SC308934 representing NM_013982. Blue=Insert sequence Red=Cloning site Green=Tag(s)</pre>	
	GUIGE THIGHTE SEQUENCE NEW EXAMINING STEE GLEEN HUG(S) GETCEGTTAGTEAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATTGCTCGCCGCCGCCGCCCCTGGAGAAGGGTCGGTC	
Restriction Sites:	Sgfl-Mlul	
ACCN:	NM_013982	
Insert Size:	2577 bp	

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ORIGENE NRG2 (NM_013982) Human Untagged Clone – SC308934

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 <u>custsupport@origene.com</u> or by calling 301.340.3188 option 3 for pricing and delivery.
	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. <u>More info</u>
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:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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:	<u>NM 013982.2</u>
RefSeq Size:	3963 bp
RefSeq ORF:	2577 bp
Locus ID:	9542
UniProt ID:	<u>014511</u>
Cytogenetics:	5q31.2
Protein Families:	Druggable Genome, Transmembrane
Protein Pathways:	ErbB signaling pathway
MW:	92.6 kDa

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GRIGENE NRG2 (NM_013982) Human Untagged Clone – SC308934

This gene encodes a novel member of the neuregulin family of growth and differentiation Gene Summary: 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 (3) includes an additional in-frame exon in the central coding region, compared to variant 1, resulting in an isoform (3, also known as alphav or alpha1) that is longer 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.

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