

## Product datasheet for **SC326761**

### NRG1 (NM\_001160002) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	NRG1 (NM_001160002) Human Untagged Clone
Tag:	Tag Free
Symbol:	NRG1
Synonyms:	ARIA; GGF; GGF2; HGL; HRG; HRG1; HRGA; MST131; MSTP131; NDF; NRG1-IT2; SMDF
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001160002, the custom clone sequence may differ by one or more nucleotides ATGTCCGAGCGCAAAGAAGGCAGAGGCAAAGGGAAGGGCAAGAAGAAGGAGCGAGGCTCC GGCAAGAAGCCGAGTCCGCGGGCAGCCAGAGCCCAGCCTTGCCTCCCGATTGAAA GAGATGAAAAGCCAGGAATCGGCTGCAGGTTCCAACTAGTCTTCGGTGTGAAACCACT TCTGAATACTCTCTCTCAGATTCAAGTGGTTCAAGAATGGGAATGAATTGAATCGAAAA AACAAACCACAAAATATCAAGATACAAAAAAGCCAGGGAAGTCAGAACTTCGCATTAAC AAAGCATCACTGGCTGATTCTGGAGAGTATATGTGCAAAGTGATCAGCAAATTAGGAAAT GACAGTGCCTCTGCCAATATCACCATCGTGAATCAAACGAGATCATCACTGGTATGCCA GCCTCAACTGAAGGAGCATATGTGTCTTCAGCTACATCTACATCCACCACTGGGACAAGC CATCTTGTAAAAATGTGCGGAGAAGGAGAAAACCTTCTGTGTGAATGGAGGGGAGTGCTTC ATGGTGAAGACCTTTCAAACCCCTCGAGATACTTGTGCAAG
Restriction Sites:	Please inquire
ACCN:	NM_001160002
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.



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<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>	<u>NM_001160002.1, NP_001153474.1</u>
<b>RefSeq Size:</b>	1643 bp
<b>RefSeq ORF:</b>	585 bp
<b>Locus ID:</b>	3084
<b>Cytogenetics:</b>	8p12
<b>Protein Families:</b>	Druggable Genome, Secreted Protein, Transcription Factors, Transmembrane
<b>Protein Pathways:</b>	ErbB signaling pathway
<b>Gene Summary:</b>	<p>The protein encoded by this gene is a membrane glycoprotein that mediates cell-cell signaling and plays a critical role in the growth and development of multiple organ systems. An extraordinary variety of different isoforms are produced from this gene through alternative promoter usage and splicing. These isoforms are expressed in a tissue-specific manner and differ significantly in their structure, and are classified as types I, II, III, IV, V and VI. Dysregulation of this gene has been linked to diseases such as cancer, schizophrenia, and bipolar disorder (BPD). [provided by RefSeq, Apr 2016]</p> <p>Transcript Variant: This variant (HRG-gamma2), which uses the type I promoter, lacks an internal in-frame exon and multiple 3' exons, but contains an alternate 3' terminal exon and thus differs in the 3' coding region and 3' UTR, compared to variant HRG-beta1. The resulting isoform (HRG-gamma2, also known as gamma protein isoform 1) lacks an internal segment, has a distinct C-terminus, and is shorter than isoform HRG-beta1. 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>