

## Product datasheet for **SC329305**

### EGF (NM\_001178130) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	EGF (NM_001178130) Human Untagged Clone
Tag:	Tag Free
Symbol:	EGF
Synonyms:	HOMG4; URG
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001178130, the custom clone sequence may differ by one or more nucleotides

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ATGCTGCTCACTTTATCATTCTGTTGCCAGTAGTTTCAAATTTAGTTTTGTTAGTCTC
TCAGCACCGCAGCACTGGAGCTGTCCTGAAGGACTCTCGCAGGAAATGGGAATTCTACT
TGTGTGGGTCCTGCACCCTTCTTAATTTTCTCCCATGGAAATAGTATCTTTAGGATTGAC
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ACAGACTATGGAAGCTGCTCAGCCAGCAGATGGGAATGGTTTATGCCCTAGATCATGAC  
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 AGGCTGTGACTGAGGATGGGATGTCCTCTTGCCCTCAACCTTGGTTTGTGGTTATA  
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 GAGCGAAGCTTTTATATGCCCTCCTATGGGACACAGACCTTGAAGGGGGTGTGCGAGAAG  
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 CAAATGGAGCTGACTCAGTGA

- Restriction Sites:** Please inquire
- ACCN:** NM\_001178130
- 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.
- 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).

<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_001178130.1, NP_001171601.1</u>
<b>RefSeq Size:</b>	5477 bp
<b>RefSeq ORF:</b>	3501 bp
<b>Locus ID:</b>	1950
<b>UniProt ID:</b>	<u>P01133</u>
<b>Cytogenetics:</b>	4q25
<b>Protein Families:</b>	Adult stem cells, Druggable Genome, Embryonic stem cells, ES Cell Differentiation/IPS, Induced pluripotent stem cells, Transmembrane
<b>Protein Pathways:</b>	Bladder cancer, Cytokine-cytokine receptor interaction, Endocytosis, Endometrial cancer, ErbB signaling pathway, Focal adhesion, Gap junction, Glioma, MAPK signaling pathway, Melanoma, Non-small cell lung cancer, Pancreatic cancer, Pathways in cancer, Prostate cancer, Regulation of actin cytoskeleton
<b>Gene Summary:</b>	<p>This gene encodes a member of the epidermal growth factor superfamily. The encoded preproprotein is proteolytically processed to generate the 53-amino acid epidermal growth factor peptide. This protein acts a potent mitogenic factor that plays an important role in the growth, proliferation and differentiation of numerous cell types. This protein acts by binding with high affinity to the cell surface receptor, epidermal growth factor receptor. Defects in this gene are the cause of hypomagnesemia type 4. Dysregulation of this gene has been associated with the growth and progression of certain cancers. Alternative splicing results in multiple transcript variants, at least one of which encodes a preproprotein that is proteolytically processed. [provided by RefSeq, Jan 2016]</p> <p>Transcript Variant: This variant (2) lacks an in-frame exon in the coding region, compared to variant 1. The encoded isoform (2) is shorter than isoform 1. This isoform (2) may undergo proteolytic processing similar 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>